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Investigating the modern human settlement of Mainland Southeast Asia using mitochondrial DNA

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Abstract

Many questions remain about the settlement of anatomically modern humans in Mainland Southeast Asia (MSEA). During the last Ice Age, the Sunda shelf was exposed and the Sunda continent connected MSEA with western ISEA (Java, Sumatra and Borneo), but global warming after about 20,000 years ago (20 ka) led to rises in sea levels which flooded a large part of Sundaland. This region is a key area of initial settlement of anatomically modern humans, who likely expanded along the coastal route from the Horn of Africa via Arabia and South Asia towards Australasia. In this work, I aimed to investigate the first arrival of modern populations in MSEA, clarify the timing and process, and study the subsequent demographic history of its populations from the perspective of the maternal line of descent.

I have studied phylogeographic and phylogenetic relationships of populations in North, South, and Southeast Asia using mitochondrial DNA (mtDNA) genome variation, using both control-region sequence and whole mitogenomes, in order to gain a more comprehensive insight into the evolutionary history of the MSEA population. Using next-generation sequencing I have analysed 909 new complete mtDNA sequences from MSEA population, including 506 Lao, 387 Vietnamese and 16 Burmese samples in the context of the available published world-wide database.

Most of the basal lineages within the major non-African founders, the roots of haplogroups M and R, represent the indigenous inhabitants who first arrived in the region from the west. The founder ages for M and R were dated by maximum likelihood in this study to ~61 ka and ~64 ka, with a 95% confidence range of 55 ka to 73 ka, confirming that this was most likely and shortly after the volcanic eruption of Mount Toba in Sumatra at 74 ka, with MSEA and ISEA beginning to diverge as early as ~54 ka.

I have used founder analysis with the new mitogenomes in order to quantify the fraction of maternal lineages that arrived at various times throughout prehistory. This showed that approximately 11-21% of modern mtDNA lineages date to the first settlement, with several subsequent major waves of arrival, mainly from the north in what is now South China, since the Last Glacial Maximum. These subsequent events are primarily focused on three time intervals, and suggest a strong demographic impact from climatic changes following the end of the last Ice Age.

The first is the Late Glacial, ~13 ka, at the time of the first major sea-level rise (17-19% of modern mtDNAs), but the largest fraction dates to the early postglacial, at the time of the final major sea-level rise, ~7 ka (36-37%). This early Holocene process corresponds to the middle Neolithic, or coastal Neolithic, a dispersal of primarily hunter-gatherer groups adapted to coastal resources and possibly practising early forms of horticulture and/or arboriculture. Only a minority of lineages, amounting to 18-24%, date to the spread of late Neolithic rice agriculture from South China ~4 ka.

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Abbreviations

AMHs	Anatomically modern humans
ATP	adenosine triphosphate
BAM	binary alignment map
BC	Before Christ
bp	base pairs
BMP	Bayesian migration partition
BP	Before Present
COI	cytochrome c oxidase subunit I
COII	cytochrome c oxidase subunit II
COIII	cytochrome c oxidase subunit III
CSB	conserved sequence block
D-loop	displacement loop
DNA	deoxyribonucleic acid
dNTPs	deoxynucleoside triphosphates
GUI	graphical user interface
HVS-I	hypervariable segment I
HVS-II	hypervariable segment II
ISEA	Island Southeast Asia
ka	thousand years
LGM	Last Glacial Maximum
LSP	light-strand promoter
MCMC	Markov Chain Monte Carlo
ML	Maximum likelihood
MP	Maximum Parsimony
MRCA	most recent common ancestor
mRNA	messenger RNA
MSEA	Mainland Southeast Asia
MSY	Y-chromosome
mtDNA	mitochondrial DNA
NJ	neighbour-joining

np	nucleotide position
OL	light-strand origin of replication
OSL	optically stimulated luminescence
OXPHOS	Oxidative phosphorylation
PAML	Phylogenetic Analysis by Maximum Likelihood
PCA	Principal Component Analysis
PCR	polymerase chain reaction
rCRS	the revised Cambridge Reference Sequence
RFLP	restriction fragment-length polymorphism
RNA	ribonucleic acid
rRNA	ribosomal RNA
RSRS	reconstructed sapiens reference sequence
SAM	sequence alignment map
SBS	Sequencing by Synthesis
SE	standard error
SEA	Southeast Asia
SNPs	single nucleotide polymorphisms
TAS	termination-association sequence
TBE	tris-borate-EDTA (ethylenediaminetetraacetic acid)
TCA	tricarboxylic acid cycle
tRNA	transfer RNA
VCF	variant call format files
ya	years ago

1. Introduction

1.1 Mitochondria

1.1.1 Features of mitochondria

Mitochondria are cellular organelles that are mainly responsible for energy production in eukaryotic organisms. These organelles were first described by Albert Von Kolliker in 1857 (Yuenyong, 2014) and visualised for the first time in 1890 by Richard Altmann who defined them as “bioblast” (life germs). Altmann believed that they were independent organelles responsible for metabolic and genetic roles (O'Rourke, 2010). The term ‘mitochondrion’ was coined by Carl Benda in 1898 and the first clear micrograph image appeared in 1952 by Palade (Ernster & Schatz, 1981). Mitochondrial size is large enough to be seen by light microscopy, and mitochondria are bean-shaped organelles, ranging from 0.75 μm to 3 μm in length (Bereiter-Hahn, 1990; Rafelski & Marshall, 2008; Wiemerslage & Lee, 2016).

1.1.1.1 Structure of mitochondria

Mitochondria are encompassed by outer and inner mitochondrial membranes which are separated by an intermembrane space. The inner membrane has numerous folds that are known as cristae, which connect to each other through small tubular structures called crista junctions, and the volume bounded by the inner membrane is known as the matrix (Figure 1). The matrix contains the enzymes required by the tricarboxylic acid (TCA) cycle (also defined commonly as the Krebs cycle or the citric acid cycle). The matrix also contains other molecules including ribosomes, ATP synthase (F0F1 complexes) and mitochondrial DNA (mtDNA) (Lodish et al. 2008).

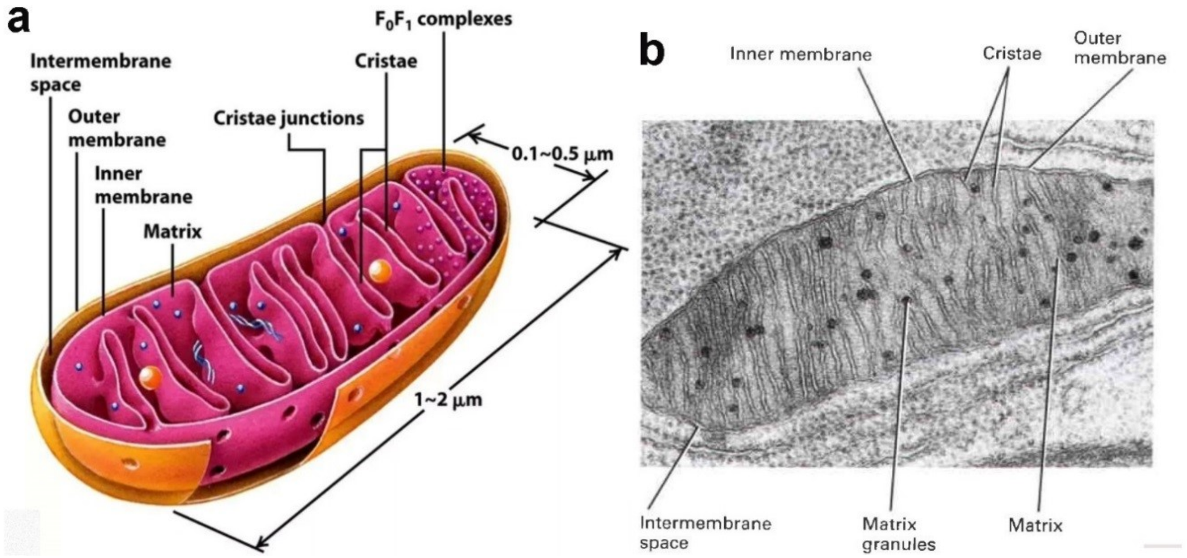


Figure 1. (a) A three-dimensional view for internal structure of a mitochondrion. (b) Electron microscope of a mitochondrion: internal membranes are visible (Lodish, 2008).

1.1.1.2 Function of mitochondria

Mitochondria are best known as energy powerhouses through their oxidative phosphorylation process, which produces adenosine triphosphate (ATP). The ATP molecule is the energy sources used for all important metabolic processes within the cell. Mitochondria participate in numerous cellular processes in addition to ATP production, including the process of programmed cell death (apoptosis), calcium homeostasis (Rutter & Rizzuto, 2000), and part of multiple cell signalling cascades (McBride, Neuspiel, & Wasiak, 2006), cellular innate antiviral immunity in mammals (Koshiba, Bashiruddin, & Kawabata, 2011) and in the metabolism of other macro-molecules such as nucleotides, amino acids, and lipids, among other functions (P. Chinnery, 2006).

1.1.1.3 Mitochondrial division and fusion

Mitochondria have been described as dynamic organelles engaged in a permanent process of division, fusion, movement, and morphological changes. Mitochondrial dynamics can take place in response to every physiological change in the cell (Youle & Van Der Bliek, 2012), and they can be controlled by dedicated proteins (Bui & Shaw, 2013; Okamoto & Shaw, 2005). The majority of these proteins are located in the nucleus and enter the mitochondria using specific receptors on the mitochondria membranes (Pfanner & Geissler, 2001).

During the lifetime of eukaryotic cells, mitochondria divide and fuse (Figure 2) several times, according to the cell's requirements. These features maintain the mitochondrial numbers and adequate amounts of their products (ATP) inside the cell.

Mitochondrial division is needed for dividing and growing cells to provide sufficient numbers of mitochondria. It is not known completely why mitochondrial division and fusion are also required in non-dividing cells, but the importance of these processes is found within the neurons, which cannot be survived without mitochondrial division and fusion, so that any defect affecting these processes will lead to diseases such as Charcot-Marie-Tooth disease (Type 2A) and dominant optic atrophy (Youle & Van Der Bliek, 2012).

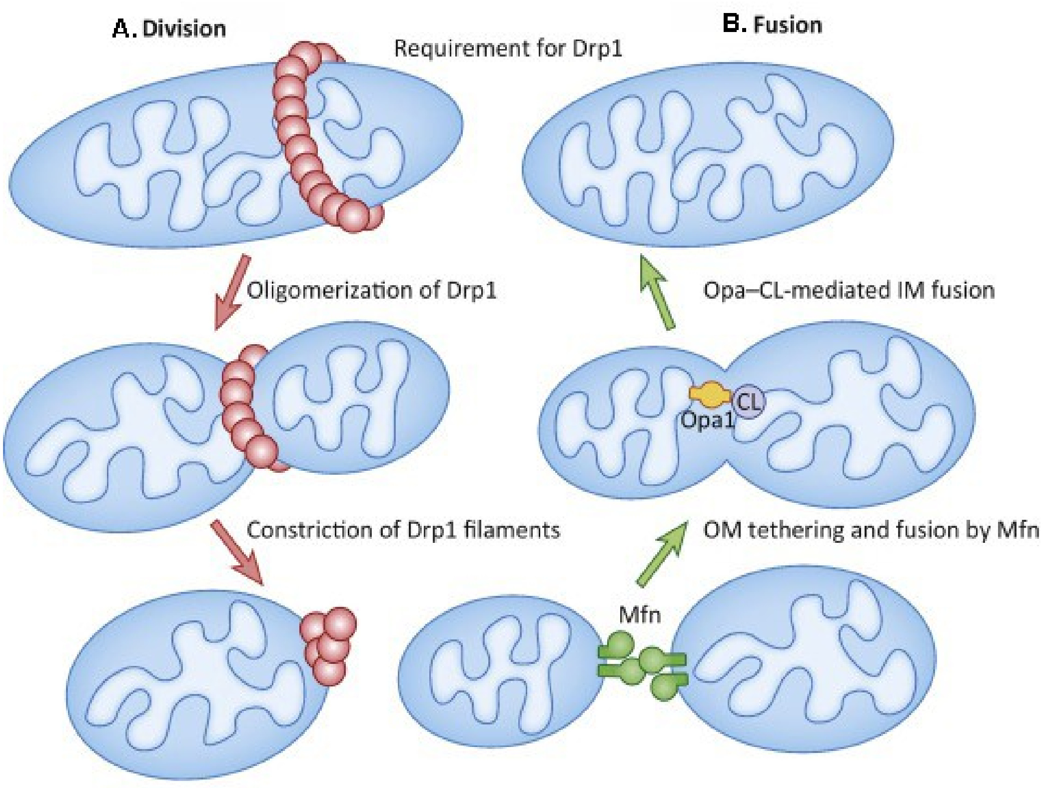


Figure 2. Mitochondrial fusion and division (Kameoka et al., 2017). In mammalian cells the mitochondrial division is mediated by a cytosolic dynamic protein called Drp1, creating spirals around mitochondria that constrict between two forming daughter mitochondria. The fusion process between mitochondrial outer membranes (OM) is mediated by a family proteins known as mitofusin (Mfn), and between the inner membrane (IM) by heterotypic interaction of Opa1 and cardiolipin (CL) (Youle and Van Der Bliek, 2012, Ban et al., 2017).

1.1.2 Mitochondrial genome.

Mitochondrial genome, or mtDNA, is a circular double-stranded molecule (Andrews et al., 1999). Anderson and colleagues published the first mtDNA sequence, of length 16,569 base pairs (bp) (S. Anderson et al., 1981). In 1999, Andrews and colleagues re-sequenced and reviewed of a placental mtDNA sample, as published by Anderson et al. This revision revealed errors which had resulted from artefacts in sequencing as well as the use of bovine samples instead of human mtDNA, as well as HeLa cells, to cover regions that had been technically difficult to sequence in the human sample.

As a result, the new version of the mtDNA sequence replaced the original and came to be defined as the “revised Cambridge Reference Sequence” (rCRS). The length of the mitochondrial genome varies between different species (between ~15 - 17 kbp). This is in contrast to human mitochondrial genome whose length is about 16,568 bp (Andrews et al., 1999). The two strands of mtDNA are distinguished by their nucleotide composition: namely the light strand (L-strand) and the heavy strand (H-strand). The human mtDNA is composed of the coding region, which contains some of the genes responsible for oxidative functions in the phosphorylation pathway. This region begins with base 577 and ends at base 16,023. The second region is known as the control region or D-loop (displacement loop) and contains the two main hyper-variable segments: the first one defined as (HVS-I) and the second (HVS-II). The two segments comprise bases 16,024-16,400 and 44-340 (Figure 04). There is also a rarely used third segment HVS-III, at bases 438-576 (P. Chinnery, 2006).

The two main hypervariable regions include the replication of origin of heavy-strand (O_H), light-strand transcription promoter (LSP), and the heavy strand promoters (HSP1 and HSP2) (Falkenberg, Larsson, & Gustafsson, 2007). These latter regions are likely to participate in replication and transcription, although their function is not clearly elucidated.

The mtDNA contains 37 genes in the coding region, with 28 genes found on the heavy strand and 9 on the light strand (Figure 3). The mitochondrial respiratory chain (RC) contains thirteen genes encoding a polypeptide component as well as cellular energy production sites through OX-PHOS. The thirteen genes mentioned above, which encode the other seven sub-units of complex I (NADH-ubiquinone oxidoreductase), also control the production of enzymes that regulate the production of ATP by ND1-ND6, ND4L and oxidative phosphorylation (OX-PHOS).

The cytochrome-b is a complex III gene that contains ubiquinol cytochrome-c oxidase reductase. The COI-COIII performs some functions including encoding three of the complex IV (cytochrome-c oxidase, or COX) subunits as well as the ATP 8 and ATP 6 genes encoding the two sub-units of complex V (ATP - synthase). The remainder of the thirteen genes encode to the two ribosomes RNAs which are; rRNAs 16S, rRNAs 12S and 22 transfer RNAs also known as tRNAs which are respectively required to aid in the synthesis of proteins (S. Anderson et al., 1981; DiMauro & Schon, 2003; Douglas C Wallace, 1994).

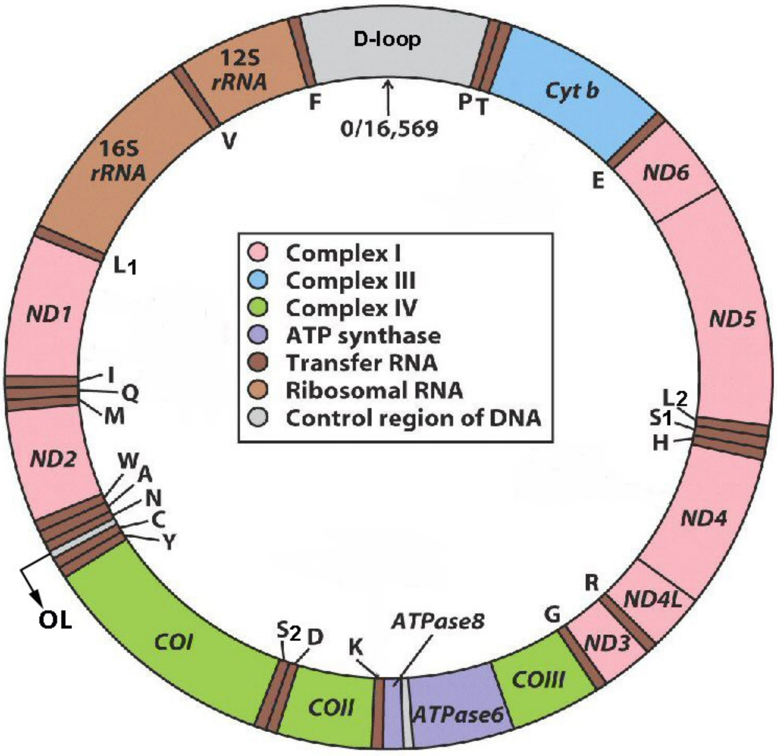


Figure 3. Schematic shows mammalian mtDNA (~16,569 bp). It contains a control region (or D-loop) in gray colour and the non-coding region in different other colors. The origin of lagging strand (OL). Two rRNAs (16S and 12S rRNA), 13 mRNAs (ND4L, ND1–6, Cytb, ATP8, ATP6, and COI–III), and 22 tRNAs (V, L1,F, M, I, W, K, D, R, G, H, S2, L2, P, E, T, S1, C, Y, Q, A, and N) are indicated by letters (Rajender, Rahul, & Mahdi, 2010).

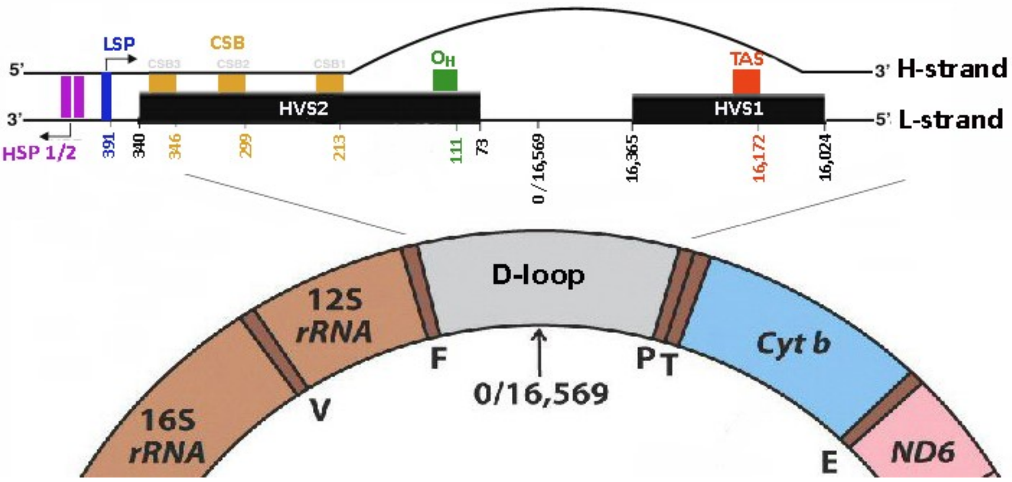


Figure 4.. Control region (D-loop) of the mitochondrial DNA, which contains the promoters for transcription process of both strands (LSP 1/2 and HSP), the origin of leading strand replication (OH), termination-association sequence (TAS) and conserved sequence block (CSB). Edited from (Rajender et al., 2010; Uhler & Falkenberg, 2015)

Mitochondria depend on the nuclear genome to carry out the majority of its OXPHOS functions, maintain and replicate mtDNA, and also proliferation and destruction of organelle network. Recent studies have recognized 92 structural OXPHOS subunit genes (P. F. Chinnery & Hudson, 2013), 79 genes coded by the nuclear genome and 13 coded by mtDNA (Angerer et al., 2011; P. M. Smith, Fox, & Winge, 2012; Vogel, Smeitink, & Nijtmans, 2007; Z.-G. Wang, White, & Ackerman, 2001).

1.1.2.1 Nuclear Mitochondrial DNA segment (NUMTs)

In his evolutionary work, Jose V. Lopez describes NUMTs as an insertion of any type of mtDNA into the nuclear genome of the eukaryotic organisms (Lopez, Yuhki, Masuda, Modi, & O'Brien, 1994). There are varied numbers of NUMT sequences with different size and length that have been detected in diverse eukaryotes (Bravi, Parson, & Bandelt, 2006). It is not common for NUMTs to have the same common features in all species as they come in different shapes and sizes (Mishmar, Ruiz-Pesini, Brandon, & Wallace, 2004; Sacerdot et al., 2008; Schizas, 2012).

NUMTs have been used by scientists as genetic markers to estimate the relative rates of nuclear and mitochondrial mutations and to help with reconstructing evolutionary trees (Bensasson, Zhang, Hartl, & Hewitt, 2001).

For the human evolutionary tree, NUMTs become useful for exemplary observation for their isolative nature and slow response to nuclear content changes as evolution goes on. It is possible that NUMTs may not or may slowly evolve over a long time with some difficulty in observation. The most significant issue with NUMTs is the analytical problems, they might cause due to the unstable nature of NUMTs. NUMTs could conflict with the actual mtDNA and provide incorrect sequences of mtDNA that could lead to wrong interpretations in population genetics, forensic genetics and archaeogenetics. The most recent estimate of NUMTs recorded in the human genome is 755 fragments which range in size from 39 bp to almost the entire mitochondrial sequence (Dayama, Emery, Kidd, & Mills, 2014). Ramos et al. (Ramos et al., 2011) reported that in more than 80% of people, there are 33 paralogous (duplicated) sequences with a length of over 500 bp. Not all NUMTs in the genome are the direct result of migration of mtDNA; some are the outcome of amplification after the nuclear insertion has taken place. The new inserted NUMTs are found to be less abundant in the human genome than the old NUMTs, indicating that mtDNA fragments can be amplified once inserted into the nuclear genome (Dayama et al., 2014).

1.1.2.2 Replication

DNA polymerase independent continuously replicates the DNA in the mitochondria from the cycle of the cell as well as the non-dividing parts like brain and the skeletal muscle (Birky Jr, 2001; Bogenhagen & Clayton, 1977). In 1982, Clayton, (Clayton, 1982) proposed that through strand-asymmetrical (traditional model), mtDNA molecules of a mammalian should replicate in a one-way direction. The replication on the H-strand frequently stops 700 bp downstream in length between the termination-association sequence (TAS) and the origin of replication region (Figure 04), which creates a triple-stranded structure (a new synthesised strand, L-strand and H-strand) known as displacement loop or D-loop. The H-strand continues to replicate in a clockwise direction up to a point the origin of the L-strand replication (OL) is exposed. Moving from the point of OL, the replication at the L-strands turns a counter-current to an anti-clockwise direction (Figure 05). This mode of replication led probably to generate a strand-specific mutational bias. The mutational damage level in the H-strand will be probably higher, since this strand spends more time as a single-stranded (Bielawski & Gold, 2002). Another study suggests an alternative strand symmetric-model (Figure 05). This suggestion shows that replication can start at any or several points in a 5.5 kb between the ND4 and control region (Bowmaker et al., 2003). At this stage, the replication continues in all directions while stopping at OH and shortly at OL before cycle completion.

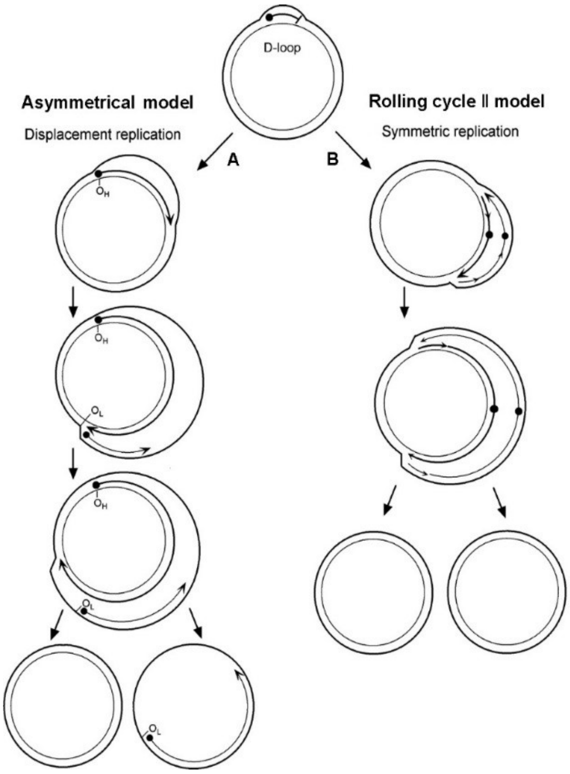


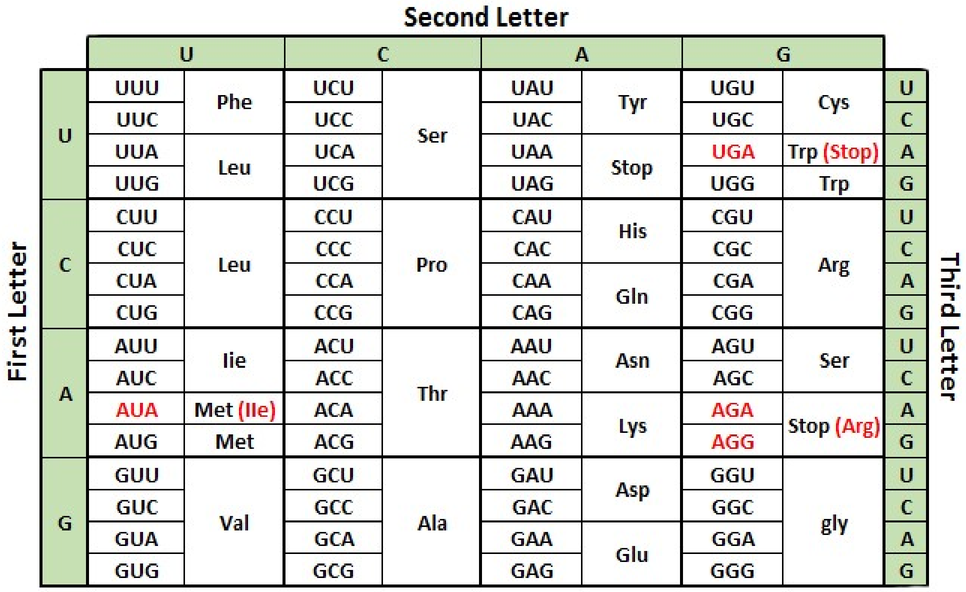
Figure 5. Two models of mammalian mtDNA replication *(T. A. Brown, Cecconi, Tkachuk, Bustamante, & Clayton, 2005)*

1.1.2.3 Transcription

The transcription process of mtDNA is similar to what happens in the prokaryotic organisms and it is controlled by three promoters, namely; the heavy-strand promoter-1 (HSP1), heavy-strand promoter-2 (HSP2) and light-strand promoter (LSP). The heavy-strand transcription is initiated with a short transcription starting from (HSP1) and ending at rRNA 16S, or starting from (HSP2) to encode a polycistronic message in two rRNA genes, 12 mRNA and 14 tRNA. While the light-strand transcription starts from the LSP, and encodes the ND6 mRNA gene and 8 tRNAs genes (Taylor & Turnbull, 2005). The full-length product of the transcription process is divided into functional molecules units of tRNA, rRNA, and mRNA. Although, more and more regulatory proteins have been identified, but still the knowledge on the regulation process for both of mRNA transcription and translation, and also the ribosomal biogenesis remains low (Z. Wang, Cotney, & Shadel, 2007).

1.1.2.4 Mitochondrial Genetic code

In 1966, the genetic code was defined for the first time, at that time, it was labelled as ‘universal’ but, less than 15 years since the code was discovered, some codons in vertebrate’s mitochondria were found different from the universal code (Barrell, Bankier, & Drouin, 1979). The mitochondrial DNA requires four codons (‘UAA’, ‘UAG’, ‘AGA’ and ‘AGG’) to stop the translation process (Figure 06) (compared with three stop codons; UAA, UGA and UAG in nDNA) (Temperley, Richter, Dennerlein, Lightowlers, & Chrzanowska-Lightowlers, 2010). The stop codon ‘UGA’ in the universal code was encoded to tryptophan in the mitochondria. Additionally, AUA found in the nDNA is encoded with isoleucine, while in the mitochondrion DNA encodes for methionine (P. F. Chinnery & Hudson, 2013).



	Second Letter								
First Letter	U		C		A		G		Third Letter
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA	Stop	UGA	Trp (Stop)	A
	UUG		UCG		UAG		UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	Iie	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC		ACC		AAC		AGC		C
	AUA	Met (Ile)	ACA		AAA	Lys	AGA	Stop (Arg)	A
	AUG	Met	ACG		AAG		AGG		G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	Glu	GGA		A
	GUG		GCG		GAG		GGG		G

Figure 6. Mitochondrial Genetic code. In red color is indicated to the differences between the vertebrate mtDNA code and the nuclear genomic codes, and amino acids between brackets are indicated the corresponding code system for that codon in the nuclear genome.

1.1.2.5 Translation.

The cytoplasmic and mitochondrial translation takes place simultaneously to make nuclear-encoded proteins destined for the mitochondria. It is in the mitochondria that the translation of the 13 mtDNA gene encoding proteins takes place by using mitochondrial ribosomes.

1.1.3 Features of mitochondrial DNA.

1.1.3.1 Genetic inheritance mode.

Mitochondrial DNA is maternally inherited. During the fertilization process, the paternal gamete (sperm) shares its haploid nuclear DNA with the female gamete (ovum) which contains the mitochondria DNA (mtDNA) in addition to the haploid nuclear DNA. It is now commonly known that paternal mitochondria does not enter the ovum, because of their position in the spermatozoa body (spiralled around the midpiece part of the sperm tail), and also the low copy number, which is about 50-75 copies in each sperm (Hecht, Liem, Kleene, Distel, & Ho, 1984). The spermatozoa mainly use the mitochondria for producing the required energy (ATP) during the fertilization journey inside the female cervix, uterus and uterine tubes (Ishijima, Oshio, & Mohri, 1986). In rare cases, sperm mitochondria may successfully enter the ovum during fertilization, but they can be degraded by the ovum's ubiquitin-proteasome dependent system which marks the sperm mitochondria and targets them for degradation (Sutovsky, 2003; Sutovsky & Schatten, 1999; Thompson, Ramalho-Santos, & Sutovsky, 2003).

There has been one case of paternal mtDNA transmission observed in a 28 years old patient who had maternal and paternal mtDNA in his muscle tissue, and all the other tissues had only maternal mtDNA (Schwartz and Vissing, 2002). However, the consensus is that paternal transmission of mtDNA is exceptionally very rare and even if that happens, there is no chance for the recombination between paternal and maternal mtDNAs. Therefore, the traditional theory of maternal inheritance, at least from the population genetics view, still stands.

1.1.3.2 Homoplasmy and Heteroplasmy

Each eukaryotic cell varies the number of the mitochondria considerably depending on the function and type of the cell. On average, the mtDNA of somatic mammalian cells is considered to be about 1000-10000 copies per cell (Falkenberg et al., 2007). All mtDNA copies normally have identical sequences (homoplasmy), but some mtDNA copies may have a different mutation compared to the majority of the molecules, this situation is called heteroplasmy. These heteroplasmic copies can be maternally transmitted to the next generation or they can be somatic copies. The level of heteroplasmic mutations is likely to be determined by two main mechanisms; relaxed replication and vegetative segregation. Relaxed replication occurs when mtDNA replication process continuously and randomly occurs even in non-dividing cells. Since this type of replication happens randomly, this leads to changes in the ratio between the mutant and wild mtDNA copies after a period of time through random intracellular genetic drift. Vegetative segregation occurs as a result of unequal distribution between wild-type and mutant mtDNA during the cell division. This can also lead to changes in the heteroplasmic level within the proliferative tissue (P. Chinnery, 2006).

During mtDNA transmission from mother to offspring, there is a rapid change in the levels of heteroplasmy (D. Brown, Samuels, Michael, Turnbull, & Chinnery, 2001; P. Chinnery, 2006). This is probably caused by a genetic bottleneck effect which acts to reduce the genetic diversity in a population. The bottleneck mechanism (Figure 07) during oogenesis is still not completely understood, but could be due to either a reduction in the number of mtDNA genome within the fertilized oocyte or the mtDNA may be partitioned into a few homoplasmic units of segregation in the germline (Cree et al., 2008; Khrapko, 2008).

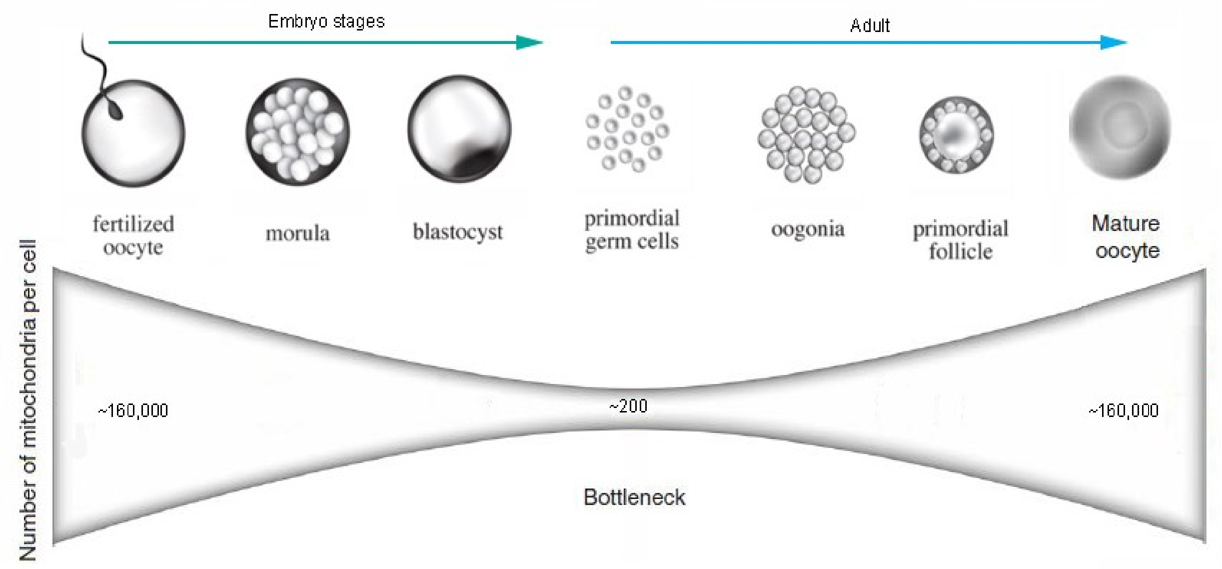


Figure 7. Diagram represents the bottleneck effect and the changes in the number of mtDNA copies during development of the female germ line edited from (Shoubridge & Wai, 2007; Wai et al., 2010).

1.1.3.3 The mtDNA mutation rate.

As a haploid genome, the mtDNA is maternally transmitted without undergoing recombination as it passes to the next generation unless new mutations occur, so the only source of variability is mutation. The mitochondrial mutation rate is about ten times higher than that of nuclear DNA (W. M. Brown, Prager, Wang, & Wilson, 1982; Neckelmann, Li, Wade, Shuster, & Wallace, 1987; Douglas C. Wallace et al., 1987). There are several factors that may explain the higher mutation rate in mtDNA: fewer proteins protect the mtDNA compared with the nuclear DNA, oxidative phosphorylation in mitochondria produces a high concentration of mutagenic oxygen free radicals, more replication is required and during the replication process the mtDNA spends more time in its single-stranded form which makes it more vulnerable to mutation (Fernández-Silva, Enriquez, & Montoya, 2003).

However, the rate of mutation is not equal throughout the whole mtDNA genome (16.5-kb molecule); each site has a different rate. The control region has a mutation rate over ten times faster than that of the coding region. This high mutation rate in the mtDNA genome leads to produce a large number of different sequences in human populations and it makes this genome an important tool for human evolutionary studies (for more details see **1.2.4**).

1.2 Phylogeography.

1.2.1 Phylogeography of mitochondrial DNA.

Phylogeography as a term was used for the first time by Avise (Avise, 2000), to describe the geographic distribution of lineages within a phylogeny. The phylogeographic approach combines three main elements: the geographic distribution of lineages, a phylogeny (a phylogenetic tree or network) and the time depth of lineages (using a molecular clock).

The geographic distribution of lineages is the first element required for this approach, tested by sampling genetic markers at different locations and the identification of similar lineages between these locations (P. Soares et al., 2010). The uniparental genetic markers, the mitochondrial DNA and the male-specific region of the Y chromosome (MSY), are usually used as in this approach, since they are haploid and non-recombining systems (transmitted in a non-Mendelian mode). The absence of recombination in these markers, makes mutations the sole source of allelic difference between lineages (Macaulay & Richards, 2008). These mutations in the genetic marker will produce haplotypes, which are combinations of alleles that are transmitted together from one generation to another (Tishkoff et al., 1996).

The second element is a phylogeny of the lineages. A phylogeny represents a hierarchy of relationships between different lineages, and it can establish hypothetical ancestral lineages from which two or more lineages descend (Macaulay & Richards, 2008). Therefore, a group of uniparental genetic markers that share mutations derived from a common ancestor (or MRCA) produce monophyletic units, or clades, commonly known as haplogroups.

The third element in the phylogeographic approach is the application of a molecular clock to the phylogeny. During human evolution, diversity on the uniparental genetic markers accumulates along maternally or parental inherited lineages, and by converting this diversity into age estimates, a phylogenetic timescale can be inferred (Kivisild et al., 2006; Sudhir Kumar, 2005). Therefore, once phylogenetic trees have been produced from human genetic markers, given sufficiently high resolution, it may be possible to geographically follow migrations that have occurred throughout history (Richards et al., 1998).

In early human mtDNA population studies, assaying the mtDNA as genetic marker was implemented by using "the restriction fragment length polymorphism" analysis (RFLP) of the whole mtDNA sequence and then screening the control-region sequence region. The first complete genome of mtDNA was published by Anderson and colleagues (1981), and was later revised by Andrews and colleagues (1999) (S. Anderson et al., 1981; Andrews et al., 1999). The rCRS is well established and widely accepted, and using the RSRS can lead to many problems (Bandelt et al. 2013), so in this study I used the rCRS system. Since then, the Cambridge reference sequence (rCRS) signed as commonest reference sequence for screening the polymorphisms in mtDNA sequences (Hans-Jürgen Bandelt, Kloss-Brandstätter, Richards, Yao, & Logan, 2014; van Oven & Kayser, 2009).

In mtDNA sequences, the variants can be reported against the reference sequence when a pyrimidine base is changed into another pyrimidine such as "C16188T", which means that pyrimidine C is substituted for T in position 16,188 on the mtDNA sequence, or a purine is substituted for another purine (for example, G for A) such as "G16145A"; in this case the change is called a transition. When a pyrimidine is exchanged for a purine, or vice versa (for example, C for G) such as "C16256g", this is a transversion. While substitutions of bases lead to mutations in the mtDNA sequence, insertion of a new base, for example adding C in position 16169 (16169.1C), or deleting bases such as removing T in position 15,944 (15944d), can change the mtDNA sequence (Jobling, Hollox, Kivisild, Tyler-Smith, & Hurles, 2013).

1.2.2 Using other lines of evidence with the phylogeographic analysis.

The phylogeographic approach requires complementary line of evidence to achieve reliable findings. For instance, a phylogeographic analysis that employs and considers other evidentiary sources such as linguistics, archaeological evidence, climatic change trends, and radiocarbon (C^{14}) dating has a better chance to provide a reliable explanation (Gamble, 2015; Jobling et al., 2013). A phylogeographic approach should be conducted in very close relationship with these lines of evidence from other research fields, which provide a model-based framework within which to test hypotheses.

1.2.3 Constructing and using mtDNA phylogenetic trees.

The phylogenetic tree (or phylogeny) is built from links or branches that intersect and terminate at nodes (individual sampled sequences or ancestral branching points) (Macaulay and Richards, 2008). The mtDNA haplogroups consist of related haplotypes of mtDNA sequences that share some common genetic mutations (e.g. single nucleotide polymorphisms) inherited from a common ancestor.

Phylogenetic trees are constructed using one of two main types of methods, character-based and distance methods. In the latter type, such as neighbour joining (NJ) and “The unweighted pair group method with arithmetic mean” (UPGMA) (Hall, 2004), the algorithm attempts to construct a phylogeny based on the genetic distance estimation for all pairs of sequences.

The distance methods are nowadays usually considered as character-based methods because these methods reduce the phylogeny information of the sequences to one value for each sequence pair (Van de Peer, 2009). Therefore, in constructing phylogenetic trees from DNA sequences one should prefer a character-based method. There are three types of methods: Maximum likelihood (ML), which is concerned with generating the best hypothesis (tree topology or branch lengths) having observed the outcome (sequence variation); maximum parsimony (MP), where the best tree is the one that requires the fewer number of changes to reconstruct phylogeny of the sequences (Fitch, 1977); and Bayesian inference, based on posterior probabilities, meaning probability estimates based on a specific model after analysing the data (Hall, 2004). The ML and the Bayesian inference methods use hypotheses of the evolutionary process, and their estimates are often not easy to depart from the proposal hypotheses and are very computer-intensive. The haplotypes of complete mtDNA sequences are usually used to construct the phylogenetic tree with the MP method, using PhyloTree as a guide, since the topology of the human mtDNA tree has been intensively studied over many years and is very well understood.

There are problems with using the MP method. The major one is that parallelisms (or recurrent mutation), the same mutation site occurring in two different sequences independently (Hans-J Bandelt, Forster, Sykes, & Richards, 1995; Hein, 1993), which can lead to two (or more) trees that are equally parsimonious, with no further criterion for choosing one of them. In some cases the MP analysis could also provide a putative tree which is longer than the actual most parsimonious tree (Felsenstein, 1978). In practice, all the parsimonious trees that were produced by this method have to be checked to correct their topological structure against the guide tree and our knowledge of the evolutionary process in mtDNA (such as the relative mutation rates of different sites).

However, some evolutionary processes (such as recombination, although more relevant for mtDNA are the high rates of homoplasy) can cause two or more lineages to appear identical. The result of these processes can be represented as a four-sided closed loop commonly known as a reticulation or cycle, and the resulting diagram is described as a phylogenetic network (Sneath, 1975). The phylogenetic analysis of the fast-evolving and low-resolution mitochondrial DNA control region is usually performed using networks, and they can be a valuable step in building up most-parsimonious trees of complete mtDNAs. (Kong et al., 2008).

Several phylogenetic network methods can be implemented using the Network 4.6 software. This software uses the median-joining (MJ) and reduced-median (RM) algorithms. Despite they are parsimony-based methods, they do not produce a single most parsimonious phylogenetic tree for a set of data, but they summarise many equally and less parsimonious trees by representing alternative evolutionary pathways in a single network diagram (Bandelt et al., 1995) (for more details see 2.11).

1.2.4 The mtDNA molecular clock.

Amongst the highly important components of phylogenetic analysis is genetic dating, the component that provides a chronology for the evolutionary history of human populations (Hans-Jürgen Bandelt, Macaulay, & Richards, 2002). We can estimate the time of a branching event or divergence in an evolutionary tree from the mutations accumulated in descendant branches over time and by employing a well-calibrated molecular clock (P. Soares et al., 2009). We therefore need an accurate estimation for the rate of mutations to provide a calibration of the molecular clock (Hans-Jürgen Bandelt et al., 2002). However, these estimations are challenging.

To begin with, a high mutation rate means that some positions in a mtDNA sequence change many times and some of these events pass without detection in the phylogenetic tree leading to an under-estimation of the true mutation rate (Hasegawa, Di Rienzo, Kocher, & Wilson, 1993). Additionally, some positions in the mtDNA sequences mutate very fast and others very slowly or not at all, so there is very high heterogeneity in the rate of mutations (Hasegawa et al., 1993, Stoneking, 2000). This problem in estimation the mutation rates was initially detected by Vigilant et al. (1991) when they reported that the mutation rate of control region over five times higher than that of the coding region (Vigilant, Stoneking, Harpending, Hawkes, & Wilson, 1991). Since then several attempts have carried out to estimate the mutation rates both in the control region (Forster, Harding, Torroni, & Bandelt, 1996; Torroni et al., 1994), and in the coding region (Ingman, Kaessmann, Paabo, & Gyllensten, 2000; Kivisild et al., 2006; Mishmar et al., 2003; P. Soares et al., 2009).

The HVS-I was estimated by Forster and colleagues (1996) to have about 1.80×10^{-7} transitions per nucleotide per year (or one transition per 20,180 years). This rate was calibrated using the diversity which accumulated in the Eskimo and Na-Dene by assuming 11,300 years for the time of expansion of these groups in North America.

A commonly used mutation rate was established by Mishmar et al. (2003) who suggested 1.26×10^{-8} base substitutions per nucleotide per year for the coding region (nps 577-16024).

However, non-synonymous mutations in the coding region have a higher level rate at the tips of branches than the deeper in the phylogenetic tree. This suggested that the purifying selection is working gradually on mtDNA (Kivisild et al., 2006; Pereira, Soares, Radivojac, Li, & Samuels, 2011). Kivisild and his colleagues (2006) suggested a mutation rate of one transition base in 6884 years for only the synonymous substitutions. This synonymous rate was revised downwards by Soares et al. (2009), to one mutation per 7884 years. However, the imprecision of rates based only on synonymous rates is substantial. More significantly, therefore, Soares et al. (2009) developed a correction for purifying selection that enabled them to provide a clock for complete mtDNA sequences, with an MS Excel-based calculator for implementing the correction, that is now widely used, and which I use here.

1.2.5 Founder analysis

Founder analysis is a phylogeographic tool for non-recombining data (mtDNA or Y-chromosome) that aims to identify all potential founders in a certain sink population, and determine their time of arrival from an assumed source region, in order to identify, date and quantify migrations between different regions (M. Richards et al., 2000). To achieve these objectives, the first step is to identify the founder sequence using a phylogenetic tree or network that includes data from both regions. An enormous amount of human mtDNA sequence data has been published, and can be used to construct phylogenetic trees or networks. Most of these published data are from the control region, especially HVS-I. Although HVS-I haplotypes do not have sufficient information to reconstruct the level of genealogical resolution that complete mtDNA sequences do, the fact that there is so much data can nevertheless provide valuable phylogeographic information in network form that can complement complete mtDNA trees (Macaulay & Richards, 2008).

In Figure 8, a hypothetical network represents two populations (source and sink populations) that both carry a hypothetical haplogroup (named K9). For calculating the founder age for the sink population, this approach uses the branches present only in the sink population, which means the founder age calculations will include the mutation diversity that has accumulated only in the sink population and will not use any mutation that has already been carried from the source population.

For this purpose, the source and sink populations must be considered separate entities (M. Richards et al., 2000). This diversity accumulated in the sink population can be calculated by using the ρ (rho) statistic; the mean number of mutations from the founder sequence to the branches in the sink population.

Two founders exist in the hypothetical network (Figure 8), corresponding to nodes K9b and K9a1. The founder age for each of these expected founders can be calculated using the sub-branches of K9b and K9a1 present only in the sink population. Logically, the founder ages of K9b and K9a1 are not the same of the age estimates K9b and K9a1. The age of these sub-haplogroups of K9 will be calculated by using diversity in the source population data as well. This means that the age of these haplogroups will be higher than the founder ages (for more details see **2.11.3**).

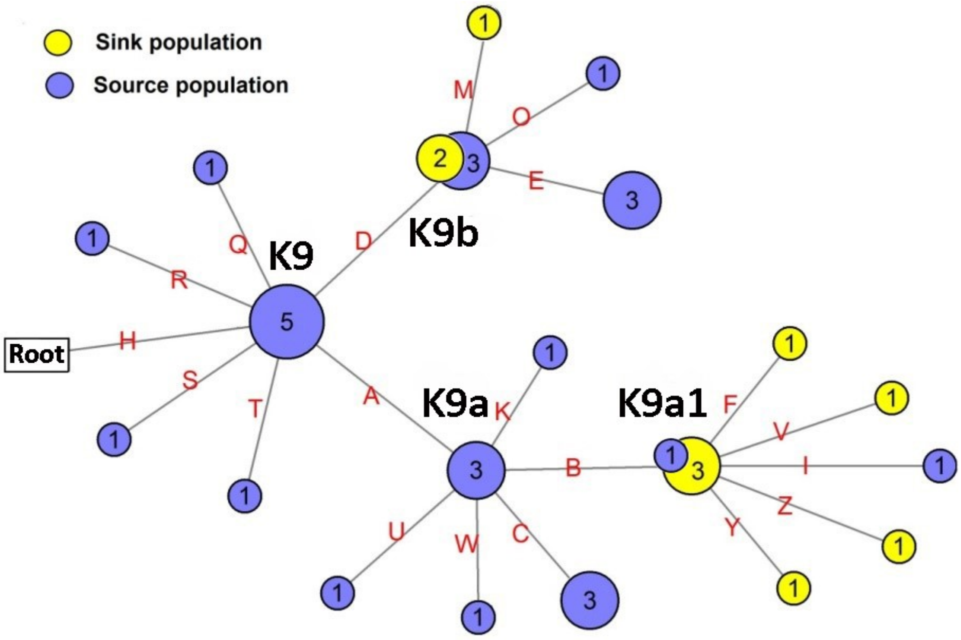


Figure 8. A hypothetical network represents a source and sink populations in one haplogroup (as an example the haplogroup is named as K9). Mitochondrial mutations are shown in red. Hypothetical numbers are used for each node in this network.

1.2.6 mtDNA tree nomenclature

Haplogroups named clades within a phylogenetic tree. Traditionally, the main mtDNA haplogroups are expressed in terms of uppercase roman letters (D, F, G, etc.), while sub-haplogroups are expressed using positive integers and lowercase roman letters (D1, F1b, G2b1, etc.) (M. Richards et al., 2000). The “macro-haplogroups”, if not symbolised by a single letter such as M or N (Figure 09), are labelled by merging the names of the combined haplogroups, such as the HV haplogroup. When a large clade contains small groups of unnamed clades, it receives the prefix “pre-”; exemplified by the pre-JT haplogroup. Paraphyletic lineages with a common ancestor can be clutered into paragroups (which are not clades as some descendant named haplogroups are excluded) and are indicated by appending an asterisk, such as for HV* (Richards et al., 1998).

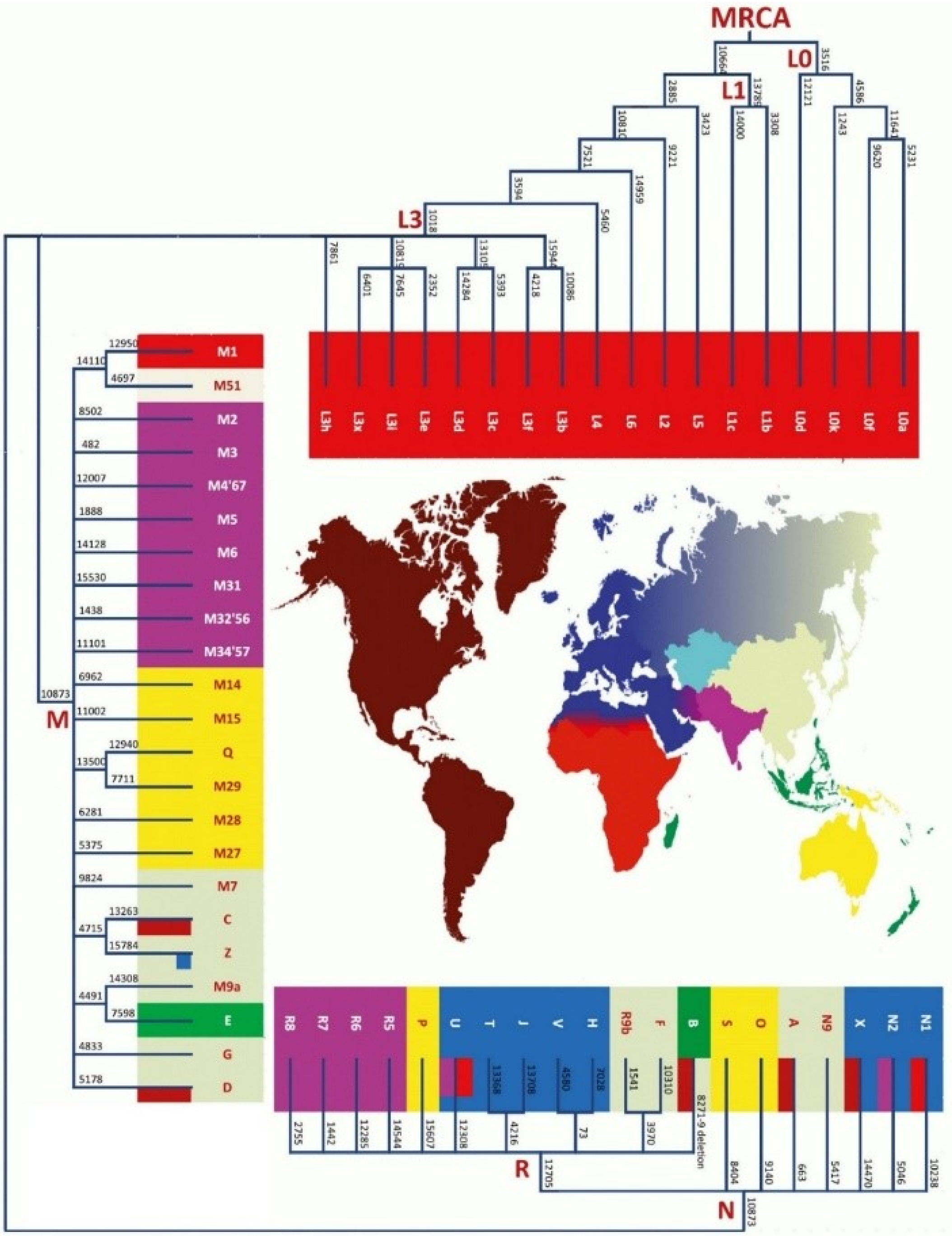


Figure 9. A schematic mitochondrial DNA phylogenetic tree (Kivisild, 2015).

1.2.7 “Mitochondrial Eve” and the root of the human mtDNA tree

“Mitochondrial Eve” is the hypothetical female at the root of the maternal human tree, also known as the most recent common ancestor (MRCA) female of all living humans in the world (Figure 09) (Cann, Stoneking, & Wilson, 1987). Eve’s mitochondrial sequence represents a theoretical ancestor to all the current human mitochondrial lineages. The expected age of Mitochondrial Eve is nearly ~200,000 years using the Mishmar coding region rate (Mishmar et al., 2003), about 186,000 years with a synonymous rate, and ~190,000 years with whole mtDNA sequence corrected for the purifying selection (P. Soares et al., 2009).

Traditionally, the human mitochondrial tree was rooted using the outgroups such as bonobo, chimpanzee and gorilla mitogenomes (Arnason, Xu, & Gullberg, 1996), but recently a complete mitochondrial genome of the Neanderthal became available (Green et al., 2008). In 2012 Behar and colleagues (Behar et al., 2012) used six *H. neanderthalensis* mitogenomes with 18,843 complete mitogenomes of modern humans to place the root, which they termed “the Reconstructed Sapiens Reference Sequence” or (RSRS) between the Homo sapiens haplogroups L0 and L1’2’3’4’5’6 using the inferred Reconstructed Neanderthal Reference Sequence (RNRS) (the expected reference for the six *H. neanderthalensis* mitogenomes), although this has been corrected by Bandelt and collaborators (Hans-Jürgen Bandelt et al., 2014).

1.1.8 The modern human dispersal out of Africa

Africa as the place of origin of all modern humans is increasingly supported by many of genetic and fossil evidence (Reyes-Centeno, 2016). The oldest modern human remains of what are known as anatomically modern humans (AMH) have been recovered in different regions in Africa (Hublin et al., 2017). Most recently, there have been new excavations at the late Pleistocene site of Jebel Irhoud, Morocco, which are directly associated with AMH remains, dated to about 315,000 years ago (~315 ka) by using optically stimulated luminescence (OSL), supported through the recalculated uranium series date of ~280 ka for a tooth (Richter et al., 2017).

In east Africa, the Middle Pleistocene Age at Gademotta, Ethiopia occurs before ~270 ka (Sahle, Morgan, Braun, Atnafu, & Hutchings, 2014), in Baringo, Kenya before about 284 ka (Deino & McBrearty, 2002), and in Ethiopia both human cranial remains and some human fossils and artefacts are dated around 198 and 155 ka respectively based on the 40Ar/39Ar-dating technique, while, in southern Africa, a redeposited late Pleistocene assemblage at Kathu Pan dates to before ~290 ka (Porat et al., 2010) based on OSL ages.

All of this evidence suggests the consistent presence of early AMH in Africa during the late Pleistocene (Reyes-Centeno, 2016), and most molecular genetic evidence suggests that non-African populations are descended primarily from only one successful late Pleistocene expansion out of Africa (M. B. Richards, Soares, & Torroni, 2016).

The ‘out of Africa’ proposal was originally based on inferences from the mitochondrial genome tree. Within the human mitochondrial DNA tree, the most recent common ancestor (MRCA), “Mitochondrial Eve”, represents the root of the seven deepest branches in the mtDNA tree. All seven of these branches – L0, L1, L2, L4, L5 and L6 – represent sub-Saharan African lineages, while L3 also includes the non-African lineages (M and N and their descendants).

This suggests that the deepest separations within all of these mtDNA branches are present in Africa, but that part of the L3 branch evolved outside of Africa into two non-

African haplogroups, M and N, prior to human spread to rest of the world (Forster, 2004).

Therefore, the L3 age (around 70 ka) represent the maximum age of human dispersal out of Africa (P. Soares et al., 2012) and the ages of two non-Africans branches, M and N, are estimated at about 50-65 ka (P. Soares et al., 2009). The similar ages between L3 and its two non-African branches suggests the possibility of similar environmental conditions that led to expansion of the L3 inside Africa, and its two lineages outside of Africa at the same time. According to climatological records, there were dramatic changes in climate conditions around 70 ka, which served to stimulate migration and expansion among early modern human populations (Scholz et al., 2007). Moreover, the similar ages of the L3 daughters (M and N) and their global non-African distributions may imply that they arose and dispersed rapidly together outside Africa in a single event, possibly along the southern coastal route from the Horn of Africa via Arabia and the Indian Ocean (Macaulay et al., 2005).

1.2.9 Southern coastal route to Southeast Asia

The southern route model is used to describe the initial peopling along the south coast of Asia through India to reach Southeast Asia and Australia, about 60 ka (Macaulay et al., 2005). It is linked to the distribution of the two non-African haplogroups, M and N, as well as a subclade of N, haplogroup R. Haplogroup R is dated close to the age of M and N and is globally considered a third main founder. Each region outside Africa, including the southern route regions (South Asia, Southeast Asia, East Asia and Australia) has different sub-branches, descending from the roots of these three basal haplogroups, M, N and R (Friedlaender et al., 2007; gounder Palanichamy et al., 2004; Kong et al., 2006; Sun et al., 2005; Thangaraj et al., 2006).

In other words, each region was settled by an initial group of people who were carrying the root sequences of three founders in their mitogenom pool, and because further mutations accumulated independently and locally, this gave rise to the differentiation between these regions into new M, N and R sub-branches (Macaulay et al., 2005; Metspalu, Kivisild, Bandelt, Richards, & Villems, 2006).

Currently, West Eurasia is unusual in having a set of N- and R-specific lineages, with M sub-branches being virtually absent (Macaulay et al., 2005), with the exception of haplogroup M1 in the Near East/Arabia. Recently, however, ancient mtDNA samples were used by Posth and colleagues to report a novel sub-branch from haplogroup M in Western Europe, and to re-date the basal roots of M and N to similar ages, about 55 ka (Posth et al., 2016). This recent result suggests that the twin haplogroups M and N were moving together toward both Europe and Asia at a similar time and strongly supports the model of single rapid expansion out of Africa after about 60 ka (Macaulay et al., 2005; M. B. Richards et al., 2016). The age of haplogroup M, which is often dated a few thousand years younger than N (and R), and its absence from modern populations in West Eurasia, seemed to suggest that M appeared a little later than N (and R), and it was not exist among the initial settlers of West Eurasia, but succeeded in spreading to only the eastern part of Eurasia (M. B. Richards et al., 2016). An anomalously young age for M in the Indian Subcontinent has also recently been addressed (Silva et al., 2017).

Therefore, the three basal roots, M, N and R, effectively represent the entire mitogenom pool in Eurasia (Macaulay et al., 2005), with a further widespread presence of their branches in the Pacific and the Americas. Macaulay and his colleagues (2005) reported the existence of M, N and R in the Orang Asli groups on the Malay Peninsula, with an estimated age about 50-65 ka (before the clock correction). This evidence supported the southern route model and the quick movements of these basal root types along the south coast of Asia, reaching islands in Southeast Asia and Australia by about 50 Ka (Mellars, 2006; Shi et al., 2010; P. Soares et al., 2012) (Figure 10). Recent archaeological studies have suggested new minimum ages for the human settlement of Sumatra by about 63 ka and of North Australia by about 59 ka (Clarkson et al., 2017; Westaway, Olley, & Grün, 2017).

According to some paleo-environmental studies, the initial peopling of Southern Asia might have occurred at a much earlier time, prior to the volcanic eruption that happened in Mount Toba in Sumatra, about 74 ka (Clarkson et al., 2017; Haslam et al., 2010). This volcanic eruption is the largest of the past two million years, depositing a blanket of volcanic ash over the South China Sea, the Indian Ocean, and the Arabian Sea (Jones, 2007), blocking the sunlight over the whole of South Asia and causing a six-year volcanic winter (Ambrose, 1998). Consequently, global environmental conditions were as severe as, or worse than, at the Last Glacial Maximum, 19-25 ka, suggesting a potential drop in the number of human populations at this time.

Petraglia and colleagues dug beneath the Toba ash layer in the Jurreru Valley in India and found stone artefacts dating between 77-74 ka, crossing the Toba boundary layer (Petraglia et al., 2007). This led them to suggest that humans had been living in the valley before the Toba eruption, and had survived the eruption and persisted, possibly to the present day, contradicting the genetic data (Petraglia et al., 2007). There are thousands of complete mtDNA sequences from Southeast Asia, but none of them carry any pre-L3 non-African lineage, which could indicate the existence of a modern human population in Southern Asia prior to the Toba event (Appenzeller, 2012; Mellars, Gori, Carr, Soares, & Richards, 2013).

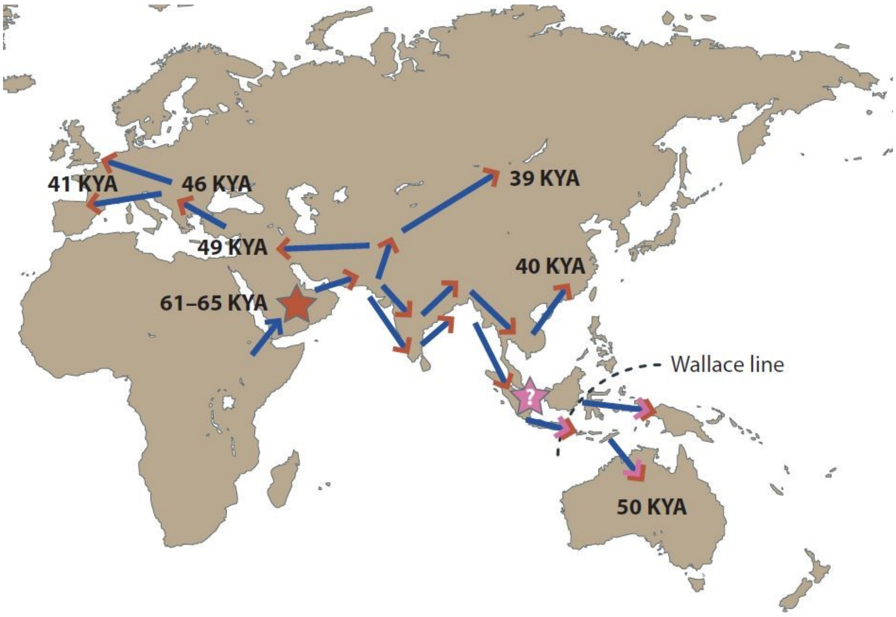


Figure 10. Possible dispersal routes out of Africa (Jobling et al., 2013).

1.3. Mainland Southeast Asia

1.3.1 Southeast Asia

Southeast Asia (SEA) is a sub region of the Asian continent and consists of countries that are geographically bordered east of India, south of China, north of Australia and west of New Guinea (Figure 11). Southeast Asian countries can be divided into two main regions: Island of Southeast Asia (ISEA) and Mainland Southeast Asia (MSEA). MSEA is also historically known as Indochina and includes Myanmar (Burma), Laos, Vietnam, Cambodia, Thailand, and West Malaysia (Peninsular Malay). ISEA includes, Indonesia, Singapore, East Malaysia, Philippines, Brunei, East Timor, Cocos (Keeling) and Christmas Island. The SEA region lies geologically near tectonic plate interactions, which exhibit volcanic and seismic activity (Hutchison, 1989).

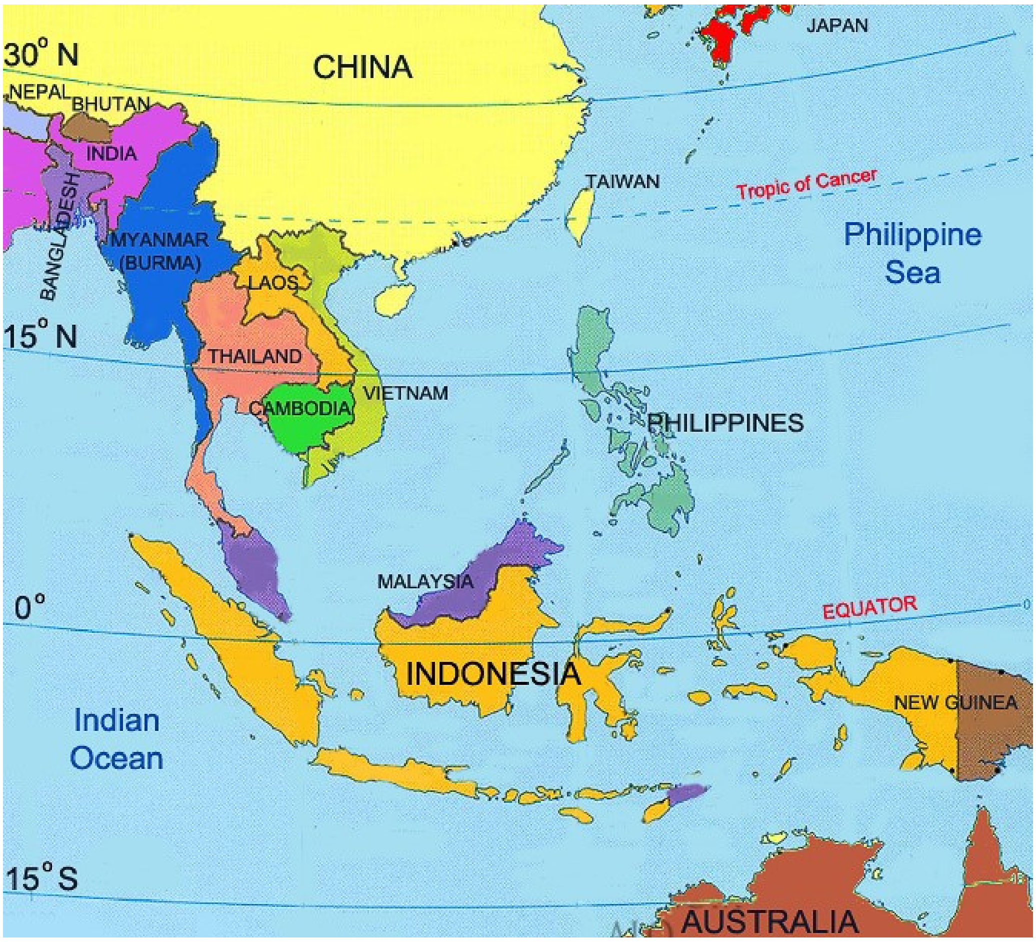


Figure 11. Map of Southeast Asia (PlantsGalore, 2018).

SEA's climate is largely tropical – humid and hot, with high level of rainfall most of the year. Myanmar Himalayas and North Vietnam are perhaps the only location in Southeast Asia that have a cold winter with high level of snowfall. Other regions have dry and a wet season due to monsoon conditions or seasonal shifts in winds. SEA is covered by tropical soils that generally lack nutrients. Often, the expansion of plants is related more to heat and moisture than to soil quality, even though SEA climatic conditions increase both the rate of bacterial action and chemical weathering, which generally helps to improve soil fertility. The most fertile soils can be found in regions of volcanic activity, *e.g.,* parts of Sumatra and the island of Java in Indonesia.

Southeast Asia comprises only 4% of the entire earth's land, but is considered a major global biodiversity region that contains about 20% to 25% of animal and plant species (Corlett, 2014; Myers, Mittermeier, Mittermeier, Da Fonseca, & Kent, 2000). Wallace (1876) biogeographically divided Southeast Asia using Wallace's line into two main parts (Woodruff, 2010). The first part includes MSEA, including the Peninsular Malay, and the three islands of western Indonesia (Sundaland, defined by the boundary of the Sunda shelf), and the Philippines; and the second comprises the Eastern Indonesian islands of Wallacea (Figure 12). Wallace's line defines the sea boundary between the Asian continental shelf and the Wallacean islands during the last glacial period.

Wallacea is a collection of Indonesian islands that are isolated by a deep level of water between the Australian and Asian continental shelves. During the glacial age, Sundaland was a single landmass forming part of the Asian mainland, but following the most recent glaciation, after about 20 ka, global warming led to rises in sea levels, subsequently covering many parts of Sundaland. These sea-level rises are thought not to have occurred only gradually, but were punctuated by rapid bursts around 14 ka, 11.5 ka and 7-8 ka (Oppenheimer, 1998; Pelejero, Kienast, Wang, & Grimalt, 1999). The final rise led to the drowned island landscape of today (Figure 11).

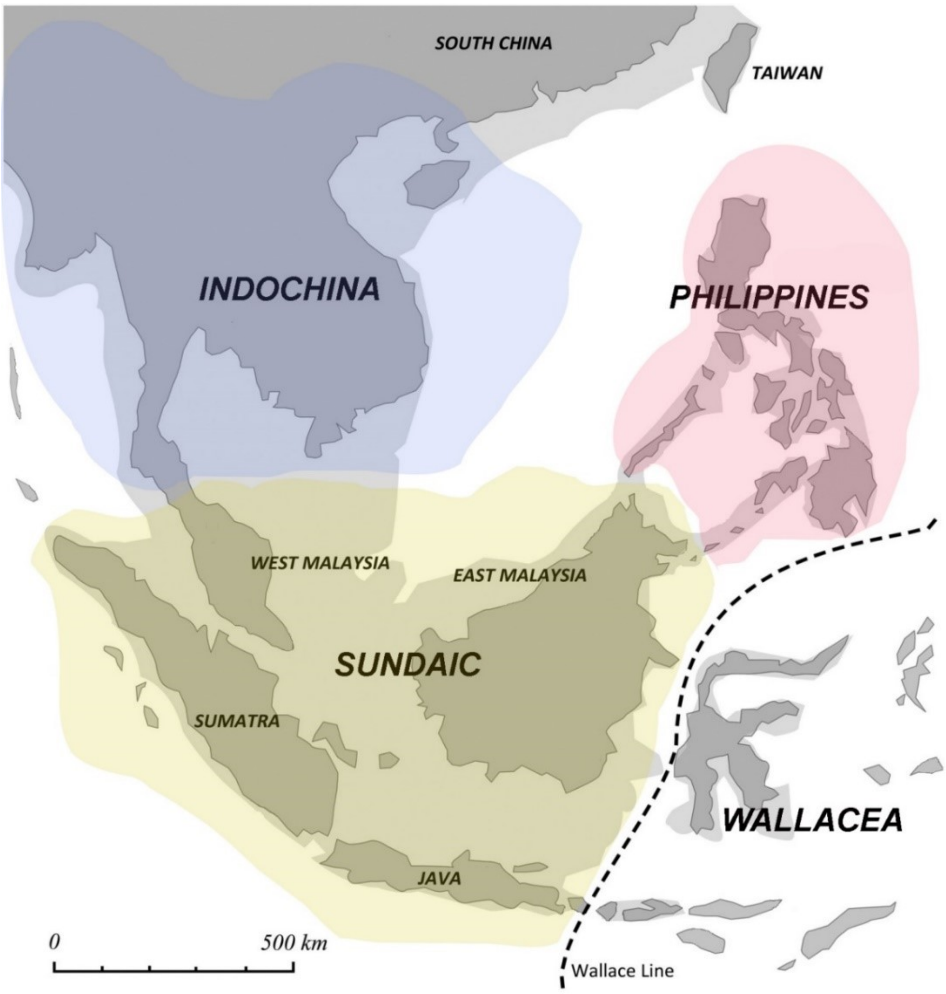


Figure 12. Map of Southeast Asia. Dark shading indicates modern lands while the light shading corresponded to the shorelines during the Last Glacial Maximum. (Jinam et al., 2012).

1.3.2 First settlement of MSEA by modern humans

Early evidence for anatomically modern humans (AMH) in SEA comes from the Niah Cave in Sarawak, Malaysian Borneo (Hunt, Gilbertson, & Rushworth, 2007), the Tam Pa Ling Cave in northern Laos (Demeter et al., 2012) and most recently from teeth in Sumatra (Westaway et al., 2017). The human cranium known as the Deep Skull from the Niah Cave was dated to about 39-45 ka using three different comparative dating techniques including the ABOX radiocarbon method, optically stimulated luminescence (OSL) dating and the uranium-series (U-series) technique (Barker et al., 2007); in Tam Pa Ling Cave, human bones were excavated and dated to between 46-63 ka using uranium-thorium dating (Demeter et al., 2015). The latter cave has been recently experienced more investigation, with a new partial mandible being found (Shackelford et al., 2017), this specimen may have been over-dated at about 43-78 ka using the luminescence technique. This raises the upper age limit for MSEA, although in the past doubts have been raised about the use of luminescence dating (Allen & O’Connell, 2003; O'Connell & Allen, 2004; M. Smith et al., 2001). Archaeological remains have also been found in the Lang Rongrien Cave in Thailand and dated to around 38 ka using the radiocarbon technique (D. D. Anderson, 1997). Most recently, teeth argued to belong to AMH at Lida Ajer in Sumatra have been dated to around 63-73 ka (Westaway et al., 2017).

The oldest clear dates for the Sahul region are from Madjedbebe, a rock shelter in northern Australia, where the earliest settlement has been estimated at 65.0 ± (3.7, 5.7) ka (Clarkson et al., 2017) and occupation of the Papua New Guinea highlands dates to at least 43-49 ka (Summerhayes et al., 2010). There are remain at the Jo’s Creek site in North-east of New Guinea and Lachitu Cave, close to the border of Indonesia, dating about 40 and 35 ka, respectively (Lilley, 2008). Moreover, near the Sahul shelf, the Jerimalai shelter in Timor presented a settlement age for modern humans of ~42 ka (S. O'Connor, 2007). To the north, skeletal remains similar to present-day modern humans were excavated from the Tianyuan Cave in China, its age estimated at about 40 ka (Shang, Tong, Zhang, Chen, & Trinkaus, 2007); furthermore, genetically, the ancient DNA of Tianyuan Cave’s skeleton belongs to a unique basal branch of haplogroup B not seen in extant populations (Fu et al., 2013).

In many cases, the range dates of archaeological records still converge with the DNA analysis that is used for current human populations in terms of timing and the origin of the first modern human settlement in Southeast Asia (Charles Higham, 2014). Genetic analysis results of the Orang Asli in the Malay Peninsula suggested that modern human settlement along the southern route in Southeast Asia was ~63 ka (Macaulay et al., 2005), a date that reduced only slightly when the mtDNA clock was corrected for purifying selection; M, N and R in East Asia have been re-estimated to ~54-61 ka, albeit with wide errors of more than 10 ka (P. Soares et al., 2009). To date, genetic evidence from modern human populations in Asia and Africa, as well most of the archaeological evidence from Southeast Asian sites suggest that the initial expansion of modern humans occurred after to the Mount Toba volcano eruption, at ~74 ka (Mellars et al., 2013), although all estimates remain imprecise.

1.3.3 Archaeological evidence in MSEA from Pleistocene to Holocene

The archaeological record in SEA was divided by Bellwood into two branches: the pre-ceramic (flaking and polishing the working surface of stone tools during the Late Pleistocene until Middle Holocene); and ceramic (the manufacture of fired pottery) (Bellwood, 1997; Charles Higham, 2014).

In the pre-ceramic period, most of the stone tools are flaked rather than polished. The earliest flaking tools are estimated to be more than 40,000 years old, and probably indicate the arrival of the first modern humans in SEA (Bellwood, 1997; Simanjuntak, Pojoh, & Hisyam, 2006). The similarity in making these tools in different archaeological sites from MSEA in the west to New Guinea and Australia in the east could suggest a single origin of the populations in these regions (Bellwood, 1997; Topich & Leitich, 2013).

As regards the Late Palaeolithic evidence, the best-known human industry in MSEA is the Hoabinhian. These are related to a hunter–gatherer lifestyle, and characterised by a distinctive cobble stone flaked on all of one or both sides (Charles Higham, 2013; Saidin, 2006). The Hoabinhian industry is pre-ceramic, but it probably overlaps with the pottery industry at some sites, e.g. in Vietnam. The Hoabinhian is found at many different sites in SEA countries (mainly in MSEA) including Vietnam, Myanmar, Thailand, South China and Peninsular Malaysia, but also Sumatra, New Guinea and Australia (Bowdler, 2006). They have been dated recently at ~43,500 years old in Yunnan, South China (X. Ji et al., 2016), from at least ~20,000 years old in north Vietnam (Seonbok, June-Jeong, Seongnam, Yongwook, & Dongwan, 2008), and between 20,000 and 5,000 years old in many regions of MSEA (Bowdler, 2006). According to a recent study, the oldest, and indeed the only, Hoabinhian site in China was found at a large rock shelter in Yunnan, about 40 kilometres from the Myanmar border (X. Ji et al., 2016). The variation in stone tools across SEA and the pre-ceramic evolution among the Late Pleistocene to Early Holocene transition have been connected with the environmental and ecological changes (Marwick, 2013; Patole-Edoumba et al., 2015). A description of some important pre-ceramic sites in MSEA follows.

Vietnam

The first evidence for a prehistoric hunter–gatherer group was established in 1906 at Tham Khoach cave in Lang Son province, northern Vietnam. Subsequently, the foundations for more detailed prospecting and excavations were laid at Hoa Binh province sites by Madeleine Colani and Henri Mansuy. Since then, the name of the Hoa Binh province has widely been used for many prehistoric sites, in the form “Hoabinhian” (Charles Higham, 2014), to describe stone artefact in SEA that contain flaked, cobble tools (Kipfer, 2000), spanning the Late Pleistocene to Early Holocene period. The second earliest hunter–gatherer location was found in Bac Son province, north of the Red River, where a certain kind of ground and polished stone artefacts were recovered and described as belonging to the Bacsonian industry (Charles Higham, 2014). The Bacsonian is an Early Holocene stone tool industry, dated between 8 and 4 ka, and is characterised by a higher frequency of edge-grounded cobble tools compared to the earlier Hoabinhian artefacts (Bellwood, 2007; Kipfer, 2000). The Hoabinhian and Bacsonian industries have never been linked to each other by Vietnamese prehistorians, although the two stone-working traditions were discovered in the same regions (Charles Higham, 2014).

However, the earliest human settlement in northern Vietnam has been reported mainly in three groups of sites. The first sites are the Dieu rock shelters in Thanh Hoa province, which produced the largest lithic assemblage found in Vietnam – almost 2000 large pebble tools and thousands of flakes. The early dates were established for the Dieu sites using the radiocarbon technique, and estimated at between 24 and 30 ka (Doi, 2005). The second grup of sites, at Nguom, in Bac Thai province, primarily contain flakes (amorphous in shape) and a few pebble core tools. The lithic technology is known as the Nguomian industry and is dated to more than 25 ka (Reynolds, 1990; Van Tan, 1997). The Son Vi sites are the third group of sites in northern Vietnam, most of which are located above the Bac Bo plain, in Vinh Phu province. The lithic industry in Son Vi sites is characterised by pebble tools flaked only on the edges and known as the Sonvian industry. More than 140 Sonvian sites were discovered, all of them dated before the Holocene (between 23 and 13 ka) (Van Tan, 1997). Ha Van Tan (1997) suggested that the Sonvian industry could have developed progressively into the Hoabinhian.

In Vietnam, Hoabinhian sites are found mainly in caves and rock shelters, located in the north of the country, close to Thailand and China (Yi, Lee, Kim, Yoo, & Kim, 2008). The most reliable chronology of these Hoabinhian archaeological sites is dated by Yi et al. (2008) at Han Cho cave in Luong Son district, Hoa Binh province (Singthong, Zeitoun, Pierret, & Forestier, 2016). Sixteen Hoabinhian levels were tested at Han Cho cave and 44 radiocarbon dates were obtained from these levels, ranging between 8.4 and 19.5 ka. This indicates that the Hoabinhian industry was already found in northern Vietnam by 20 ka (Yi et al., 2008). Another date, of 29 ka, from an unexcavated layer below the 16 Hoabinhian levels is congruous with dates established for sites in northern Thailand (Singthong et al., 2016). This suggests an even earlier emergence of the Hoabinhian in northern Vietnam (Yi et al., 2008).

Thailand

Spirit Cave in north-west Thailand was one of the earliest prehistoric sites to be investigated in Southeast Asia. This site provided the first documentation for understanding the prehistoric human lifestyle spanning the Pleistocene to Holocene periods (Conrad, Higham, Eda, & Marwick, 2016). It is the first site in MSEA reliably dated to the Pleistocene to Holocene transition (Gorman, 1969; CFW Higham, 1972) and also established the first well-defined evidence about how the hunter–gatherer groups adapted to this region during this period (Conrad et al., 2016). The radiocarbon dating indicated that Spirit Cave was occupied from about 12 to 7.5 ka, around a 5000-year time span of continuous occupation and uninterrupted use (Gorman, 1970).

In northern Thailand, the Tham Pha Chan cave in Mae Hong Son province was reported to have been occupied between 7.5 and 5.1 ka. This site was dated using radiocarbon and produced about 200 stone tools with a large amount of flake debitage (White & Gorman, 2004). Another three sites in the north of Thailand produced

Hoabinhian materials. The first site is Ban Rai which has eight radiocarbon dates ranging from 10.6 to 7.2 ka; the second site is Tham Lod which has four radiocarbon and two thermoluminescence dates spanning 32.4 to 12.1 ka (R Shoocongdej, 2004; Rasmi Shoocongdej, 2006); and the earliest dates were estimated between 30 and 28 ka at the Tham Khuong site (Nguyen, 1991). In the north-west of Thailand, near the Burmese border, a recent excavation recovered 181 Hoabinhian stone tools from the Huai Hin site (Forestier, Zeitoun, Winayalai, & Métais, 2013).

In southern Thailand, three cave sites near the village of Ban Kao; Khao Talu, Heap and Ment, produced archaeological material such as flakes and large worked cobbles that was related to the Hoabinhian industry and dated between 11 and 2 ka (Pookajorn, 1990). More archaeological evidence in peninsular Thailand, recovered at Moh Khiew in Krabi and Sakai cave in Trang province, dated the human occupation to more than 25 ka (Pookajorn, 1991, 1996; Pookajorn, Sinsakul, & Chaimanee, 1994). The Moh Khiew cave produced raw material in the form of large pebble tools nearly similar to those excavated at the Lang Rongrien rock site located nearby the Moh Khiew cave (D. D. Anderson, 1990), which was estimated to about 37 ka. Other levels of excavation in the Moh Khiew cave unearthed many significant archaeological finds, such as abundant flake and pebble tools, dated between 25 and 8.4 ka, some axes and polished stone adzes spanning 7 to 4.2 ka (Pookajorn, 1991, 2001; Pookajorn et al., 1994), and also well-preserved human skeletal remains dated by radiocarbon to about 25.8 ka. The features and measurement of the skeletal remains at the Moh Khiew site were found to be similar to Australian samples, especially those found in Coobool creek. This could suggest that the Moh Khiew remains may represent one of first group of people who invaded the ancient Sundaland region during the Late Pleistocene period (Matsumura & Pookajorn, 2005).

Laos

Archaeologically speaking, Laos is situated between two well-documented Hoabinhian industry areas, in Vietnam and northern Thailand. Recent excavations in north-eastern Laos have produced a modern human cranium from Tam Pa Ling Cave, dated, using the U/Th-series technique, to between 63 and 46 ka, and this is considered important evidence of the first occupation of early humans in MSEA (Demeter et al., 2015). In north-western Laos, Hoabinhian lithic material was collected from the Ngeubhinh Mouxeu rock shelter. Zeitoun and colleagues described some of these stone tools as pre-Hoabinhian and dated them between 56 and 45 ka, using the optically stimulated luminescence technique (Zeitoun et al., 2012). Although it has been argued that the luminescence technique may overestimate ages (O'Connell & Allen, 2004; M. Smith et al., 2001), these stone tools provided a good diagnosis about the stone industry and interduced more details about the Hoabinhian lithic production system (Singthong et al., 2016). Three other sites have Hoabinhian tools and human remains in Laos: Tam Hang site in the Khan river catchment, Tam Pong in the Seuang basin, and Tam Nang, on the right side of the Mekong river (Saurin, 1935, 1966). Many excavations delivered about 900 knapped stones, mainly located to the south of the Tam Hang site, dated between 10 and 13.2 ka, and in the central area of the same site, there were some lithic assemblages dated between 9.3 and 9.7 ka (Patole-Edoumba et al., 2015). The dating of, and the culture associated with, the Tam Hang site are similar to the classical Hoabinhian industry which was found in Vietnamese sites. Therefore, this site is considered as an important cultural marker for the Hoabinhian industry in Laos (White & Bouasisengpaseuth, 2008; White, Lewis, Bouasisengpaseuth, Marwick, & Arrell, 2009; Zeitoun et al., 2012). In Tam Pong (Saurin, 1966) some partially and fully polished stone tools corresponding to flaked Hoabinhian tools were found (Singthong et al., 2016).

Cambodia

The Hoabinhian evidence in Cambodia emerged for the first time in the 1960s, in the Laang Spean cave in the karst region, in the north-west of the country (Mourer, 1970, 1977; Stark, 2004). The lower layers excavated at the Laang Spean site were rich in lithic materials and stone tools which are affiliated to the Hoabinhian lithic industry. The oldest age of these lower layers was estimated at about 6.8 ka, by radiocarbon (Mourer, 1970, 1977). Since 2009, subsequent investigations have led to the discovery of Hoabinhian tools and earthenware potteries at several caves and rock shelters, near to the Laang Spean cave. This recent investigation establishes a new timeline for the occupation of Laang Spean sites, claimed to stretch back to 70 ka (Sophady et al., 2016). Stone cobble-shaped tools have been found in the lowest layers of the new Laang Spean sites. Sophady and colleagues have classified these stone tools as pre-Hoabinhian artefacts because they are different from the Hoabinhian industry pattern and date between 71 ± 6 and 26 ka, using OSL. Although the dating aspect is open to doubt because of the technique used, the lithic technology of these stone tools could shed light on an older phase of human activity, earlier than the Hoabinhian lifestyle in Cambodia.

Numerous Hoabinhian tools have been found near to the Laang Spean Cave such as pebble and cobble tools, a chopping tool and a few small flake tools originating from river deposits and shaped from hard and homogenous sandstone (Forestier et al., 2015). The age of these Hoabinhian tools has been estimated at 5 to 10 ka using the radiocarbon technique (Forestier et al., 2015) and their industry pattern is very similar to the Palaeolithic Hoabinhian industry in Vietnam, Thailand, Laos, Burma and also the island of Sumatra in Indonesia (Bellwood, 2007; Rabett, 2012) (Bellwood, 2007; Zeitoun et al., 2012).

Myanmar

Myanmar is located at the crossroads between India to the west and Southeast Asia to the east. With increasing archaeological evidence and the construction of chronological frameworks, it has the potential to provide significant more evidence about early human migration, human adaptation and technical innovation during the Late Pleistocene and Early Holocene in MSEA (T. H. Aung, Marwick, & Conrad, 2015).

The Hoabinhian industry in Myanmar is known as the "Anyathian Culture", derived from Anyatha, which is another name for Upper Myanmar (Movius, 1948; Topich & Leitich, 2013) referring to the central and northern area of Myanmar. The Anyathian culture is one of the pioneering stone industries in MSEA, which used a flaked stone made from a river cobble for hunting animals and gathering wild fruits and vegetables (Charles Higham, 2013; Saidin, 2006), and spans the Late Pleistocene and Holocene periods at different archaeological sites in the central belt of Myanmar (T. H. Aung et al., 2015).

In Upper Myanmar, there are about 14 archaeological sites thought to be part of the Anyathian industry, and the hand tools of stone in these Anyathian sites are similar to Hoabinhian artefacts (Aung-Thwin & Aung-Thwin, 2013). In Shan state, small assemblages of animal bone associated with some Palaeolithic stone tools were discovered at the Luyo Taung site, and a substantial animal bone assemblage, in association with 1600 stone artefacts, some fragments of pottery, a few pieces of charcoal and red ochre were discovered at the Padah-lin site. At the latter site, the oldest artefact tool is dated about 13.4 ka, suggesting that at least some of the human settlement probably dates to the Pleistocene–Holocene transition, while the youngest artefact is dated to 1.7 ka (T. H. Aung et al., 2015). In Upper Myanmar, there were more Anyathian artefacts discovered in two other caves in the Shan hills, Maung-Pa and Tin-Ein, dating between 5,000 and 3,500 years ago. Most of these artefacts were polished and shaped like axes and chisels (Aung-Thwin & Aung-Thwin, 2013).

In Kayin state, Waiponla cave is claimed to have been occupied around 12–6 ka, based on the similarity of the stone artefacts found there with those found in the Padah-lin cave (Thein et al., 2001), which was dated by radiocarbon to the end of the Pleistocene (M. Aung, 2000).

The archaeological sites in Myanmar are still under exploration, compared with those in Thailand and Vietnam. Therefore, we do not yet have enough information about the Anyathian culture (Tun, 2015). However, at other archaeological sites like the Choukoutien Lan sites in China, the Soan site in northeast India, and the Lalmai hills and Chaklapunji sites in Bangladesh, a type of stone tool was found which is similar to that in the Anyathian sites in Myanmar. This similarity in making stone tools in different archaeological sites in South East Asia suggests connections over a wide area of Southeast Asia during prehistoric times (Topich & Leitich, 2013).

1.3.4 The Neolithic and the origins of agriculture in MSEA

The Neolithic (or New Stone Age) begins with the rise of agriculture, and ends when metal tools start expanding during the Copper/Bronze Age, or shifting directly into the Iron Age, depending on the geographical region.

In Southeast Asia, agriculture can be traced back to sources on the Yangzi and Yellow River regions since it was in these regions that rice and millet started to be domesticated. Current evidence shows that the advancement of the farming societies from Yangzi and Yellow River valleys extended to most of MSEA from about 4000 ka; the earliest radiocarbon dates associated with rice agriculture in MSEA are ~3.8 ka (Charles Higham, 2014).

There are two contrasting theories that explain the beginning of agriculture in Mainland Southeast Asia. The first theory argues that farming expanded and was taken up after the adoption and dissemination of agricultural technology by the offspring of hunter-gatherers, a view that has received support from physical anthropologists (Pietrusewsky, 2010). The alternative theory argues that the relocation of early rice farmers into MSEA from centres of domestication in South China resulted in the expansion of farming. The debate is very similar to the debate between migration and assimilation of rice farmers through Taiwan to ISEA (Bellwood 1997, Bellwood 2005).

The later theory was supported by the only human genome-wide study published to date which was collected from five ancient sites in MSEA; Myanmar, Thailand, Cambodia, and two sites in Vietnam (Lipson et al 2018) and reported that the agriculture was first practiced in the region from southern China about 4 ka. The majority of ancient DNA samples from Vietnam represent a homogeneous Neolithic component, with local contact between the hunter-gatherers and the incoming farmers who had acquired about 25-30% hunter-gatherer ancestry (Lipson et al 2018).

This interpretation of how farming communities expanded into Mainland Southeast Asia revolves around a research that incorporates isotopic, human biological, and archaeological examination. The initial requirement is to establish where and when both millet and rice were farmed.

According to Yang et al. (2012), foxtail millet, which is the only species of millet to become established in Southeast Asia, was first planted on the plains of the Yellow River, with Nanzhuangtou, Cishan, Peiligang, Dadiwan, and Jiuahi having been amongst the earliest locations. There was a similar sequence for rice domestication in the Yangzi River basin, at sites such as Baligang, Shangshan (dating to 10,000-8000 ka) and Huxi (7000-6400 ka) (Deng et al., 2015; Fuller et al., 2009; Y. Zheng, Crawford, Jiang, & Chen, 2016). Both led to the outward spread of farming societies into the Sichuan Basin as well as south into Yunnan, Guangxi and Guangdong. Before that, hunters and gatherers occupied South China and MSEA.

The hunter-gathers who occupied South China, are often described in the Chinese and Vietnamese archaeological literature as Neolithic, because of the presence of pottery as well as polished stone adzes (X. Yang et al., 2012), and their sites on the coasts of South China and Vietnam are commonly termed as "coastal Neolithic", which seems to reflect a widespread adaptation by hunters and gathers in the rich resources of the estuaries and shore of Southeast Asian (Charles Higham, 2004). However, the term is disliked by many western archaeologists who associate "Neolithic" with agriculture, and Oxenham and Matsumura (2011) use the phrase "pre-Neolithic pottery using culture" to differentiate them from the farmers (Oxenham & Matsumura, 2011). The following paragraphs will summarise some information concerning the archaeology of Neolithic settlements in MSEA.

In northern Vietnam, the earliest first farmer settlements are represented by the Phung Nguyen cluster of sites in the Red River plains, dating to ~3800 ka. The Red River provides access from Yunnan into northern Vietnam and produced important evidence in the material sequence for beginning of agriculture and the Hoabinhian culture at that time. Most of the Neolithic sites in north Vietnam are similar to Chinese sites, which indicates that these hunting and gathering groups may have maintained contacts with the farming societies of the Yangtze valley (Charles Higham, 2003). In southern Vietnam, by contrast, the agricultural events at the Son site in the Dong Nai River region started with an occupation stage and cemetery that can be tracked from 3700–3300 ka. Excavations produced fossilized particles of rice in the basal layer and some Neolithic material comprising shouldered and quadrangular stone adzes and barbed fish hooks (Bellwood et al., 2013).

The occupation of farmers in inner central Thailand can be divided into two main regions. In the west, there are sites categorized as Ban Kao after the first site to be studied (Sørensen & Hatting, 1967). In the East of the Chao Phraya River, most of the settlements are concentrated in the Lopburi Province. Human remains were found along with ceramic utensils, shell decorations and stone carvings, and the initial occupation in these regions has been traced to the first half of the second millennium BCE. The pots were mainly decorated with multifaceted engraved and impressed designs that suggest a common Southeast Asian Neolithic “syntax” even though it had regional variations such as the pottery utensils belonging to the Ban Kao group and the Lopburi groups (Charles Franklin Higham, 2017).

In Northeast Thailand, the initial farmer occupation is evidenced by three locations on the Khorat Plateau. The early occupation appears later than the coastal sites since, as explained by Higham et al. (2015), it comprises Non Nok Tha 1500–1300 BC, Ban Chiang 1600-1450 BC and Ban Non- Wat, 1750-1550 BC. The three have in common the protracted the existence of domsticated animals such as pigs, cattle, and dogs, and domesticated rice (Charles FW Higham, Douka, & Higham, 2015).

In Cambodia, some of the earliest known ceramics were found in Laang Spean cave in Battambang Province. Some of these overlap with Hoabinhian artifact layers, complicating the relationship between the Neolithic and Hoabinhian settlements.

Archaeological sites in other MSEA countries, such as Myanmar, are still under-explored compared with those in Thailand and Vietnam. The evidence of a Neolithic age in Myanmar appears in three caves in the Shan hills, Maung-Pa, Tin-Ein and Padah-lin, dating ~4000 years ago (Aung-Thwin & Aung-Thwin, 2013; Tun, 2015).

1.3.5 The people of MSEA and language dispersals

Five language families overlap within MSEA: Daic or Tai-Kadai, Austroasiatic (Mon-Khmer), Hmong-Mien, Sino-Tibetan and Austronesian. Among these, Austroasiatic is represented across MSEA, stretching all the way down into Peninsular Malaysia, as well as west towards the Andaman Sea and northeast India. Austroasiatic languages are diverse and numerous throughout inland areas across central MSEA. The languages of numerous sub-branches are spoken throughout northeast Cambodia, southern and central Laos and Vietnam (Enfield, 2005).

The Sino-Tibetan stretches northwards through China as well as northwest into the Himalayas (Benedict, 1972; Matisoff, 1991; Thurgood & LaPolla, 2003). The branches of Sino-Tibetan family that are present in MSEA like the Loloish languages that are spoken in Myanmar’s highlands, northern Thailand and northern Laos as well as south-western China (Goudineau, 2003). In addition, expansive and thriving minority communities in South China primarily speak Hmong-Mien languages which are thought to migrate southward into Laos, Vietnam and Thailand (Culas & Micraud, 1997).

The Tai-Kadai family includes two key branches: Tai, a homogeneous branch that mainly spreads towards the west across MSEA into northeast India and Myanmar's highlands, and Kadai, an offshoot of minority languages that are spoken in Guizhou, Yunnan, Guanxi, and Guangdong provinces across south-western China (Diller, Edmondson, & Luo, 2004).

The two main families, Tai-Kadai (TK) and Austroasiatic (AA), are spread widely throughout Asia; as many as 167 AA languages are spoken by a population of ~102 million people from India and Bangladesh to MSEA and South China, including Malaysia; on the other hand, ~80 million people in South China, northeast India, Myanmar, Vietnam, Thailand, Cambodia and Laos speak 92 TK languages (Lewis, Uchiyama, & Nunnari, 2016). It has been suggested that TK arose in southeast China maybe before 2.5 ka and subsequently spread through MSEA (R. A. O'Connor, 1995; Pittayaporn, 2014). While the origin as well as expansion of AA is contentious, it has been suggested that the AA population descended from the region's earliest inhabitants (Condominas, 1990; Penth, 2000). Alternatively, Higham (2014) suggests that Austroasiatic was carried into MSEA by the first rice farmers, by analogy with the language-farmer dispersal model for the spread of Austronesian in ISEA and the Pacific (Bellwood 1997).

In MSEA, the Austronesian family is only represented by the Chamic languages (Thurgood, 1999). Austronesian languages are primarily dominant across Taiwan, ISEA and the Pacific (Adelaar & Himmelmann, 2005). The Chamic group comprises a set of ten languages that are spoken in some parts of Cambodia, China, Vietnam and Aceh (in Sumatra, Indonesia), related to a subgroup of languages that are part of the Malayo-Sumbawan culture. Genetically, the mtDNA of Chams shares a close affinity with AA-speaking populations within MSEA, as compared to the Austronesian populations belonging to ISEA. Therefore, this could suggest that the Chams' origin in ISEA was a process of language shifting, thus the diffusion of Austronesian in MSEA may primarily have been mediated by a cultural diffusion (Peng et al., 2010).

1.4 Objectives

The overall objectives of this study were to investigate the first arrival of modern populations in MSEA, clarify the timing and process, and study the varied settlement history of its populations from the perspective of the maternal line of descent.

According to the other complementary lines of evidence such as linguistics, archaeological and climatic changes in MSEA, the most significant settlements in the region would more likely take place during the following events:

- **The initial Pleistocene settlement,** which happened during the Ice Age in the region. The Sunda shelf was connected MSEA, western ISEA and whole of the island of Borneo. This ancient Sundaland region is considered as a key area of initial settlement of the anatomically modern humans, who likely expanded along the coastal route from the Horn of Africa via Arabia and South Asia towards Australasia. By using modern samples in this study we can ask which modern-day maternal lineages date to this initial settlement in MSEA. Do these dates fit well with the recent palaeontological and archaeological estimates for the initial settlement of Southeast Asia, especially the most recent modern human remains at Sumatra around 63-73 ka (Westaway et al., 2017) and northern Australia about 65 ka (Clarkson et al., 2017)? And when was the first signal for the separation of these maternal lineages within ancient Sundaland region between MSEA and ISEA?

- **The end of the Last Glacial Maximum and the Late Glacial warming phases,** which led to rapid climatic changes that dominated the Late Pleistocene. Melting of large amounts of Arctic ice led to a substantial rise in the sea level in the oceans affected the world shorelines for many different regions but had a particularly powerful impact on Southeast Asia. In this study we investigate how the people in MSEA, who could have been adapted to coastal regions at that time, were affected by these changes, which had a major impact on human populations in ISEA (Soares et al., 2008). Or, in another words, are there signs of an important impact of Late Glacial and postglacial climate change and sea-level rises on human population dispersals, as in ISEA?

- **The early Holocene settlement,** or the early postglacial period between ~11.5 ka to ~6 ka. Archaeologically, the best-known human industry from this time in MSEA is the Hoabinhian. These are related to a hunter–gatherer lifestyle and characterised by a distinctive cobble stone flaked on all of one or both sides (Saidin, 2006, Higham, 2013). The Hoabinhian industry is pre-ceramic, but it probably overlaps with the pottery and farming industries at some archaeological sites in MSEA. The hunter-gathers who occupied South China are often described in the Chinese and Vietnamese archaeological literature as Neolithic, because of the presence of pottery as well as polished stone adzes (Yang et al., 2012), and their sites on the coasts of South China and Vietnam are commonly termed as “coastal Neolithic”. This seems to reflect a widespread adaptation during the early Holocene by hunters and gathers in the rich resources of the estuaries and shorelines of Southeast Asia (Higham, 2004). For this settlement event we need to address if there are significant dispersals from the north to MSEA in the early Holocene that might be associated with the so-called “coastal Neolithic” expansion of foraging populations.

- **The rice Neolithic expansion.** There are two main alternative theories concerning the beginning of rice agriculture in MSEA. The first argues that farming expanded via the offspring of hunter-gatherers who adopted food cultivation, a view that has received support from some physical anthropologists (Pietrusewsky, 2010). The alternative theory argues that the relocation of early rice farmers into MSEA from centres of domestication in South China resulted in the expansion of farming – the “farming-language dispersal hypothesis” that has also been discussed for ISEA, sub-Saharan Africa and Europe (Bellwood, 1997, Bellwood and Dizon, 2005). According to the latter expansion model, the earlier settlers were replaced in the last ~4 ka by Neolithic rice agriculturalists from South China. By this time, MSEA and ISEA were already separated by water. By using the maternal line of descent, I have investigated which of these theories is better supported, and what fraction of maternal lineages date to arrivals at the time of the rice Neolithic, around 3.8 ka.

By using a high-resolution phylogeographic analysis with a well-estimated molecular clock (P. Soares et al., 2012; P. Soares et al., 2009), the latter events can be investigated and discussed to address the direction and timing of modern human dispersals and expansions in MSEA.

2. Materials and methods

2.1 Samples

The samples used in this study were already present in Martin Richards and Maria Pala's laboratory since the beginning of my study. We used 466 samples in this study which were collected from Myanmar, 550 from Laos and 398 from Vietnam. All of them were already partially sequenced (HVS-I) by Pedro Soares (Burmese samples) and Andreia Brandão (Laos) and Maru Mormina (Vietnamese). 41 Burmese samples were already sequenced for a complete mtDNA sequence by Pedro Soares.

I produced 909 complete mitochondrial genomes; 387 from Vietnam, 506 form Laos and 16 samples from Myanmar. Sequence data was inserted in database (Excel file) with more details about the geographical locations, ethnicity, and languages. More 1645 complete mtDNA genome and 4,699 partial mtDNA sequence (HVS-I) published data from different locations in MSEA were added in the database (Table 01). Also 11,811 published, 456 unpublished complete mtDNA sequence and 28,913 (HVS-I) data were added from 24 different Asian countries (obtained from GenBank and Archaeogenetics Research Group, Huddersfield). In this study, all the ID samples and accession numbers were colour coded according to their geographic location.

Table 1. List of partial and complete mtDNA genomes in MSEA that uses in this study.

MSEA's mtDNA Data was used in this study	Myanmar		Laos		Thailand		Vietnam		Cambodia		Total
	CR	**CS**	**CR**	**CS**	**CR**	**CS**	**CR**	**CS**	**CR**	**CS**	
This Study	/	16	/	506	/	/	/	387	/	/	909
(Bodner et al., 2011)	/	/	220	/	/	/	/	/	/	/	220
(Kutanan et al., 2017)	/	15	/	49	/	1170	/	/	/	/	1234
(Irwin et al., 2008)	/	/	/	/	/	/	186	/	/	/	186
(Jin, Tyler-Smith, & Kim, 2009)	/	/	/	/	40	/	42	/	/	/	82
(H. Li et al., 2007)	/	/	/	/	/	/	65	2	/	/	67
(Summerer et al., 2014)	256	71	/	/	/	/	/	/	/	/	327
(Oota et al., 2002)	/	/	/	/	1	/	19	/	/	/	20
(Y.-C. Li et al., 2015)	713	135	/	/	/	/	/	/	/	/	848
(Fucharoen, Fucharoen, & Horai, 2001)	/	/	/	/	215	/	/	/	/	/	215
(Y. G. Yao et al., 2002)	/	/	/	/	32	/	/	/	/	/	32
(Zimmermann et al., 2009)	/	/	/	/	189	/	/	/	/	/	189
(Hartmann et al., 2009)	/	/	/	/	/	/	/	/	/	2	2
(Zhang et al., 2013)	/	/	/	/	/	/	/	/	921	133	1054
(Peng et al., 2010)	/	/	/	/	/	/	285	4	/	/	289
Archaeogenetics Research Group, Huddersfield	420	46	44	/	131	15	11	3	/	/	671
Total:	1389	283	264	555	608	1185	608	396	921	135	6344

(CS) Complete mtDNA genome sequence and (CR) Partial mtDNA sequence (Control Region 'HVSI').

Figure 13. Geographical locations of all the samples which are used in this study. Keys: Andaman (AND), Australia (AUS), Australia (AUS), Bangladesh (BNG), Bhutan (BTN), Burma (BUR), Cambodia (CMB), East China (CHE), North China (CHN), Northwest China, Gansu NW (CNW), South China (CHS), West China (CSW), Central China (CHC), Southwest China (CSW), Christmas (CHR), Cook Island (COO), India (IND), Indonesia (INS), Iran (IRA), Japan (JAP), Kazakhstan (KAZ), Laos (LOS), Malaysia (MLY), Mongolia (MOG), Nepal (NEP), Pakistan (PAK), Papua New Guinea (PNG), Philippines (PHL), Samoa (SAM), Siberia (SIB), Singapore (SNG), South Korea (KOR), Sri Lanka (SRI), Taiwan (TWN), Taiwan (TWN), Thailand (THI), Uzbekistan (UZB), Vanuatu Island (VAN) and Vietnam (VIT).

2.2 DNA Extraction

Consented buccal swabs were taken from 16 Burmese people by using sterile cotton swabs. These swabs were air dried and then stored at -20 ^{0}C. DNA was extracted from the samples using the QIAamp® DNA Investigator kit. The following protocol was used to obtain high molecular weight DNA from buccal swabs. This method yields approximately 200 µg of DNA.

1. Before using the kit for the first time both the concentrated buffers AW1 and AW2 were diluted with ethanol, and before starting each extraction batch, the buffers ATL and AL were incubated at 70^{0}C in a water bath to dissolve any precipitates.
2. Swabs taken out from the freezer for 10 minutes to thaw, and then the cotton tip of each swab was cut out using a sterile scalpel and placed in a 1.5ml tube.
3. 20µl of proteinase K and 400µl buffer ATL were added to the 1.5ml tube and were mixed by vortexing for 10 sec. All the 1.5ml tubes were incubated at 56^{0}C with shaking at 900 rpm for 1 hour.
4. 300µl buffer AL was added to the 1.5ml tube and mixed by the vortex for 10 sec before placing it in a water bath at 70^{0}C with shaking at 900 rpm for 10 minute.
5. 150µl ethanol (96–100%) was added to the 1.5ml tube and it was again mixed by vortexing for 15 sec, and then about 700µl lysate of the 1.5ml tube was then transferred to the QIAamp MinElute column with 2ml collection tube.
6. Each MinElute column was subjecting to a centrifugation step (6000 x g for 1 minute) and discard the flow-through from the collection tube.
7. 500µl buffer AW1 was added to column and then the centrifugation step repeated with discarding the flow-through from the collection tube again.
8. After moving the MinElute column back into the collection tube, 700µl buffer AW2 was added and then the centrifugation step applied again.
9. The previous step is repeated by using 700µl of ethanol (96–100%) instead of 700 µl buffer AW2, and then centrifuge the empty column at full speed (20,000 x g) in order to dry the membrane. After that each column was placed into a new 1.5ml tube, which was then incubated at 56^{0}C for 3 minutes.

10. 60µl buffer ATE (PH 8.0) was added to the MinElute column assembly and incubated at room temperature for 1 minute before subjecting it to centrifuge at full speed (20,000 x g) for 1 minute to obtain the DNA from the column.

2.3 Amplification (Long range PCR)

A routine Polymerase chain reaction (PCR) is a technique used to amplify a certain segment of DNA molecule, generating thousands to millions of a particular DNA sequence. Basically, this technique requires several components to prepare the PCR reaction, including: a DNA template (DNA target region to amplify), a heat-stable DNA polymerase (*Taq* DNA polymerase), two DNA primers (a forward and a reverse), deoxynucleoside triphosphates (dNTPs), and buffer solution (a suitable chemical environment). This method relies on thermo-cycling PCR reaction (cycles of DNA denaturation, primer annealing and DNA extension).

Long range PCR indicates to the amplification of longer DNA lengths than what is a typically be amplified using routine PCR methods. Polymerases optimized for Long Range PCR can amplify about 20 kb. In our study the GoTaq® Long PCR Master Mix kit was used from Promega to amplify the whole mtDNA genome, where the amplification of complete mtDNA is performed in two overlapping fragments (about 8 kb for each) by using four primers (table 02). The first fragment extends from np 5871 to np 13829, and the second fragment np 13477 to 6151 and includes the control region. The long range PCR reactions were prepared for a final volume of 29 µl for each fragment as described in (table 03). For each mtDNA fragment, two Master Mix were always prepared according to the number of our samples with including just one blank sample as a negative control. After optimization, all the PCR reactions were exposed to the same conditions as described in (table 04).

Table 2. Primers used to amplify the human mtDNA genome in two fragments.

Fragment ID	DNA fragment length (bp)	Primer ID	Primer Length	Sequence 5→ 3
1.	7958	5871For	22	GCTTCACTCAGCCATTTTACCT
		13829Rev	22	AGTCCTAGGAAAGTGACAGCGA
2.	9243	13477For	22	GCAGGAATACCTTTCCTCACAG
		6151Rev	22	ACTAGTCAGTTGCCAAAGCCTC

Table 3. Amplification protocol used in this study

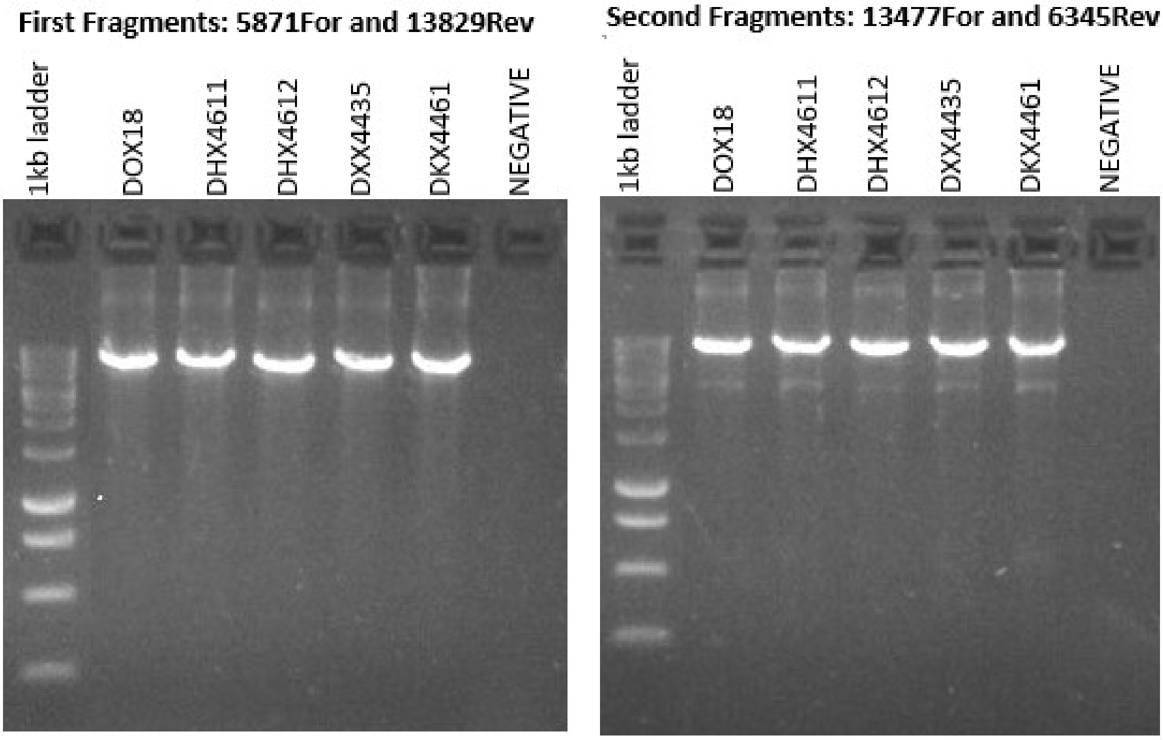
Reagent	concentration	Quantity (µl)
Nuclease-Free Water	-	12.5
GoTaq® Long PCR Master Mix (PROMEGA)	2X	14.3
Forward primer	10 pmol/µl	0.6
Reverse primer	10 pmol/µl	0.6
DNA template	<0.3µg/30µl	1

Table 4. PCR reaction protocol used in this study.

Step	Temperatures (^{0}C)	Time
1. Initial denaturation	94 ^{0}C	2 minutes
2. Thermo-cycling (30 times):		
a. Denaturation	94 ^{0}C	30 seconds
b. Annealing	55 ^{0}C	30 seconds
C. Extension	72 ^{0}C	9 minutes
3. Final extension	72 ^{0}C	10 minutes

2.4 Gel electrophoresis

The agarose gel electrophoresis was used to check all the PCR products. Gel electrophoresis is a technique for separation of macromolecules (nucleic acid and proteins) and their fragments according to their size and charge in a gel matrix inside electric field. After preparing 1% agarose gel, the PCR products were loaded beside 1kb DNA ladder (0.1µg/µl) to estimate the size of the DNA bands (Figure 14). In the 0.5% TBE tank the agarose gel was run at a constant voltage of 75 V for about 45 min.


First Fragments: 5871For and 13829Rev

Second Fragments: 13477For and 6345Rev

Figure 14. Agarose gel of two different long range PCR fragments. The first well in each row contains a molecular weight ladder of 1Kb.

2.5 Clean-up of PCR Amplification Products

PCR amplification products are commonly purified to eliminate excess nucleotides and primers before doing DNA sequencing. In this study, the membrane-based system (the Wizard ® SV Gel and PCR Clean-Up System kit) was used to clean the PCR products. This system is based on the ability of DNA bands to bind to silica membranes. The target DNA fragments can be isolated using micro-centrifugation to force PCR amplification product through the membrane while simultaneously binding the DNA fragments on the Silica surface. After washing the isolated DNA fragment by the washing buffer, the yield DNA eluted in elution buffer.

Three main steps were used to purify the PCR amplification product:

A. Binding of DNA

1. The equal volume of Membrane Binding Solution to the PCR product was added.
2. After placing Mini-column into a collection tube, the prepared PCR product was transferred to the Mini-column assembly and incubated at room temperature for 1 minute.
3. I centrifuged the Mini-column at 16,000 × g for 1 minute, discard flow-through and replaced Mini-column into collection tube again.

B. Washing step

1. For each Mini-column assemble I added 700µl Membrane wash solution (95% ethanol added).
2. I centrifuged the Mini-column at 16,000 × g for 1 minute, discard flow-through and replaced Mini-column into Collection Tube again.
3. I repeated the step 4 with 500µl Membrane Wash Solution, and centrifuged at 16,000 × g for 5 minutes.

4. The collection tube was drained and re-centrifuged the Mini-column assembly for 1 minute to allow evaporation of any residual ethanol.

C. Elution step

1. Mini-column was transferred into a clean 1.5ml tube.
2. I added 50μl of Elution buffer (0.01 μmole/μL Tris-HCl, pH 8.5) to the Mini-column, and incubated at room temperature for 1 minute.
3. Finally, I centrifuged the Mini-column at 16,000 × g for 1 minute and collected the DNA in the 1.5 ml tubes.

2.6 Quantification

Quantification is commonly performed to determine the concentrations of DNA and there are two main approaches used to quantify the isolated DNA; spectrophotometric quantification and UV fluorescence tagging. In this study, the fluorescence tagging method was applied by using the Qubit® 3.0 Fluorometer. The Qubit Fluorometer utilizes fluorescent dyes that are specific to the target the DNA. The dyes have very low fluorescence levels, but once they bind to their targets DNA the fluorescence level will increase intensely. The Qubit fluorometer can measure the fluorescence level and then convert it into a DNA concentration measurement using DNA standards of known concentration. The Qubit dsDNA HS Assay Kit was used to measure the purified DNA. This kit contains concentrated assay reagent (fluorescent dye), dilution buffer, and pre-diluted DNA standards. After calibrating the Qubit fluorometer by using the DNA standards, a Master Mix was always prepared according to the number of purified samples. Each reaction contains 1μl of the fluorescent dye,198 μl of the dilution buffer and just 1μl of the purified DNA. The assay is highly selective for double-stranded DNA (dsDNA) and is accurate for initial sample concentrations from 10 pg/μl to 100 ng/μl.

2.7 NGS sequencing

During this study, I did not prepare the samples for the sequencing step. All the purified samples are sent to Earlham institute in Norwich to do the Next-generation sequencing (NGS). In this study, 931 purified samples were sent for the NGS by using the 96-well plate, aiming to have 200x coverage by using the Illumina MiSeq platform (Micro flow cell 150bp PE read). Each purified sample had 40 µl volume (20 µl for each fragment), and their concentration is 1 ng/µl.

NGS is also known as non-Sanger-based high-throughput sequencing technology. Millions of DNA fragments can be sequenced in parallel, increasing throughput substantially and minimising the time and cost of DNA sequencing beyond that which is possible with the fragment cloning methods that are often used in Sanger sequencing (Schuster, 2008).

The principle of NGS technology is similar to capillary electrophoresis sequencing (CE). The DNA polymerase catalyses fluorescently labels the deoxyribonucleotide triphosphates (dNTPs) into a DNA template fragment during sequential cycles of DNA synthesis. In each cycle, the nucleotides are detected by fluorophore excitation (Bentley et al., 2008).

There are a number of different NGS technologies, such as Illumina Solexa, Roche 454 pyrosequencing, Ion torrent and SOLiD sequencings, which can be used by different sequencing platforms (Behjati & Tarpey, 2013). In this project, the Illumina Solexa (also known as the Sequencing by Synthesis – SBS) technology was applied to analyse our samples using the Illumina MiSeq platform (Micro flow cell 150bp PE read). However, Illumina NGS workflows include four main steps:

1. NGS Library Preparation: the NGS library is prepared by cutting the DNA genome into random fragments, followed by the tagmentation step by adding 3′ and 5′ adapters ligation.

2. Cluster generation: In this step, the NGS library is loaded into a flow cell which contains two types of surface-bound oligos complementary to the adapter sequences. Each fragment is then captured and amplified in a distinct way, known as the PCR bridges, to generate clusters of DNA templates for sequencing.

3. Sequencing: in the Sequencing by Synthesis (SBS) technology, nucleotides are detected as they are incorporated into DNA fragments by using "the proprietary reversible terminator-based method". To determine the sequence, all the four reversible terminator-bound dNTPs nucleotides are added during each sequencing cycle. Once a nucleotide base is added to the new DNA stand, the fluorescent dye molecule is imaged by using a camera to detect and read the nucleotide base and then cleaved to allow the addition of the next nucleotide. This method minimises the incorporation bias because of the natural competition between the dNTPs molecules that are present as single and separate molecules (Bentley et al., 2008).

4. Data Analysis: Millions of new sequence reads are generated in FASTQ format, which can be aligned to a certain reference genome (rCRS).

2.8 EAGER software

The Efficient Ancient Genome Reconstruction (EAGER) free software was used in this project to align the FASTQ files with the Revised Cambridge Reference Sequence (rCRS) (GenBank ID 251831106) and create a report of sequence variants. EAGER consists of tools and methods addressing read pre-processing, read mapping and genotyping large-scale NGS data from NGS platforms (Figure 15). It offers a graphical user interface (GUI) that helps to configure the complex pipelines (Peltzer et al., 2016).

For the pre-processing stage, EAGER prepares all steps necessary to process large genome data in FastQ format, including the initial analysis of raw sequencing reads using FastQC method (which can assess the basic quality of the generated NGS data), and removing forward and reverse read adapters from the sequencing reads by using the adapterRemoval method.

In EAGER, mapping the raw NGS reads against the reference genome (rCRS) can be implemented by using a set of state-of-the-art mapping methods such as BWA-aln, Bowtie2, or BWA-mem. In this project we used the BWA-mem method which produces the sequence alignment map (SAM) and/or the binary alignment map (BAM) files. SAM and/or BAM files can be viewed, sorted and indexed by using the SAMtools programme, which allows the EAGER to work more efficiently with the data and to remove the duplicate alignment reads. To ensure that the resulting SAM and/or BAM files are processed appropriately, EAGER has a duplicate removal method called DeDup. This method removes duplicates and is tailored specifically to merged paired-end reads.

In the last stage, the EAGER pipeline can be used to perform full genotyping by identifying the SNPs and indels using the genotyper, which is called the

HaplotypeCaller in GATK (McKenna et al., 2010) along with the GATK variant filtration method to perform downstream analysis of called variants inside the pipeline and creating the variant call format files (VCF).

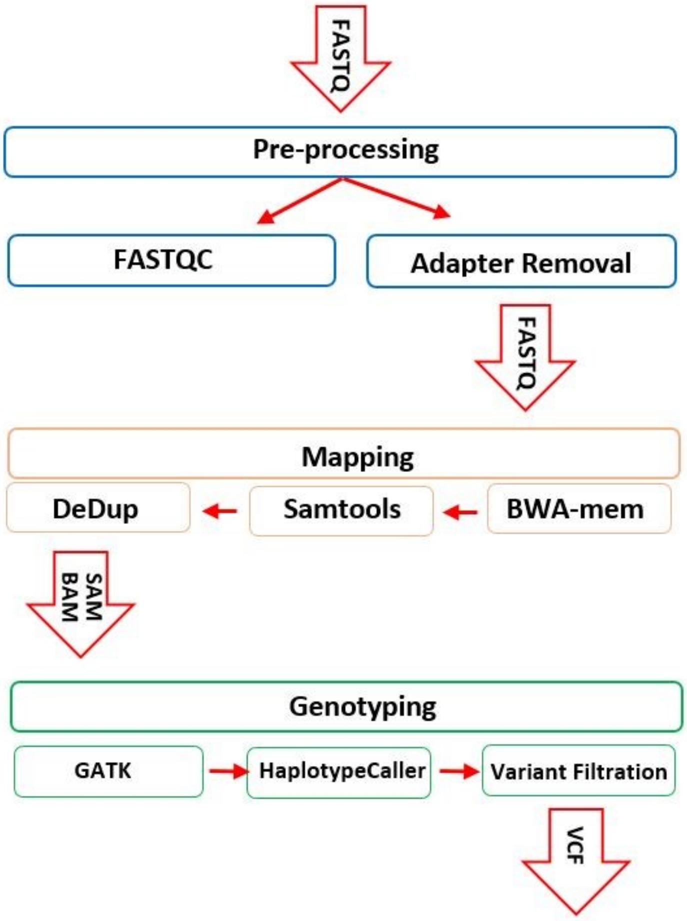


Figure 15. Workflow diagram of the three distinct main components in the EAGER pipelines (Peltzer et al., 2016).

EAGER has been executed in the Java programming language and can be run on several types of operating system. In this project, the Linux (Ubuntu 16.04.3 LTS) was used to download the EAGER pipeline at a certain location by using the command line:

```
“singularity pull shub://apeltzer/EAGER-GUI:master”
```

Once the NGS data was prepared, the EAGER graphical user interface (GUI) can be opened by using the command line:

```
"singularity exec -B /path/to/your/data:/data /path/to/apeltzer-EAGER-GUI-
master.img eager"
```

The GUI allows the user to select multiple NGS samples and to conFigure all the analysis tasks as XML files. (In this project, the EAGER parameters are summarised in table 05).

Table 5. the general settings for EAGER

Tasks of EAGER	**Main setting**	**Advanced setting**
CPU Cores to be used	4	-
Memory in GB	2	-
Use system tmp dir	Unchanged	-
FastQC Analysis	Ticked	Unchanged
Adapter RM/Mergin	AdapterRemoval	Unchanged
Mapping	BWAMem	Unchanged
Complexity Estimation	Unchanged	Unchanged
Remove Duplicates	DeDup	Unchanged
PMDtools	Unchanged	Unchanged
Contamination Estimation	Unchanged	Unchanged
Coverage / Statistics Calculation	Unchanged	-
Damage Calculation	Unchanged	Unchanged
SNP Calling	Ticked and HaploCaller	Ploidy of organism = 100
SNP Filtering	Ticked	Unchanged
VCF2Genome	Unchanged	Unchanged
CleanUp	Ticked	Unchanged
Create Report?	Ticked	Unchanged

In the last step, the actual EAGER analysis procedure can be run with eagercli by issuing the following command line:

```
singularity exec -B /path/to/your/data:/data /path/to/apeltzer-EAGER-GUI-
master.img eagercli /data
```

The eagercli should then find all the generated configuration files (which are saved in a XML format), then subsequently execute them and run the required analysis tasks to obtain the VCF files.

2.9 Creating FASTA files

All the variants and sample ID in the output EAGER files (VCF) were copied in an Excel file (one sample per raw) and then converted into FASTA file by using fastmtDNA (http://www.mtdnacommunity.org/downloads.aspx). The fastmtDNA is free tool, which allows transformation of list of mtDNA haplotypes into FASTA files. The heteroplasmies per sample were checked with Geneious 6.1.8 software and eventually add manually to the Fasta. Geneious software is a powerful and comprehensive suite of molecular biology and NGS analysis tools. In this project, the Geneious was used for checking the EAGER's variant callings by mapping the NGS reads data to the reference sequence (rCRS).

2.10 MitoMap database

MITOMAP database is designed for human mitochondrial genome data (Kogelnik, Lott, Brown, Navathe, & Wallace, 1996), and has grown and improved very rapidly over the past several years. One of the distinctive features which has added to the MITOMAP database is the access to the mitochondrial DNA sequences in the GenBank Database. This feature allows users to look up human mtDNA gene loci and search or browse for more details about the published whole or partial mtDNA sequences, such as Genbank ID (accession numbers), PubMed Reference, sequence type (full sequence FL or control region CR) and predicted haplogroup by entering at least one of the single nucleotide variants in the search allele option (Lott et al., 2013).

In this project, the search allele tool in the MITOMAP database was used to browse a report about most of the published whole mtDNA sequences, matched with the haplogroups that were determined in this study by our mtDNA sequences.

In the search allele page online (https://www.mitomap.org/foswiki/bin/view/Main-/SearchAllele), the distinctive nucleotide variants for each determined haplogroup were entered to obtain all the accession numbers for the published mtDNA sequences. After copying all these accession numbers from the MITOMAP browser, they were entered into the search machine in the NCBI Nucleotide database (https://www.ncbi.nlm.nih.gov/nuccore/?term=) to obtain the published FASTA files for each accession number. The FASTA files were then used with our data to generate the phylogenetic trees by using the mtPhyl program.

2.11 Phylogeographic Analysis

Phylogeographic analysis can be defined as the analysis of the geographical distribution of the various DNA lineages within a phylogenetic tree. A phylogenetic tree is a branching tree that can describe the evolutionary relationships among various individuals based upon differences and similarities in their genetic material. However, there are two basic approaches that can be used to construct phylogenetic trees: distance-based and character-based approaches. The first approach (not used in this study) is commonly applied by implementing a clustering algorithm to construct the phylogenetic tree based on measures of genetic distances, and in traditional evolutionary studies the neighbour-joining (NJ) method is popularly used in this regard. In the second approach, there are three main types of character-based approaches, namely maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference. Character-based methods more usually use an optimality criterion, in order to select between many possible trees (Felsenstein & Felenstein, 2004; Page & Holmes; Swofford, Olsen, Waddell, & Hillis, 1996). In addition, there are the network methods such as the median-joining (MJ) and reduced-median (RM) methods, which were applied in this study by using the Network 4.6 software to produce phylogenetic network graphs (with loops) in order to summarise a set of trees in a single network diagram (Hans-J Bandelt et al., 1995). In this study, three main character-based methods were used: maximum parsimony (MP) to build the phylogenetic trees, and maximum likelihood (ML) and Bayesian inference to estimate the time events to the most recent common ancestor.

2.11.1 Reconstructing the phylogenies

For reconstructing the phylogenies from the mtDNA control region data, the reduced-median (RM) method was applied in this study by using Network V4.6.0.0, while the maximum parsimony approach was applied to analyse the complete mtDNA sequences using the mtPhyl V4.015.

2.11.1.1 Reduced median (RM)

Almost all the control region data throughout this project was carried out using the reduced median method (Hans-J Bandelt et al., 1995), and the Network 4.5 software. Although the reduced median algorithm is one of the parsimonious network methods (which includes also the median joining method), but it does not produce a single most parsimonious tree. It usually presents a series of reticulations that could represent different evolutionary histories of the sequence. This method is traditionally used to construct the phylogenies, since distance method and MP often do not succeed in building nested sets of haplotypes for mtDNA data due to parallel or reverse mutations.

The reduced median algorithm works with the binary data (0 – 1), where only a descendant and an ancestor can exist per position. In this approach, the first step is assuming all the descendants arise directly from the same ancestor, and after constructing the initial network, analysis is carried out to ascertain whether any other possibility seems more appropriate.

A median network structure consists of nodes, and between these nodes there are links which connect them. The nodes represent either sequences from the data set, or what is known as median vectors. A median vector (mv) is an assumed sequence which could represent unsampled data or extinct ancestral taxa (Hans-J Bandelt et al., 1995), and it is required to link existing sequences within the median network with maximum parsimony. For resolving the reticulations (parallel mutations) between an existing sequence and a median vector, a reduction parameter is available in the Network software. The reasoning is that parallel mutations are more likely to be found between existing sequences than between an existing sequence and a median vector. The Reduced Median method will generate a reduced network if the reduction parameter “r” is set to a sufficiently high number (two or other low numbers greater than two). The reason for reducing the initial median network (full median network with median vector nodes) is to improve clarity for data size, and because a full median network usually contains too many median vectors and links to visualise and interpret.

2.11.1.2 Network 4.5 and Network Publisher

I checked all sequence data and aligned them against the human mitochondrial reference sequence (rCRS) to assign the data into different types of haplogroups. After checking and determining the haplogroups, the HVS-I variants (minus 16000) of samples that share the same haplogroup were used to build the mtDNA phylogenies. Through this study, the mtDNA phylogenies were constructed using the reduced-median algorithm (RM) of the Network 4.5 software and Network publisher (http://www.fluxus-engineering.com/sharenet.htm), using all the substitution information on the mtDNA molecule (except for 16182C, 16183C and 16194C in poly-cytosine tracts containing the 16189C variant).

The ‘fm2net’ software is used to produce a ‘.Tor file’ that can be imported into Network v4.5 software (Snell, 2008). In the Network software, each haplotype was represented by binary data (0 or 1); 0 for absence, 1 for presence of a character (mutation) and each character was weighted according to their evolutionary values. Some mutations can be more important than others, and a weighing scheme can be used when using a reduced-median algorithm in order to eliminate some of the less plausible pathways. For each mutation, the default weight usually is 10, although this weight value may range between 0 and 99. Fast mutations in the HVS-I such as nps 16311, 16189, 16129, 16093, and 16362 were down-weighted from 10 to 3, while other mutations such as nps 16086, 16319, 16278, 16172, 16192, 16223, 16291 and 16390 were reduced to 5. This ranking is implemented according to (P. Soares et al., 2009). After checking or editing the requirement values, all the data can be then saved as a ‘.rdf file’ that can be imported to apply the reduced-median calculations in the network software. Once the phylogenetic network has been constructed, the nodes can be coloured according to their geographic locations by using the Network publisher. Node colouring is increasingly used within network graphics to visualise more information in a network, such as the haplogroup, geographic affiliation, or ethnic affiliation of each sequence. Colour-coded nodes can also be used to help in analysis and some interpretation, for example whether the geographic origins of DNA sequences correlate with their relationships within the phylogenetic network.

2.11.1.3 Maximum Parsimony (MP)

A basic concept of constructing a parsimonious tree is that the best possible phylogenetic tree has the shortest tree length (minimum evolutionary changes from the common ancestor). Thus, the best phylogenetic tree is the one that requires the minimum number of mutations to account for sequences in the alignment. There are some problems with using MP, however. The major one is recurrent mutation (or parallelisms; the same mutation site occurring in two different sequences independently). More problems can be found if the sequences are related and there are many recurrent mutations; two (or more) trees may be equally parsimonious leaving MP with no criterion for choosing one of them. Including many samples will lead to more computational demands, and in many cases the MP algorithms could only provide a putative tree, which may be longer than the actual parsimonious tree. In these circumstances, the MP approach can provide a parsimonious tree with the wrong topological structure. Therefore, all the parsimonious trees that were produced in this study were manually checked and reviewed according to the mtDNA phylotree Build 17 (http://www.phylotree.org/tree/index.htm). After checking all the parsimonious trees in their output excel files, they were converted into XML trees.

2.11.1.4 mtPhyl v4.015

This is a free tool that can perform different types of Human mtDNA analyses, such as reconstructing maximum parsimony trees, calculating coalescence time for each cluster, exporting a list of mutation sites in particular mtDNAs into an Excel table, defining mitochondrial haplotype, and downloading complete mtDNA sequences from the GenBank (Eltsov & Volodko, 2009). The mtDNA sequence can be imported in a FASTA format or as '.txt' files containing partial (control region) or complete mtDNA sequences for each sample, since the program does not accept one concentred file with multiple mtDNA sequences. mtPhyl aligns the mtDNA sequences against the reference sequence (rCRs) to reconstruct and produce a maximum parsimony tree in Microsoft PowerPoint or Excel formats. With the tremendous advancement of sequencing technology today, the amount of published sequence data is increasing rapidly, and mtPhyl can integrate this massive amount of sequence data into the phylogenetic trees. Additionally, the undesired mutations that will not be used in reconstructing the tree can be specified by using this software. In our case, we used the molecular clock that was proposed by Soares (2009), which takes into account all substitutions except the 16183C, 16182C, 16194C, 16519, and indels (deletions and insertions). Therefore, these excluded mutations and indels were specified as undesired mutations with mtPhyl before generating the trees. However, this tool has to be used with caution: all the output trees have to be carefully checked, and age calculations are not reliable.

2.11.2 Age estimate

I used two approaches to estimate the time events to the most recent common ancestor; the rho (ρ) statistic and maximum likelihood (ML).

2.11.2.1 The rho (ρ) statistic and variance ($\sigma 2$)

A rho statistic (ρ) is the average number of mutations between a set of sequences and a root or most recent common ancestor (MRCA) of the phylogenetic tree or network. This statistical approach was described for the first time by Morral et al. (1994) and then developed by Peter Forster and collaborators (Forster et al. 1996). The rho statistic formal can be expressed as $\boldsymbol{\rho} = \frac{\sum_{i=1}^{k} n_i m_i}{N}$, where ni represents number of sequences and mi the number of observed mutations along the ith link, and N is the total number of sequences in a very parsimonious tree or network.

The variance formula was originally obtained as $\boldsymbol{\sigma^2} = \rho \,/\, N$, where n is the total number of sequences in the clade, but assuming that all the mutations in the estimate are independent, which does not happen very often (because it only occurs if the tree is perfectly star-like). Therefore, the revised formula of the variance that takes into account the tree shape and the type of mutations counted (if they are independent or not) in the estimate of ρ is given as $\boldsymbol{\sigma^2} = \sqrt{\frac{\sum_{i=1}^{k} n_i^2 m_i}{N^2}}$, (Saillard, Forster, Lynnerup, Bandelt, & Nørby, 2000). The 95% lower and upper confidence intervals were estimated by $(\rho - 1.96 \times \sigma^2;\ \rho + 1.96 \times \sigma^2)$. In this study, the ρ and σ^2 values were converted into years by using the rate of non-linear mutation corrected for purifying selection, which was applied by the calculator (ρ Genetic Distance Value Conversion calculator) provided in Soares et al. (2009)

How to calculate ρ and σ^2:

Practically speaking, the rho ρ statistic can be computed manually for each node by adding the total number of mutations in each sample, and then dividing by the total number of individuals. The variance σ2 can be calculated in the same way as ρ, but by squaring the number of samples each time when calculating the mutations, and then dividing by the square of the total number of samples.

For example, in Figure 16, the hypothetical network (K9a) has a root node which is the most frequent node (n = 6), and a total number of 46 mutations (red star shape) in 28 samples. We can directly calculate the average number of mutations (ρ) for the hypothetical network (K9a) when dividing the total number of the mutations by the total number of samples (ρ = 1.643). The latter value means that the clade (K9a) has accumulated an average of 1.643 mutations per sample. This value can be translated into time (i.e. years) using a molecular clock. However, we can also mathematically try to calculate ρ and σ2 values for K9a and K9a1 nodes as follows:

- K9a

$$\rho = \frac{(3 \times 2) + (3 \times 2) + 1 + (10 \times 1) + (2 \times 1) + 1 + (5 \times 1) + (2 \times 1) + 1 + (4 \times 1) + 1 + (3 \times 1) + (2 \times 1) + (2 \times 1)}{28} = 1.643$$

$$\sigma^2 = \sqrt{\frac{(3^2 \times 2) + (3^2 \times 2) + 1 + (10^2 \times 1) + (2^2 \times 1) + 1 + (5^2 \times 1) + (2^2 \times 1) + 1 + (4^2 \times 1) + 1 + (3^2 \times 1) + (2^2 \times 1) + (2^2 \times 1)}{28^2}} = 0.513$$

- K9a1

$$\rho = \frac{(10 \times 1) + (2 \times 1) + 1 + (5 \times 1) + (2 \times 1) + 1}{10} = 2.1$$

$$\sigma^2 = \sqrt{\frac{(10^2 \times 1) + (2^2 \times 1) + 1 + (5^2 \times 1) + (2^2 \times 1) + 1}{10^2}} = 1.162$$

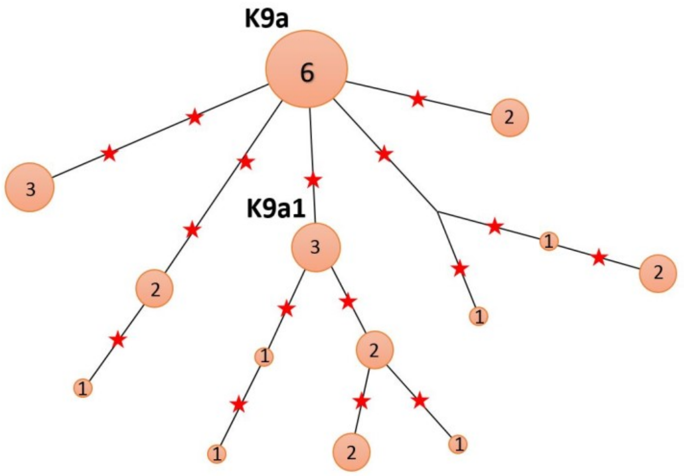


Figure 16. Hypothetical network for illustrating the rho calculations. Mitochondrial mutations are shown in red stars. Hypothetical numbers are used for each node and taxon in this network.

2.11.2.2 Maximum Likelihood (ML)

ML is a standard statistical method for inferring probability distributions to assign probabilities to particular possible phylogenetic trees, and it is based on an explicit substitution model to assess the probability of particular mutations when estimating the phylogenetic tree. Therefore, using appropriate calibrated mutation rates can provide a more realistic estimation of coalescence time with less confidence intervals. Statistically speaking, the likelihood (L) formula is often written as L=Prob(A/H), where Prob(A/H) is the probability of obtaining the data (A) given the hypothesis (H). In phylogenetic analysis, the likelihood estimation is given by the probability of observing the nucleotidic sequence data given a particular model of mutation processes, hence A will be the set of DNA sequences being compared and H is a phylogenetic tree (with a certain topology and set of branch lengths). Therefore, from this formula, we need to find the likelihood of obtaining the observed DNA sequence given a particular phylogenetic tree and/or branch length. The assumption of ML has several limitations when constructing phylogenetic trees. There is no very clear idea about how the evolutionary process happens, and ML estimates are often not strong enough to depart from the hypotheses. In addition, when comparing likelihoods across all possible trees, the ML is extremely computationally demanding.

ML was performed using PAML software (Phylogenetic Analysis by Maximum Likelihood (Z. Yang, 1997)) to estimate just the branch lengths in a pre-defined phylogenetic tree using a molecular clock in a given substitution model. It is not used to build the tree since there are other methods (such as reduced-median (RM) network and maximum parsimonious (MP) methods) that are more adequate for this.

2.11.3 Founder analysis (FA)

Founder analysis is a phylogenetic approach that aims to identify all potential founders in a certain population and determine their source and time of arrival. This approach for calculating founder age uses the links present only in the sink population, which means the founder age calculations will include the diversity that has accumulated in the sink population, and it will not use any mutation that has already been carried from the source population (P. Soares et al., 2009). This diversity within the sink population can be measured using the statistic ρ (rho), which is the average number of transitions from the founder sequence type to the sub-branches in the sink population.

Two factors can interfere with the signals of the founder analysis. One is the back-migration whereby migration must take place in one direction: from the source to the sink population. Back-migration may lead to an overlap between the sources and migrated reverse sequences; therefore, the source itself must be determined. The second factor is a recurrent mutation, which could affect the identification of the founders by matching these mutations in terms of state rather than descent (Macaulay

& Richards, 2008). These factors can lead to undesirable sequence matches, leading to an effect on the estimation of the founder age. In order to overcome these obstacles, two criteria (*f1* and *f2*) were designed to minimise the levels of stringency when identifying founders were created.

In Figure 17, a hypothetical network represents seven founder site assumptions (N1-N7) for both criteria. The founder criteria *f1* and *f2* are used to consider every single candidate founder as a real founder, and they should be a reasonable estimate of founder ages due to the risk of false mutations that could occur in both source and sink population sequences because of the recurrent mutation (especially at fast sites) and back-migration. Therefore, the false matches should be specified in the source phylogeny which should have 1 (*f1*) or 2 (*f2*) derived branches. For example, the founder site assumptions N5 and N6 (Figure 17), present a derived branch in the source population so they are considered as (*f1*) founders. Meanwhile, founders' nodes N1, N2 and N3 have at least two derived branches in the source population and would be considered (*f2*) founders.

However, these two thresholds of calculating the founder age for each founder node will help to reduce the back-migration factor, since more common clades in the sink population would be more likely to back-migrate into the source population than rarer clades. Although, all the HVS I networks in this study does not contain reticulations (See chapter 3), but in case of the parallel mutations (reticulations), the founder approach assumes that the fast-mutating evolutionary site is the recurring site where the mutation could happen more than once, and the other site is slower and the mutation happens just once. Founder N4 (Figure 17) might be a possible founder site. It depends which mutation site is faster, m or n. If the (m) mutation is slower, the founder approach will consider the N3 site as founder site that is linked to one sink population sequence with the (n) mutation. If the (n) mutation is slower, the (m) mutation will produce two recurrent events and there is no founder site that could link the sink population sequence with the N3 node.

The founder analysis v1.4 was performed using the complete sequence and HVS-I data to estimate the founder ages of the migrants in MSEA. This approach used the output files of the Network publisher to perform the age calculations. All the populations (except the MSEA populations) in the network were selected as ascendants (source), while the MSEA population was selected as descendants (sink population). Founder analysis results (*f1* and *f2* files) were analysed using the ρ (rho) Genetic Distance Value Conversion calculator (an excel file developed by Soares) (P. Soares et al., 2009), which can calculate the settlement age by using two values, the ρ (rho) statistic and the standard error (se), which were already obtained from each of the *f1* and *f2* files.

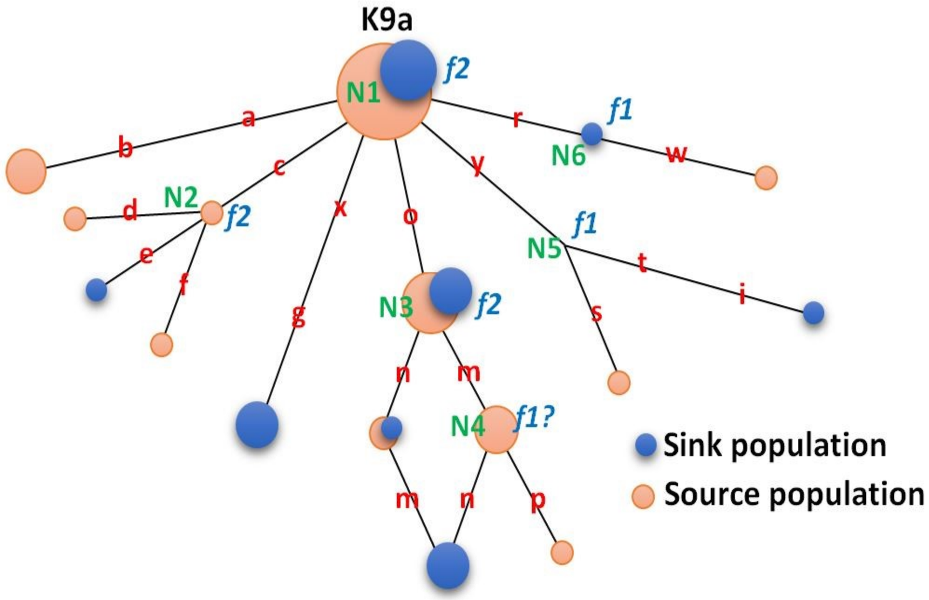


Figure 17. Hypothetical network for the founder analysis. The network (not the real haplogroup K9a) containing different assumed founders' sites (N1 to N6) in green colour and the *f1* and *f2* criteria in which those founders are included is indicated in blue letters (P. Soares, 2009).

2.11.3.1 Bayesian migration partition (BMP)

This approach is an application of the founder analysis that allows us to fractionate founder lineages into migration events at pre-defined time windows (Richards et al. 2000). The time windows used can be defined by scanning the ρ values at regular intervals and identifying peaks of migration, or by inputting the known ages of particular cultural changes (such as then Neolithic transition). Each founder type is then probabilistically assigned to each specific defined migration events using the Bayesian migration partition software. In this study, after obtaining the ρ values for each founder type by using the founder analysis, a five-migration model was assigned (100, 3,800, 7,000, 14,200 and 50,000 years) using the BMP software, corresponding to recent gene flow, the arrival of the rice Neolithic, the peak of migration during the coastal Neolithic, the first sea-level rise during the Late glacial, and an approximate age for the first modern human settlement.

2.11.4 Splitting Analysis

This analysis focused on basal lineages in MSEA and ISEA, which are putatively the ones that are associated with the first settlement, and uses a reciprocal founder analysis to study the times at which lineages separated between ISEA and MSEA into regionally specific subclades, with minimal gene flow from one region to another. To do this, the BMP software tool was used to obtain a probabilistic distribution of the founder age estimates corresponding to 200-years intervals ranging from 0 to 70 ka, from both ISEA to MSEA and from MSEA to ISEA.

3. Results and Discussion: Phylogeographic analysis using the control region (HVS-I)

- Phylogeographic analysis using the control region (HVS-I)

The first step of the overview examination of the populations was implemented in this study by reconstructing phylogenetic networks of hyper-variable segment 1 (HVS-I) sequences for each haplogroup, in order to build a portrait of the genetic variation in MSEA. I identified a number of mitochondrial tree branches of previously characterised clades and fine-tuned their branching structure in order to gain some insight into the maternal evolutionary history of the region and understand the processes that determined the present genetic array of the MSEA populations.

As mentioned in the first chapter, the genetic diversity outside Africa derives from three major haplogroups (or macrohaplogroups): M, N and N's nested haplogroup R. Each of these clades splits into a number of further clades and sub-clades with a specific geographic distribution and characteristic frequencies, probably reflecting the combined action of migrations and genetic drift. The haplogroups M, N and R are widely distributed across Southeast Asia, with some sub-clades spreading through wide areas, while others are more restricted to specific populations. The phylogenetic relationship between MSEA and other Southeast Asian lineages will be analysed by using the HVS-I in the course of this chapter.

- Haplogroup profile

In this study, haplogroup M accounts for about 60% of the total diversity in MSEA. The most frequent haplogroups within M are M7b (Kong et al., 2003; Tanaka et al., 2004), D4, C, M12 (Kong et al., 2006) and M74. As shown in in table 7, M7b is widely distributed across Southeast Asia, reaching its highest frequency in South China, MSEA and ISEA, while the sister haplogroup M7c (Kong et al., 2003) and haplogroup

E exhibit relatively higher levels in ISEA. In this study (tables 7 and 8), M7b is most commonly found in north Laos and north Vietnam, while it is almost absent from south Vietnam (tables 8). In contrast, the basal M haplogroups such as M51, M52, M53, M54, M55, M56, M57, M58 and M61 (in 'M others') are detected in south Vietnam and completely absent from the north of Vietnam. This Vietnamese pattern could suggest that the south Vietnam pool has more ancient components surviving than the northern genetic pool. Haplogroups C and D4 are relatively frequent in MSEA but reach their highest levels in North-Central Asia and North-Central and East China. By contrast, the rare M12 and M74 (table 6) are most frequent in MSEA, where they have mainly been detected in the Austro-Asiatic speakers in Cambodia.

Other Southeast Asian lineages in haplogroup M, such as M21 and M20, are restricted to the Malay Peninsula, MSEA, ISEA and South China. M21 is more frequent in the Malay Peninsula. It has been mainly detected in the *Orang Asli* people in Malaysia, the Stieng people in South Vietnam, the Sakai of south Thailand and the Jarai of east Cambodia. M20 is more frequent in north Thailand, Yunnan in China, south Vietnam, east Cambodia and Indonesia in ISEA. The lineages C, D4, D5, G, M8, M9, M10 and Z are most frequent in North, East and Central Asia (including North, East and Central China) and are found mainly in Sino-Tibetan speakers in these regions. M3, M2, M5, M49 and M33 are the most frequent M lineages in South Asia (primarily India). The latter haplogroups were mostly detected in Dravidian and Indo-European speakers, and the Sino-Tibetans in Myanmar (Silva et al., 2017).

Other M lineages appear as more locally distributed and were found in MSEA and ISEA. For instance, between them, M24, M50, M51, M54, M55, M57, M58, M59 and M72 account for ~18% of the total diversity in MSEA and ~14% in ISEA. Most of these lineages seem to have a restricted distribution within Mainland and Island SEA.

Within haplogroup N, lineages found in MSEA include haplogroups A (Torroni et al., 1993), N9a (Kivisild et al., 2002), and N21(Macaulay et al., 2005). Haplogroup A is not common in ISEA and South China, reaching its highest frequency in Tibet (~13%), but it is relatively frequent in Sino-Tibetan speakers in Myanmar. Haplogroup N9a shows the highest frequencies in East Asia, within the Japanese population and the Han people in South, North, East and Central China. Haplogroup N21 is restricted to Myanmar in MSEA, the Sundaic region (including the Malay Peninsula) and South China, and it is completely absenting in North, East and South Asia.

Within haplogroup R, the main haplogroups detected in East and Southeast Asia are B (Torroni et al., 1993) and R9 (Y.-G. Yao & Zhang, 2002). Haplogroup B ostensibly includes three major branches, B4, B5 and B6, although the reconstructed phylogeny is more complicated. In this study (tables 7 and 8), B4 and B5 are the most common branches within haplogroup B of North Lao and Vietnamese samples. B4 is one of the highest frequent East and Southeast Asian haplogroups, particularly in the ISEA region (~18%) and among the Taiwanese population (~28%), while in MSEA and Malaysia, its frequency is about 6 and 10%, respectively, with ~12% in South China.

In contrast, the frequency distribution of B5 shows a different gradient. B5a particularly is frequent among MSEA, Malaysia and South China (populations south of the Yangtze River), with levels decreasing to the North, Central and East China provinces, and it is absent from North Asia.

B6, which cluster with R11 and may not be closely related to B4’5, forms only ~2% of the total haplogroup B diversity and is commonly found in the northern parts of Thailand and the Kayin state in Myanmar, while in this study, B5a is very commonly detected within Hmong speakers in north Laos (table 7).

Haplogroup R9 consists of three main haplogroups: the minor R9b and R9c and the major haplogroup F. Haplogroup R9b is most frequent in the Malay Peninsula, MSEA and in the South Chinese provinces (Guangxi, Hainan and Yunnan), its frequency decreasing from Central China to North Asia, and it is absent from the Japanese and Korean populations in East Asia. In ISEA, it is just found in Indonesia.

Haplogroup F consist of four subclades, F1, F2, F3 and F4, where F1 is by far the most frequent. F1 shows exceptionally high frequencies in MSEA, accounting for nearly 20% of the region’s total diversity. It is also very frequent (12%) in the Malay Peninsula, ISEA and in many parts of South China. F1 is the most common haplogroup detected in this study within north Laos and Vietnam (tables 7 and 8). The most diverse and frequent branch within the F1 subclade is F1a, which is most frequent in north Laos while the other branches such as F1b are most frequent within the Tibetan population (F1b1 is most frequent in Japan and Korea, in East Asia), F1c is commonly found in Myanmar, F1f is detected commonly in north Laos, whereas F1d, F1e and F1g are more recent branches and are distributed in different regions in Southeast Asia. Among the other three F subclades, F2 is most frequent in South China, while F3 and F4 are primarily detected in Taiwan and South China. The F4 subclade includes F4b, which is locally restricted within the Aboriginal Taiwanese.

The other R haplogroups include R11, R2, R22, R23, R30, R5, R6, R7, U2 and U7, which are present in MSEA at significantly lower frequencies (except R22 which appears commonly in Cambodia), probably reflecting their more recent arrival into the MSEA genetic pool (especially from South Asia).

In summary, the frequencies of haplogroups A, D4, D5, G, M8 (including C), M9 (excluding E), M10 and Z tend to increase from south to north, whereas the frequencies for haplogroups B4, B5, M7c, N21, M21, R9c and the local M lineages tend to decrease from south to north. Furthermore, haplogroups F1, M12, M7b, B5a and R9b appear to have frequencies decreasing both to the north and to the south from MSEA and South China.

Table 6. Estimated frequencies of principal mtDNA haplogroups in MSEA compared with other different regions of eastern Asia.

Main Haplogroups		MSEA Region *n=6183*	West Malaysia *n=914*	ISEA *n=2440*	Taiwan *n=1058*	South China *n=4873*	China Tibet *n=962*	N, C & E China *n=1756*	South Asia *n=4218*	East Asia *n=2505*	Central Asia *n=728*	North Asia *n=1528*
M	**E**	0.05%	5.36%	12.54%	11.06%	0.02%	0.10%	0.11%	0.33%	0.08%	-	-
	M8	0.36%		0.12%	0.09%	1.44%	0.62%	2.96%	-	1.20%	0.55%	0.79%
	M10	0.42%	0.11%	0.29%	0.38%	1.35%	0.94%	1.48%	0.05%	1.20%	0.96%	0.20%
	M33	0.44%	0.11%	-	-	0.80%	0.31%	-	1.33%	-	0.14%	-
	D	0.63%	0.44%	1.60%	0.47%	2.65%	1.04%	7.29%	0.26%	12.10%	9.75%	7.92%
	Z	0.99%		0.41%	-	1.42%	1.77%	3.13%	0.17%	1.00%	3.71%	2.49%
	M7c	1.29%	4.38%	8.32%	6.33%	1.81%	0.10%	2.16%	0.26%	1.48%	1.92%	0.52%
	D5	1.31%	0.33%	1.80%	4.16%	2.91%	3.33%	4.50%	0.43%	4.07%	3.98%	2.29%
	M21	1.34%	9.41%	0.98%	-	0.08%	-	-	0.02%	-	-	0.13%
	M20	1.39%	1.53%	0.90%	-	0.47%	-	-	0.12%	-	-	-
	M9	1.63%	0.11%	0.08%	0.19%	1.72%	22.45%	3.36%	0.62%	2.16%	1.24%	0.33%
	G	1.91%	0.77%	0.08%	0.47%	3.10%	8.11%	5.24%	1.14%	8.34%	7.69%	14.40%
	A	2.31%	0.33%	0.08%	0.47%	4.19%	13.51%	9.68%	0.95%	6.67%	6.18%	11.78%
	M74	2.44%	0.88%	1.48%	0.09%	1.40%	1.25%	0.57%	0.12%	0.24%	0.82%	0.13%
	M12	2.60%	0.77%	0.45%	0.28%	1.17%	0.10%	0.06%	0.12%	0.12%	0.14%	-
	C	2.98%	0.55%	0.33%	0.19%	4.08%	4.89%	5.41%	0.81%	0.88%	11.13%	24.02%
	D4	3.15%	1.09%	0.90%	1.51%	7.84%	11.54%	10.65%	1.33%	18.56%	10.30%	7.85%
	M7b	6.13%	2.41%	2.79%	11.63%	9.95%	0.10%	4.21%	0.31%	4.23%	1.65%	0.20%
	M Others	13.10%	13.68%	12.99%	0.76%	6.53%	11.23%	5.18%	57.44%	11.34%	3.85%	1.24%
N	**N Others**	1.34%	3.06%	4.02%	1.23%	1.70%	0.83%	1.82%	2.80%	2.87%	1.65%	7.85%
	N21	1.60%	4.38%	0.33%	-	0.35%	-	-	-	-	-	-
	N9a	1.73%	2.63%	0.94%	1.61%	2.44%	0.31%	2.68%	-	4.63%	2.34%	0.72%
R	**B5***	0.34%	3.06%	3.57%	0.28%	0.82%	0.83%	1.82%	0.45%	2.48%	1.24%	0.92%
	R9c	0.39%		3.11%	1.70%	0.70%	-	0.23%	0.02%	-	-	-
	U2	0.87%	0.11%	0.08%	-	0.04%	0.31%	0.40%	7.71%	-	0.55%	0.39%
	B	1.41%	1.31%	0.94%	-	0.80%	0.10%	0.46%	0.02%	0.12%	-	0.07%
	F others	2.25%	1.20%	3.52%	17.49%	6.55%	1.04%	4.27%	0.12%	0.76%	3.30%	0.98%
	R9b	3.25%	3.50%	0.61%	0.57%	2.54%	0.21%	0.28%	0.07%	-	0.27%	0.59%
	R Others	3.46%	11.16%	3.65%	0.09%	1.44%	2.81%	4.67%	21.12%	0.72%	15.93%	9.16%
	B4	6.24%	10.18%	17.83%	27.41%	12.35%	2.08%	6.72%	0.19%	8.54%	5.63%	2.49%
	B5a	11.90%	4.49%	2.70%	4.63%	5.62%	0.10%	1.77%	0.05%	0.88%	0.82%	-
	F1	20.73%	12.69%	12.54%	6.90%	11.72%	9.98%	8.88%	1.66%	5.35%	4.26%	2.55%

Total = 27,165. C = central, N = north, E = east

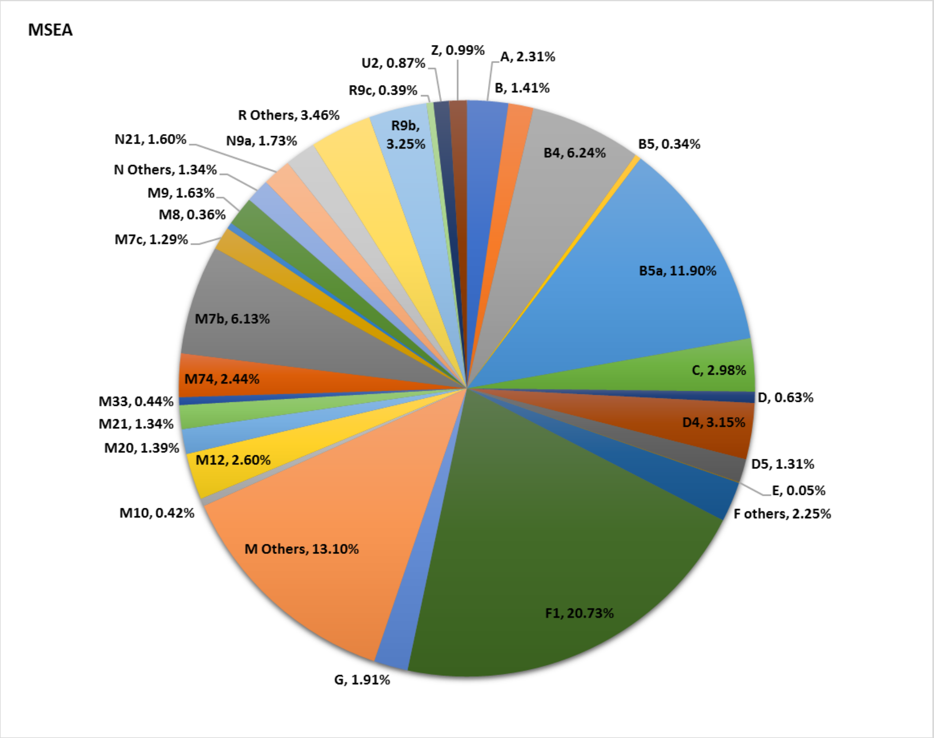


Figure 18. The main haplogroup frequencies in MSEA overall.

Table 7. The main haplogroups frequencies of 8 different locations in North Laos (in this study)

Main Haplogroups	1.Ban Long (Hmong) *n* = 102	2.Ban Naxai *n* = 44	3.Ban Xat *n* =100	4.Houay Thong *n* = 31	5.Long Lao Ning (Kao) *n*=99	6.NongTok *n*= 50	7.Tinpha *n*=54	8.Xiang Mouak *n*= 70
A	2.94%	-	-	-	-	-	-	-
B	-	-	-	-	-	-	-	1.43%
B4	12.75%	4.55%	9.00%	-	1.01%	10.00%	7.41%	22.86%
B5	-	-	3.00%	-	-	-	-	-
B5a	30.39%	2.27%	14.00%	-	3.03%	2.00%	-	2.86%
C	7.84%	9.09%	3.00%	9.68%	-	6.00%	1.85%	5.71%
D4	5.88%	-	3.00%	-	-	-	-	-
D5	-	-	-	-	6.06%	4.00%	3.70%	2.86%
F others	11.76%	-	8.00%	3.23%	-	-	-	1.43%
F1	8.82%	27.27%	22.00%	38.71%	40.40%	44.00%	53.70%	24.29%
G	-	2.27%	-	6.45%	2.02%	-	-	-
M Others	1.96%	13.64%	10.00%	-	18.18%	16.00%	18.52%	2.86%
M12	-	2.27%	-	3.23%	1.01%	-	-	1.43%
M20	-	-	2.00%	3.23%	5.05%	-	1.85%	-
M74	2.94%	2.27%	-	3.23%	3.03%	4.00%	5.56%	-
M7b	0.98%	9.09%	14.00%	-	10.10%	4.00%	-	12.86%
M7c	-	2.27%	2.00%	-	1.01%	2.00%	5.56%	1.43%
M8	-	-	-	-	1.01%	-	-	-
M9	-	2.27%	1.00%	6.45%	-	-	-	1.43%
N Others	-	-	-	3.23%	-	-	-	1.43%
N9a	13.73%	2.27%	-	-	-	-	-	-
R Others	-	13.64%	2.00%	-	-	4.00%	-	4.29%
R9b	-	4.55%	6.00%	12.90%	8.08%	4.00%	-	11.43%
R9c	-	2.27%	1.00%	-	-	-	-	-
Z	-	-	-	9.68%	-	-	1.85%	1.43%

Table 8. The main haplogroups frequencies of north and south Vietnam.

Haplogroups	N Vietnam *n* = 589	S Vietnam *n* = 388
A	0.51%	-
B	1.36%	-
B4	12.39%	9.54%
B5	0.51%	1.29%
B5a	10.19%	14.43%
C	3.40%	0.52%
D	0.68%	0.26%
D4	2.89%	0.77%
D5	2.55%	-
E	-	0.52%
F others	4.75%	0.26%
F1	19.35%	23.71%
G	1.36%	0.26%
M Others	5.43%	16.49%
M10	1.19%	-
M12	1.36%	4.90%
M20	0.34%	3.61%
M21	-	3.87%
M33	0.34%	0.26%
M74	0.68%	1.03%
M7b	13.07%	2.84%
M7c	4.24%	1.03%
M8	0.68%	0.77%
M9	1.19%	0.52%
N Others	1.53%	-
N21	-	1.55%
N9a	2.55%	4.64%
R Others	1.19%	3.35%
R9b	3.40%	2.58%
R9c	1.02%	1.03%
Z	1.87%	-

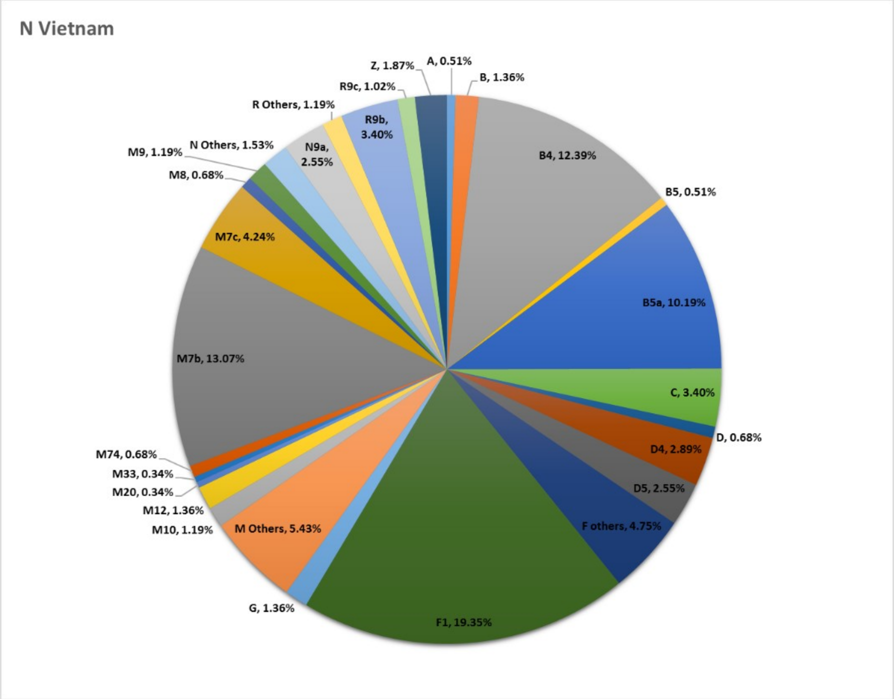


Figure 19. The main haplogroup frequencies of north Vietnam's population.

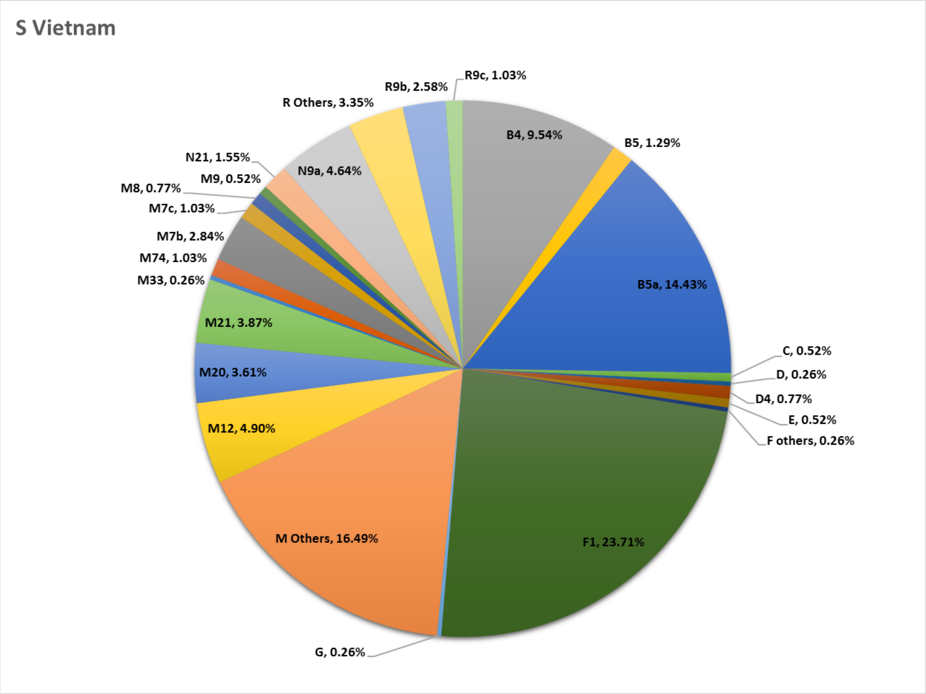


Figure 20. The main haplogroup frequencies of south Vietnam's population.

Table 9. The main haplogroups frequencies of the Vietnamese ethnic groups (in this study)

Haplogroups	**STIENG** ***n* = 184**	**KINH** ***n* = 112**	**TAY-NUNG** ***n* = 102**
B	-	0.89%	0.98%
B4	2.17%	8.93%	13.73%
B5a	14.67%	8.93%	10.78%
C	-	3.57%	2.94%
D4	-	2.68%	5.88%
D5	-	-	8.82%
F others	-	7.14%	2.94%
F1	34.24%	25.89%	14.71%
G	-	1.79%	2.94%
M Others	21.20%	5.36%	2.94%
M10	-	0.89%	2.94%
M12	8.70%	0.89%	0.98%
M20	6.52%	-	-
M21	5.98%	-	-
M74	1.09%	0.89%	1.96%
M7b	-	10.71%	15.69%
M7c	-	8.93%	2.94%
M9	-	0.89%	0.98%
N Others	-	-	0.98%
N21	1.63%	-	-
N9a	2.17%	1.79%	2.94%
R Others	0.54%	0.89%	1.96%
R9b	1.09%	3.57%	0.98%
R9c	-	2.68%	-
Z	-	2.68%	0.98%

3.1 Principal Component Analysis (PCA)

PCA is used in this study to produce two-dimensional representations of genetic distances between populations of interest using allele frequencies. Here, I used the frequencies of the main South, North and East Asian haplogroups to perform PCA in order to visualise molecular genetic distances between the MSEA populations and the other Asian populations. To avoid any biases because of sample size, we excluded all the populations that have less than 30 samples. For each PCA plot, each mtDNA haplogroup was also represented to understand which were contributing to the observed arrangement.

The first PCA included populations from South, North and East Asia (Figure 21). The PCA represents a clear geographical pattern for the 38 regions in Asia (25,057 samples) along the first (F1) and second (F2) components, accounting for 22.6% and 15.1% of the observed variation, respectively. This PCA result could help to confirm our selection to the Chinese provinces that represent the South Chinese region in this study. In Figure 21, all South Chinese provinces cluster together between ISEA, MSEA, South Asia, North-East Asia and the other provinces in North, East and Central China. This position of South Chinese population could reflect a significant genetic contribution in the South Chinese population and the other surrounding populations, especially MSEA and ISEA populations. Yunnan and Guangxi appear the closest Chinese provinces to MSEA; geographically, they are located on the borders of Myanmar and Vietnam. Vietnam, Laos and Thailand are closer to ISEA and South China (probably due to their high frequency of haplogroups F1, B5a, B4 and M7b) than Myanmar, which falls closer to South Asian populations because of the presence of haplogroup M33, while Cambodia was placed at one extreme pole of the F2 component (mainly due to the relatively high frequency of haplogroup M12).

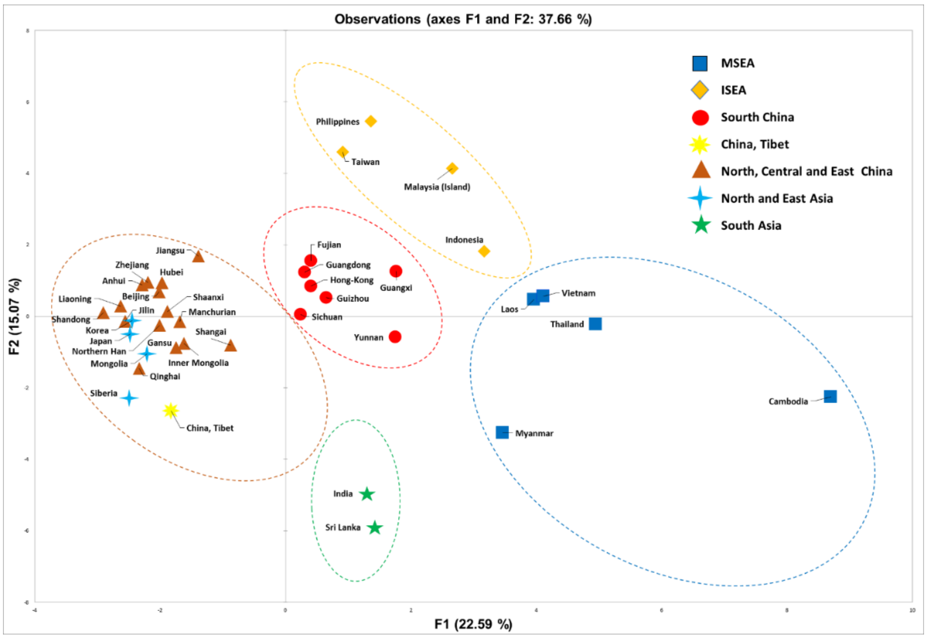


Figure 21. Representation of the first and second components of genetic variation in Asia.

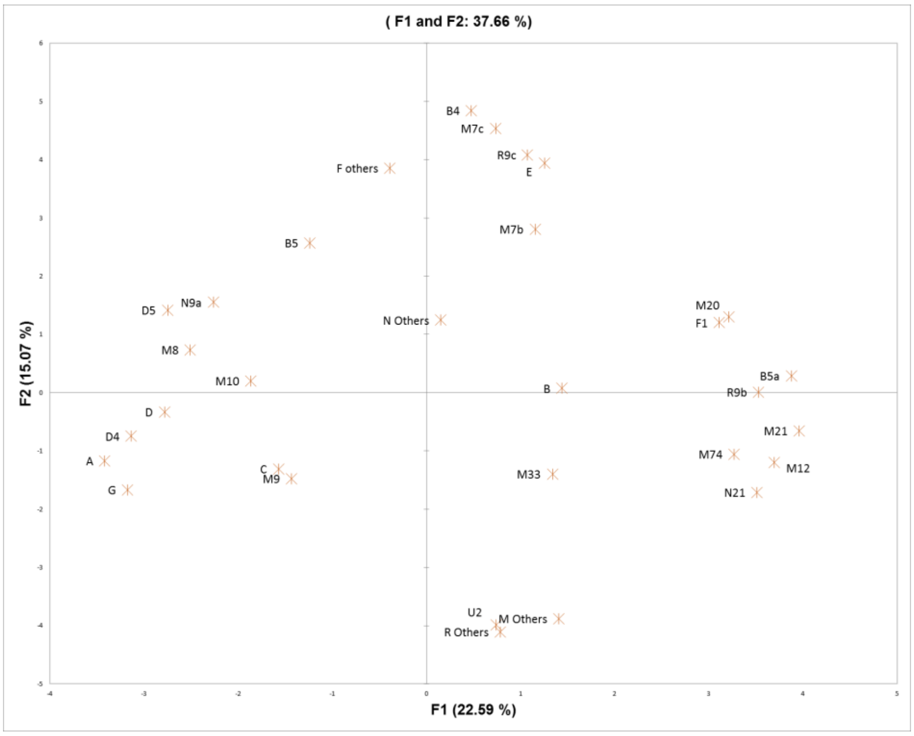


Figure 22. Representation of the first and second components of the main haplogroups in Asia.

To investigate the linguistic relationship between MSEA population and the surrounding Asian populations and to have more details about the Laos samples that were collected form eight different regions in this study, I performed a second PCA analysis dividing the samples into the main languages families in Southeast Asia (Austro-Asiatic (AA), Austronesian (AE), Tai-Kadai (TK), Sino-Tibetan (ST) and Hmong-Mien (HM)), and I numbered the Laos samples to eight groups (Lao-01 to Lao-08) according to their locations with their linguistic families (Lao-01; Ban Long Lao Mai (HM), Lao-02; Ban Naxai (mainly AA with few TK), Lao-03; Ban Xat, Lao-04 (TK); Houay Thong, Lao-05; Long Lao Ning (HM), Lao-06; NongTok (AA), Lao-07; Tinpha (AA) and Lao-08; Xiang Mouak (mainly TK with few AA)).

The results are shown in Figure 23. Again, almost all the language families in Yunnan and Guangxi are the closest groups to the MSEA, especially the Austro-Asiatic group in Yunnan province (Va ethnic group from Yao and Zhang (2002), Bugan group from Li et al (2007) and Wa group from Qian et al (2001)) clustered within the MSEA groups. Peng et al. (2010) revealed that, regarding the Vietnamese Austronesian group (Cham people), more affinities with Austronesian groups existed in ISEA, and the Vietnamese Tai-Kadai group (Tay–Nung people from this study) clustered with the Southern Chinese groups. The Vietnamese Austro-Asiatic groups, which represent mainly both the Stieng and the Kinh in this study and the Hanoi ethnic group in Irwin et al. (2008), are clustered within the MSEA linguistic groups. Seven Laos groups (02–08) in this study appear more genetic affinity with the Austro-Asiatic and Tai-Kadi groups within the MSEA region, while the first group (Lao-01) clustered close to Hmong-Mien family group in the Guangdong province, confirming our results since we already know that this Laos group is one of the Hmong-Mien family. Sino-Tibetan linguistic groups in Myanmar and Thailand draw different genetic distance. The first one in Myanmar showed a close genetic affinity with South Asia in Northeast India, while the Thailand group clustered within the Southern Chinese groups.

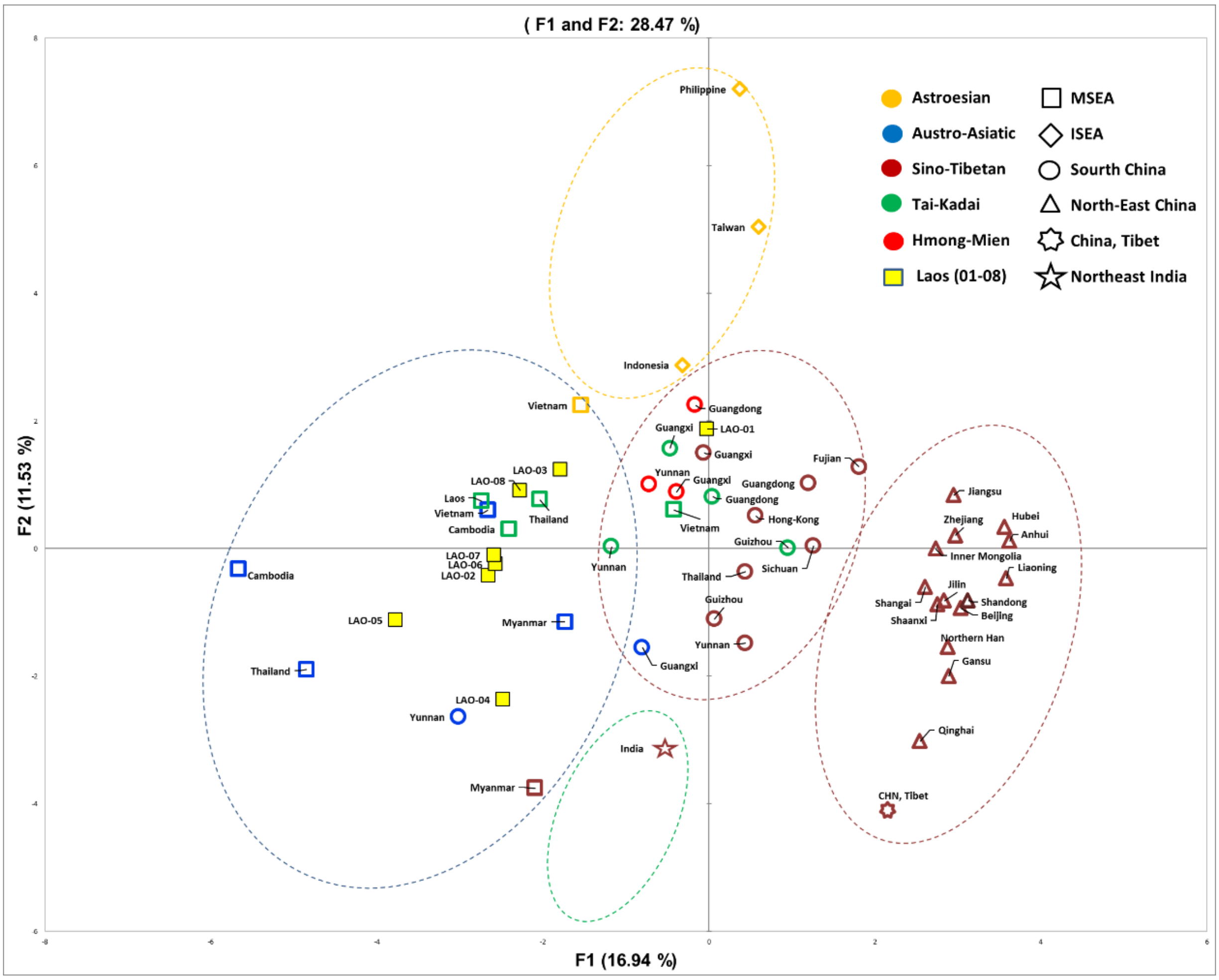


Figure 23. Representation of the first and second components showing genetic distances between linguistic groups and Southeast Asian populations. Laos linguistic families: Lao1 (HM), Lao2 (AA with a few TK) Lao3 (TK), Lao4 (TK), Lao5 (HM), Lao6 (AA), Lao7 (AA) Lao8 (TK with few AA) Lao9 (AA).

3.2 Haplogroup M

Haplogroup M accounts for about 60% of the total diversity in MSEA. The most frequent lineages within M are M7b, D4, M12, M74 and M9. Haplogroup M is defined by four transitions mutations at np489, np10400, np14783 and np15043. It also represents more than half of the total mtDNA diversity in India (Kivisild et al., 2002; Kivisild & Villems, 2000; Metspalu et al., 2004) and is widely distributed in East and Island Southeast Asia, where it contributes more basal haplogroups to the total mtDNA pool with more than either N or R (Kivisild et al., 2002; Kong et al., 2003; Y.-G. Yao & Zhang, 2002). This extraordinarily high number of these basal haplogroups suggests a rapid local radiation within Southeast Asia, similar to the expansion of haplogroup M in India (Sun et al., 2005).

Besides the basal haplogroups, other branches of haplogroup M in MSEA such as C, D, G, M12, M7b and M21, and other Southeast Asian haplogroups such as Z, M8a, M9 and M10 will be represented using the phylogeographic analysis in the following sections.

3.2.1 Haplogroup M12

M12 is the second haplogroup of the M12'G cluster, alongside haplogroup G. It is defined by transitions np 16234 and np 16290 in HVS-I (Figure 24) and is divided into M12a and M12b. M12a is divided into M12a1 and M12a2 (Figure 24). M12a1a1 dates roughly to the Younger Dryas ~12 ka and the origin appears to lie between South China and northern MSEA, as the basal lineages are found in Thailand, Vietnam and South China (Fucharoen et al., 2001; Peng et al., 2010; H.-X. Zheng et al., 2011). M12a1b1 appears to have an LGM origin in MSEA or South China (dates to ~ 12.8 ka). It is seen in the Stieng people in South Vietnam (this study) and nested within a subclade found in India, Myanmar, Yunnan and China (H. Li et al., 2007; Y.-C. Li et al., 2015; Peng et al., 2010; Y. G. Yao et al., 2002). M12a1a1 and M12a1b1 have estimated their founder age in MSEA, ~19 and ~11 ka, respectively, which reflects the two migrations waves from South China into MSEA during the LGM and Holocene ages. The M12b branch is the most representative of MSEA pool within the M12 haplogroup, dated to LGM age ~ 24 ka and is commonly detected in East Cambodia, North Laos and Myanmar.

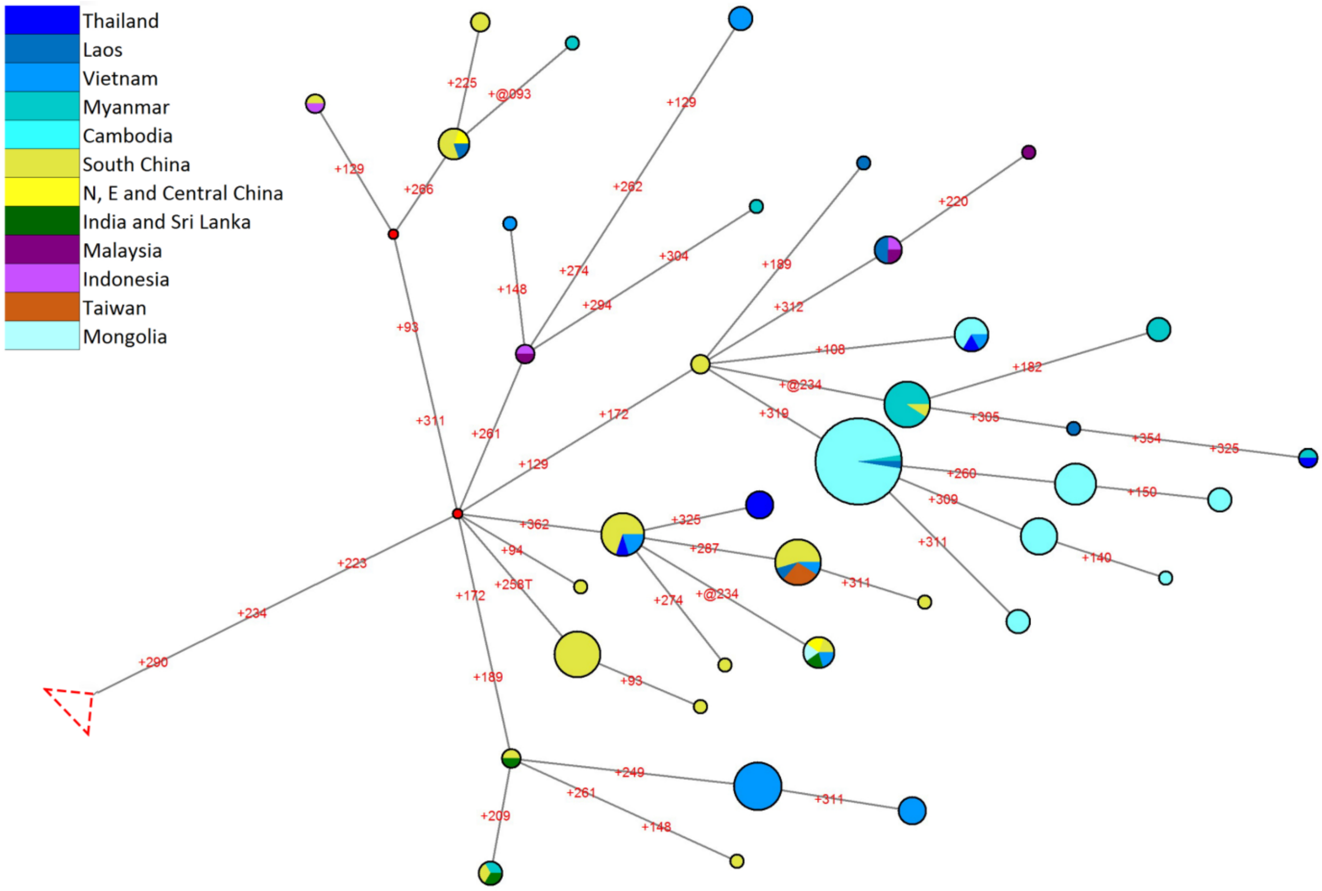


Figure 24. HVS-I phylogenetic network of haplogroup M12

3.2.2 Haplogroup M3

M3 is a South Asian haplogroup (Kivisild et al., 2003), dating to ~23 ka, and is subdivided into four branches M3a, M3b, M3c and M3d. M3a and M3b are defined by a transition in the coding region, while M3c and M3d are defined by the control region (Figure 25). M3 appears to be almost restricted to the Indian population with some samples from MSEA (Myanmar and Vietnam), the Malay Peninsula and one sample from South Central Russia. The founder age for this haplogroups has a high standard error value (~10 ka), and hence, the migration age to the sink population (MSEA) is estimated before the Holocene age between 17–27 ka. This high standard error is due to the size sample of the sink populations (8 samples).

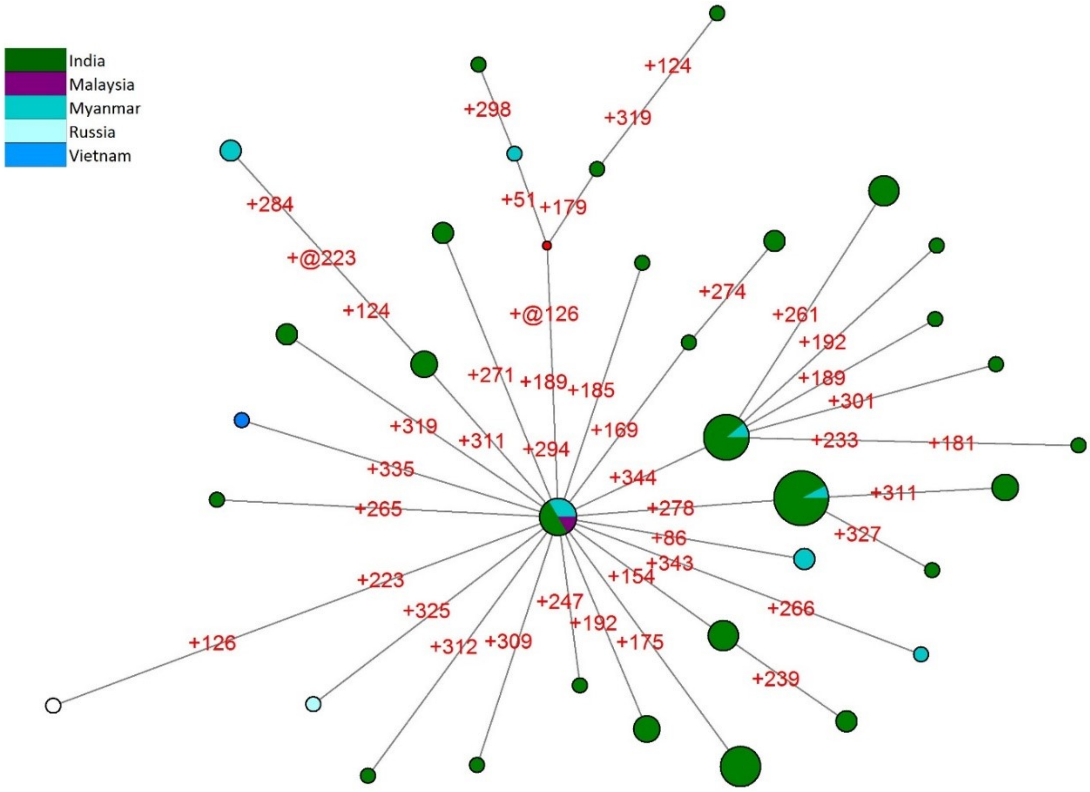


Figure 25. HVS-I phylogenetic network of haplogroup M3.

3.2.3 Haplogroup M7b

M7b is defined by a transition at np16297 in the control region and subdivides into M7b+16189 (M7b1b), M7b+16192 (M7b1a1a), M7b3 and M7b4. Additionally, all these branches share a transition at np16129 (Figure 26). M7b is dated to about 28.5 ± 9.7 ka, and found mainly in MSEA, East, Central and South China, but are more diverse in the M7b+16192. Within MSEA, M7b+16192 is defined by the transition np 16192, and mainly detected in north Laos, north Vietnam, north Thailand and central Thailand, and also in some regions in central, east Cambodia, and southwest and southeast of Myanmar. It seems to originate in South China (provinces below the Yangtze River) and invade mainly the north side of MSEA. The founder age for the M7b* paragroup is dated to the LGM, ~20 ka, M7b+16192 is likely to have entered the MSEA during the Neolithic age, ~5 ka, and M7b+16189, dates to the early Holocene, about 10 ka (table 10). In this study, this haplogroup is commonly detected in north Laos and north Vietnam.

3.2.4 Haplogroup M9

Haplogroup M9 is characterised by two transitions, at np 16362 in the control region and np 4491 in the coding region. It has two main branches, E and M9a’b. M9a’b is detected mainly in Tibet, North-central China, Korea and Japan, whereas E is commonly found in Taiwan and Indonesia. M9a’b further subdivides into the haplogroup M9a, which is characterised by a transition at np 16234 in HVS-I (Figure 27) and M9b, characterised by two transitions at np16051 and np16209 (Kong et al. 2006).

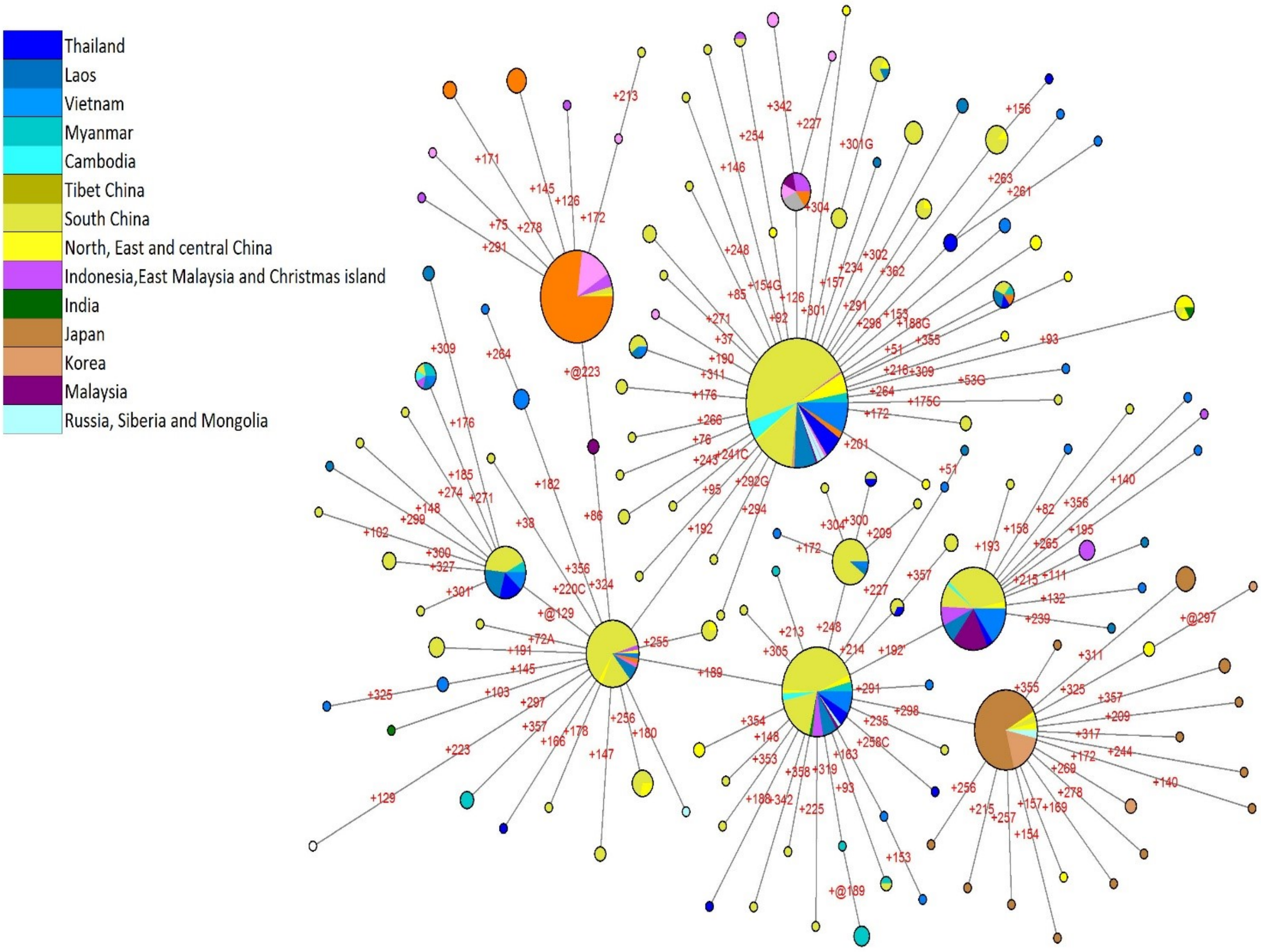


Figure 26. HVS-I phylogenetic network of haplogroup M7b

M9a subdivides into two groups, M9a1 and M9a4 and M9a5. M9a1 is characterised by a transition at np 16234 in the HVS-I and is the most common subclade. M9a4 and M9a5 are defined only by transitions at the coding region. M9a is most frequent in Tibet and then gradient to both North and Southeast Asia, dated to about 26.8 ± 11.5 ka. M9a's migration into the MSEA region is estimated by the founder analysis to ~8.3 ± 4.8 ka. The most common branch detected in MSEA is M9a1b1, which is commonly found in Myanmar, and its founder age (table 10) is dated to the Neolithic age (4 ± 1.7 ka).

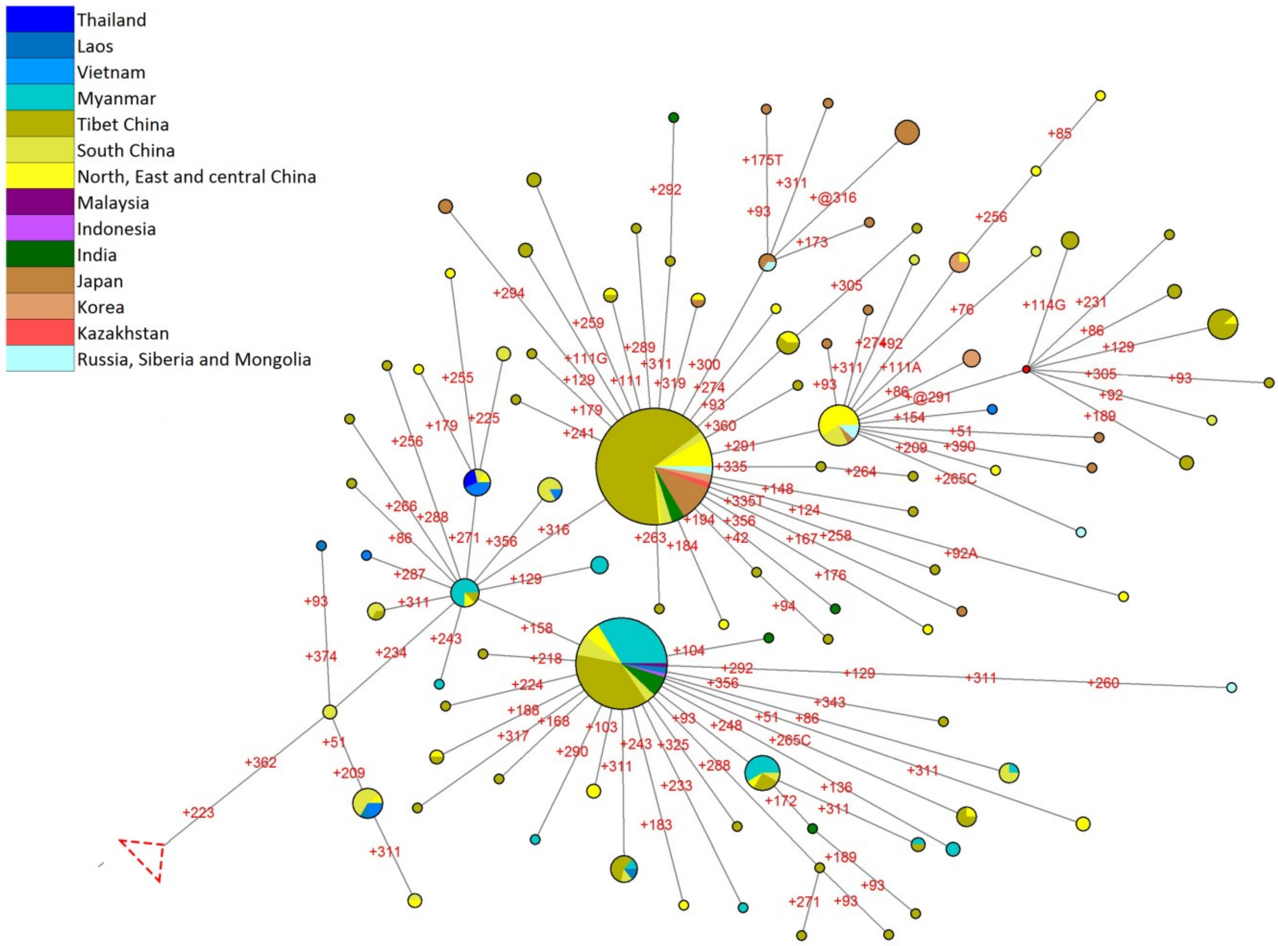


Figure 27. HVS-I phylogenetic network of haplogroup M9

3.2.5 Haplogroup D

Haplogroup D was characterised and defined by Torroni et al. (1992). This clade subdivides into two major branches, D4 and D5. D4 is defined by transitions at np 3010, np 8414 and np 14668 and is fairly commonly detected in Japan and North-East China (Inner Mongolia, Gansu, Jilin, Liaoning, Manchurian and Beijing provinces). There are many lineages within D4 haplogroup (include D1, D4a, D4b, D4c, D4d, D4e, D4f, D4g, D4h, D4i, D4h, D4j, D4l, D4m, D4n, D4q, D4s and D4t), but only D4a (defined by a transition at np16129 in the control region, and three other mutations in the coding region), D4b (defined by a transition at np16291), D4e (especially, the D4e1 branch, characterised by a transition at np 16092) and D4g (especially, D4g1 and D4g2a, defined by transitions at np 16278 and np 16274, respectively) seem to be significant in MSEA (Figure 28).

In contrast, D5 is commonly found in Taiwan, Japan and the north-eastern parts of China. It reaches its highest frequencies in Northeast China (table 6). All the three linages within D5 were detected in MSEA: D5a, D5b and D5c. D5a2a1, defined by a transition at np 16266 in the control region, is the most frequent (Figure 29). The overall age for this branch is about 11.8 ± 3.9 ka, and the founder age is dated about 1,000 years. Although there is a high frequency of MSEA samples (especially Burmese samples) within this haplogroup, the diversity is very low and the resulting founder age very recent, suggesting a spread in historical times.

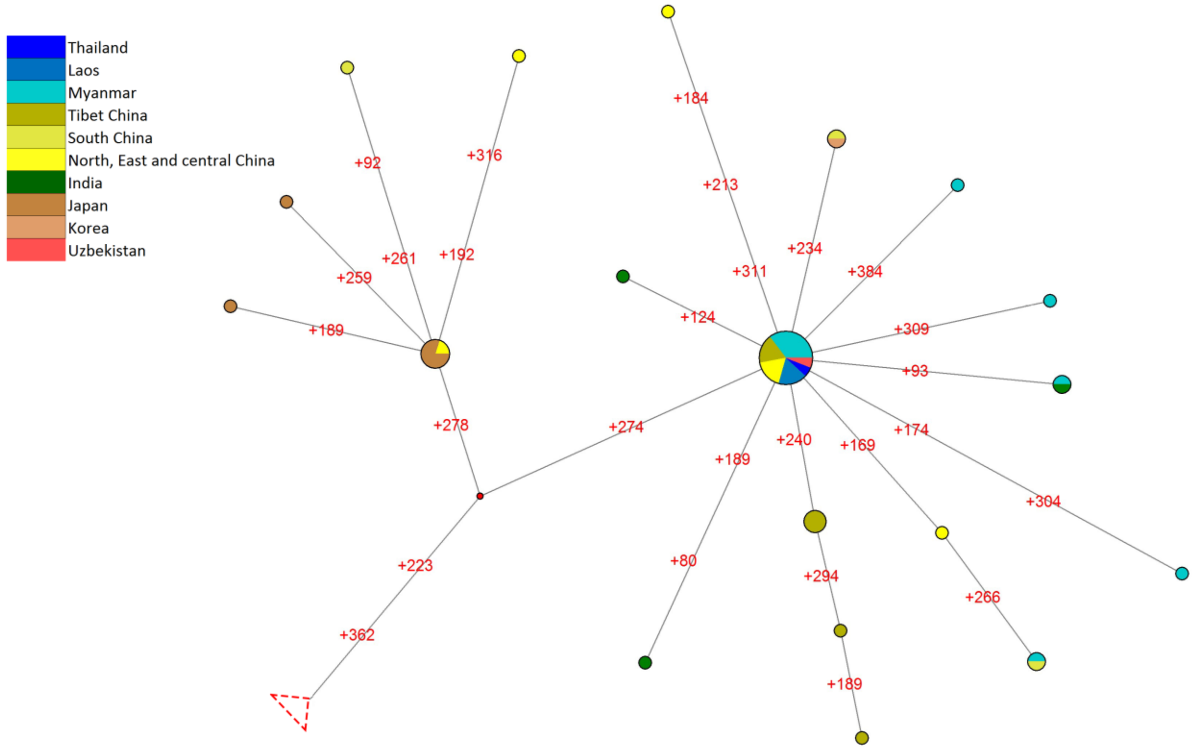


Figure 28. HVS-I phylogenetic network of haplogroup D4g

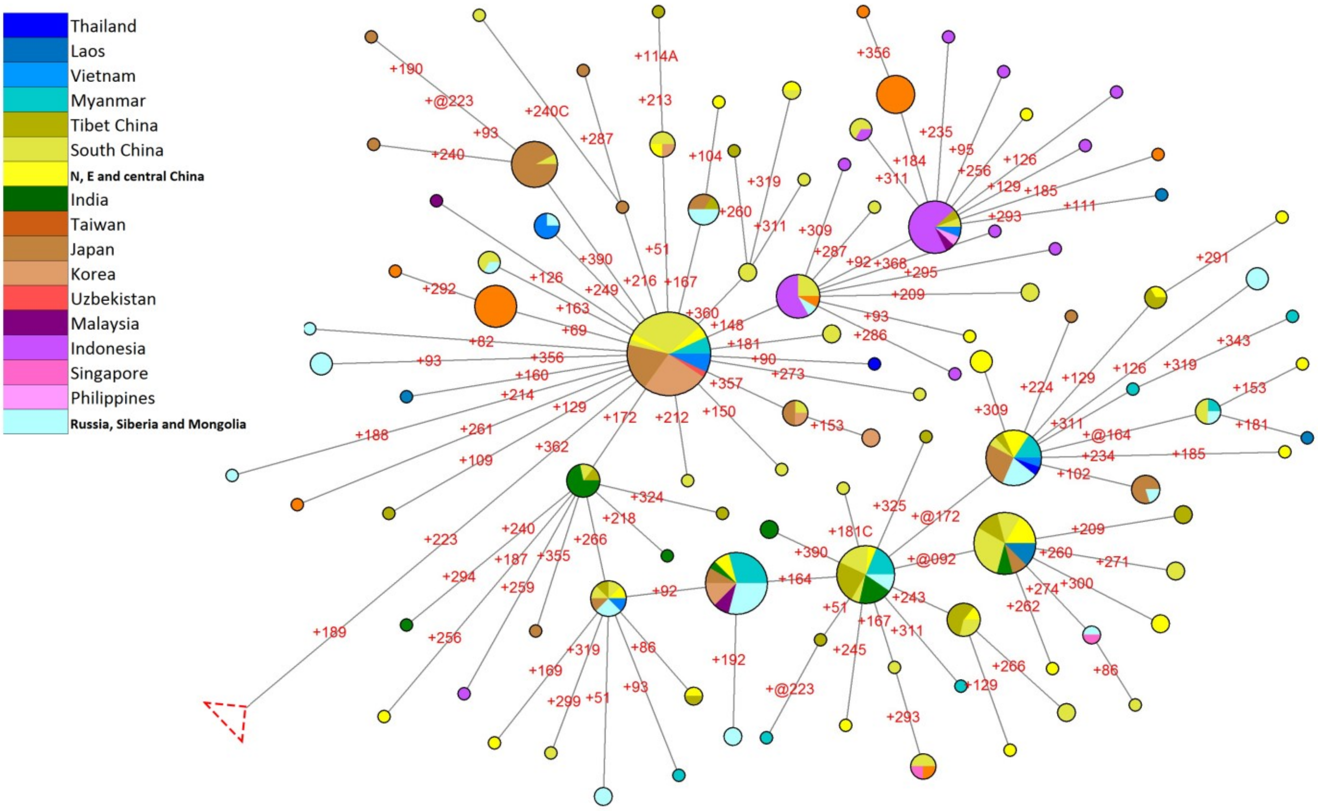


Figure 29. HVS-I phylogenetic network of haplogroup D5.

3.3 Haplogroup N

This haplogroup is globally distributed outside Africa, with descendants including almost all haplogroups found in Europe, Southwest Asia and the Caucasus, and some branches are also found in South-East Asia, which came to America. It accounts for about 12% of the total diversity in MSEA (excluding R lineages). The most frequent lineages within N are N8, N9, N10, N21 and A. This haplogroup is defined only by transitions in the coding region, at nps 8701, 9540, 10398 and 10873, and a reversion at np 15301. N basal branches in the southeast (Figure 30) are detected within Australia, Malaysia, China, India, Myanmar and Thailand, and the total age for these branches is about 60 ± 10 ka (table 11), while the founder age for the MSEA branches is dated about 37 ± 16 ka. The later estimated age for these basal branches reflects a high drift level, which is part of the first modern human gene pool in the southeast.

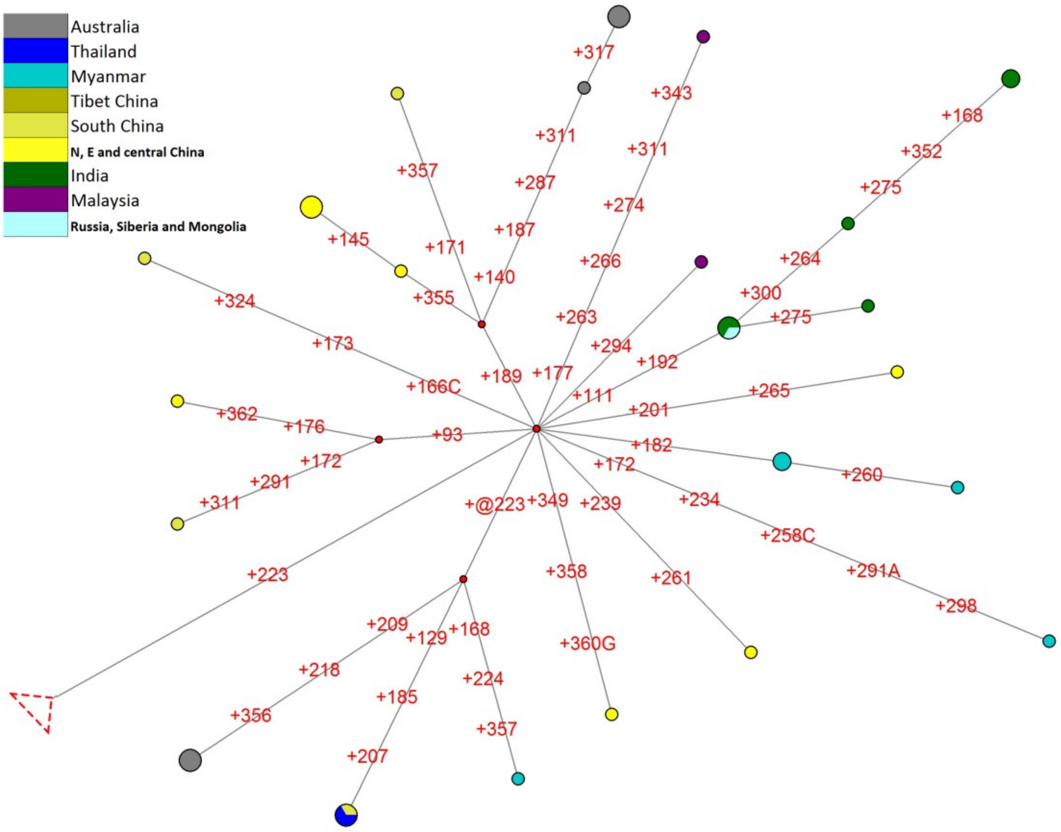


Figure 30. HVS-I phylogenetic network of paragroup N*.

3.3.1 Haplogroup N10a

N10 is an ancient basal N haplogroup dated to 64 ± 21 ka, and commonly found in South China (Yunnan and Guangdong provinces) and Northeast Thailand in MSEA, which may suggest an ancient origin in South China or Northeast Thailand. N10 diverges into two haplogroups, N10a and N10b (Figure 31). N10a has more diverse and frequent samples from MSEA (Myanmar and Thailand) than the N10b. N10a is defined by two HVS-I transitions at nps 16189 and 16111, and its founder age in MSEA is estimated to 19.5 ± 14 ka; while N10b is defined by three mutations at nps 16069, 16278 and 16298 and a transversion, 16291A, and its founder age in MSEA is estimated to ~22 ± 15.7 ka ka. The long internal branches in the phylogenetic network suggest founder effect and genetic drift, and an ancient gene flow between South China and MSEA during the LGM period.

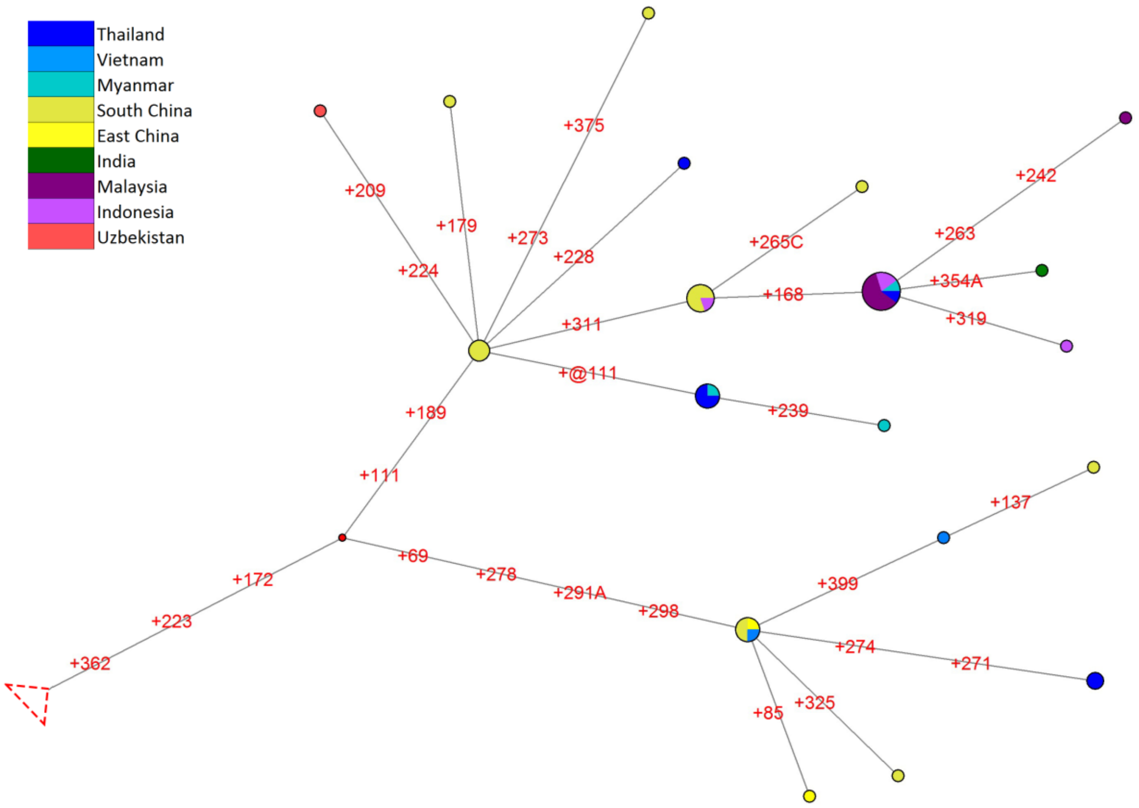


Figure 31. HVS-I phylogenetic network of haplogroup N10a.

3.3.2 Haplogroup N21

Haplogroup N21 was first described in the Malay Peninsula (Hill et al., 2006; Macaulay et al., 2005) and was subsequently identified across the ISEA (Hill et al., 2007). It represents an ancient haplogroup, dating to 25 ± 10 ka. It is defined by a transition at np16193 in the control region and np10583 in the coding region. The basal branches are mostly found in MSEA (Cambodia, Laos, Vietnam and Thailand), which could therefore represent the place of origin for this haplogroup. There are two main sub-branches of this haplogroup, which are defined by transitions at np 16291 and np 16182 (Figure 32). The first branch represents mainly Malaysia/Indonesia, while the second branch is restricted to Myanmar and Yunnan province in South China.

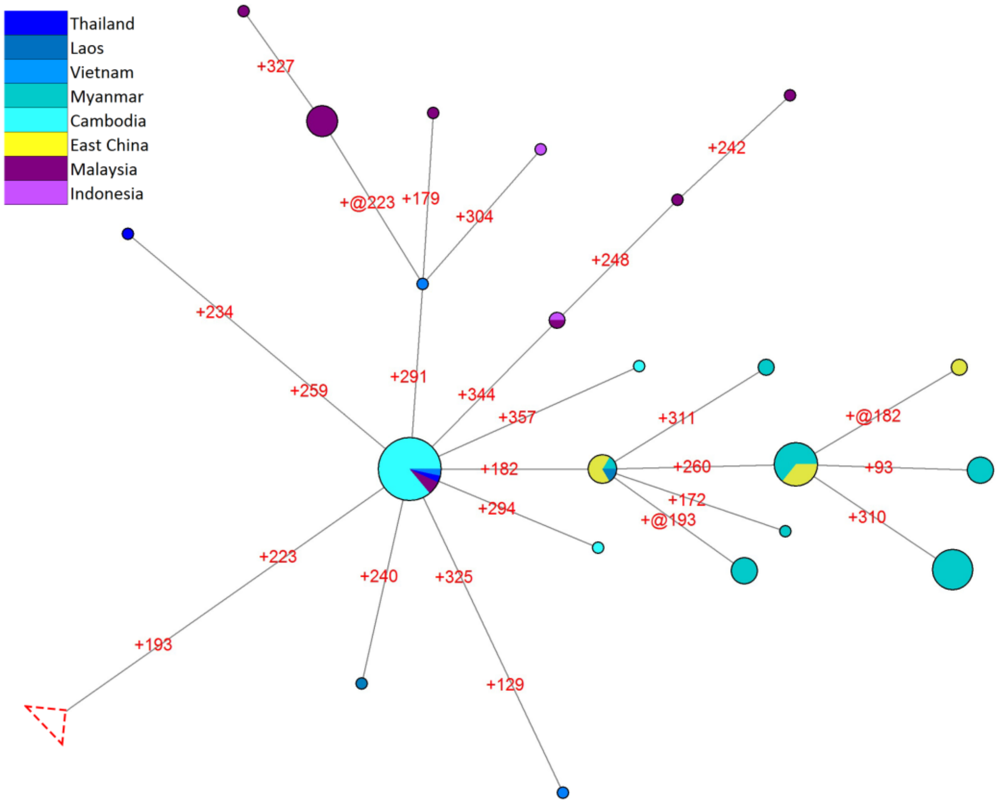


Figure 32. HVS-I phylogenetic network of haplogroup N21.

3.4 Haplogroup R

Haplogroup R is the major branch within the haplogroup N, and represents most of the Eurasian mtDNA diversity. It is defined at np 12705 and 16223, and has been dated in South Asia to ~65 ka (Silva et al., 2017). It accounts for more than 50% of the total maternal lineages in MSEA, of which more than 90% fall into haplogroups B or R9 (Figure 18; table 6).

3.4.1 Haplogroup B

Haplogroup B is regarded for convenience (*e.g.* in PhyloTree) as being nested within R+16189, divided into two main branches B4’5 and R11’B6, although whether these are genuinely having the same ancestor is not clear, as 16189 is highly recurrent. The first branch is commonly found in ISEA, and it consists of two haplogroups B4 and B5. B4’5 is characterised by a 9-base pair deletion (9bpd) at nps 8281-8289 in the coding region (Hartmann et al., 2009; Kong et al., 2010; P. Soares et al., 2012; P. Soares et al., 2008). The B4 distribution suggests an ancient ancestry in East Asia and dispersal into Southeast Asia after the LGM (P. Soares et al., 2011). B5 seems to have a more southerly origin in South China or MSEA. The second main branch, R11’B6, is characterised by a transition at 12950.

3.4.2 Haplogroup B5a

The major branch of haplogroup B in MSEA is B5, defined by transitions at np 709, np 8584, np 9950, np 16140, np 16140, and a reversion at np 10398. Most of the diversity within B5 is encompassed within two subclades, B5a and B5b. The latter shows a widespread distribution in Japan, Korea, China, ISEA and the Malay Peninsula. Additionally, a few types were found as far as Cambodia (Zhang et al. 2013), India (Kivisild et al. 2003) and Siberia (Gokcumen et al. 2008). However, this clade is not commonly found in MSEA or Taiwanese aborigines. In contrast, Haplogroup B5a is defined by transitions at np210, np3537 and np15235, and its founder age is dated to about 7 ± 3 ka. B5a is found at ~12% across MSEA, and distributed throughout MSEA and, at lower levels, ISEA and South China (Figure 33).

B5a itself has two main subclades, B5a1 and B5a2. The latter is defined in HVS-I by a further transition on top of the transversion at np16266. B5a2 is mainly detected within Taiwan, and a few types were also found in North Laos (this study), the Kihn people in north Vietnam (this study), Thailand (Zimmermann et al. 2009), Korea (Jin et al. 2006), West Malaysia (Macaulay et al 2005), East China (Nishimaki et al. 1999) and South China (Irwin et al. 2009; Wang et al. 2010). B5a2 may therefore reflect a connection between MSEA and Taiwan. B5a1 is defined by only a transition at np 6960 in the coding region, and is divided into four polytomous branches, B5a1a, B5a1b, B5a1c and B5a1d, where the latter branch is defined by a transition at np16261 and reversion at 152 in the control region, and transitions at np4086 and np11465 in the coding region. B5a1d is a major branch that spreads mainly through both the Stieng people (this study) and the Cham people (Peng et al. 2010) in south Vietnam, Malaysia (Zainuddin and Goodwin 2003; Tajima et al 2004), Myanmar (Li et al. 2015), East Cambodia (Zhang et al. 2013) and South China (Wen et al 2004; Irwin et al 2009; Wang et al 2010; Liu et al 2010; Zhou, HY et al. 2014), and its founder age is estimated to about 6 ± 2 ka (table 11).

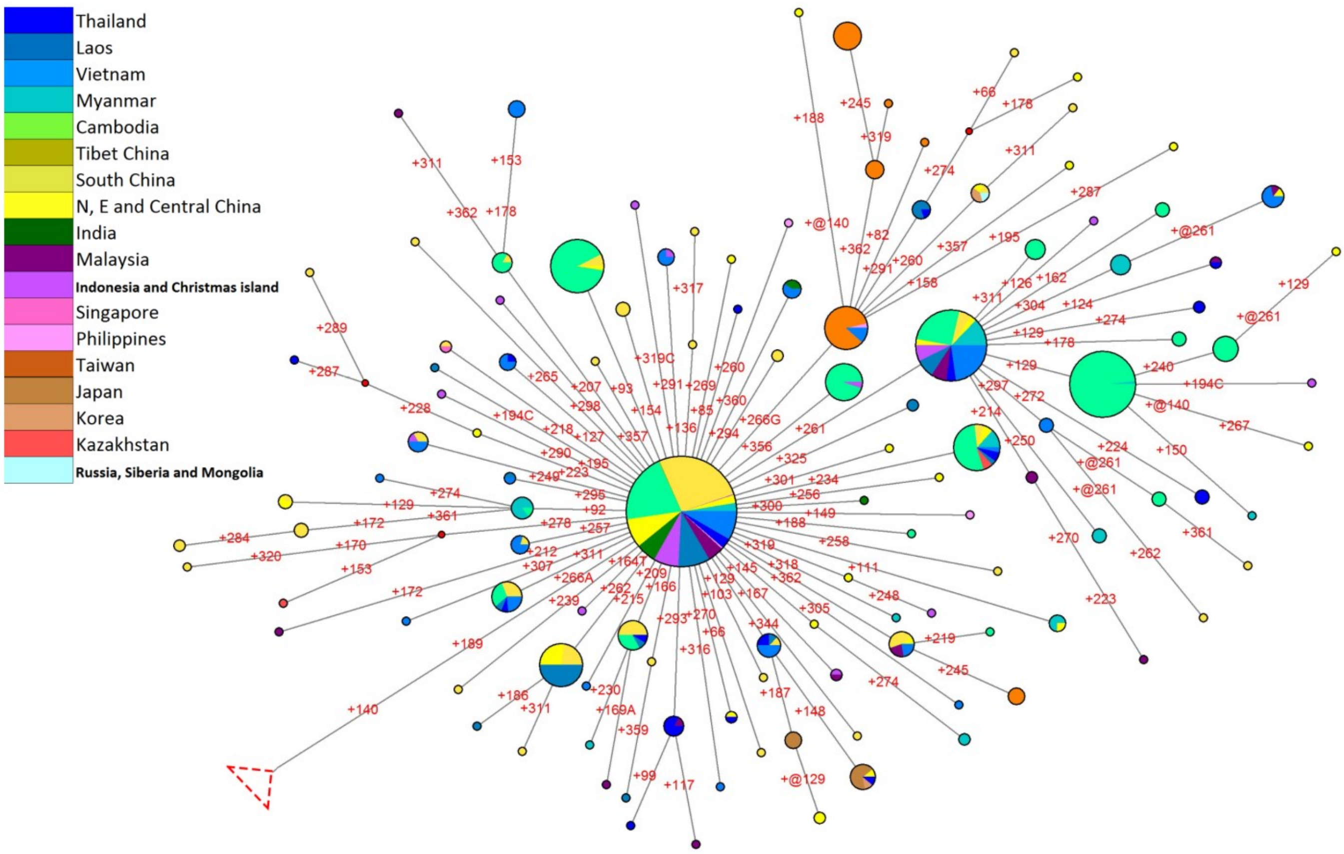


Figure 33. HVS-I phylogenetic network of haplogroup B5a.

3.4.3 Haplogroup R9

R9 is defined by transitions at nps 3970, 13928C and 16304, and it consists of three main subclades, R9b, R9c and F (Kong et al., 2003; P. Soares et al., 2009) (Kong et al., 2003b; Soares et al., 2009). The latter haplogroup is defined by a deletion of np 249 in the control region (HVS-II) along with two coding-region variants, and it has four subclades, F1, F2, F3, and F4.

R9b is widespread in MSEA and South China, and falls into two branches, R9b1 (Figure 34) defined by transitions np16309 and np16390, and R9b2 by a transition np16362. R9c only has one sub-branch visible from HVS-I variation, known as R9c1, which is defined by the transition np16157, and it is commonly found in ISEA and South China. The deeper lineages for both R9b1 and R9c1 in Figure 34 appear most diverse and frequent in South China (Guangxi, Guangdong and Yunnan), where it could have originated and then spread into two main directions, toward ISEA (R9b1) and to MSEA (R9c1). R9b1 and R9c1 are dated to 35 ± 14 ka and 30 ± 16 ka (table 11), respectively, and the founder age for both in MSEA is about 11 ka. This suggests that the latter branches spread together further toward MSEA during the Holocene period. The second branch within R9b, R9b2, is dated to ~ 9 ± 2.6 ka, and is most commonly detected in the northern parts of MSEA (north Thailand, north Laos, north Vietnam and east Cambodia), where it could have originated.

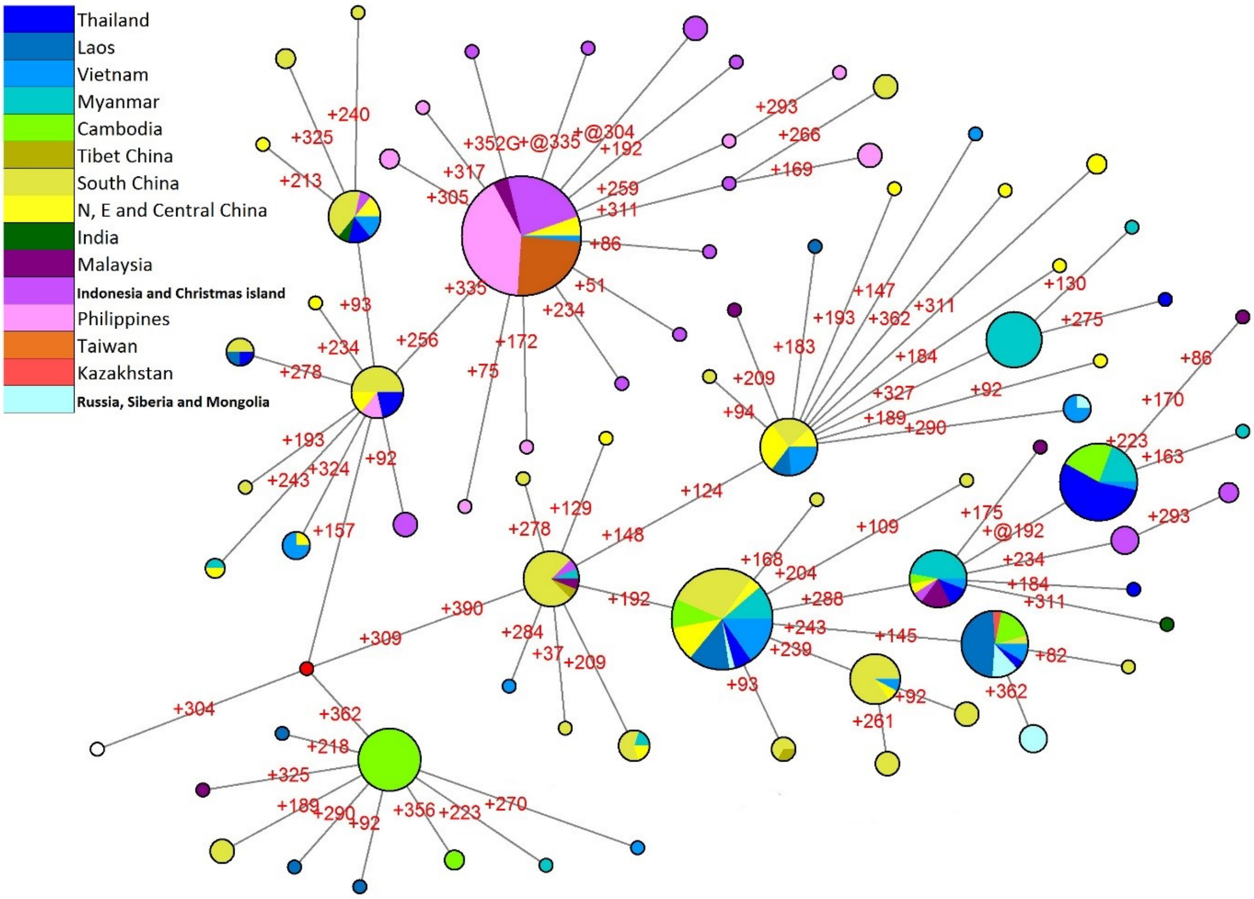


Figure 34. HVS-I phylogenetic network of haplogroup R9.

3.4.4 Haplogroup F1a

F1a is the main branch within haplogroup F1, and it is most common haplogroup in Southeast Asia (Ballinger et al. 1992). It is commonly detected in MSEA, where it represents more than 20% of the samples, a higher proportion than the frequency of F1 haplogroup in other regions where it is also very common, such as South China, West Malaysia and ISEA, where it is ~12% (table 6). F1a is defined by a transition at np16129 (which it shares with F1c) and a transition at np16172 in the control region. It can be sub-divided into three basal branches, F1a1’4, F1a2 and F1a3a. F1a is commonly distributed across East and Southeast Asia. The root type is very common in MSEA and South China, although a few types can also be found in ISEA, particularly in Indonesia and Philippines (Figure 35).

Haplogroup F1a is dated to ~15 ± 5 ka, and its founder age in MSEA is about 5 ± 2 ka (table 11). The latter founder age for F1a could potentially be due to the Neolithic farming dispersals from East Asia into MSEA. As seen in Figure 35, haplogroups F1a4a (defined by a transition at np16362) and F1a3 (defined by a transition at np16311) are two minor haplogroups distributed predominantly in ISEA (Indonesia and the Philippines) and Taiwan. Therefore, F1a3 and F1a4 were considered possible markers for Austronesian dispersal by Hill et al. (2007).

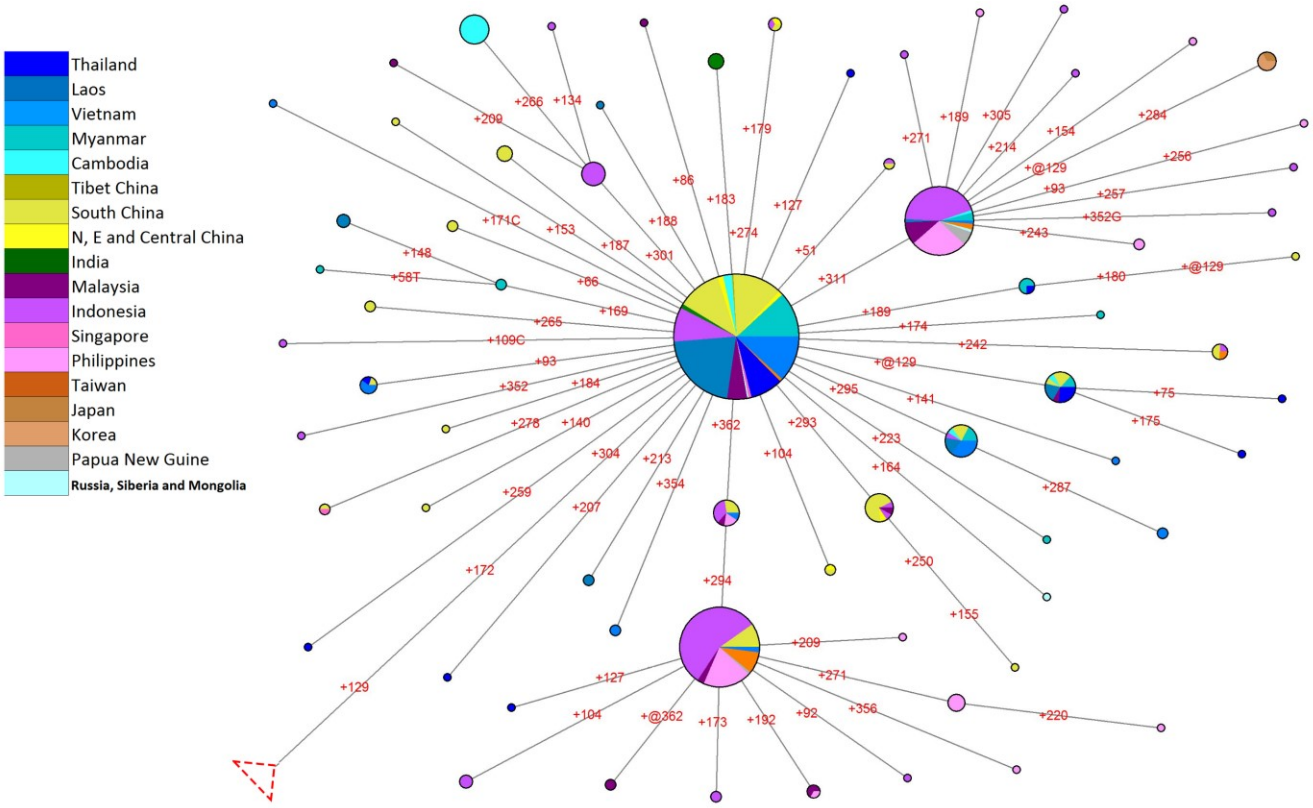


Figure 35. HVS-I phylogenetic network of paragroup F1a*.

Haplogroup F1a1 (Figure 36), characterised by a transition at np 16162, is the most common branch of F1a, with a wide distribution across Southeast and East Asia. This haplogroup is sub-divided into four main sub-lineages, F1a1a, F1a1b, F1a1c and F1a1d, and its age as a whole is dated to 7 ± 1.5 ka, while its founder age in MSEA is estimated between ~4 (*f1*) and ~6 (*f2*) ± ~2 ka (table 11). Haplogroup F1a1 is mainly detected in South China (Guangdong, Guangxi, Hainan and Yunnan), MSEA (Myanmar, Laos, Northeast-North Thailand), East China (Han people), Taiwan and Japan, and its founder age is similarly estimated between ~4 (*f1*) and ~6 (*f2*) ± ~2 ka.

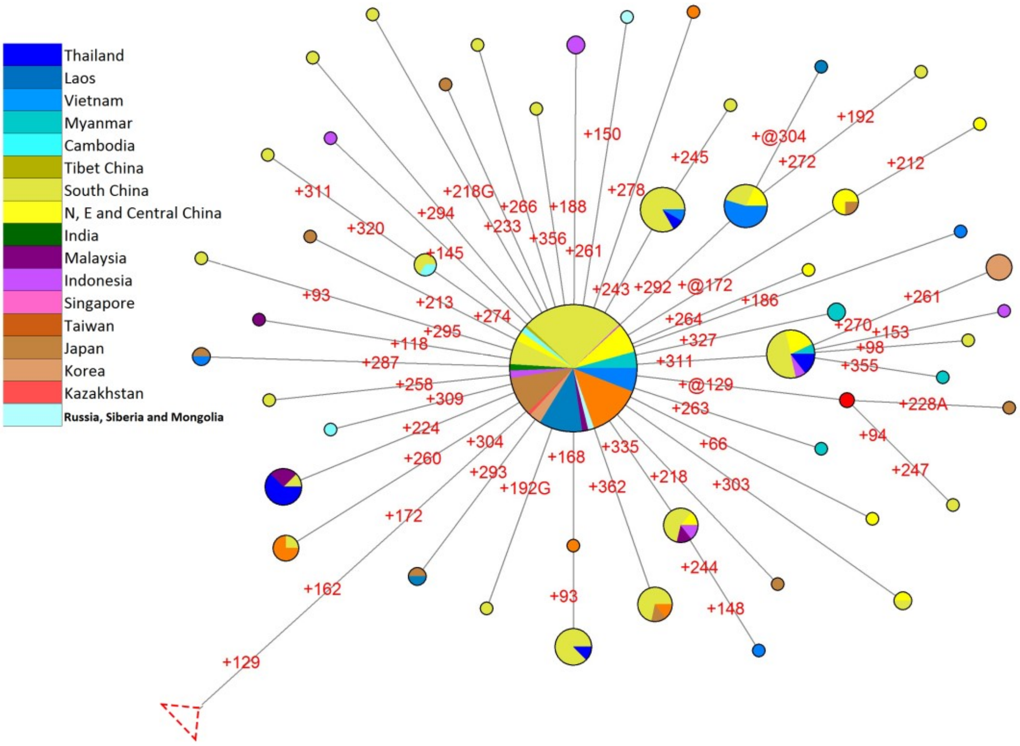


Figure 36. HVS-I phylogenetic network of paragroup F1a1*.

Haplogroup F1a1a is (Figure 37) defined by a further transition at np16108, and it is the main sub-branch within haplogroup F1a1. Overall, the age of this haplogroup is dated to 8 ± 1.5 ka (table 11), and it shows particularly high frequencies in MSEA and the Malay Peninsula. MSEA is commonly found in east Cambodia (Zhang et al., 2013), the Stieng people in south Vietnam (this study), north Laos (Bodner et al., 2011), northwest Thailand (Fucharoen et al., 2001; Jin et al., 2009; Zimmermann et al., 2009) and the Kayin people in Kayin state, in Myanmar (Summerer et al., 2014). In Malaysia, it is mainly detected within aboriginal Senoi people in West Malaysia (Macaulay et al., 2005), and also in Western Indonesia (Hill et al., 2007). However, this haplogroup is almost absent from the northern parts of Asia, Taiwanese aborigines and completely absent in Japan and Korea. This could suggest that the origin of this haplogroup was in MSEA, followed by migratory events into the Peninsular Malaysia and then to the ISEA.

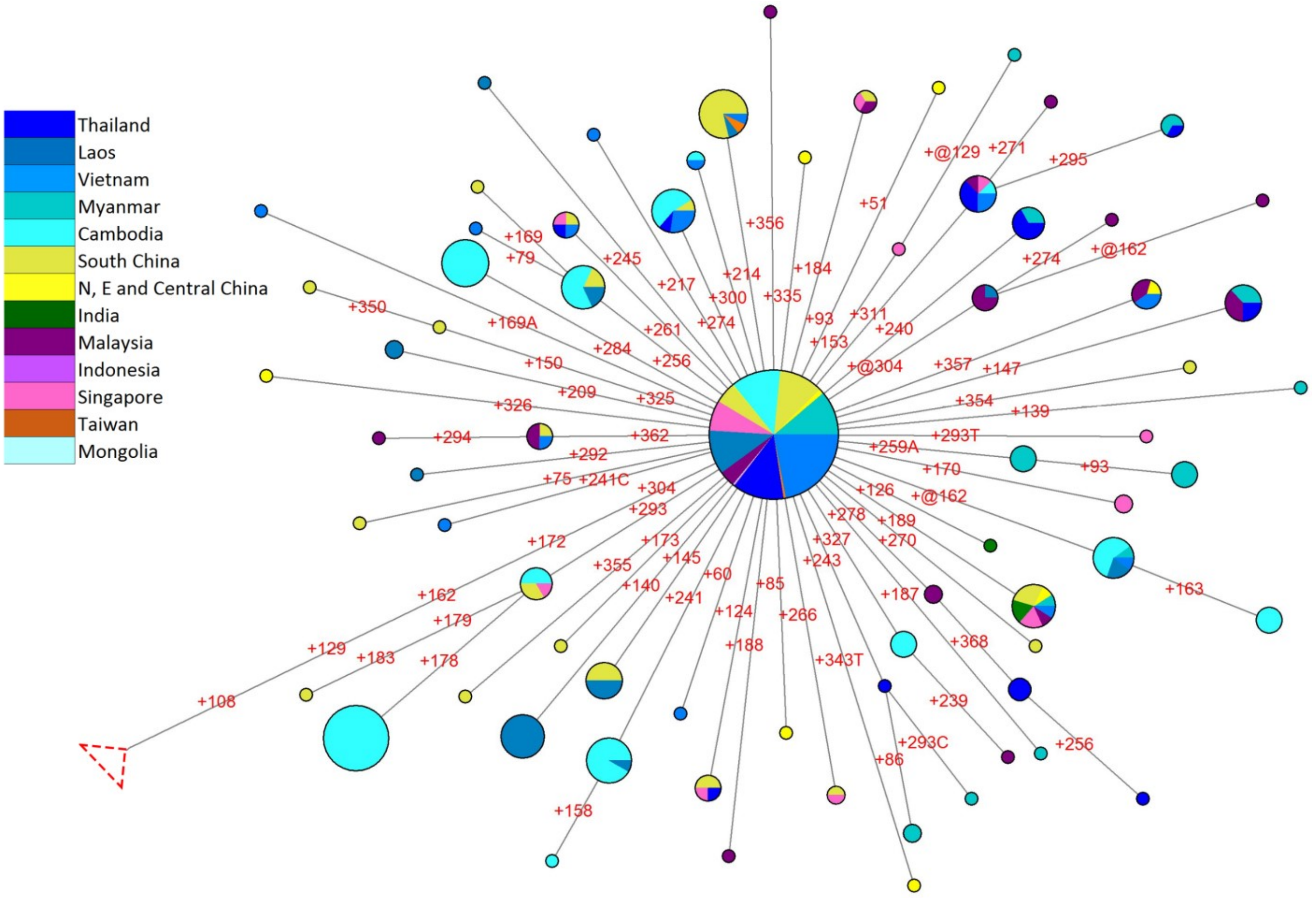


Figure 37. HVS-I phylogenetic network of haplogroup F1a1a.

4. Phylogeographic analysis using the Complete mtDNA genome

4.1 Complete sequence variation

In this study, I used in total of 951 samples from MSEA for complete mtDNA genome sequencing: 16 from Myanmar, 506 from Laos and 387 from Vietnam (see table 1). In addition, 283 from Myanmar, 1185 Thai and 135 Cambodian mtDNA genomes were taken from the literature, along with all published data worldwide from the haplogroups to which the MSEA mtDNA genomes belonged. The complete mtDNA sequences in MSEA comprised haplogroups within the three non-African haplogroups M, N and R. Haplogroup M encompassed: M7, M8, CZ, M9, M10, M12, M13, M17, M19, M20, M21, M23’75, M24, M46, M59, M61, M68, M69, M72, M73’79, M74, M76 and D; haplogroup N included N7, N8, N10, N21 and N22, while R included B4, B5, R11, B6, R9, F1a and R22. All of the non-African mtDNA haplogroups branch from the African L3 clade, which migrated to Eurasia from Eastern Africa about 55-75 ka (P. Soares et al., 2012; Watson, Forster, Richards, & Bandelt, 1997). It is thought that here was only one major prehistoric expansion of early humans out of Africa, and that both haplogroups M and N (including R) were part of the worldwide colonization process (Macaulay et al., 2005).

4.2 Haplogroup M

Haplogroup M is defined by transitions at np 489, 14783, 10400 and 15043. In this study the two-major basal haplogroups in Southeast Asia, M and R, are dated in this study by Maximum Likelihood (ML) to ~61 ka and ~64 ka respectively, with approximately 10 ka 95% confidence intervals, with upper bounds of ~67-73 ka.

4.2.1 Haplogroup M7

M7 is the most common M haplogroup in most of East and Southeast Asia. It dates to ~49 ka, and subdivides into M7a (dates to ~22.5 ka) and M7b'c (dates to ~47 ka). M7a is an East Asian haplogroup, found mainly in Japan and Korea (Kivisild et al., 2002; Tanaka et al., 2004). M7b'c is a Southeast Asian haplogroup, divided into M7b and M7c, and the basal lineages are found mostly in South China. M7c dates to around the LGM (~25.5 ka) and its branches are mostly found in China (Hartmann et al., 2009; Jiang et al., 2014; Kong et al., 2010; Lippold et al., 2014; Peng et al., 2010; Y. G. Yao et al., 2002) and Taiwan (Ko et al., 2014).

4.2.2 Haplogroup M7b

M7b is the main subclade of My found in MSEA, dates to ~50 ka, and is divided into M7b1 (dating to ~35 ka) and M7b2 (dating to ~10.6 ka). The latter subclade (Figure 38) is divided into M7b2a and a long basal lineage found in Guangxi, South China (Kong et al 2011). M7b2 is seen in South China (Kong et al 2011), Thailand (Kutanan et al 2017) and Taiwan (our unpublished data), with one sample geographically is undefined (Zheng et al. unpublished).

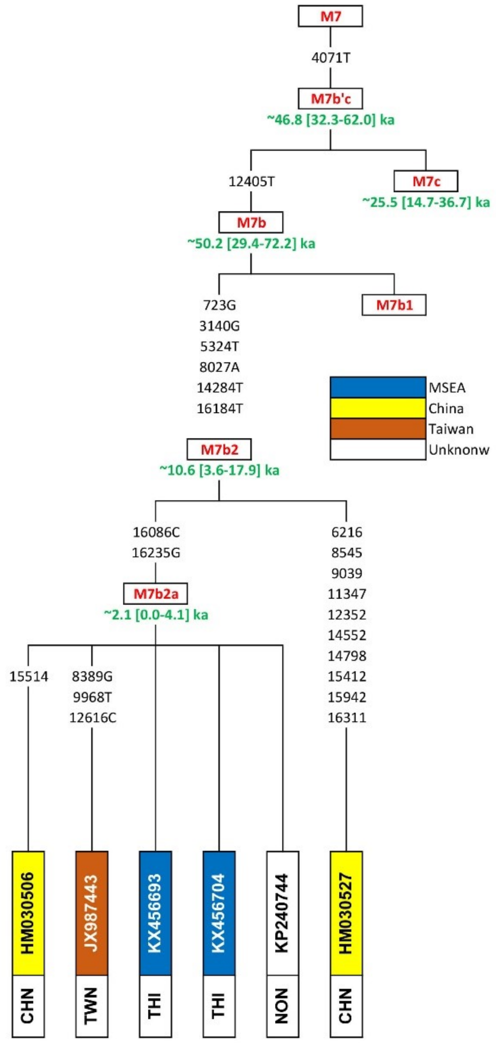


Figure 38. The tree of haplogroup M7b2. Age estimates (in ka) displayed is averaged distance (ρ) in green. (CHN – China, NON – Unknown, THI – Thailand, TWN – Taiwan).

M7b1 dates to the pre-LGM age, and is subdivided into M7b1a (~12.3 ka) and M7b1b (~ 5.2 ka). The latter subclade is mainly seen in Central China (Kong et al 2011) and south Siberia in Russia (Derenko et al., 2007). M7b1a has a wider distribution in East and Southeast Asia, dates to the LGM (~20 ka), and it is divided into M7b1a1 and M7b1a2. M7b1a2 is commonly found in south Taiwan (Ko et al., 2014; Loo et al., 2011) (Ko et al 2014; Loo et al. 2011) and also in ISEA (Delfin et al., 2014; Eng, 2014) and South China (Jiang et al., 2014; Kong et al., 2006).

M7b1a1 dates to the late Pleistocene age (~12.3 ka), encompasses three subclades, M7b1a1a, M7b1a1b and M7b1a1c as shown in Appendix B, dating to ~11.4 ka, ~8.6 ka and ~8.1 ka respectively. M7b1a1a is dated to the early Holocene age and is divided into M7b1a1a1 (dates to ~5.2 ka), M7b1a1a2 (dates to ~10 ka) and M7b1a1a3 (dates to ~5.8 ka). M7b1a1a1 is dated to the Neolithic age and mainly found in Japan (Bilal et al., 2008; Tanaka et al., 2004; H.-X. Zheng et al., 2011). M7b1a1a2 (Appendix B) dates to the early Holocene age (~10 ka), is more wider distributed in Southeast Asia and is seen in Peninsular Malaysia (Eng, 2014; P. A. Soares et al., 2016), north Vietnam (this study), Thailand (Kutanan et al., 2017), south Taiwan (Loo et al., 2014), with basal lineages found in South China (Zheng et., al 2011; 1000 Genomes Project, 1KGP). Most of the north Vietnamese branches nest under the subclade M7b1a1a2a1a1, which dates to the Neolithic age (~4.8 ka), this pattern suggests the southern Chinese origin during the early Holocene and the farming Neolithic expansion from South China to north Vietnam in MSEA during the Neolithic age.

M7b1a1a3 (Appendix B) dates to the mid-Holocene, is mainly found in Southeast Asia and is divided into two main subclades, M7b1a1a3a and M7b1a1a3b, with basal lineages found in north-east Thailand (Kutanan et al., 2017) and Vietnam (1KGP). The latter subclade (M7b1a1a3b) seems to have an origin in South China (Zhang et al. 2011), while M7b1a1a3a is mainly found more frequent and diverse in north MSEA: north Vietnam, north Laos (this study).

Both M7b1a1b and M7b1a1c are dated to around 8 ka, and are commonly found in Southeast Asia. M7b1a1b is divided into M7b1a1b1, M7b1a1b2, M7b1a1b3 and M7b1a1b4 (Appendix B). The two latter subclades are minor branches and found in two different regions, M7b1a1b3 is seen in Shandong, East China (Kong et al., 2003) and the Ami, in Taiwan (Soares et., al 2016), while M7b1a1b4 is confined south Siberia

(Derenko et al., 2007). M7b1a1b1 and M7b1a1b2 are major subclades and they are restricted to MSEA and South China (Bi, Li, Chen, Zhu, & Yao, 2011; Y. Ji et al., 2008; P. A. Soares et al., 2016; H.-X. Zheng et al., 2011) and Taiwan (Ko et al., 2014; Loo et al., 2014; P. A. Soares et al., 2016) with basal lineages found mainly in South China (Kang et al., 2016; H.-X. Zheng et al., 2011), which could suggest a South Chinese origin. M7b1a1b2 and M7b1a1b1a, which are dated to the Neolithic age about ~ 4 ka, are most frequent in MSEA. M7b1a1c (Appendix 0B) dates to the early Holocene and is divided into a major subclade, M7b1a1c1, with basal lineages found in South China (Bi et al., 2011; Zou et al., 2010). M7b1a1c1 dates to mid-Holocene (~6.5 ka) and its major subclades, M7b1a1c1a and M7b1a1c1b, are dated to during the Neolithic Age, at ~3.8 ka and ~3.2 ka, respectively. The latter major subclade is restricted to Taiwan (Ko et al., 2014; Soares et al., 2016) and South China (Lippold et al., 2014; Zheng et al., 2014), while M7b1a1c1a is confined to north MSEA (this study; Soares et al., 2016; Kutanan et al., 2017) and South China (Lippold et al., 2014).

Similar to the pattern for M7b1a1a2a1a, the subclades M7b1a1b2, M7b1a1b1a and M7b1a1c1a could all be related to the Neolithic farming expansion from South China to north MSEA and Taiwan during the Neolithic age.

4.2.3 Haplogroup M10

The minor haplogroup M10 is divided into two subclades, M10a (Kong et al., 2003) and M10b. The latter is a very minor subclade and mostly seen in the Vietnamese sequences form this study (Figure 39). The M10 tree is reconstructed from 51 complete sequences: 48 M10a and 5 M10b. M10 is mainly found in MSEA and China, and at lower levels in North (Russia and Mongolia) and South Asia (India). **M10a** is dated to the LGM, ~24.9 ka, and seen widely in Asia: North, South and Southeast Asia (Chandrasekar et al., 2009; Derenko et al., 2012; Ko et al., 2014; Tanaka et al., 2004). It is divided into three subclades, two LGM subclades; M10a1 (~22.4 ka) and M10a2 (~23.3 ka) and an early Holocene subclade M10a3 (~9.2 ka). M10a1 has a major nested sub-haplogroup (M10a1a), and a basal lineage in China (Lippold et al., 2014). M10a1a (Figure 40) is defined by a transition np 13135A, and divided into four main subclades: M10a1a1, M10a1a2, M10a1a3 and M10a1a4, which dated between the Late glacial and early Holocene ages.

However, M10b is much younger (2.2 ka) compared to the other M10 subclades. This could indicate a heavy drift event. M10b is seen in Vietnam (this study) and South China (Kong et al., 2006). Overall, M10 may have an origin somewhere in China during the pre-glacial age and then spread during the Holocene into North, East, South and Southeast Asia, including MSEA.

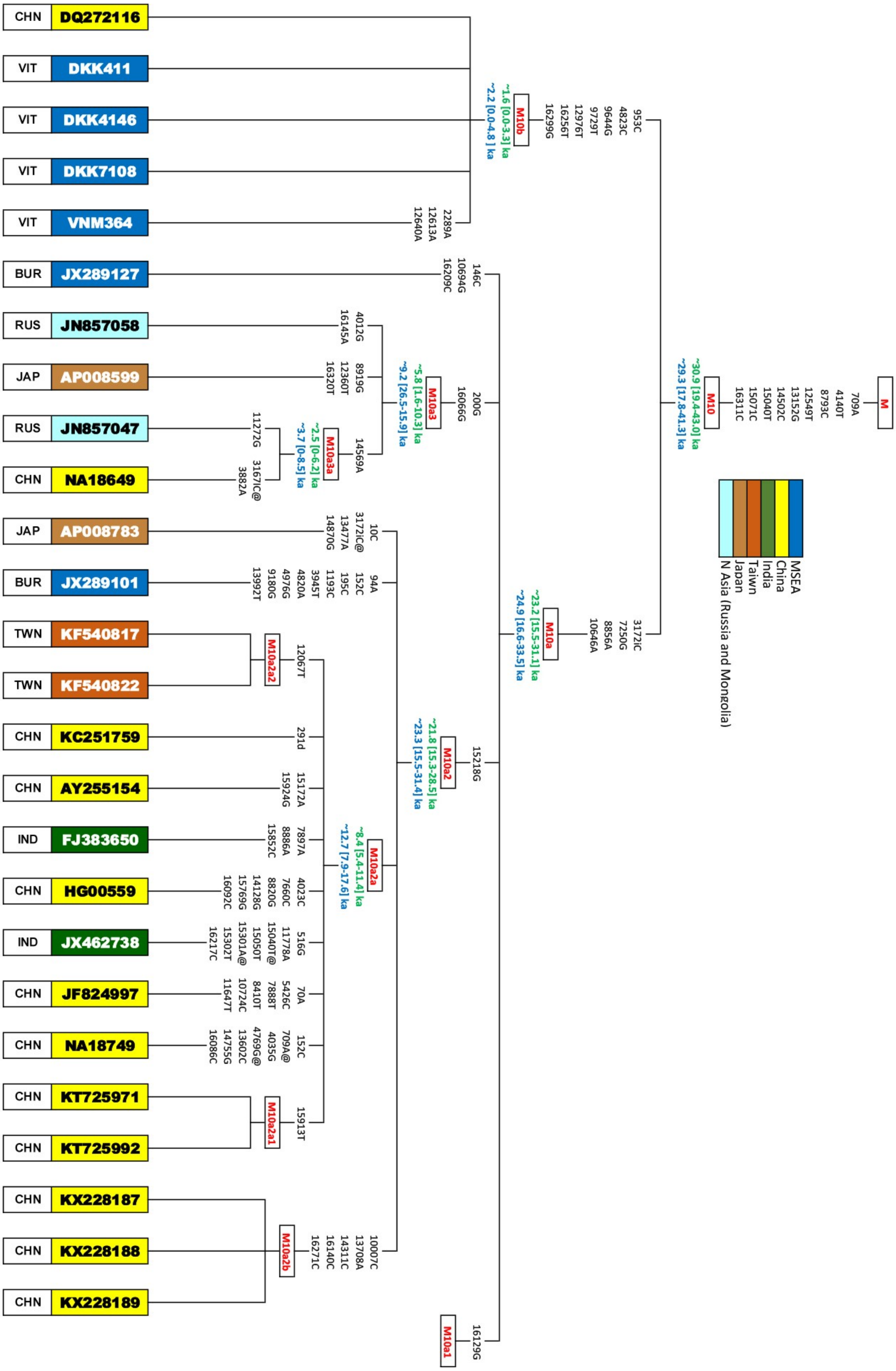


Figure 39. The tree of haplogroup M10. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, JAP – Japan, VIT – Vietnam, TWN – Taiwan, IND – India, BUR – Myanmar, RUS - Russian).

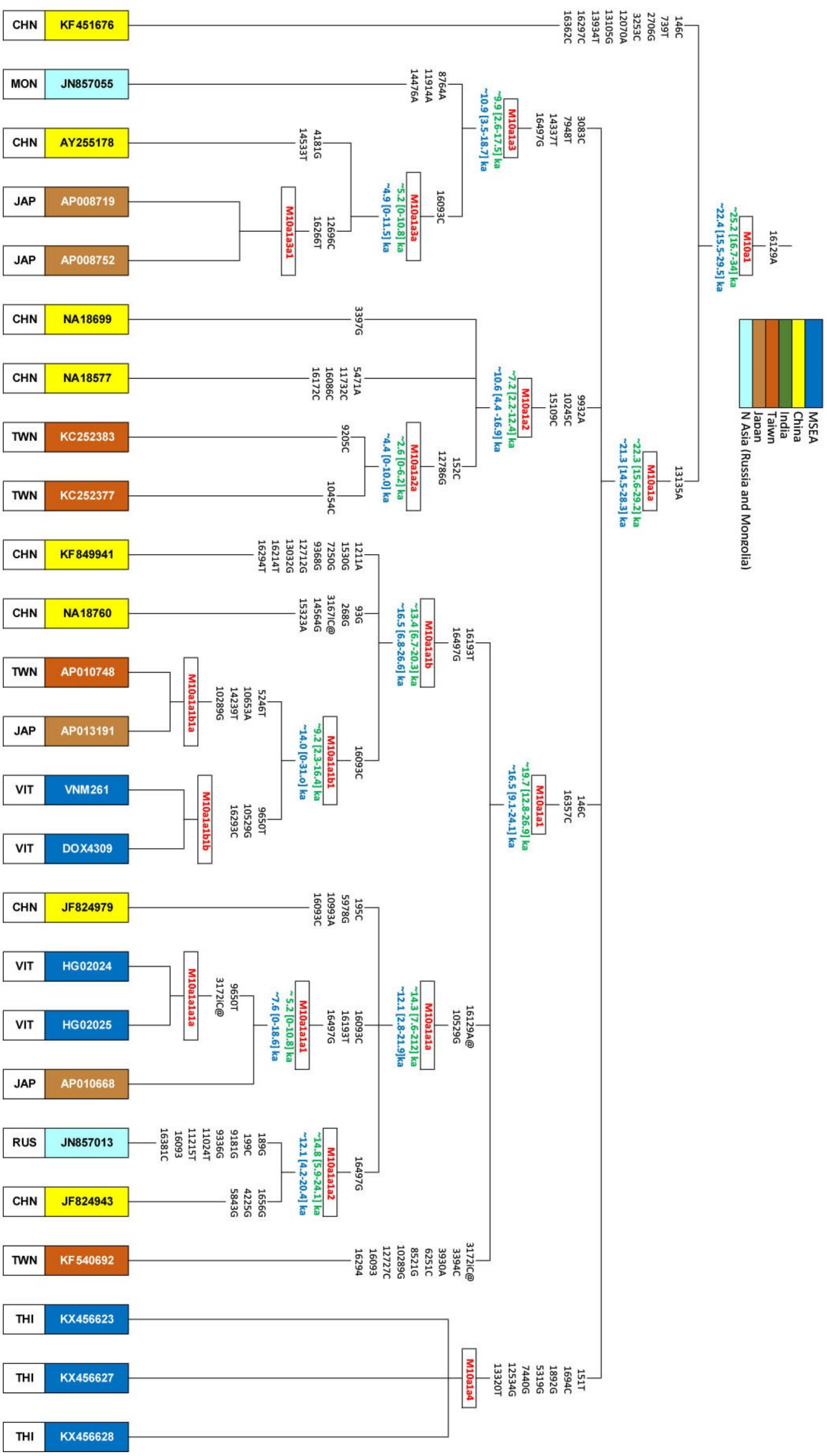


Figure 40. The tree of haplogroup M10a1. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, THI – Thailand, JAP – Japan, TWN – Taiwan, MON – Mongolia and RUS – Russian).

4.2.4 Haplogroup M12

M12 is dated to ~40 ka (Figure 41) and divided into two main subclades, M12a and M12b. M12b (Figure 42) is mainly seen in Cambodia (Zhang et al., 2013) and Thailand (Kutanan et al., 2017) within MSEA, and there is a basal branch in Northeast Malaysia (Eng, 2014).

M12a is dated to ~38 ka and is divided into two subclades, M12a1 and M12a2, which are dated to before the LGM and around the LGM, at ~34.8 ka and ~23 ka, respectively (Figure 43). M12a1 is further divided into two main subclades; M12a1a (~25 ka) and M12a1b (~27.4 ka), and seems to have an origin in northern MSEA as the basal branches are seen in north Vietnam, north Thailand and South China (Peng et al., 2011; Zheng et al., 2011, Kutanan et al., 2017), while M12a2 is a minor LGM subclade restricted to Vietnam (Peng et al., 2011), Myanmar (Summerer et al., 2014) and Peninsular Malaysia (Eng, 2014).

Both M12a1a and M12a1b seem to have a pre-LGM origin in MSEA or South China. M12a1a is dated to ~25 ka and found in Laos (this study, Kutanan et al., 2017), South China (Peng et al., 2011, Lippold et a., 2014), Indonesia (Eng, 2014) and Thailand (Kutanan et al., 2017). M12a1b (Figure 43) is divided into M12a1b1 (~21 ka), M12a1b2 (~17.9 ka) and a basal branch from Guangdong in South China (Kong et al., 2003). M12a1b1 is restricted to MSEA, including Vietnam (this study, Peng et al., 2011), Thailand (Kutanan et al., 2017).

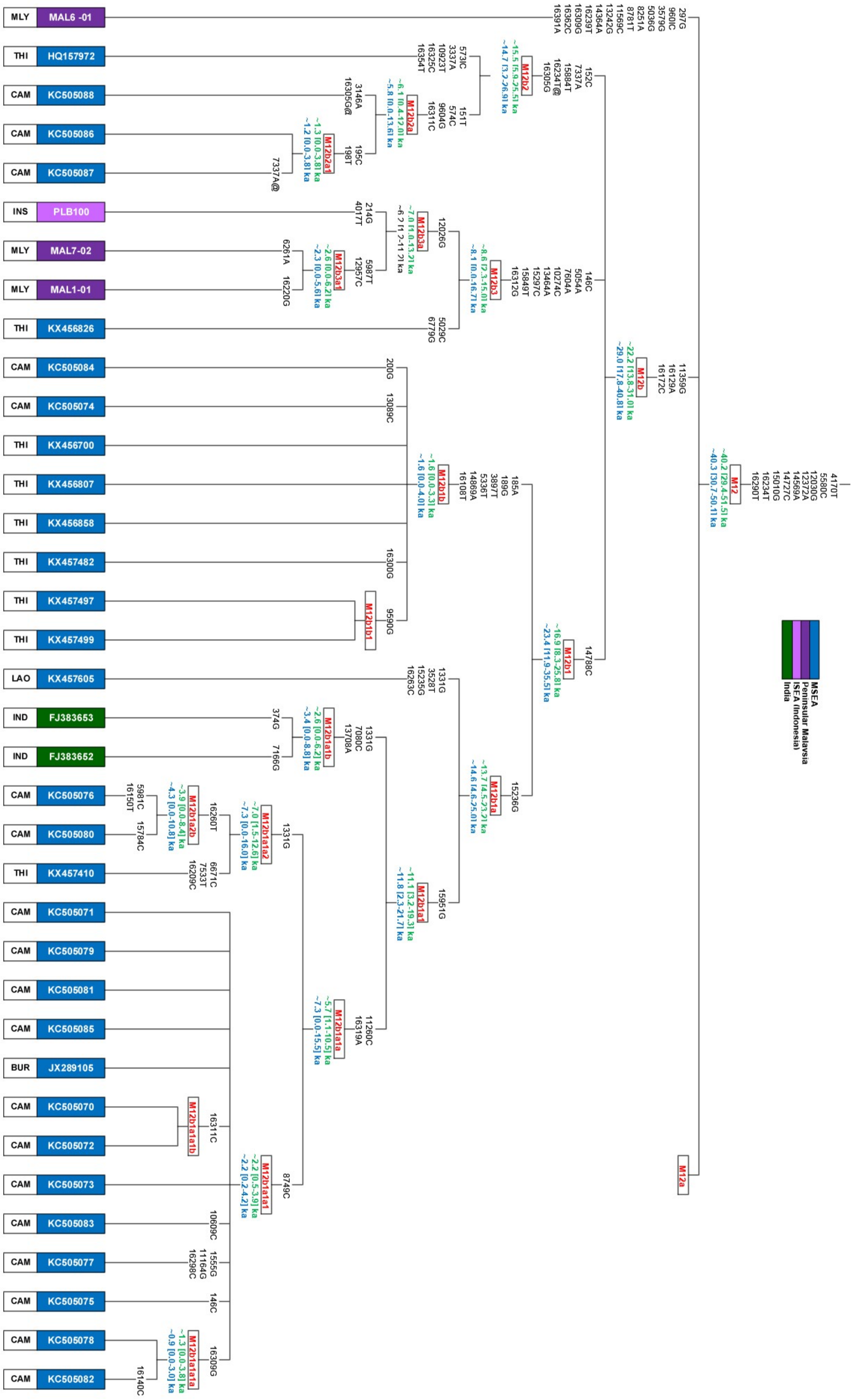


Figure 41. The tree of haplogroup M12b. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (MLY – Peninsular Malaysia, IND – India, INS – Indonsia, BUR – Myanmar, THI – Thailand, CAM – Cambodia).

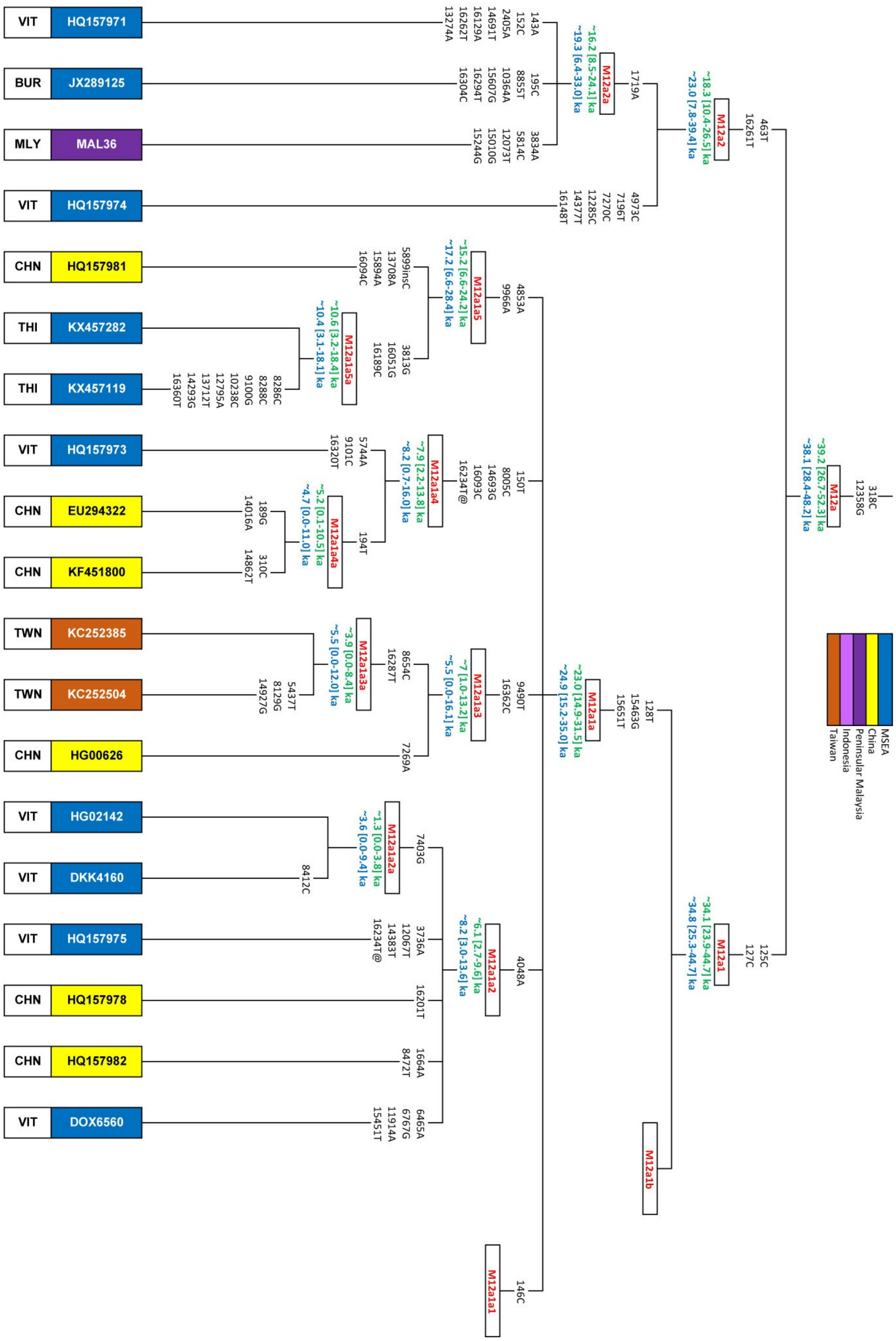


Figure 42. The tree of haplogroup M12a. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, INS – Indonsia, TWN – Taiwan, THI – Thailand, VIT – Vietnam, LAO – Laos and BUR – Myanmar).

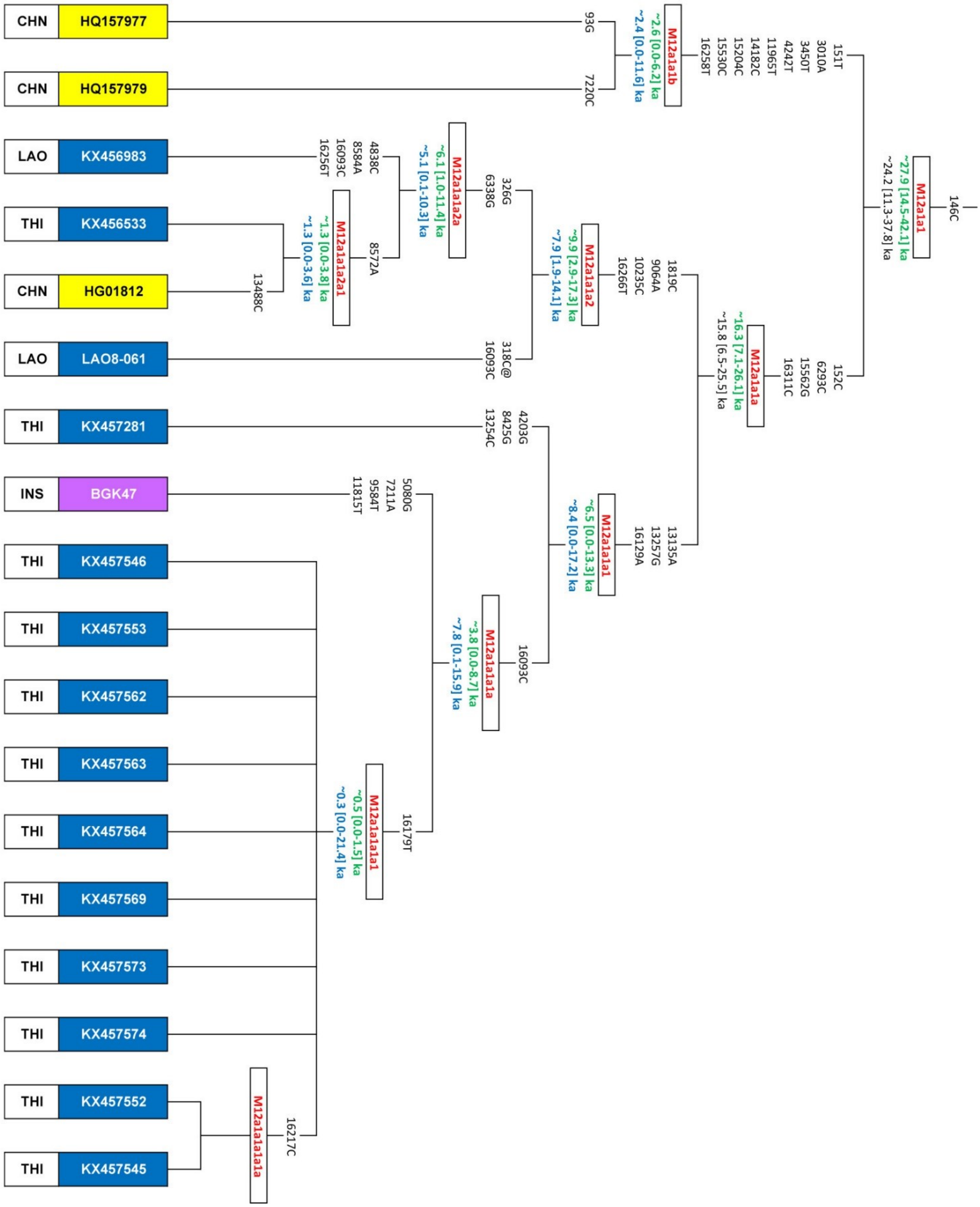


Figure 43. The tree of haplogroup M12a1a1. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, INS – Indonsia, THI – Thailand, LAO – Laos and).

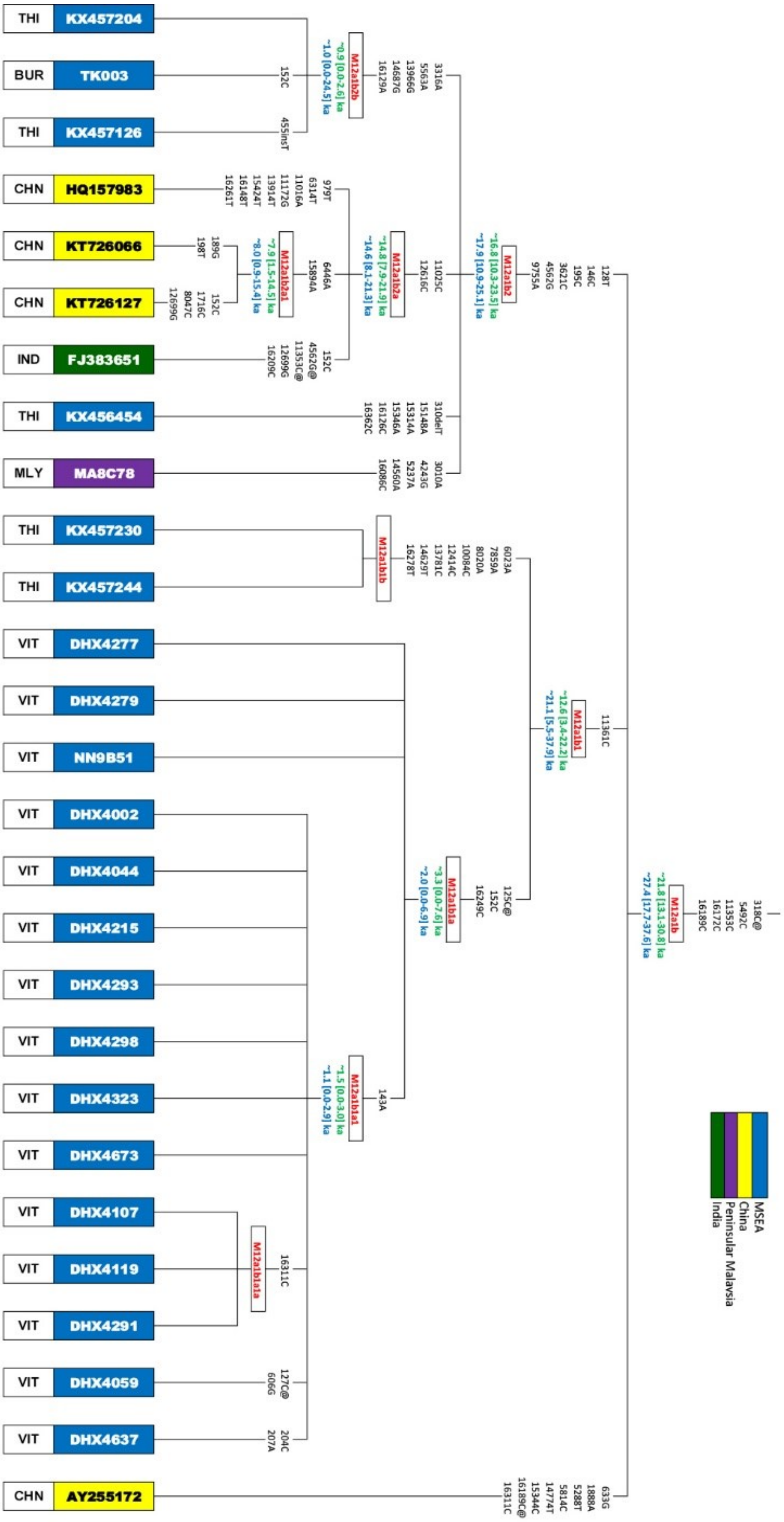


Figure 44. The tree of haplogroup M12a1b. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (IND – India, MLY – Peninsular Malaysia, CHN – China, THI – Thailand, VIT – Vietnam, BUR – Myanmar).

4.2.5 Haplogroup M13’46’61

M13’46’61 is divided into two basal subclades M13 and M46’61, dates to ~56 ka (Figure 45), and has been proposed to have an origin in MSEA or South China (Macaulay et al., 2005, Zhang et al., 2013, Summerer et al., 2014, Kutanan et al., 2017), with more recent branch having expanded into India and Nepal in South Asia (M13b2: Figure 45 and M61a1a: Figure 48), Russia, Japan and northern China (M13a1: Figure 46).

4.2.6 Haplogroup M13

M13 is characterized by a transition at np 6023, dates to ~52 ka, and is subdivided into three subclades M13a (~30 ka), M13b (~37 ka) and M13c (~48.6 ka).

M13a is commonly found in the Tibet region, China (F. Ji et al., 2012; Qin et al., 2010), and is subdivided into M13a1 (~25 ka) and M13a2 (~12.6 ka). M13a1 dates to the LGM and is divided into M13a1b which dates to the end of the Pleistocene (~12 ka) with one basal subclade found in East and Northeast Asia and a basal sister lineage found in one individual in India. Although M13a1a is present in the PhyloTree 17(van Oven & Kayser, 2009), it is excluded from this study since all Japanese samples (Tanaka et al., 2004) match the new branch M13a1b1ab (Figure 46). However, M13a1b is seen also in Inner Mongolia, south Siberia (Derenko et al., 2012) as in M13a1b1a1 (dates to ~3 ka) and Japan as in M13a1b1ab (dates to ~2.5 ka), but there are no samples from MSEA match the whole M13a subclade. This pattern could suggest that M13a has an origin in China and then expanded northward to south Siberia and eastward to Japan in East Asia during the Neolithic.

M13b dates to before the LGM (~37 ka), and is not found in MSEA, but it is found in Peninsular Malaysia (Eng, 2014), Tibet (Kong et al., 2011), Nepal (Fornarino et al., 2009) and Northeast India (Satish Kumar et al., 2009).

M13c is an ancient haplogroup (dates to ~ 48.6 ka) seen mainly in Myanmar, defined by transition np 5910, and divided into M13c1 and a long basal lineage found in Lahu people in China (Lippold et al., 2014). M13c1a is dated to pre-LGM age (~32 ka) and it is almost restricted to the Burmese people (Summerer et al., 2014, Li et al., 2015, Kutanan et al., 2017) with one sample found in Thailand (Pradutkanchana and Kimura 2010). This could suggest that M13c is ancient lineage, exposed to high level of drift in Tibetan region, and may have an origin in north Myanmar/Tibet.

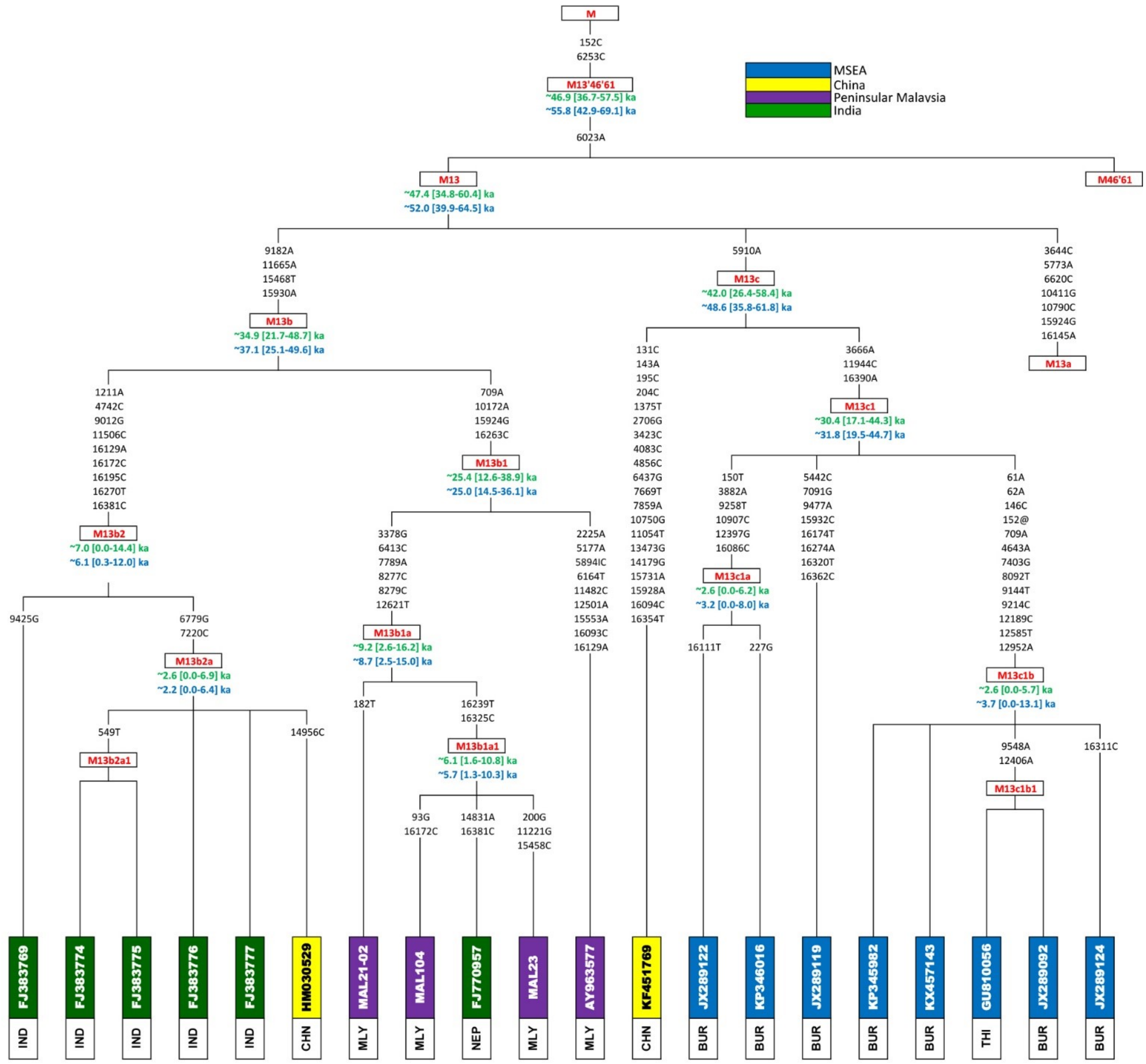


Figure 45. The tree of haplogroup M13. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (IND – India, CHN – China, MLY – Peninsular Malaysia, THI – Thailand, BUR – Myanmar and NEP – Nepal).

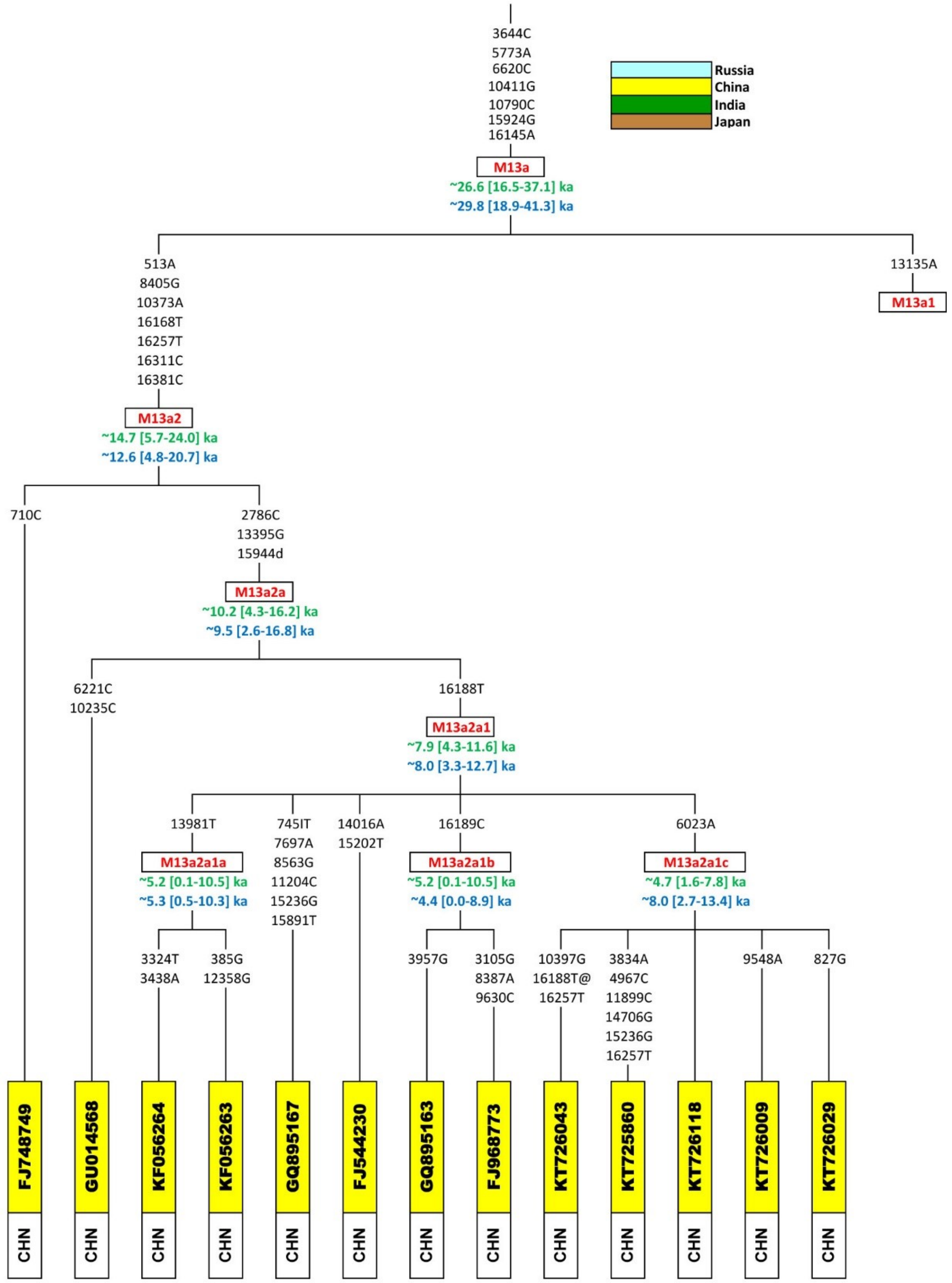


Figure 46. The tree of haplogroup M13a. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China).

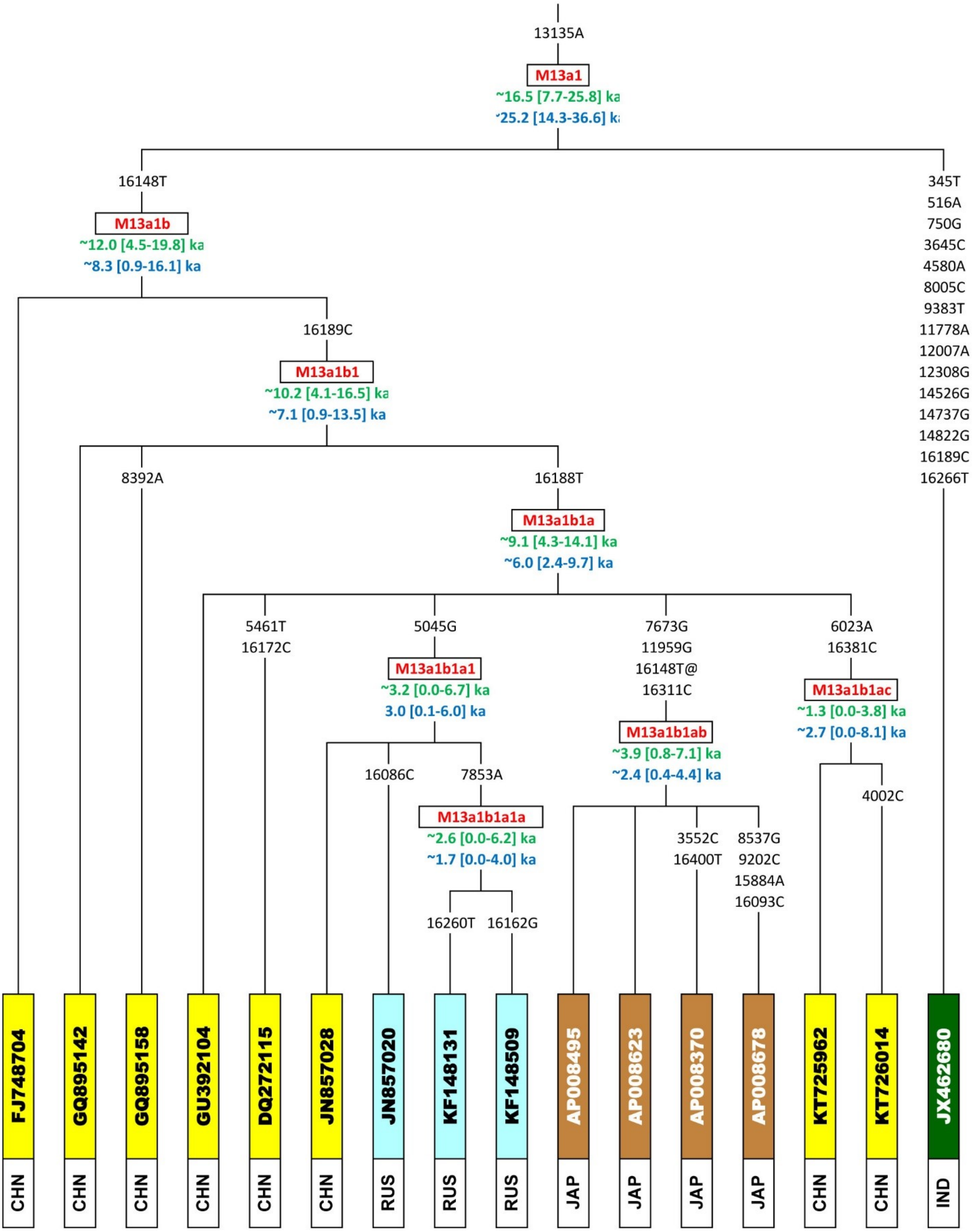


Figure 47. The tree of haplogroup M13a1. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, IND – India, JAP – Japan and RUS - Russia).

4.2.7 Haplogroup M46

M46 is an ancient haplogroup, dates to ~52.6 ka (Figure 52) and is divided into two subclades M46a (dates to ~2.7 ka) and M46b (dates to ~16 ka). M46 is restricted to the MSEA region: M64a is seen in Thailand (Dancause et al., 2009; Pradutkanchana and Kimura 2010) and Myanmar (Li et al., 2015), while M64b is found in Cambodia (Zhang et al., 2013) and Myanmar (this study). the low number samples within this rare haplogroup suggests clearly a heavy drift that maybe happen because the population subdivision in MSEA especially in Thailand.

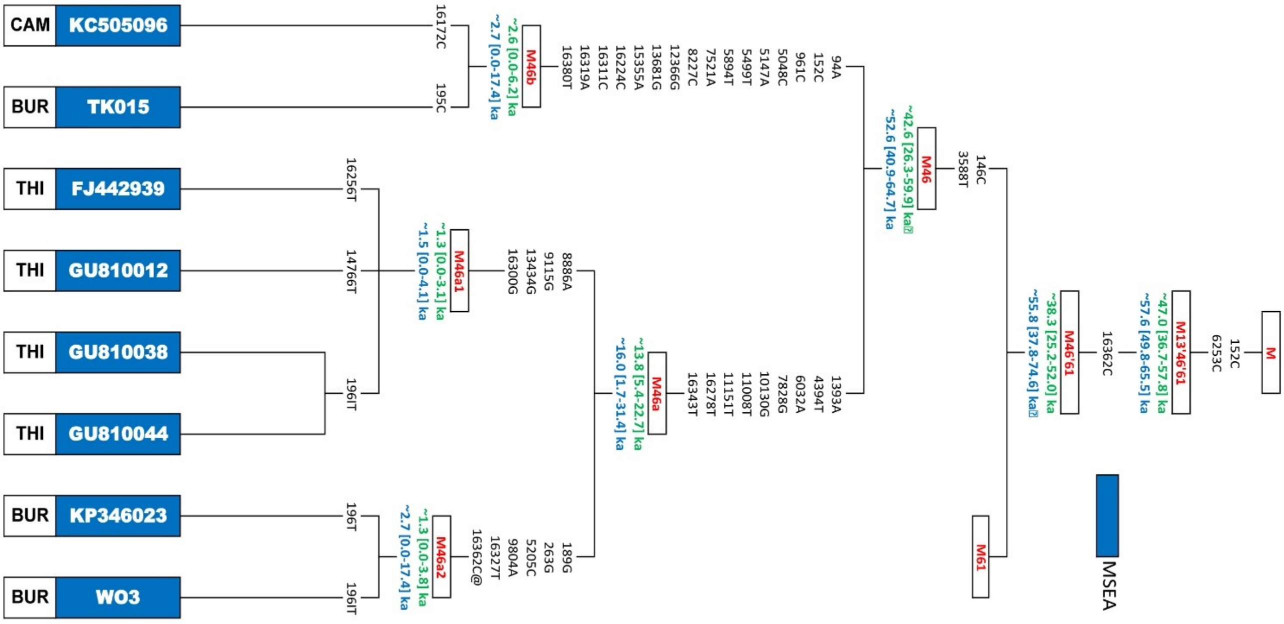


Figure 48. The tree of haplogroup M46. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CAM – Cambodia, BUR – Myanmar and THI – Thailand).

4.2.8 Haplogroup M61

M61 is dated to ~24 ka and branches into two subclades, M61a (~8 ka) and M61b (~19 ka), with different distributions. M61b is seen in Yunnan province in South China (1KGP) and Peninsular Malaysia (Eng 2014), but mainly in MSEA: Vietnam (this study), Thailand (Kutanan et al 2017), Myanmar (Sumerer et al 2014) and Laos (this study). The Vietnamese and Thai lineages fall into a very recent subclade dating to less than 1 ka. M61a is restricted to Northeast India (Chandrasekar et al. 2009) and the Tibetan region (Kong et al 2011); the Indian lineages date to only ~2 ka and nest within Tibetan lineages, suggesting a very recent expansion.

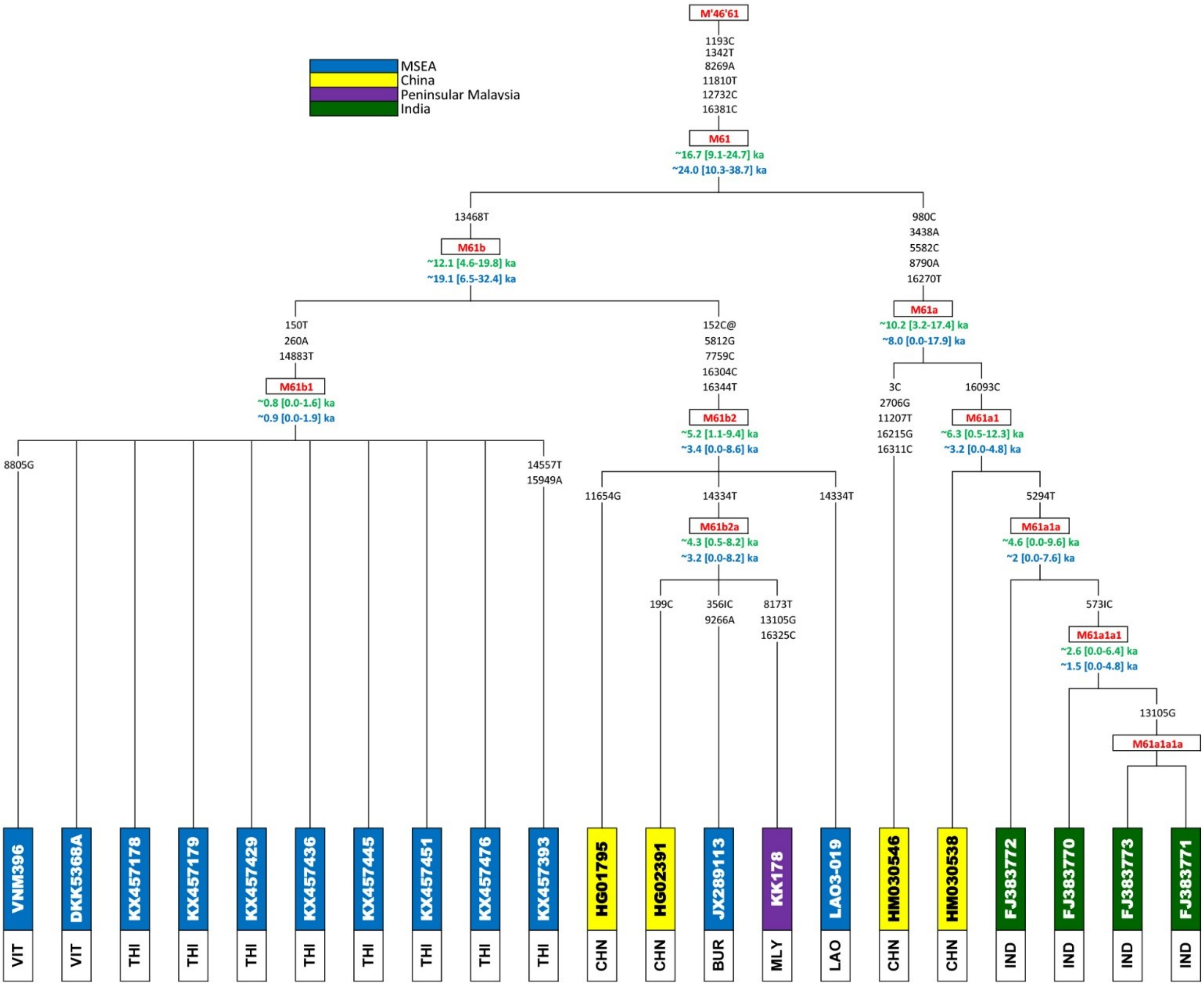


Figure 49. The tree of haplogroup M61. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, IND – India, BUR – Myanmar, VIT – Vietnam, INS – Indonesia, MLY - Malaysia and THI – Thailand and LAO – Laos).

4.2.9 Haplogroup M17

M17 is an ancient Sundaic basal M haplogroup dating to ~51 ka (Figure 50). M17 is divided into two major subclades (M17a and M17c) with a further basal lineage from Myanmar. Both main subclades are dated to ~45 ka, and seen only in MSEA and ISEA, with some samples from Peninsular Malaysia (Eng, 2014). M17a diversifies mainly around the LGM on the Sunda shelf, and divides into a major subclade M17a1 (dates to ~23 ka), with another basal lineage in Indonesia. In MSEA, M17a is found in Cambodia (Zhang et al., 2013; Lippold et al., 2014), Vietnam (Peng et al., 2010), Thailand (Kutanan et al., 2017) and Laos (this study), and in ISEA, across Philippines (Delfin et al., 2013) and Indonesia (Tabbada et al., 2009). M17c is seen in Laos (this study; Kutanan et al., 2017), Thailand (Kutanan et al., 2017) Vietnam (Peng et al., 2010), and Indonesia (Tabbada et al., 2014; Eng, 2014). M17's many long branches and wide range of node ages indicate an ancient autochthonous haplogroup that has remained within Southeast Asia for almost the entire time it has been settled by modern humans.

4.2.10 Haplogroup M19

M19 is very rare basal M haplogroup, shares a transition np 11167G with the Indian subclade M53 (Sun et al., 2006; Sharma et al., 2012) (Figure 52), although, since this is quite a variable position (Soares et al. 2009), it is not clear whether or not this is due to common ancestry. M19 is dated to the LGM (~24 ka), dividing into M19a and a basal lineage in northeast Thailand (Kutanan et al 2017). M19a is dated to the mid-Holocene (~5.2 ka), and is seen in south Vietnam (this study) and the Philippines (Scholes et al 2011). M19 appears indigenous to Southeast Asia and has undergone a high level of drift.

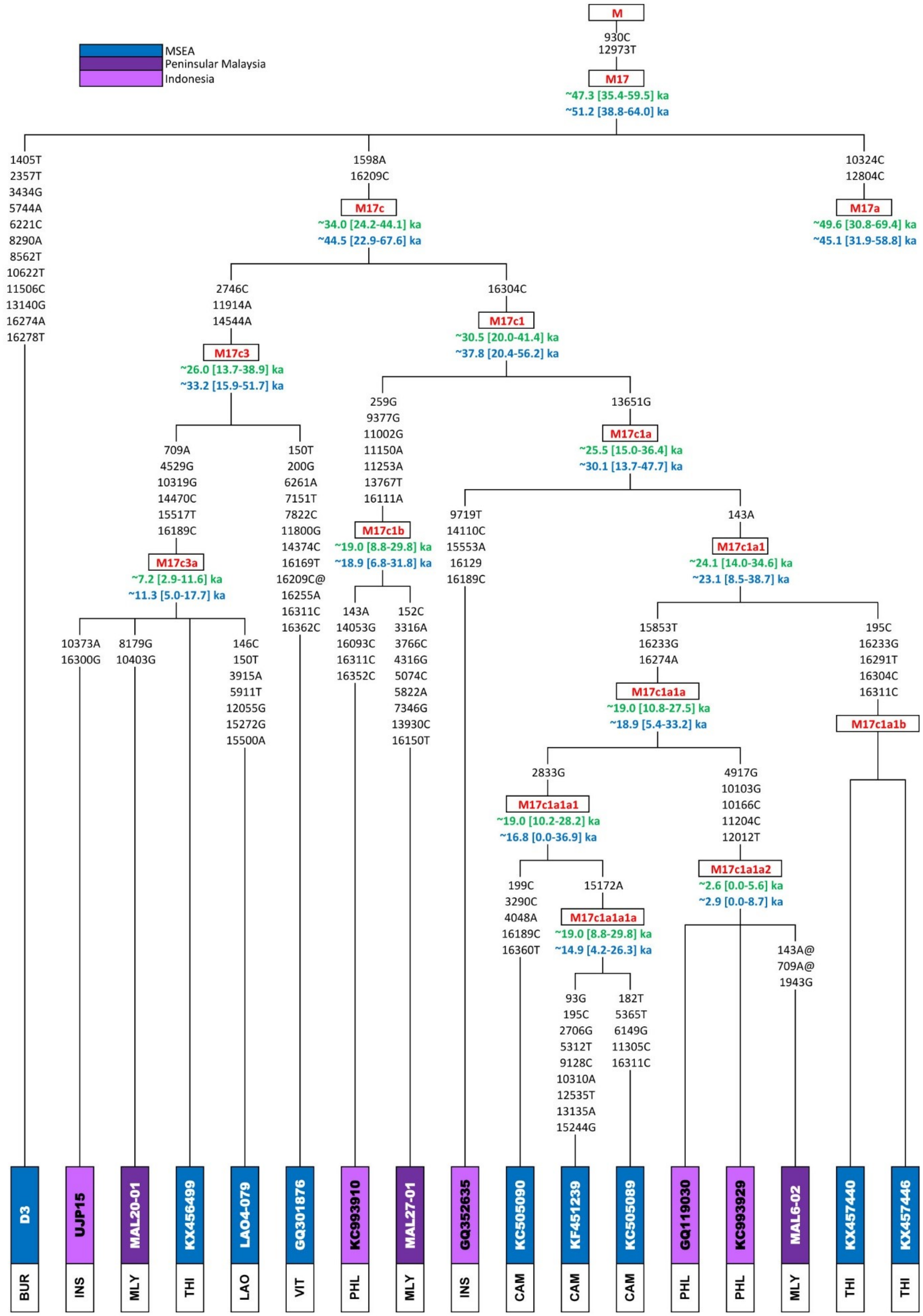


Figure 50. The tree of haplogroup M17. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (PHL – Philippines, INS – Indonesia, LAO – Laos, THI – Thailand, BUR – Myanmar and CAM – Cambodia).

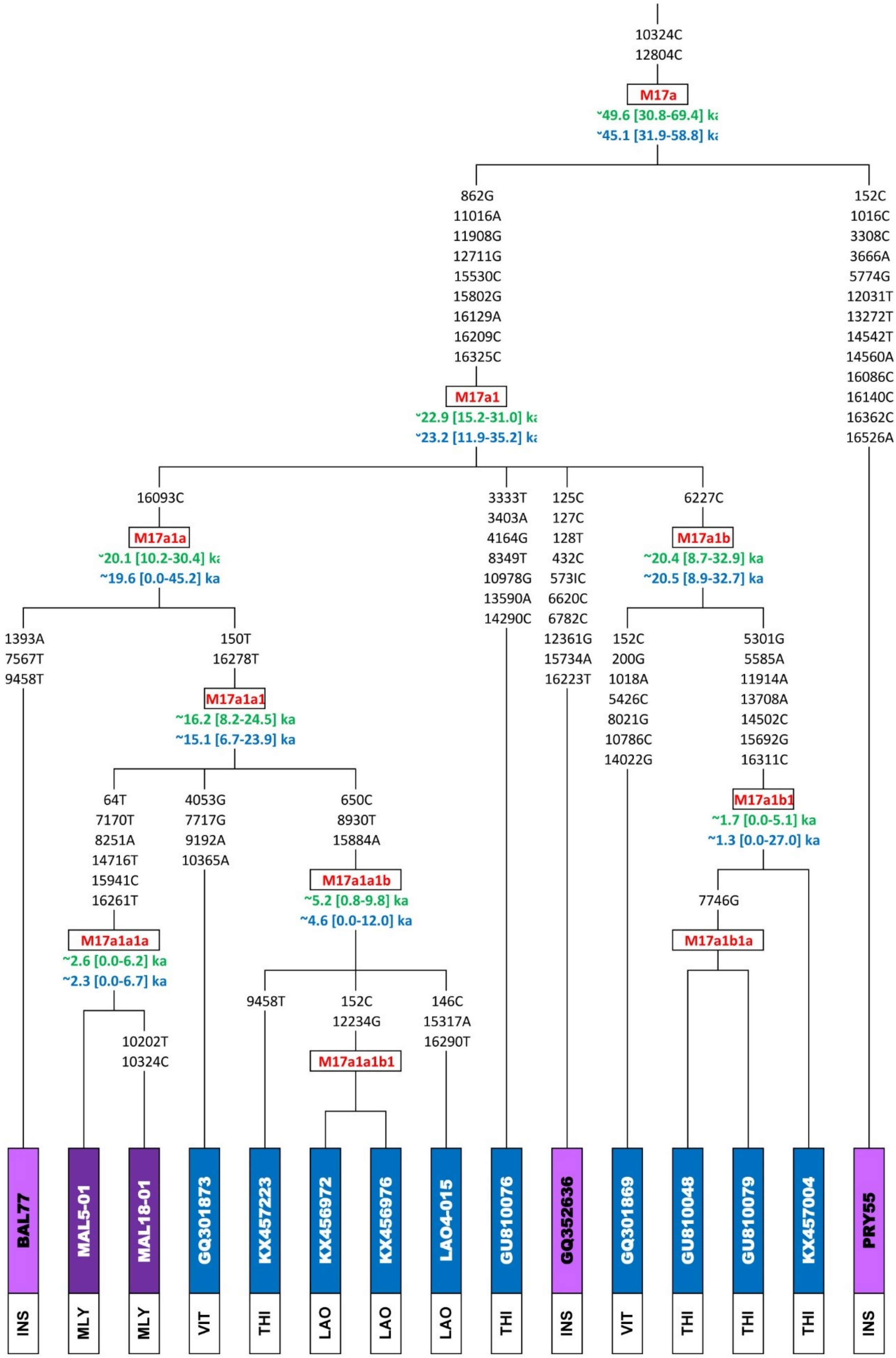


Figure 51. The tree of haplogroup M17a. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (INS – Indonesia, LAO – Laos and THI – Thailand).

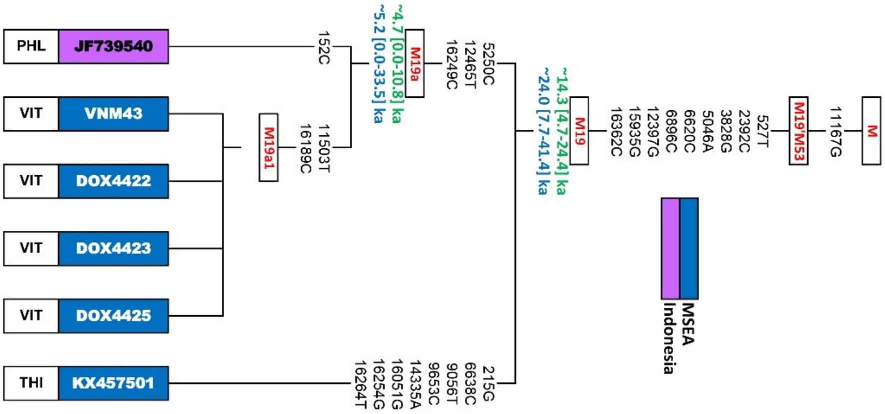


Figure 52. The tree of haplogroup M19. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (VIT – Vietnam, THI – Thailand and PHL – Philippines).

4.2.11 Haplogroup M20

M20 shares its transition at np 14110 with two other haplogroups (M1 and M51) forming a putative single cluster known as M1’20’51, which if a genuine clade would date to ~58 ka. M20 has its deepest roots within the Sunda region, in Peninsular Malaysia (Figure 53), in Northeast Peninsular Malays. It dates to before the LGM (~38.6 ka) and its subclade M20a to the Late Glacial (~17.2 ka).

M20a1 dates to early Holocene (~11 ka), before the last flooding episode of the Sunda shelf, and includes two main subclades: M20a1a (~8.8 ka) and M20a1b (~5 ka), with more basal lineages seen in North Borneo (Jinam et al., 2012) and Indonesia (Eng, 2014).

M20a1b is newly named in this study. It dates to the Neolithic age and is seen in Vietnam (this study), Thailand (Kuntanan et al., 2017) and Indonesia (Eng, 2014). M20a1a (Figure 54) is subdivided into three main subclades, M20a1a1 (~6.7 ka), M20a1a2 (~6.5 ka) and M20a1a3 (just ~1.5 ka). Both the latter subclades are commonly found in Vietnam (this study) and Thailand (Kuntanan et al., 2017), while

M20a1a1 (Figure 55) is not seen in Vietnam but is commonly seen in Laos (this study), Thailand (Kutanan et al., 2017), Yunnan in South China (Kong et al., 2011) and Peninsular Malaysia (Eng, 2014). The pattern could suggest an ancient source somewhere in MSEA and most probably recent expands northwards into South China (in Yunnan), and southwards in Indonesia, perhaps relating to the rise sea level of the Strait of Malacca during the early Holocene (Oppenheimer, 1998).

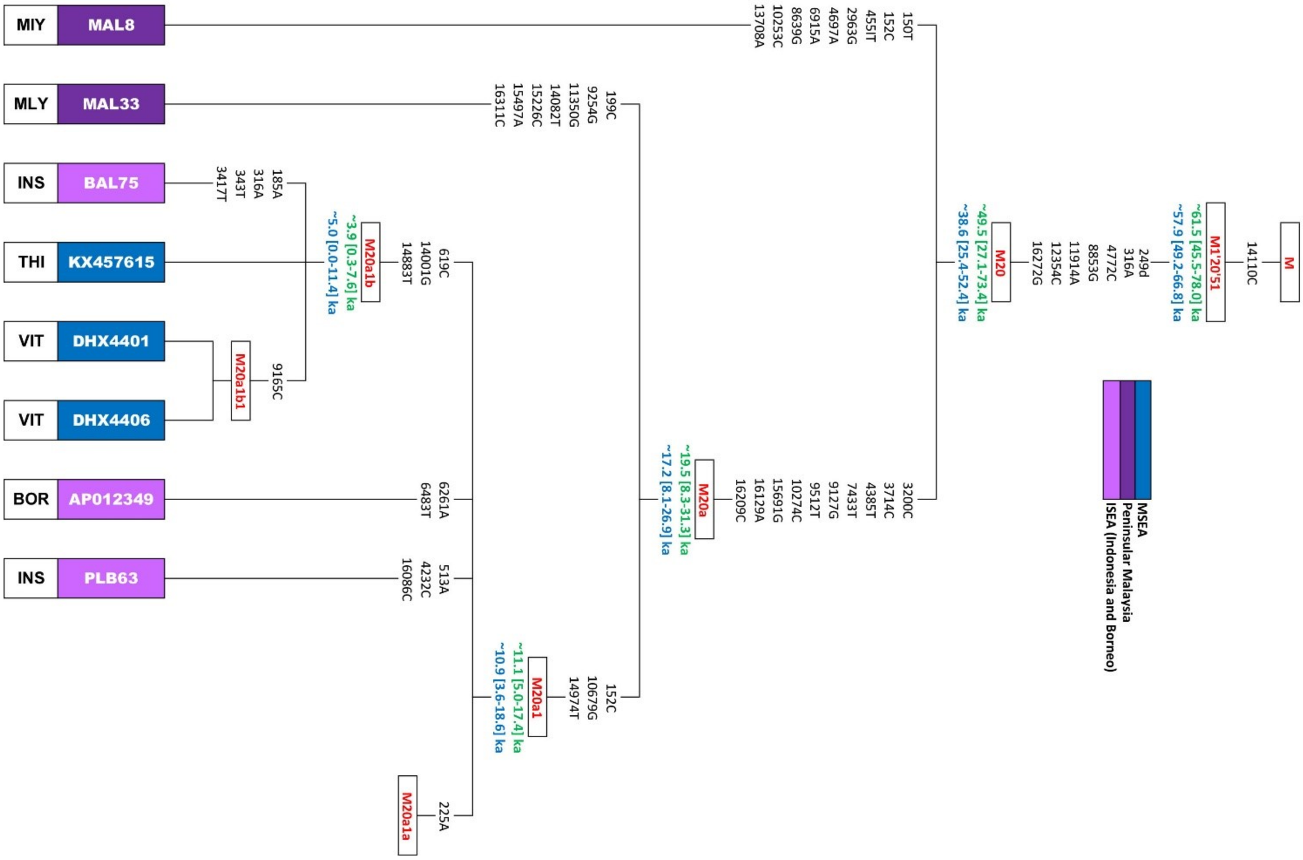


Figure 53. The tree of haplogroup M20. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (MLY –Malaysia, BOR – Borneo, INS – Indonesia, VIT – Vietnam and THI – Thailand).

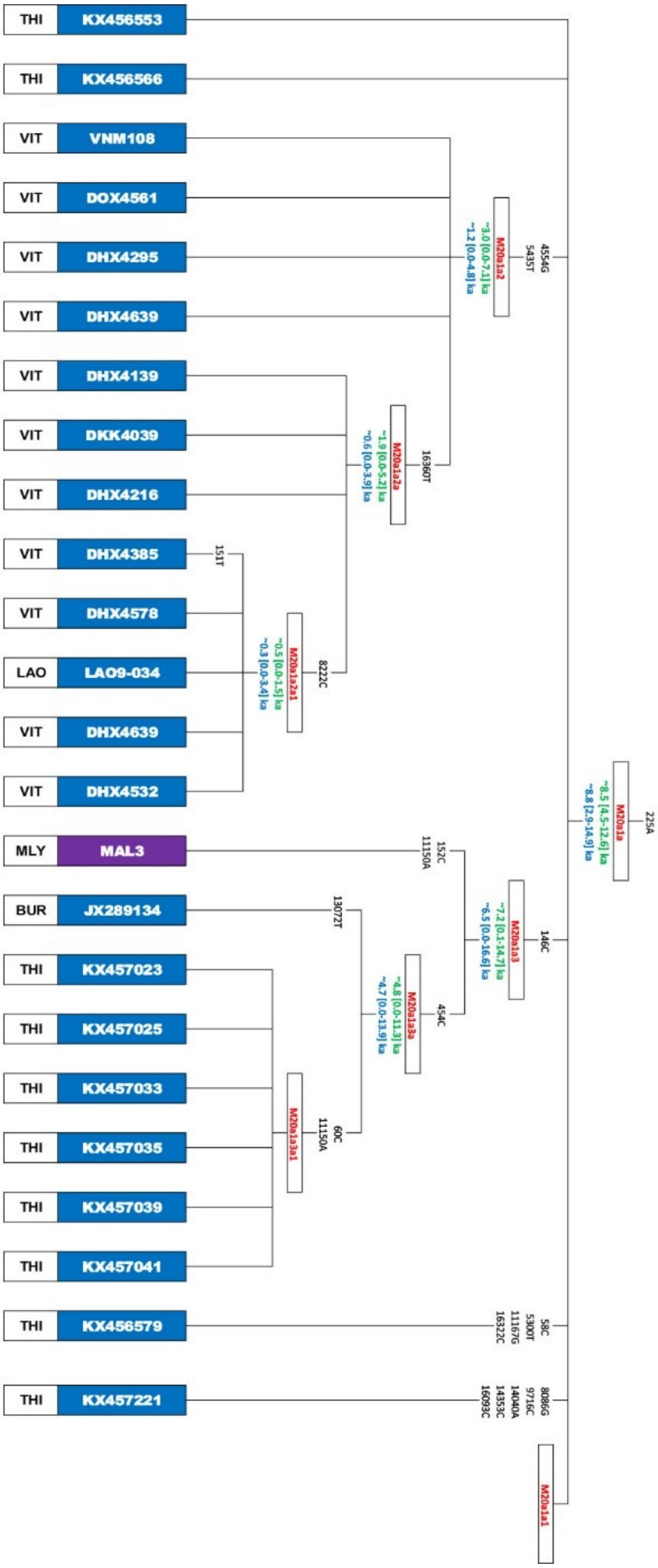


Figure 54. The tree of haplogroup M20a1a. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (MLY –Malaysia, VIT – Vietnam, THI – Thailand and LAO – Laos).

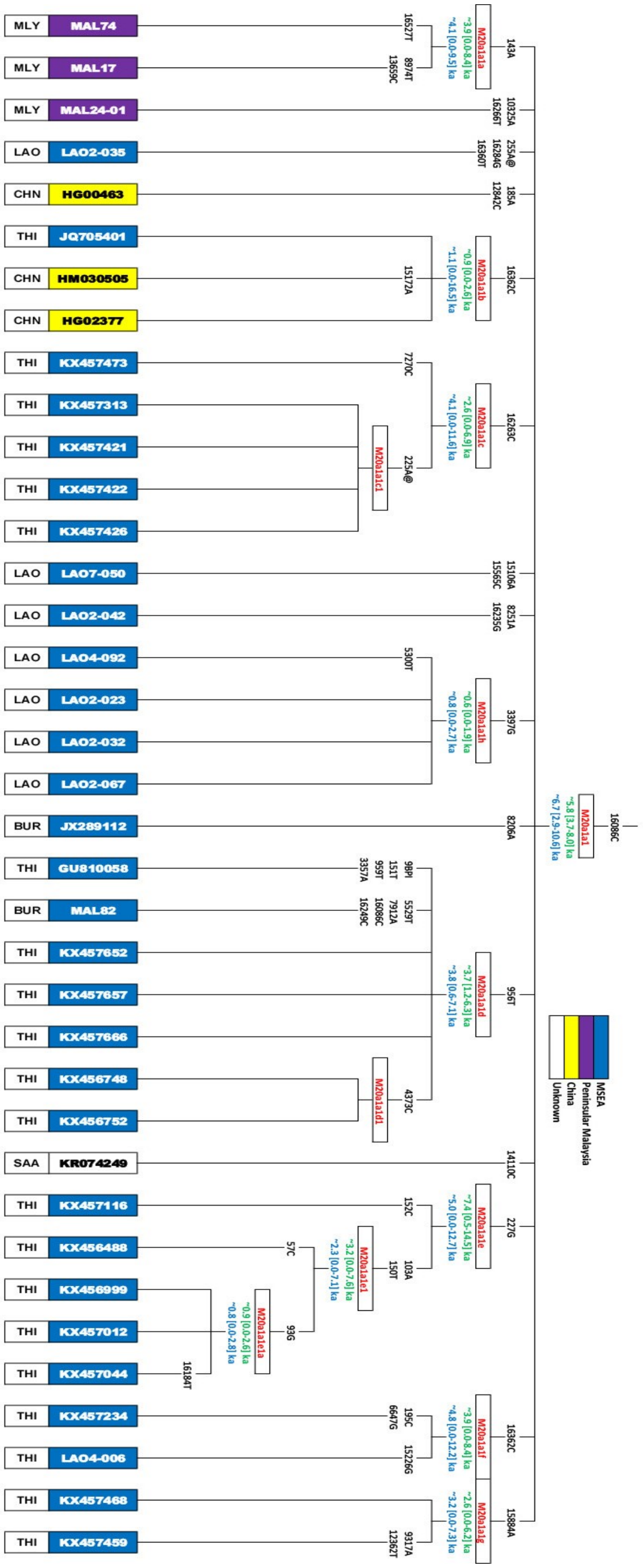


Figure 55. The tree of haplogroup M20a1a1. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, INS – Indonesia, BUR – Myanmar, THI – Thailand, LAO – Laos and SAA- Saudi Arabia).

4.2.12 Haplogroup M21

M21 is defined by a transition np 11462 (Figure 56), dates to ~56 ka, and is divided into two main clusters: M21a’c (~27.9) and M21b'd (~48.8) (Macaulay et al., 2005). M21 was proposed as Upper Pleistocene component within the Semang *Orang Asli* of Peninsular Malaysia by Hill et al. (2006), but argued to have a wider Southeast Asian ancestry by Hill et al. (2007). This study confirms that M21 has deep Sunda ancestry, as it is restricted to but distributed across MSEA and ISEA. M21a’c is subdivided into two subclades (M21a and M21c) with a basal lineage in Philippines (Tabbada et al. 2010). Both subclades date to the Late Glacial (~14 ka). M21a is mainly seen in Semang and, to a lesser extent, Senoi *Orang Asli* in Peninsular Malaysia (Hill et al., 2006; Jinam et al., 2012; Eng, 2014), while the M21c is seen in Vietnam (this study) and Indonesia, with a basal lineage in Myanmar (Li et al 2015).

M21b’d (Figure 57) is divided into two ancient haplogroups: M21b (~44.5 ka), found across the Sunda region and M21d (~33.5 ka), focused more on MSEA. M21d is constructed by three taxa found in Peninsular Malay, Indonesia (Eng, 2014) and Cambodia (Zhang et al 2013). Overall, the ancient ancestry of M21 and its distribution still indicate a Pleistocene Sunda origin, with a widespread distribution across the Sunda region, into the Philippines.

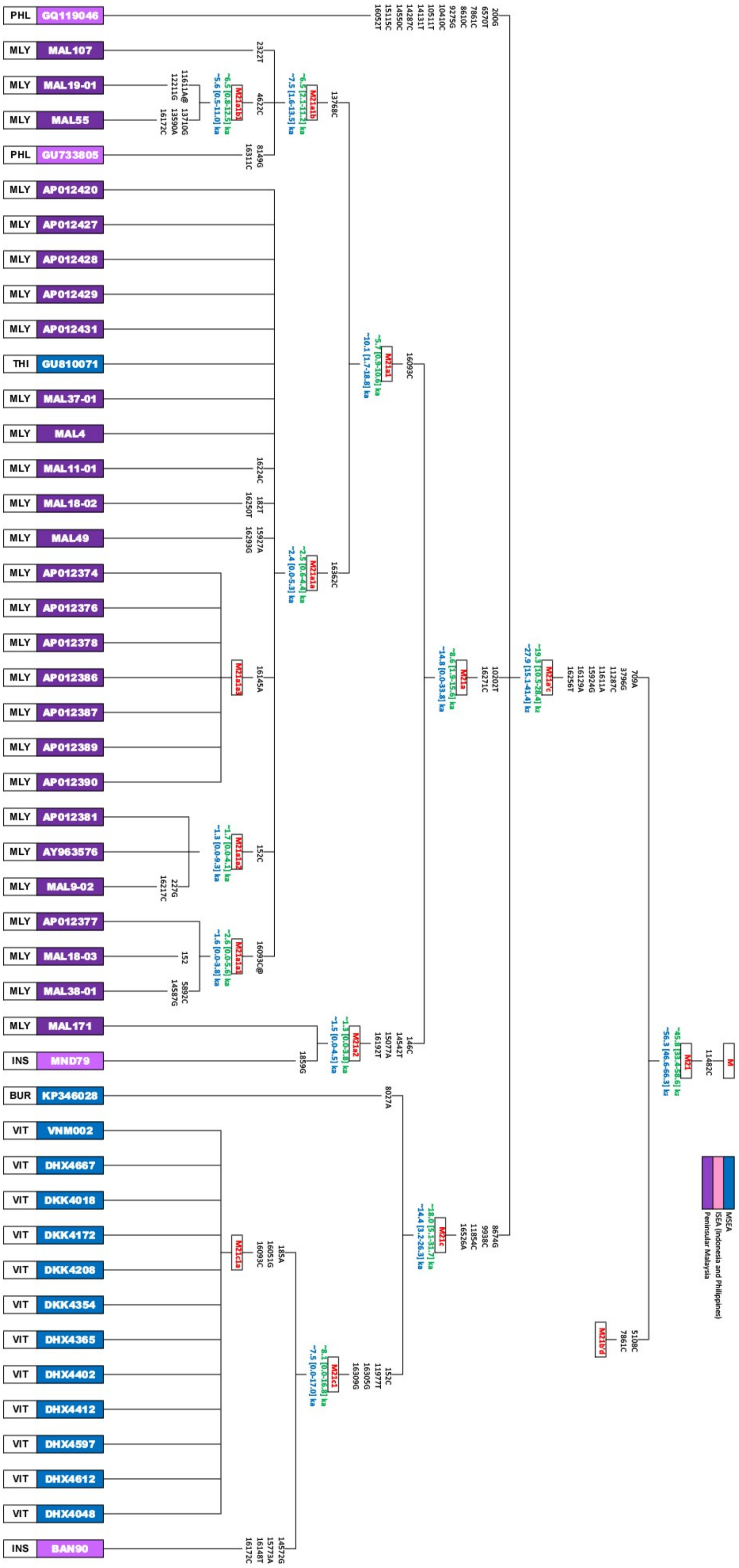


Figure 5656. The tree of haplogroup M21a'c. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (MLY – Peninsular Malaysia, INS – Indonesia, VIT – Vietnam, THI – Thailand, PHL – Philippines and BUR – Myanmar).

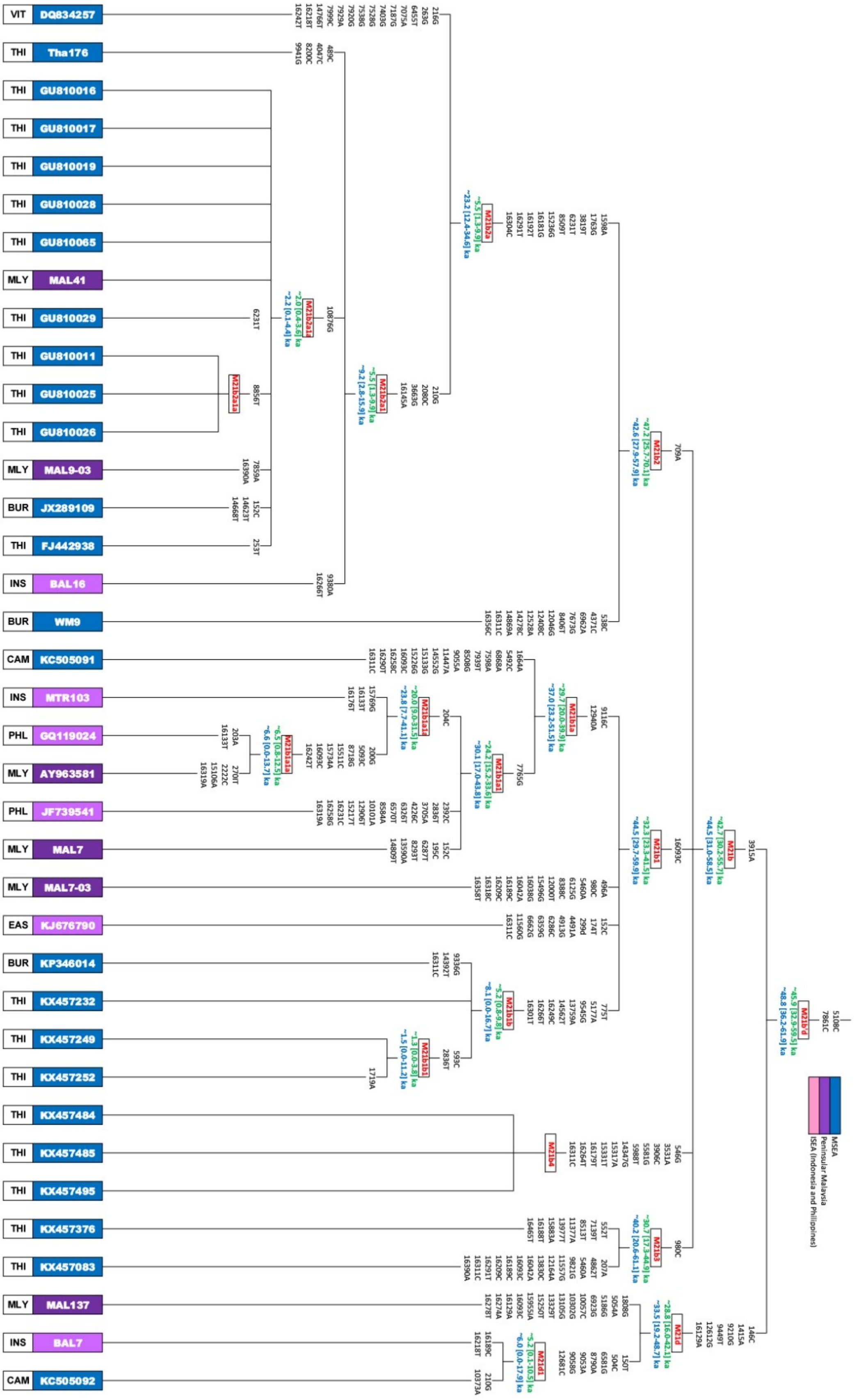


Figure 57. The tree of haplogroup M21b'd. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (MLY – Peninsular Malaysia, INS – Indonesia, BUR – Myanmar, THI – Thailand, CAM – Cambodia and VIT – Vietnam).

4.2.13 Haplogroup M75

M75 (Figure 58) shares a transition at np 12279 with haplogroup M23 in M23’75, and dates to before the LGM (~39 ka). It was reconstructed from 25 complete sequences, and divides into a major subclade, M75a (~24 ka) with a basal lineage from Qinghai in central China (Kong et al. 2011). M75a then divides into M75a1 alongside a basal lineage found in North Laos, and dates with its subclade M75a1a to the end of LGM (~16 ka). M75a1a1, dating to less than 1 ka, is restricted to North Laos, and nested within two basal M75a1a lineages in Northeast Thailand (Kutanan et al 2017) and Qinghai in central China (Kong et al. 2011). This pattern could indicate an ancient ancestor somewhere in China or North MSEA, with high drift and a very recent founder event of bottleneck in Laos.

4.2.14 Haplogroup M24

M24 (Figure 59) is an almost entirely MSEA haplogroup, which shares a transition at np 15601 with the Indian haplogroup M41, and dates to before the LGM, ~29 ka. M24 is divided into two subclades, M24a and M24b, with basal lineages in Vietnam, Thailand and Cambodia in MSEA. M24b is mainly seen in northeast Thailand (Figure 65), dates to ~9.2 ka, and divides into three Late Glacial and postglacial subclades, M24b1 (~14 ka), M24b2 (~7 ka) and M24b3 (~17.5 ka), with basal lineages in Vietnam and northeast Thailand. The latter subclade has a similar ML estimation age to M24b because of the long branch (M24b3a) that is seen in the Austro-Asiatic speakers in north Laos (this study). M24a dates to the early Holocene, and is seen in within Stieng people in South Vietnam, Hmong speakers in North Laos (this study), Sino-Tibetan speakers in Myanmar (Li et al 2015) and Cambodian people (Zhang et al 2013), Peninsular Malaysians (Eng 2014) and in a single Tagbanua individual from the

Philippines. The Tagbanua people are one of the three most common indigenous tribes in the Philippines. They practice a low level of agriculture (Migliano et al., 2007), and in the whole mtDNA (Figure 60) the individual clusters with a Burmese sample (Li et al 2015) in M24a1 (in a small subclade dating to ~4 ka).

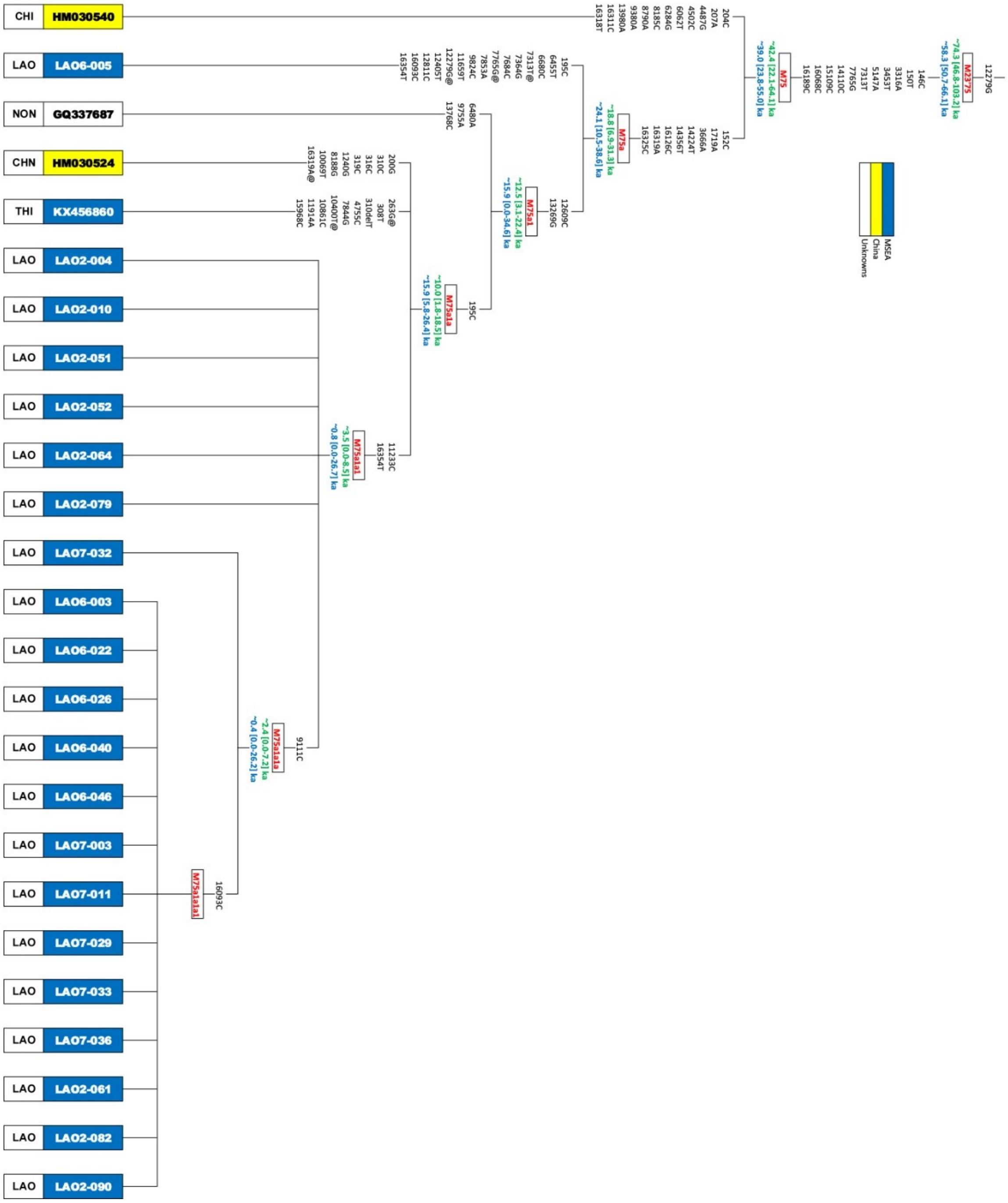


Figure 58. The tree of haplogroup M75. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, THI – Thailand, LAO – Laos and NON – Unknown).

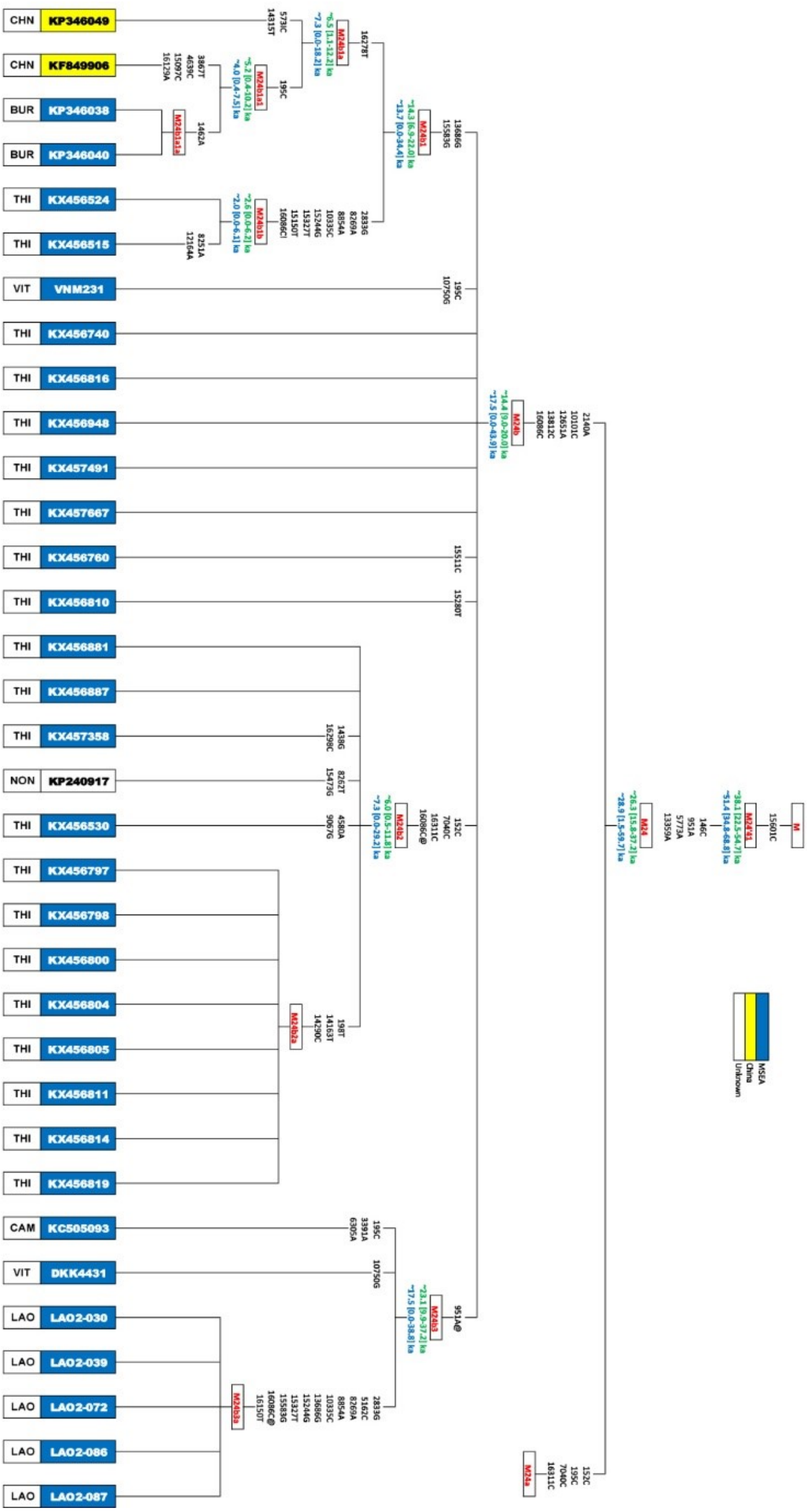


Figure 59. The tree of haplogroup M24b. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, THI – Thailand, LAO – Laos, BUR – Myanmar, and NON – Unknown)

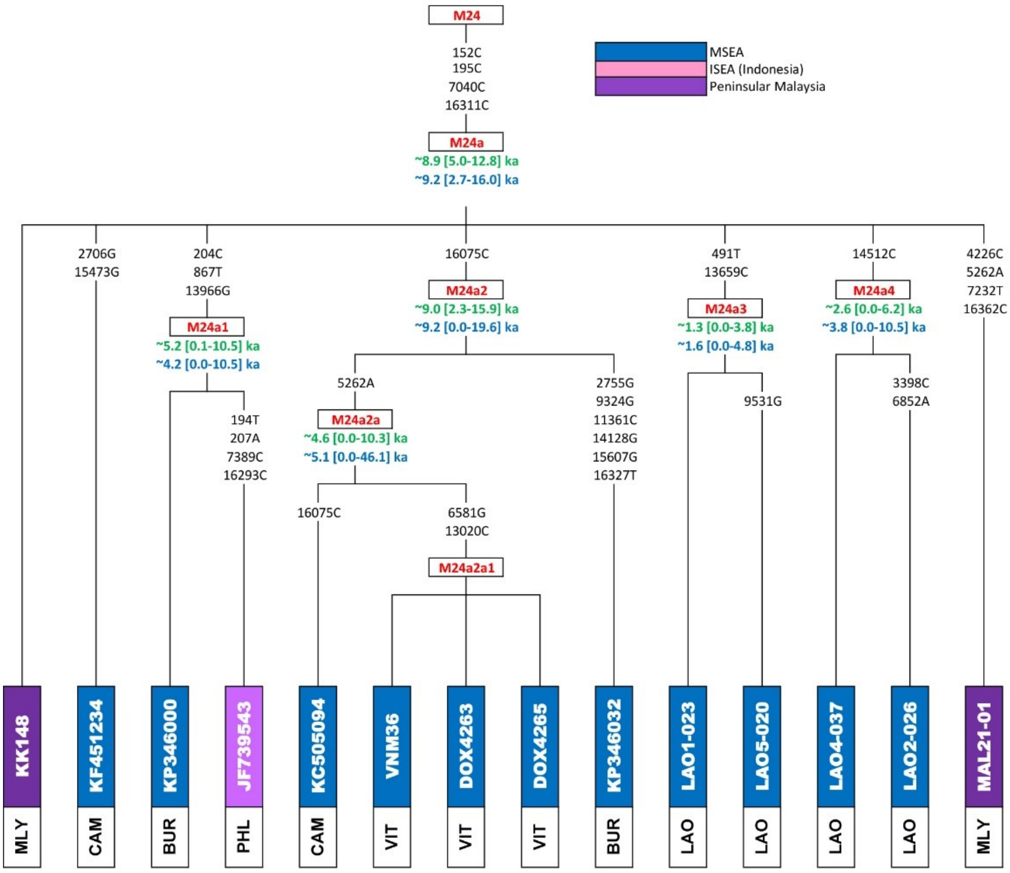


Figure 60. The tree of haplogroup M24a. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (VIT – Vietnam, BUR – Myanmar, LAO – Laos, MLY – Peninsular Malaysia, CAM – Cambodia and PHL – Philippines).

4.2.15 Haplogroup M59

M59 is a basal M haplogroup largely confined to MSEA and the Malay Peninsula (Figure 61), which dates to ~41 ka and divides into a subclade M59a (newly named in this study) and a basal lineage found in Cambodia (Zhang et al., 2013). M59a dates to the end of LGM, ~18 ka, and is subdivided into M59a1, M59a2, M59a3 and M59a4, the latter found in two samples from north Vietnam (this study). M59a1 is restricted to south Vietnam (this study, Mormina, 2007) and dates to only ~2.4 ka.

The largest and oldest subclade is M59a2, which dates to ~14 ka, the time of the first sea-level rise in Southeast Asia, and it is just found in Kedah, Peninsular Malaysia (Eng, 2014) and northern parts of MSEA: northeast Thailand (Kutanan et al., 2017) and north Vietnam (this study). A minor subclade, M59a3, dates to the mid-Holocene, ~6.3 ka, and is seen in Johor, southern Peninsular Malay, adjacent Palembang in south Sumatra (Eng, 2014) and Singapore (Behar et al., 2012).

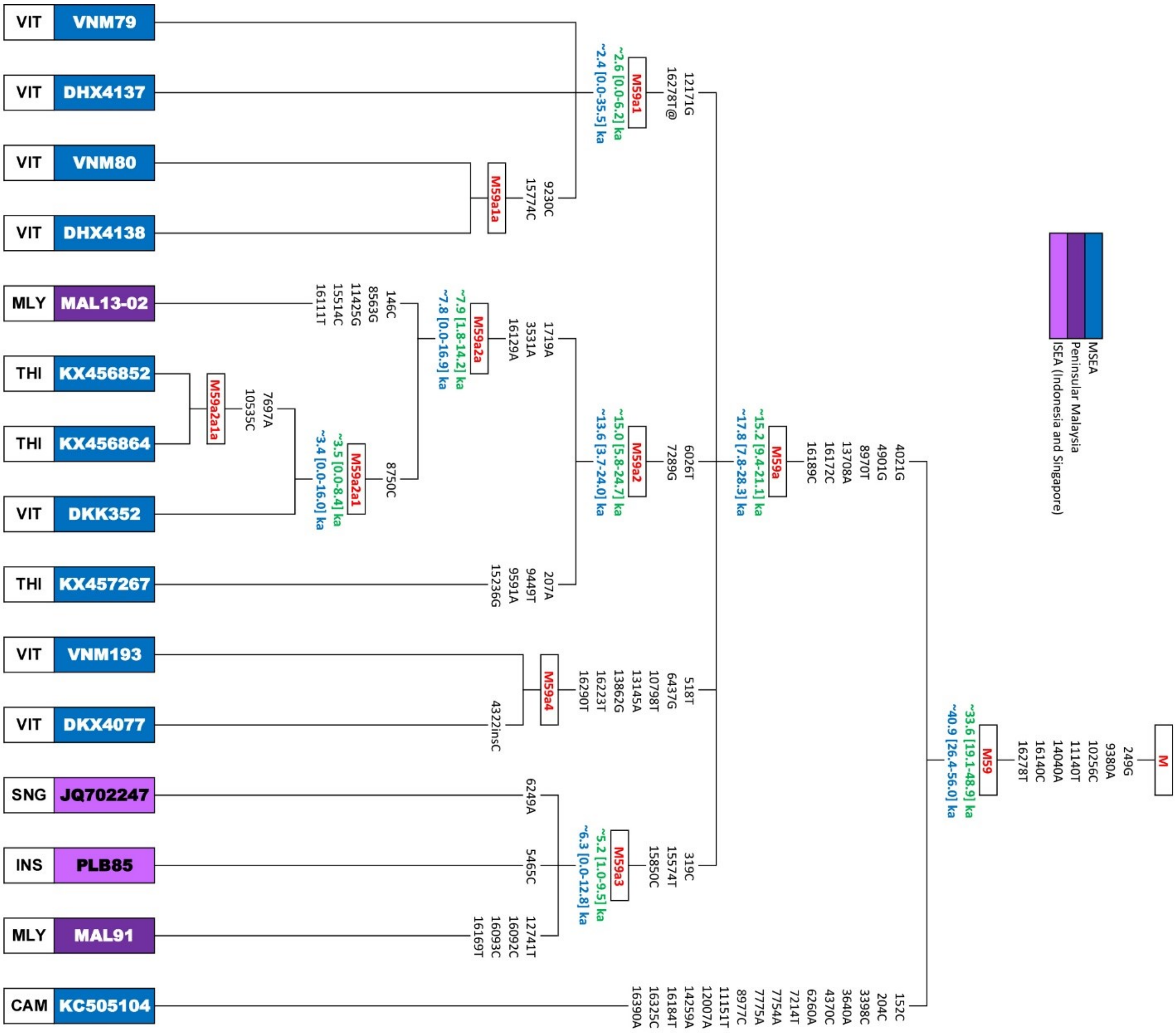


Figure 61. The tree of haplogroup M59. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CAM – Cambodia, VIT – Vietnam, INS – Indonesia, MLY – Malaysia and THI – Thailand).

4.2.16 Haplogroup M69

M69 is very rare basal M haplogroup, defined by transitions nps 4392 and 11365, and dating to ~55 ka (Figure 62). M69 is divided into a major subclade, M69a, and a long basal lineage seen in Sumatra, Indonesia (Gunnarsdóttir et al., 2011). M69a dates to the Late Glacial ~16 ka and divided into M69a1 and a basal lineage found in Thailand. M69a1 dates to only ~2.3 ka, and is restricted to Cambodia, where 12 out of the 14 samples identified carrying M69 to date have been seen.

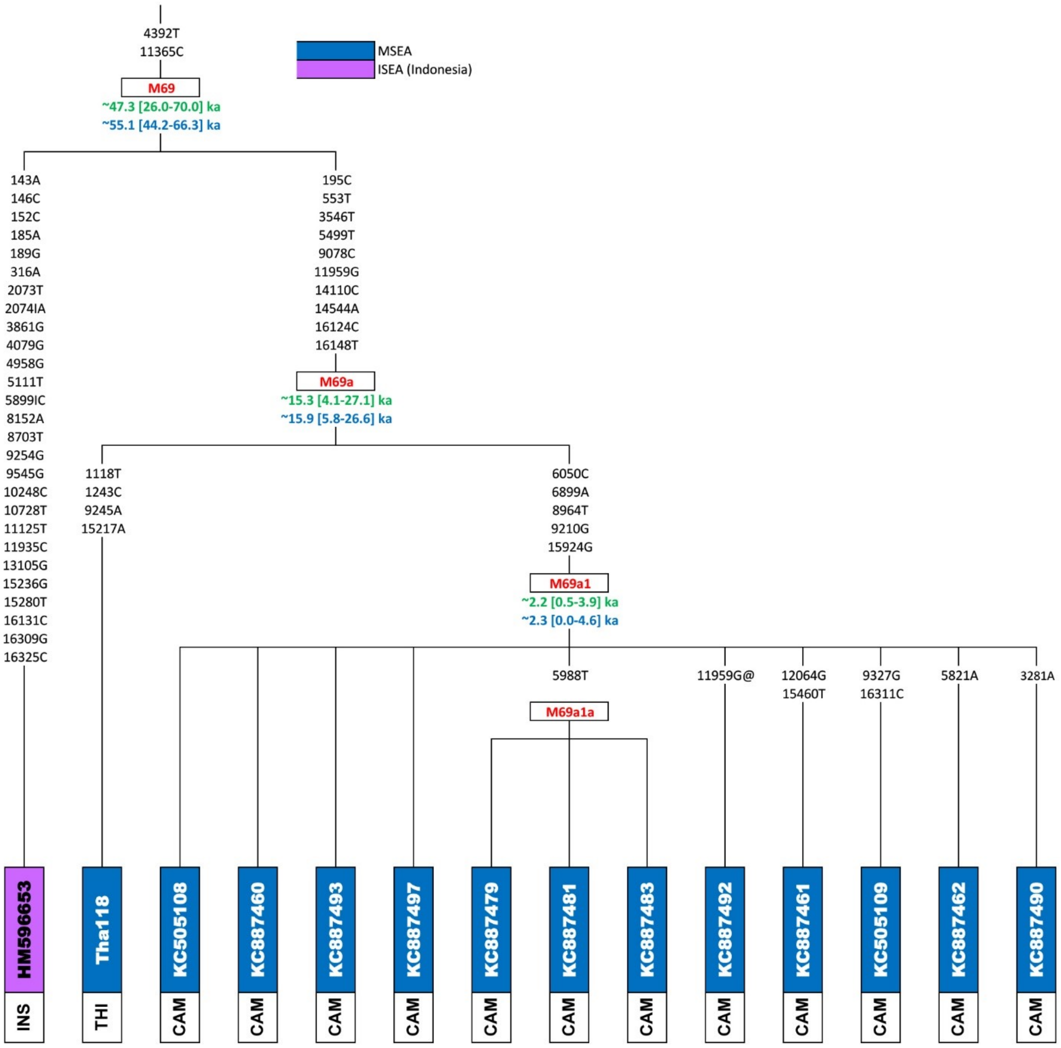


Figure 62. The tree of haplogroup M69. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CAM – Cambodia, INS – Indonesia and THI – Thailand).

4.2.17 Haplogroup M72

M72 is a basal M branch mainly seen in MSEA (Figure 63) that dates to the immediate Late Glacial, ~18 ka, with most branching during the early Holocene. Phylogenetically, M72 is divided into subclades M72a and M72b plus a single basal lineage found in

South China (Kong et al., 2011). M72a is dated to the early Holocene ~11 ka and divides into the major M72a1 (dates to ~ 7.7 ka) and the minor M72a2 (dates to only ~1.7) and M72a3 (dates to only ~1.5 ka) with a basal M72a lineage is found in the Philippines (Tabbada et al., 2009). M72a1 is confined mainly to MSEA: northeast Thailand, Central Laos (Kutanan et al., 2017), south Vietnam (this study), north Vietnam (Peng et al., 2010), Cambodia (Lippold et al., 2014), Myanmar (Summerer et al., 2014) and north Peninsular Malaysia (Eng, 2014). M72a2 is found in Mataram in eastern Indonesia and Negeri Sembilan, western Peninsular Malay (Eng, 2014). M72a3 is seen only in northeast Thailand (Kutanan et al., 2017).

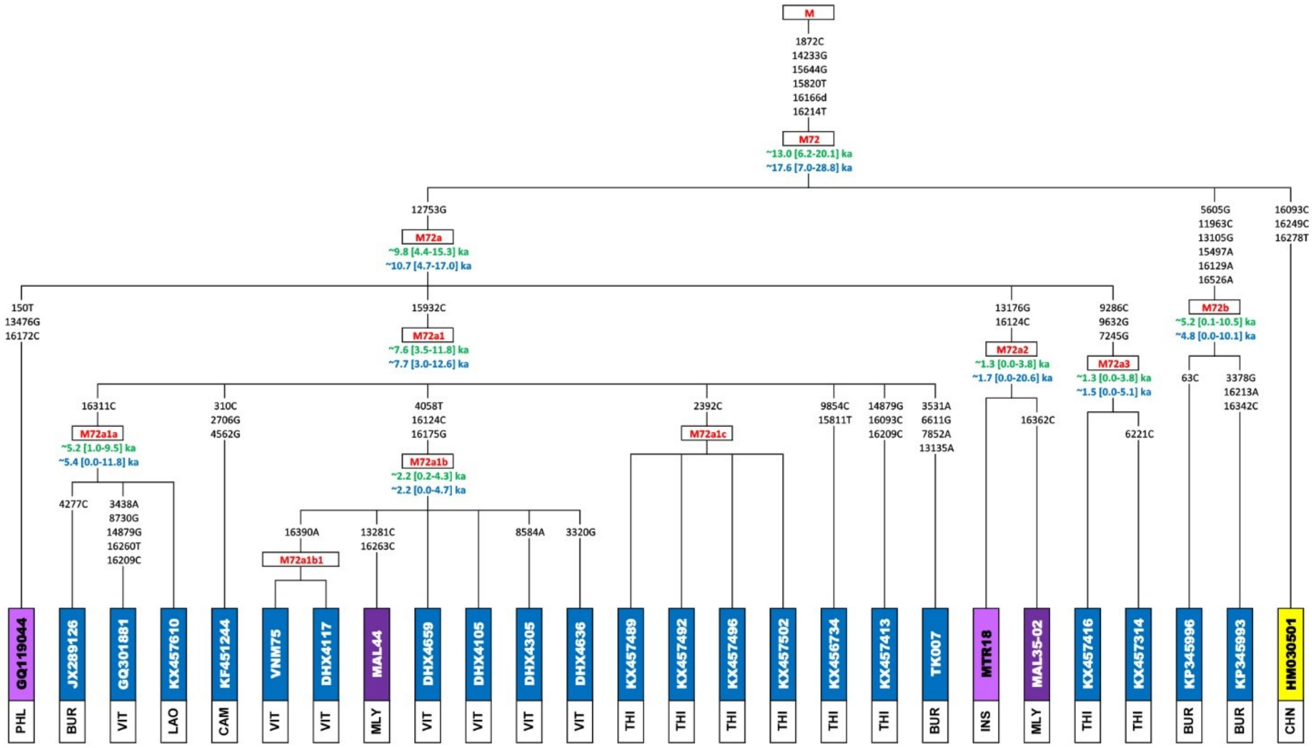


Figure 63. The tree of haplogroup M72. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, LAO – Laos, CAM – Cambodia, PHL – Philippines and THI – Thailand, INS – Indonesia, MLY – Peninsular Malaysia and BUR – Myanmar).

4.2.18 Haplogroup M73’79

M73’79 is a basal Sunda lineage, expanding widely and early in southeast Asia (Figure 64), putatively dating to ~59 ka, and is composed of two haplogroups M73 and M79 that share only a transition at np 16278. Since this is a fast-evolving HVS-I site (Soares et al., 2009), it is not clear if these two haplogroups are genuinely connected in this way.

M73 is an ancient haplogroup dating to ~43 ka and subdivided into three subclades M73a (~38 ka), M73b (~25.6 ka) and M73c (~2.2 ka). M73b is dated to before the LGM and divided into M73b1 (~27 ka) and two basal roots in Sumatra, western Indonesia and adjacent Peninsular Malaysia (Eng, 2014). M73b1 is dated to the early LGM and is seen in south Vietnam (this study; Peng et al, 2010), Cambodia (Zhang et at al 2013), western Peninsular Malaysia, Borneo (Eng, 2014) and Indonesia (Tabbada et al., 2009). M73a dates to the early LGM as well, and is seen in Philippines (Tabbada et al., 2009), Indonesia, East Timor (Gomes et al., 2015), and in Vietnam. Unusually, one M73a2 lineage clustering with a sample from Timor reaches Papua New Guinea. M73c dates to the early Bronze Age and is restricted to Northeast Thailand (Kutanan et al., 2017) and north Vietnam (this study). The long branches and dating of M73c reflect heavy genetic drift across the LGM and into recent times, especially in MSEA.

M79 is a very rare haplogroup (Figure 65), divided into two subclades. M79a and M79b (newly named in this study). and dated to the LGM, ~20.5 ka. M79a dates to only 900 ya, and is M79a is restricted to north Vietnam (this study) and northeast Thailand (Kutanan et al., 2017), and again the disparity in branch lengths within M79 likely reflects very high levels of genetic drift. M79b is defined by a transition np 16262, dates to the Late Glacial, ~17 ka, and is seen in Yunnan, South China (Kong et al., 2011) and Java, Indonesia (Eng, 2014).

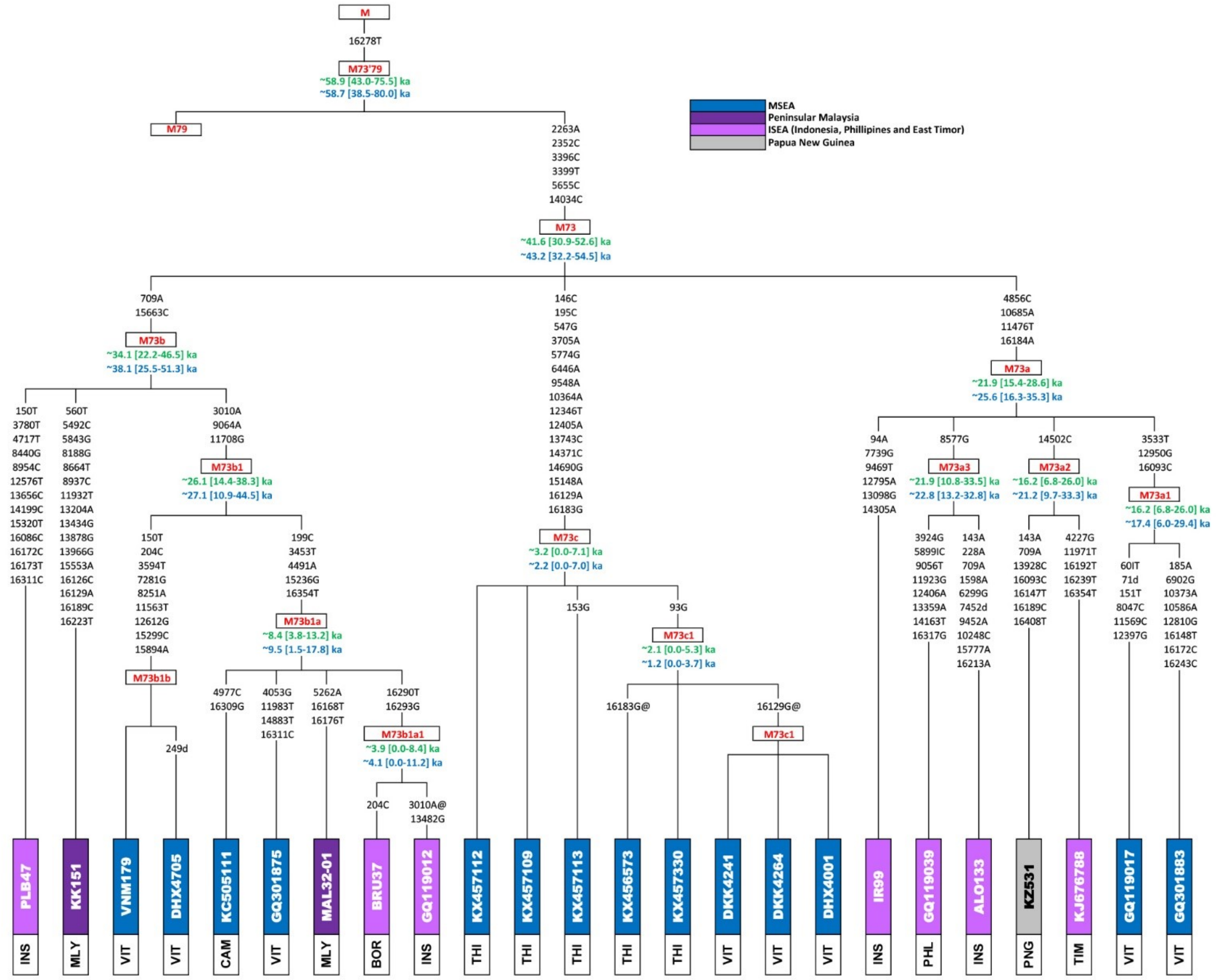


Figure 64. The tree of haplogroup M73. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CAM – Cambodia, VIT – Vietnam, INS – Indonesia, PNG – Papua New Guinea, MLY – Peninsular Malaysia, PHL – Philippines, and THI – Thailand; TIM – East Timor).

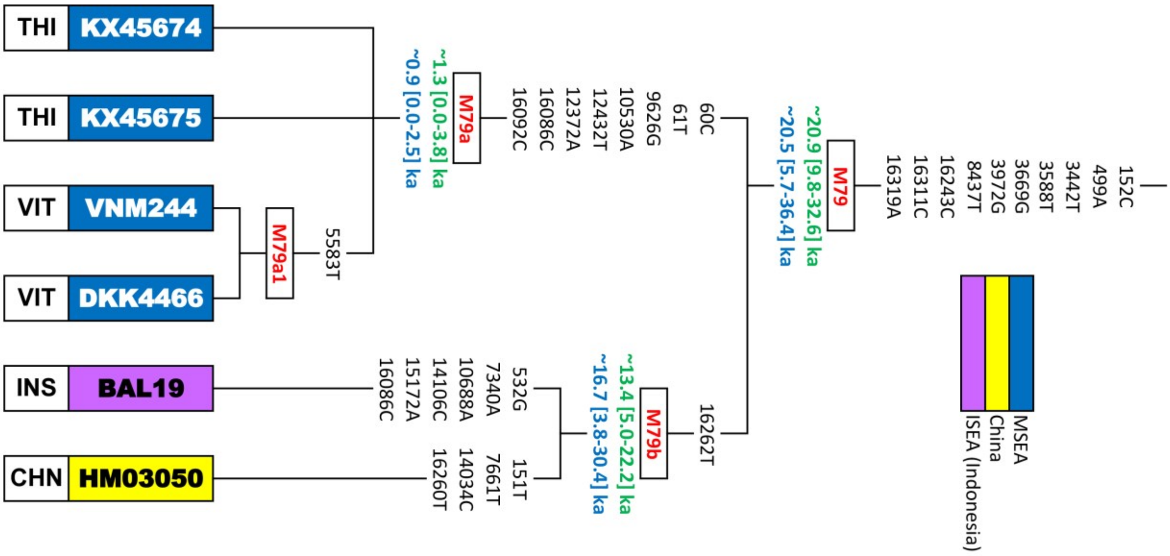


Figure 65. The tree of haplogroup M79. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, INS – Indonesia and THI – Thailand).

4.2.19 Haplogroup M74

M74 shares a transition at np 8251 with M42 to define a putative M42'74 nodes (Figure 66), that would date to ~58.4 ka. M42 is mainly found in aboriginal Australians (Ingman et al., 2000), while M74 is a Sunda haplogroup commonly seen in MSEA and ISEA. However, 8251 is a very fast-evolving site (P. Soares et al., 2009), so the link may well be spurious.

M74 dates to ~41 ka and it is subdivided into three subclades M74a (~12.4), M74b (~28.6 ka) and M74 (~6.4 ka). M74a dates to late Pleistocene age, and it is divided into M74a1 and M74a2. M74a1 dates to the Neolithic age (~5 ka) and it is confined south Vietnam (1KGP) and north Laos (this study). M74a2 dates to early Holocene (~9.5 ka), and found mainly in north MSEA: north Vietnam, north Laos (this study), northeast Thailand (Kutanan et al., 2017) and South China (Kong et al., 2011; Li et al., 2016).

M74b (Figure 67a) dates to before the LGM, and is subdivided into three subclades M74b1, M74b2, M74b3. The latter subclade dates to the end of the LGM (~19.3 ka), and is seen mainly in MSEA (this study; Kutana et al., 2017) with one basal Chinese M74b3a lineage (Kong et al., 2011) (~8.5 ka) nesting some Thai lineages (M74b3a1). Both M74b1 and M74b2 are found in ISEA and MSEA, and they date to ~10 ka and ~12.6 ka respectively.

The overall nesting pattern for M74 suggests Late Glacial and postglacial expansions in MSEA with some mid-Holocene expansions into ISEA.

4.2.20 Haplogroup M76

M76 is a basal M haplogroup, dating to ~34.6 ka, and it is subdivided into two subclades M76a and M76b (Figure 68). Although it is very rare, M76 is found in South China and the Sunda region, especially MSEA, where it is likely to have originated. M76a dates to before the LGM (~30 ka), and divides into M76a1 and a basal branch found in Bali, Indonesia (Eng, 2014). M76a1 dates to the Late Glacial (~17.6 ka) and is seen in north Thailand (Kutanan et al 2017), Cambodia (Zhang et al 2013) and South China (Kong et al. 2011). M76b is mainly found in MSEA: south Vietnam (this study), north Thailand (Kutanan et al 2017) and Myanmar (Li et al 2015). It dates to ~ 29.4 ka and divides into M76b1 and a long-branched basal lineage seen in Guizhou, South China (Kong et al. 2011). Overall, M76 seems to have an origin in MSEA/South China and once again, like so many of the basal M haplogroups in MSEA, shows signs of high level of genetic drift.

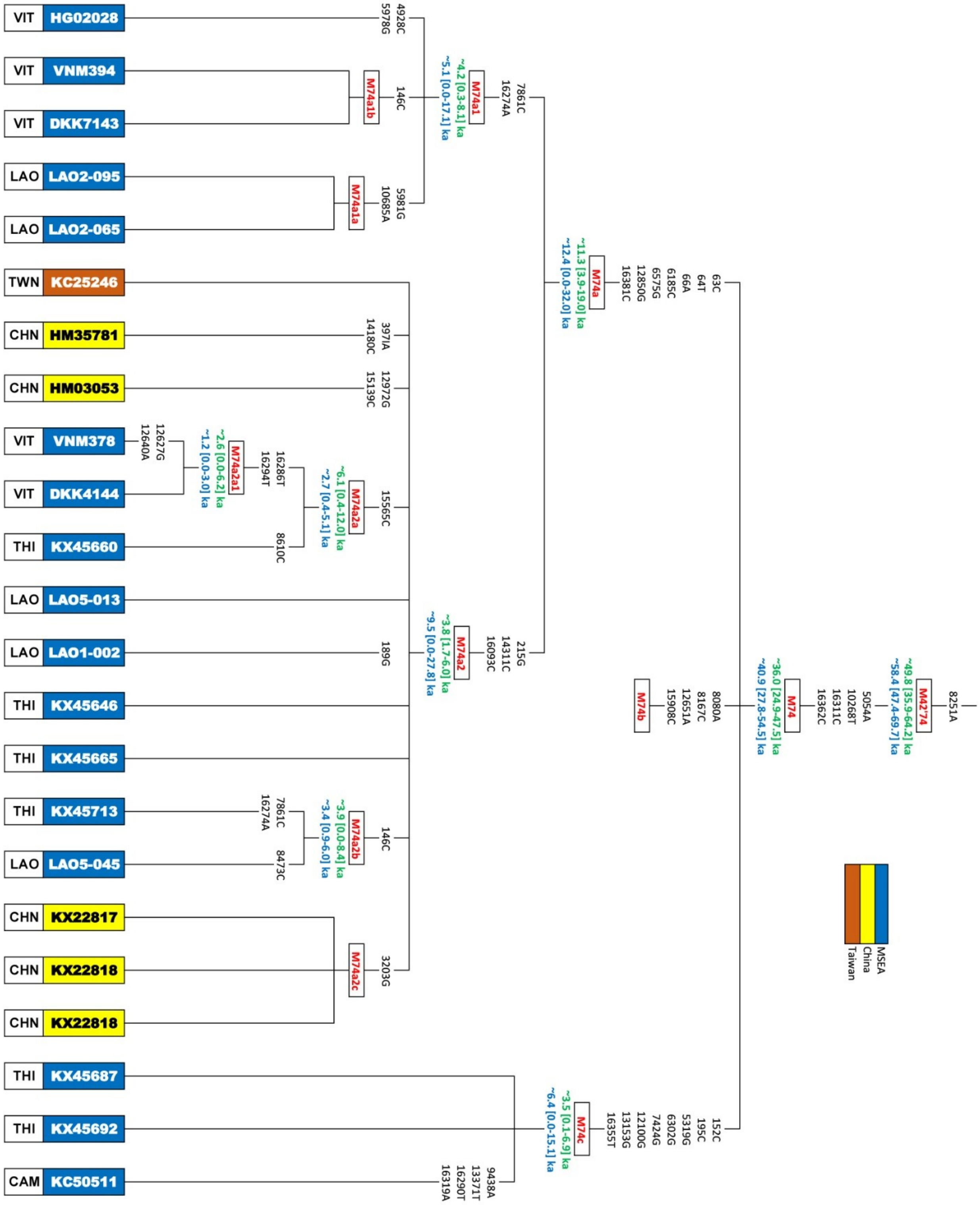


Figure 66. The tree of haplogroup M74. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, TWN – Taiwan, LAO – Laos, CAM – Cambodia, and THI – Thailand).

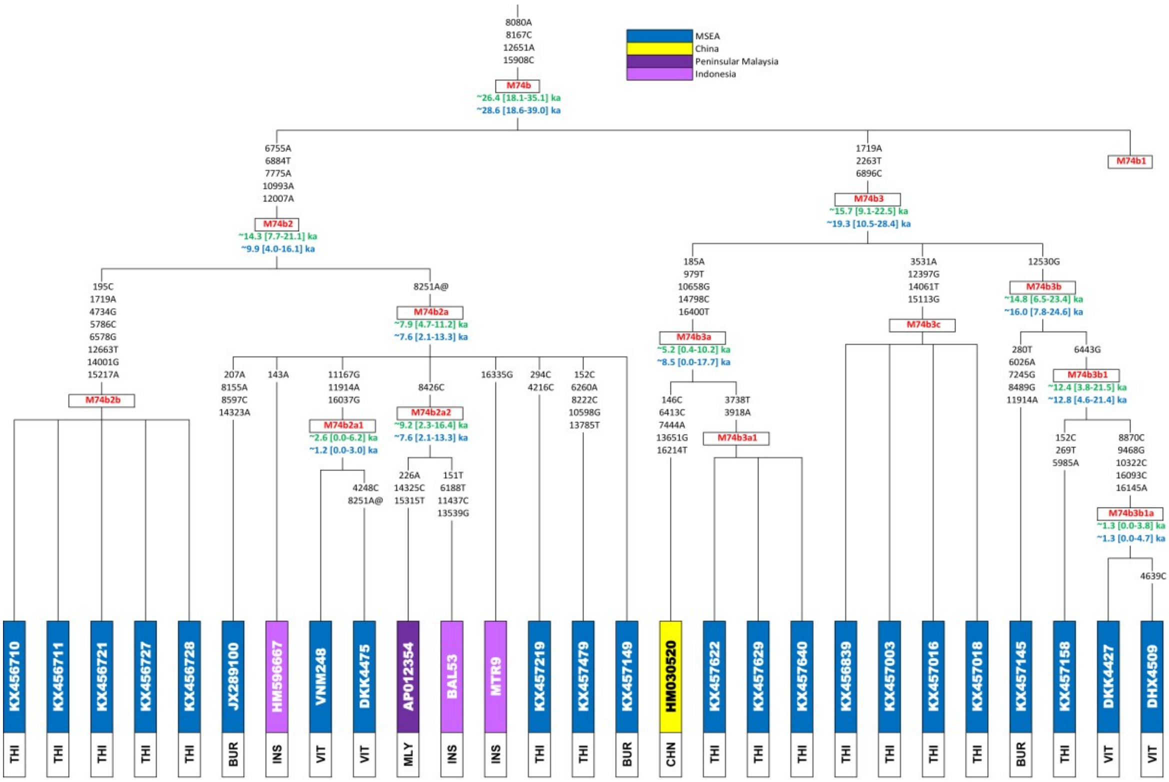


Figure 67a. The tree of haplogroup M74b. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, LAO – Laos, MLY – Peninsular Malaysia, PHL – Philippines, BUR – Myanmar, and THI – Thailand).

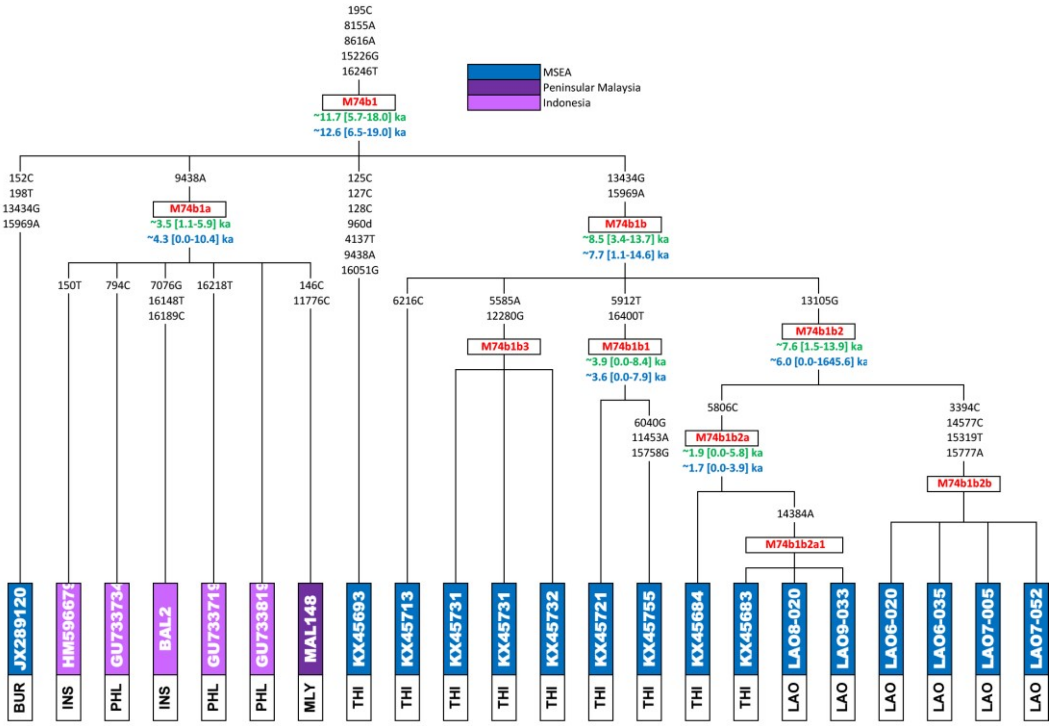


Figure 67b. The tree of haplogroup M74b1. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (VIT – Vietnam, LAO – Laos, MLY – Peninsular Malaysia, PHL – Philippines, BUR – Myanmar, and THI – Thailand).

4.3 Haplogroup N

Haplogroup N is characterized by transitions at coding region nps 8701, 9540, 10398 and 10873, and a reversion at np 15301. In Southeast Asia, this haplogroup includes some branches such as: N7 (Zhang et al., 2013), N9 (Tanaka et al., 2004; Metspalu et al., 2006; Derenko et al., 2007), N10 (Kong et al., 2011), N21, N22 (Macaulay et al., 2005; Hill et al., 2007; Tabbada et al., 2009), and subclades of haplogroup R.

4.3.1 Haplogroup N7

N7 is a basal N haplogroup seen only in Cambodia (Zhang et al., 2013), with an estimated age of ~36.4 ka (Figure 69) and it is defined by transitions at nps 723, 11617, 13542, 14668, 15945, 16129 and a transversion at np G6570T. N7 is divided into N7a and N7b. N7a has an estimated age of ~14.6 ka and can be further divided into two several sub-branches. N7b is a younger branch than N7a, dating to ~1.2 ka.

4.3.2 Haplogroup N8

N8 is a basal N haplogroup that has a long internal branch, resulting in a divergence time of ~21 ka (Figure 70). The N8 tree is reconstructed from 14 complete mtDNA sequences. It is defined by transitions at nps, 3027, 7885, 2760, 8188, 10398, 7961, 13710, 16263, 16311, 16274, 16357 and 16343. N8 is mostly found in Sundaland region, and it is largely therefore a Sundaic lineage. The deeper lineages are found in northern Mainland SEA, especially in north Thailand and Vietnam, and it therefore seems to have an origin in North Mainland SEA and then migrated into Island SEA.

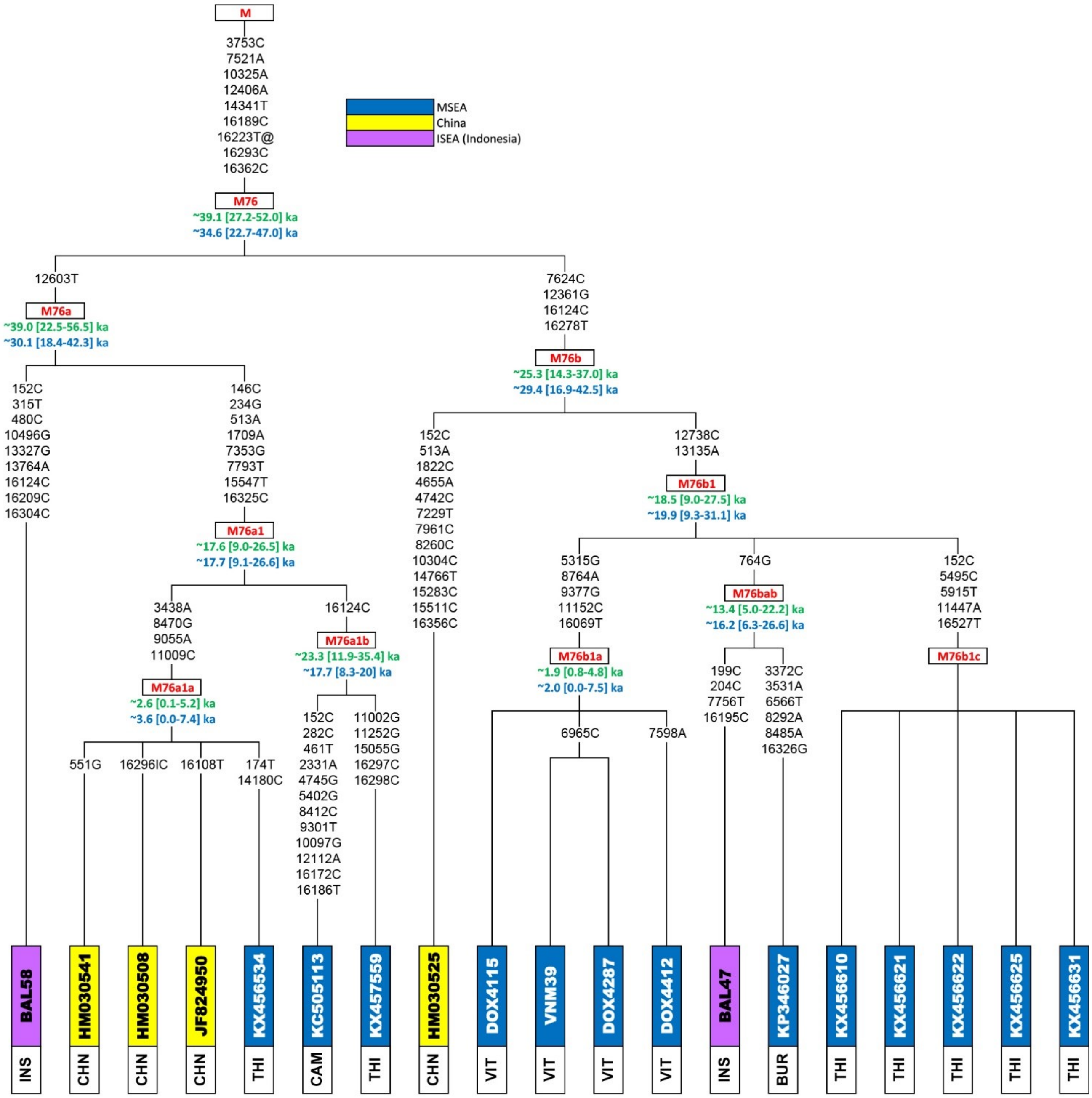


Figure 68. The tree of haplogroup M76. Age estimates (in ka) displayed are ML (in blue) and averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, INS – Indonesia, CAM – Cambodia, and THI – Thailand).

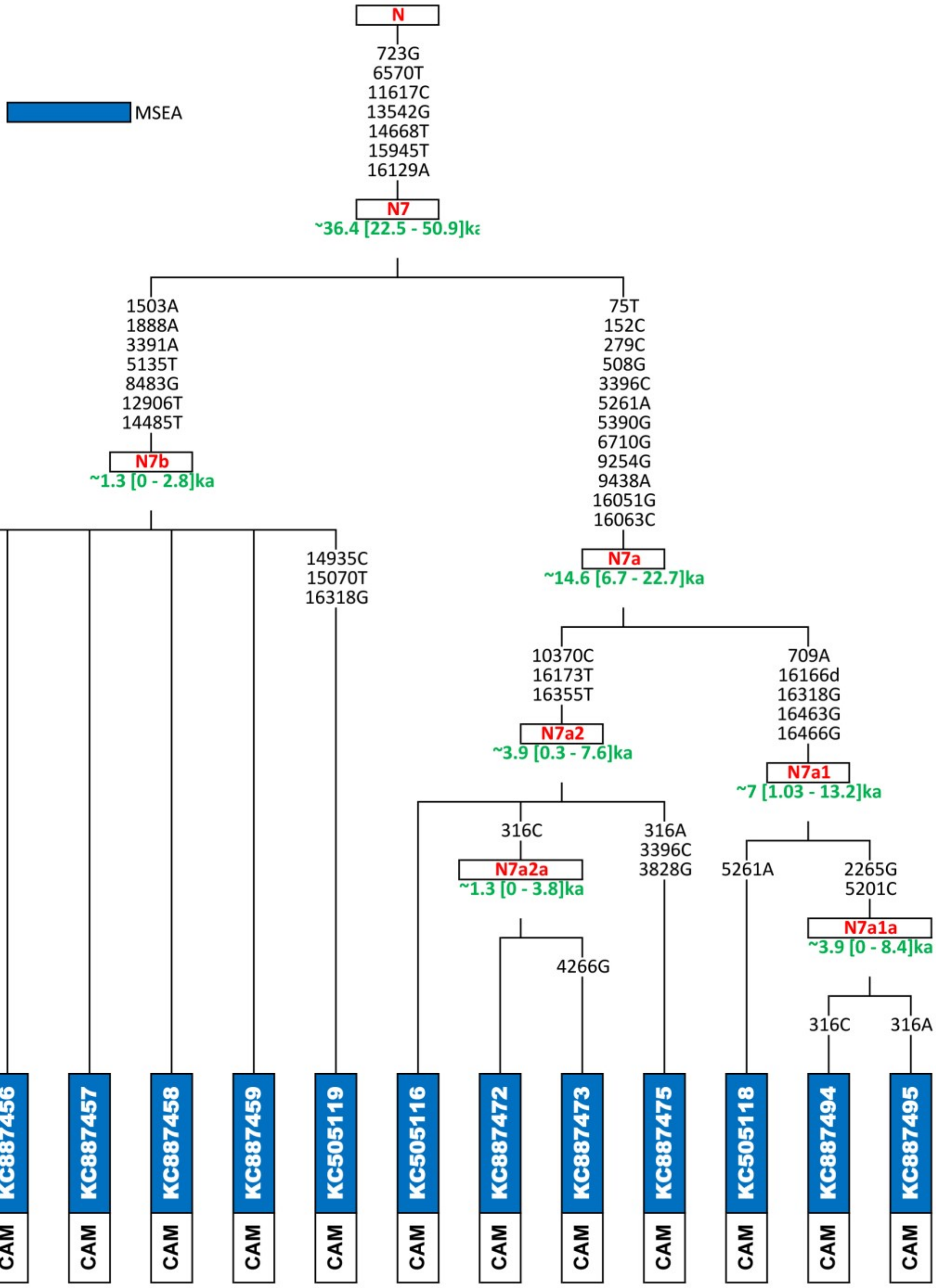


Figure 69. The tree of haplogroup N7. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CAM – Cambodia).

N8 is divided into N8a and N8b; both are defined here for the first time. N8a is characterised by np 16357C, dating to ~19 ka, which can be further divided into two subclades. It is seen mostly in north Thailand and at lower levels in Vietnam, south China and Indonesia. N8b is defined by transitions at nps 195C, 5120G, 10129A and 16318T, with an estimated date of ~2.6 ka, and it is found in Thailand and Myanmar.

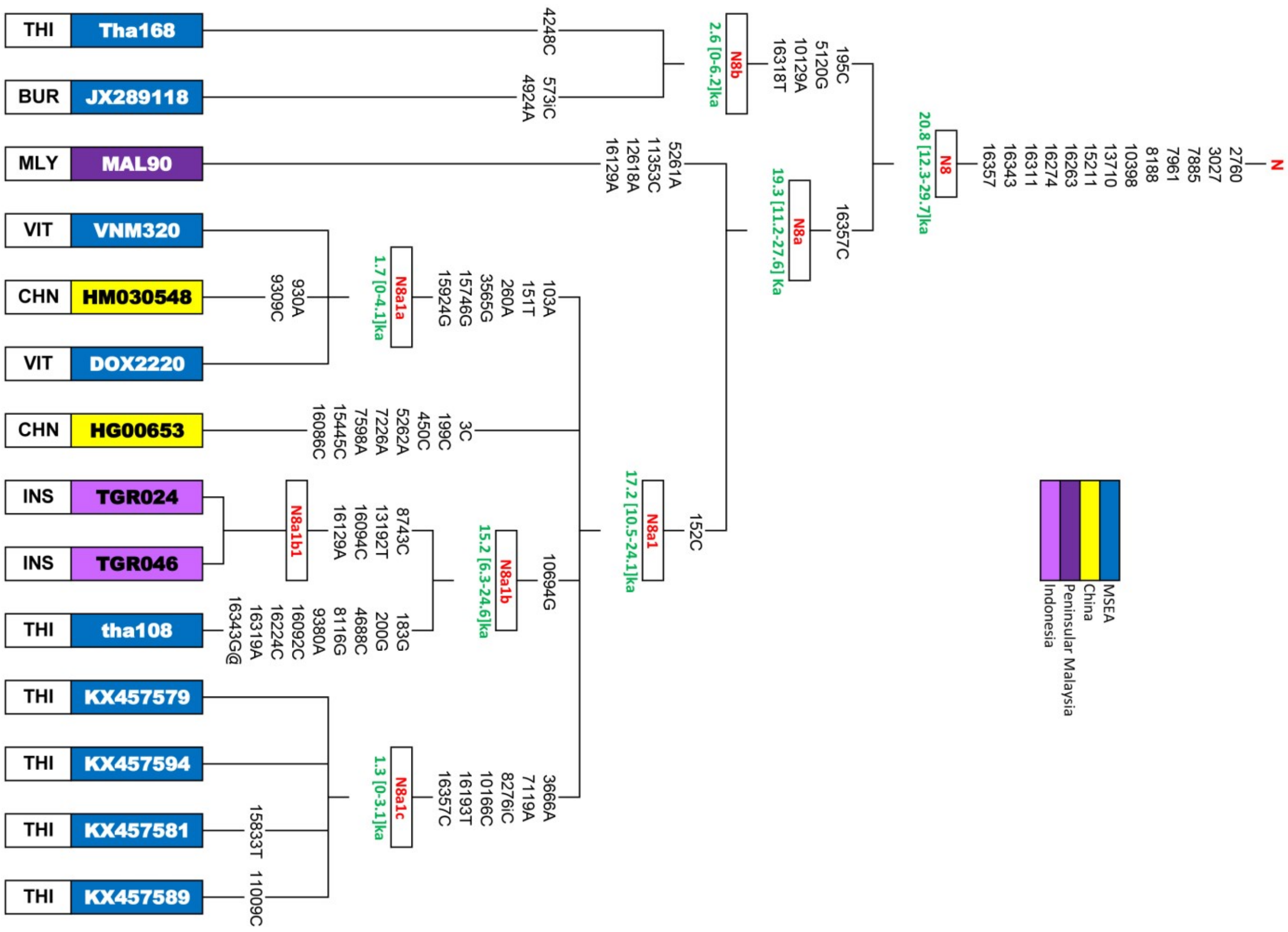


Figure 70. The tree of haplogroup N8. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI - Thailand, MLY - Malaysia, INS - Indonesia, VIT – Vietnam, BUR - Myanmar).

4.3.3 Haplogroup N9

Haplogroup N9, which is widespread in East Asia, is characterized by a transition at np 5417 and dates to ~ 37.5 ka (Figure 71) with three main sub-haplogroups; N9a, N9b and Y. The N9 tree includes a total of 448 complete mtDNA sequences. Most of the subclades are commonly found in Japan and China, with the deepest branches in China, which could suggest an origin in China. The exceptions are N9a6 and N9a10 which are found mostly in Mainland and Island SEA, and N9b, which has found mainly in Japan.

N9a dates to ~18 ka and includes nine subclades, seven of which are already known (N9a1’3, N9a2’4’5, N9a6, N9a7, N9a8, N9a9 and N9a10), while there are two subclades newly named in this study as N9a11 and N9a12 (Kutanan et al., 2017; C.-Y. Wang & Zhao, 2012) (Figure 71). N9a1’3 is defined by a single control-region transition at np 16129, and dates to ~16.5 ka. It contains two subclades, N9a1 and N9a3, both of which are commonly found in East Asia. N9a1 dates to ~7.1 ka and is commonly found in south China (Kong et al., 2003; Tanaka et al., 2004; Zheng et al., 2011; Ji et al. 2012; Lippold et al 2014). N9a3 (Figure 72) dates to ~14.8 ka, and has been reported mainly in China, Japan and south Siberia (Tanaka et al., 2004; Zheng et al., 2011; Derenko et al., 2012).

Within MSEA, N9a6 and N9a10 are commonly found in Vietnam, Thailand and Laos (this study; Peng et al., 2010; Kutanan et al., 2017). N9a6 is characterized by transitions at nps 4856 and 16292, and it dates to ~12.4 ka (Figure 73 and 74). N9a6 is found mainly in three regions; MSEA (Vietnam and Thailand), Peninsular Malaysia and Indonesia. It includes six subclades: N9a6a, N9a6b, N9a6c, N9a6d, N9a6e and N9a6f. The latter four subclades are newly named in this study and are commonly found in Vietnam (this study) and Thailand (Kutanan et al., 2017).

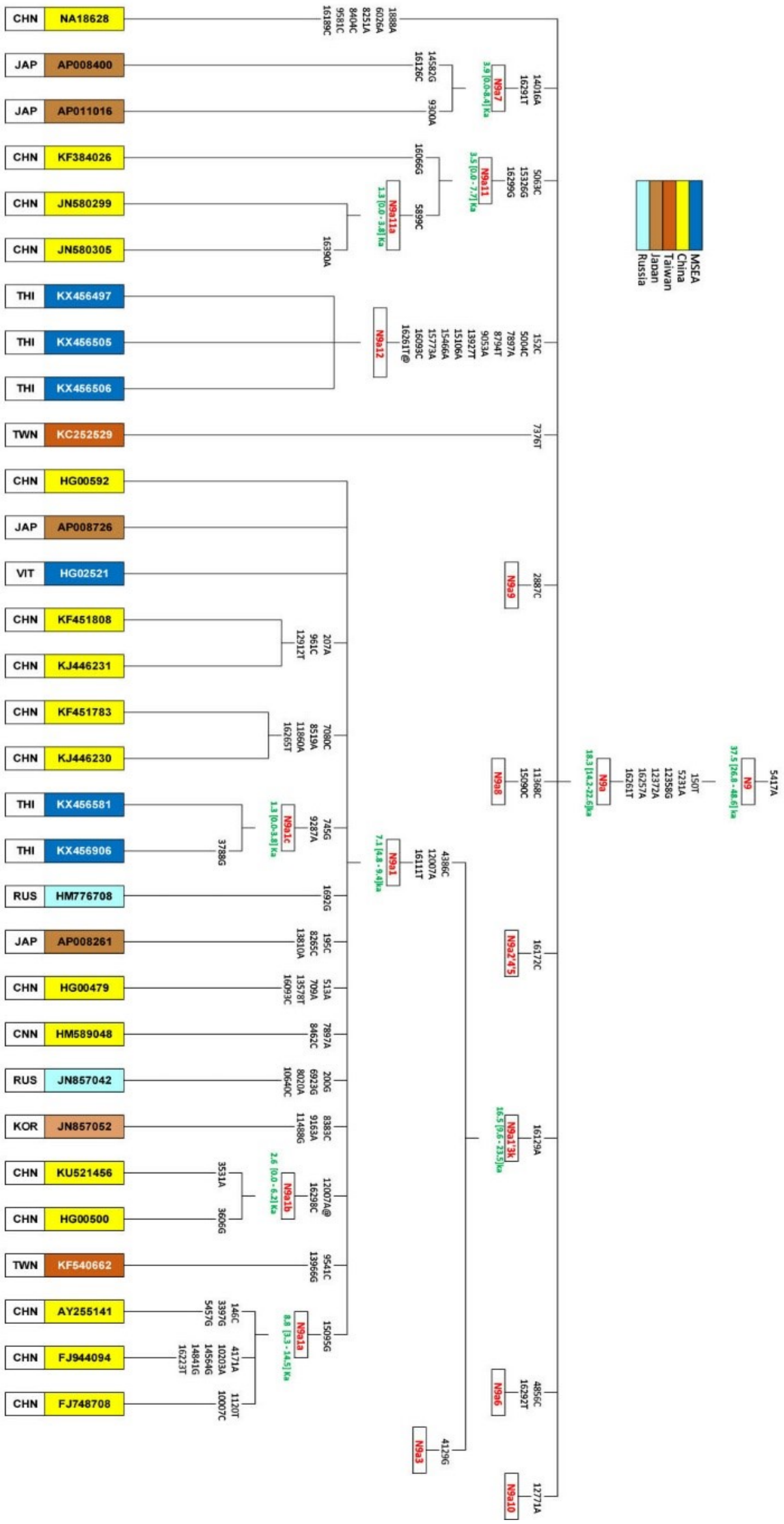


Figure 71. The tree of haplogroup N9a. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand, VIT – Vietnam, Jap – Japan and TWN – Taiwan, RUS – Russia).

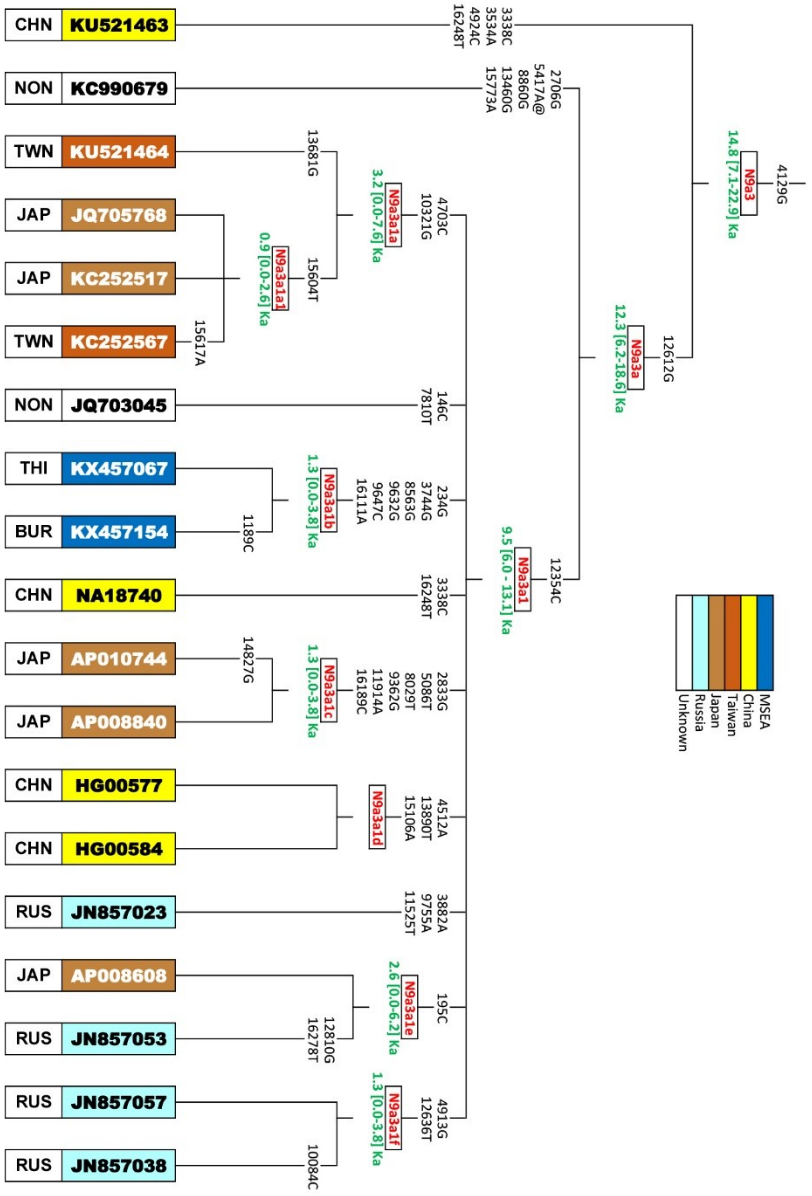


Figure 72. The tree of haplogroup N9a3. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI - Thailand, Jap – Japan, BUR - Myanmar, RUS – Russia, NON – Unknown and TWN – Taiwan).

The subclade N9a6a dates to ~12.5 ka, and is mainly found in MSEA (Vietnam, Cambodia and Thailand), Indonesia (Sumatra) and Peninsular Malaysia (Gunnarsdóttir et al., 2011; Jinam et al., 2012; Kutanan et al 2017). N9a6b dates to only ~0.2 ka and is only found in the Aboriginal Malaysian people (Jinam et al., 2012).

N9a6 seems to have dispersed southwards ad eastwards from MSEA, where it may have originated, during the early Holocene period ~12 ka, with some mid-Holocene gene flow into Indonesia.

N9a10 dates to ~15.6 ka, with the deepest-branching lineage found in Vietnam (this study), Taiwan (Ko et al., 2014) and South China (Zheng et al., 2011), and it comprises four main subclades; N9a10a, N9a10b, N9a10c and N9a10d (Figure 75). The subclade N9a10a, dating to ~8.1 ka, is seen among the Austronesian speakers in Taiwan and the Philippines (Loo et al., 2011; Ko et al., 2014). The latter subclade's age could coincide with early proto-Austronesian arrivals from the north (South China), spreading rapidly to the south, during the putative Neolithic expansion ~4 ka (Ko et al., 2014).

N9a10b is defined by a reversion mutation in the control region at np 16311, dated to ~12 ka (Figure 76), and is seen mainly in MSEA (particularly Thailand and Laos) and South China. N9a10b consists of three main subclades: N9a10b1, N9a10b2 and N9a10b3. The latter subclade dates to ~0.6 ka, restricted to the Lao samples (this study), while N9a10b1 is dated to the early Holocene age (~11.3 ka), restricted to the Thai samples (Kutanan et al., 2017), and N9a10b2 to the middle Holocene age ~8 ka and restricted to the Chinese samples (Jiang et al., 2014).

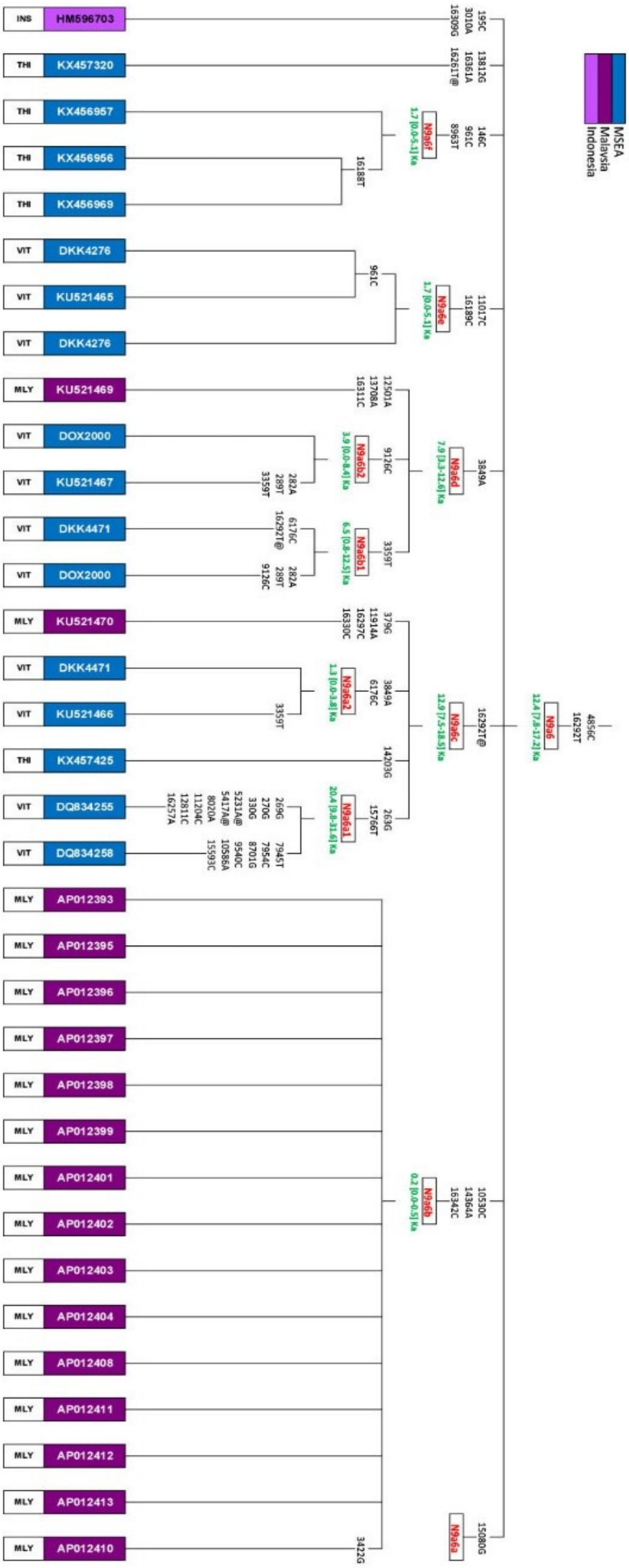


Figure 73. The tree of haplogroup N9a6. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (THI - Thailand, MLY – Peninsular Malaysia, VIT – Vietnam and INS - Indonesia).

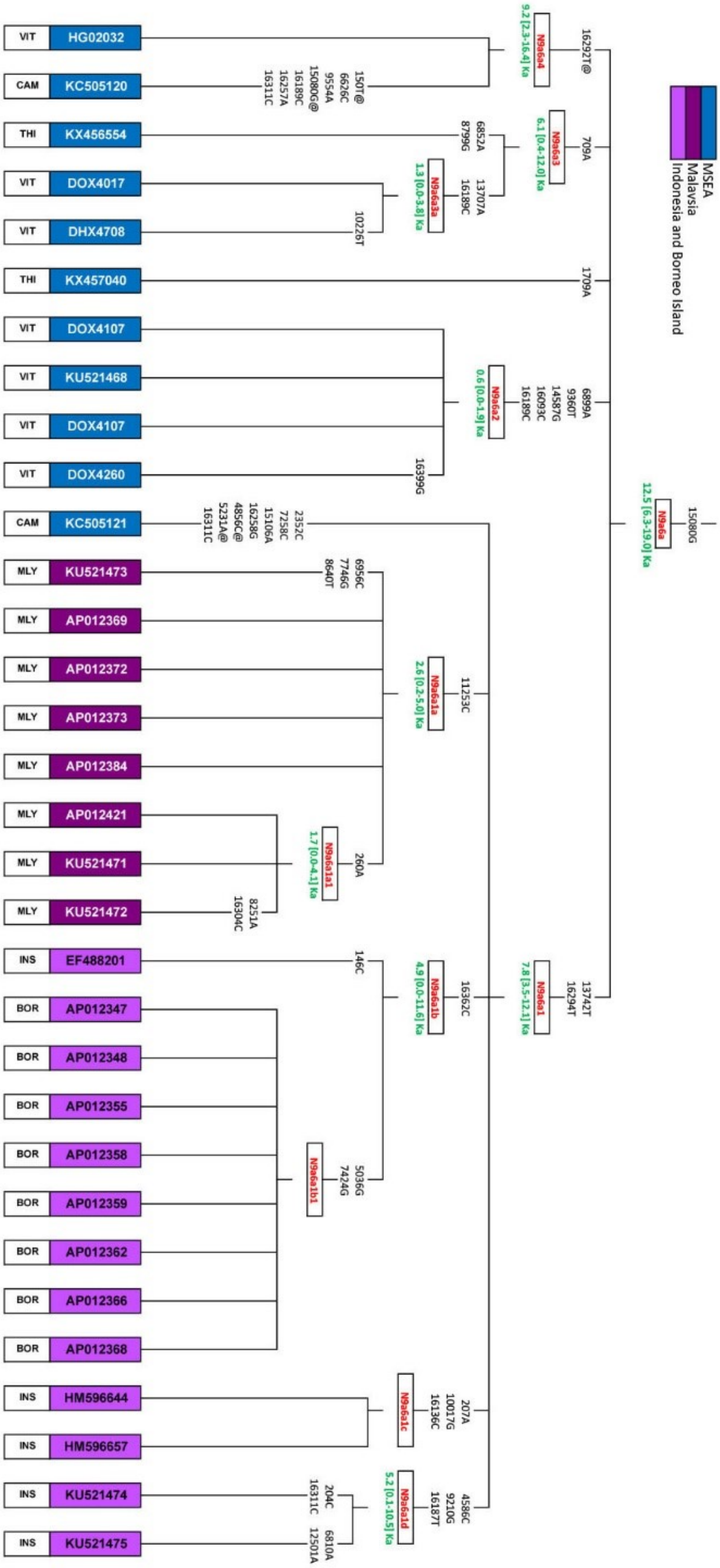


Figure 74. The tree of haplogroup N9a6a. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (THI - Thailand, MLY – Peninsular Malaysia, VIT – Vietnam, CAM – Cambodia and INS - Indonesia).

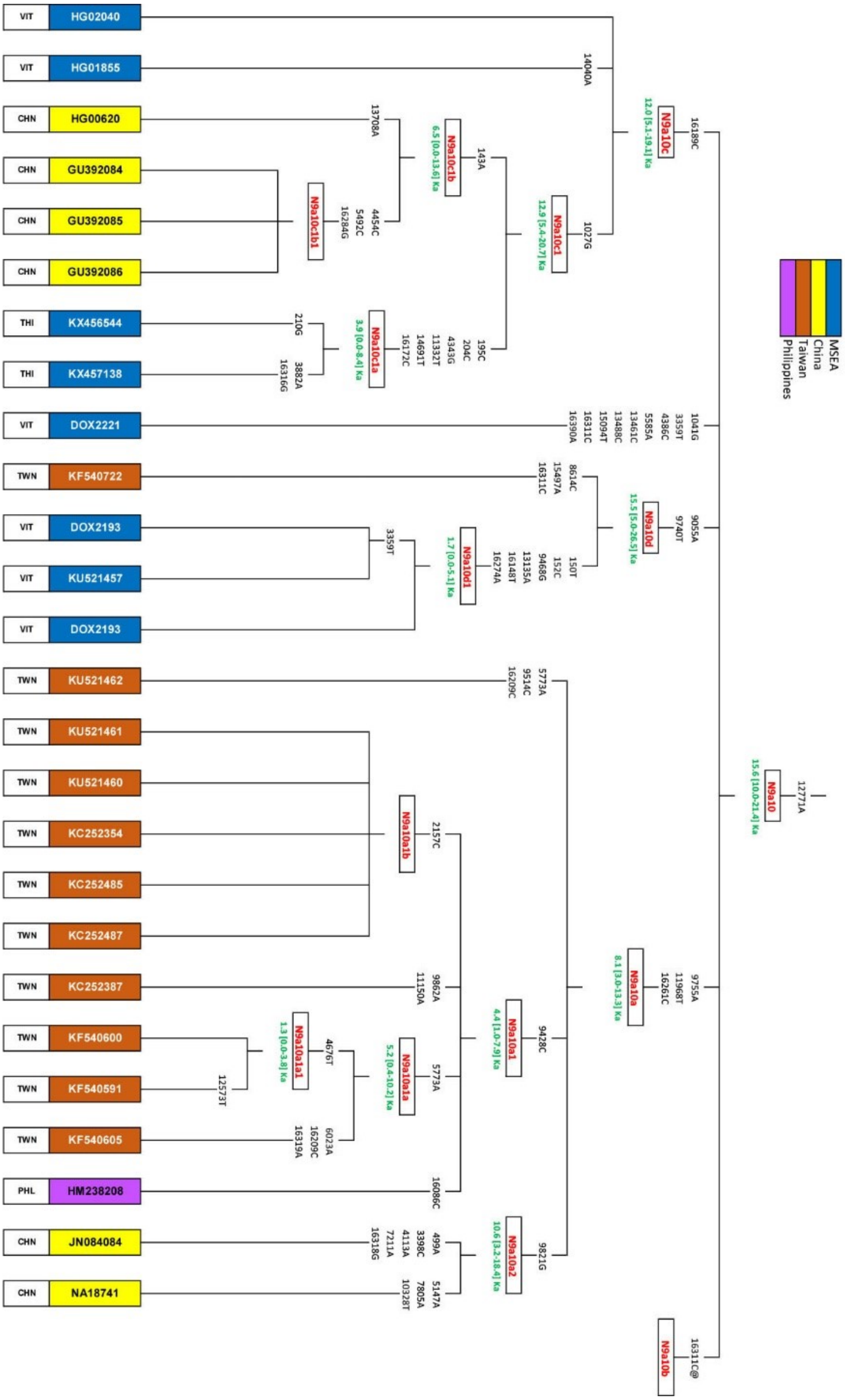


Figure 75. The tree of haplogroup N9a10. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand, PHL – Philippine, VIT – Vietnam and TWN – Taiwan).

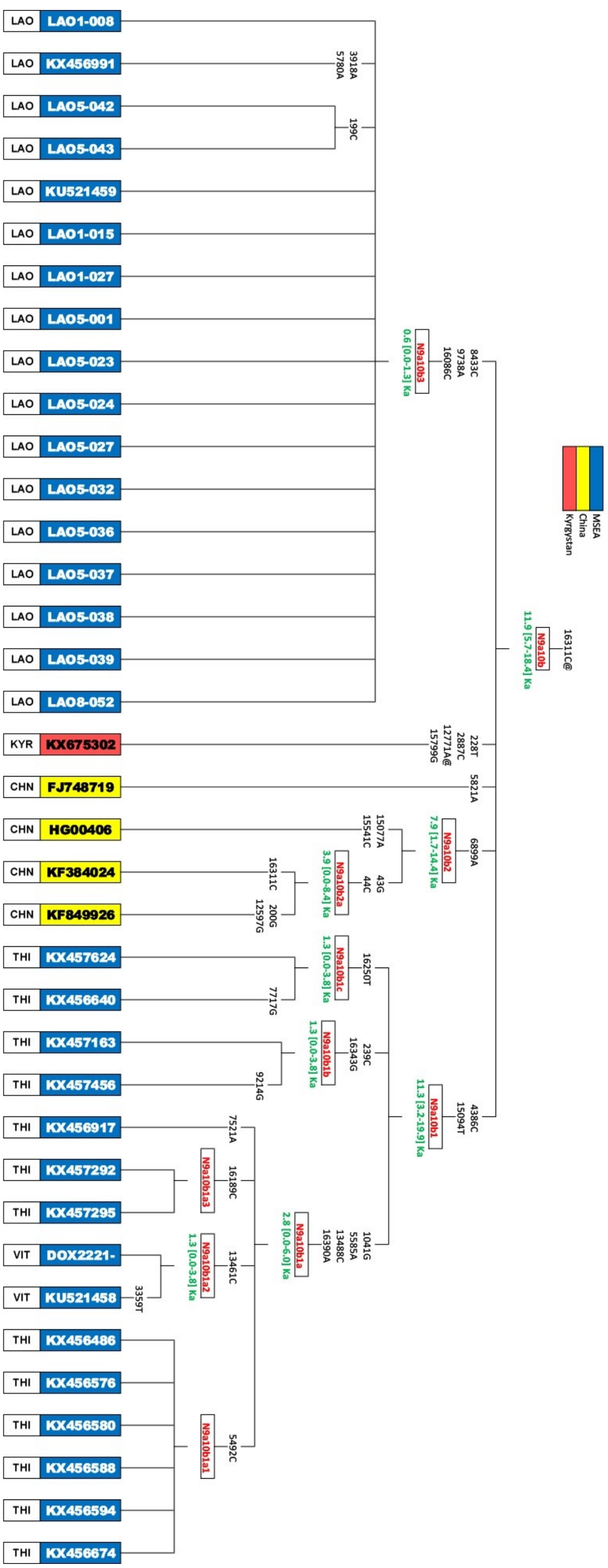


Figure 76. The tree of haplogroup N9a10b. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand, LAO – Laos and KYR – Kyrgyzstan).

4.3.4 Haplogroup N10

N10 dates to~70 ka, approximately the age of haplogroup N itself (Kong et al., 2011). The N10 tree includes eight complete mtDNA sequences from Thailand (Kutanan et al., 2017), four from south China (Kong et al., 2011), two from Myanmar and one each from northeast Peninsular Malaysia, Indonesia (Archaeogenetics Research Group, Huddersfield) and Laos (this study). But the HVS-I data (Figure 31) shows more southern Chinese branches in the N10a network which may suggest an ancient origin in South China or MSEA.

As shown in Figure 77, N10 diverges into two subclades, N10a and N10b. N10a dates to ~59 ka, and is further divided into N10a1 and N10a2. N10a1 dates to ~26 ka and is seen mainly in Thailand (Kutanan et al., 2017). N10a2 dates to a more recent age of ~2.5 ka, and is seen in only two individuals from Peninsular Malaysia and Indonesia. N10b is seen in MSEA and Guangdong, in south China (Kong et al 2011) and it is dated to around the last glacial maximum ~25 ka.

4.3.5 Haplogroup N21

N21 is a basal haplogroup within N (Macaulay et al., 2005; Soares et al., 2009) and the phylogeny is reconstructed from 36 complete mtDNA sequences. The deeper lineages appear to be restricted to MSEA, detected in Vietnam (this study) and Thailand (Kutanan et al., 2017). N21 is divided into five subclades; N21a, N21b, N21c, N21d and N21e (mostly new nomenclature) (Figure 77). All the N21 subclades except N21a are mainly found in the MSEA region (Thailand, Vietnam and Myanmar), while N21a is commonly found in Peninsular Malaysia (Jinam et al. 2012). A recent expansion brought N21a1 lineages into Peninsular Malaysia, including Aboriginal

Malays, and also Indonesia, by ~7ka (Figure 78). The age of N21 is estimated between ~15 ka, which could suggest the Late Glacial expansion in MSEA and an early to mid-Holocene expansion into ISEA (Peninsular Malaysia and Indonesia).

N21b, defined by a transition at np 16182 in the control region (Figure 79), dates to the early Holocene. It is commonly seen in Thailand (Kutanan et al., 2017) and Myanmar (Li et al., 2015) with one sample from Lijiang, South China (Kong et al., 2011).

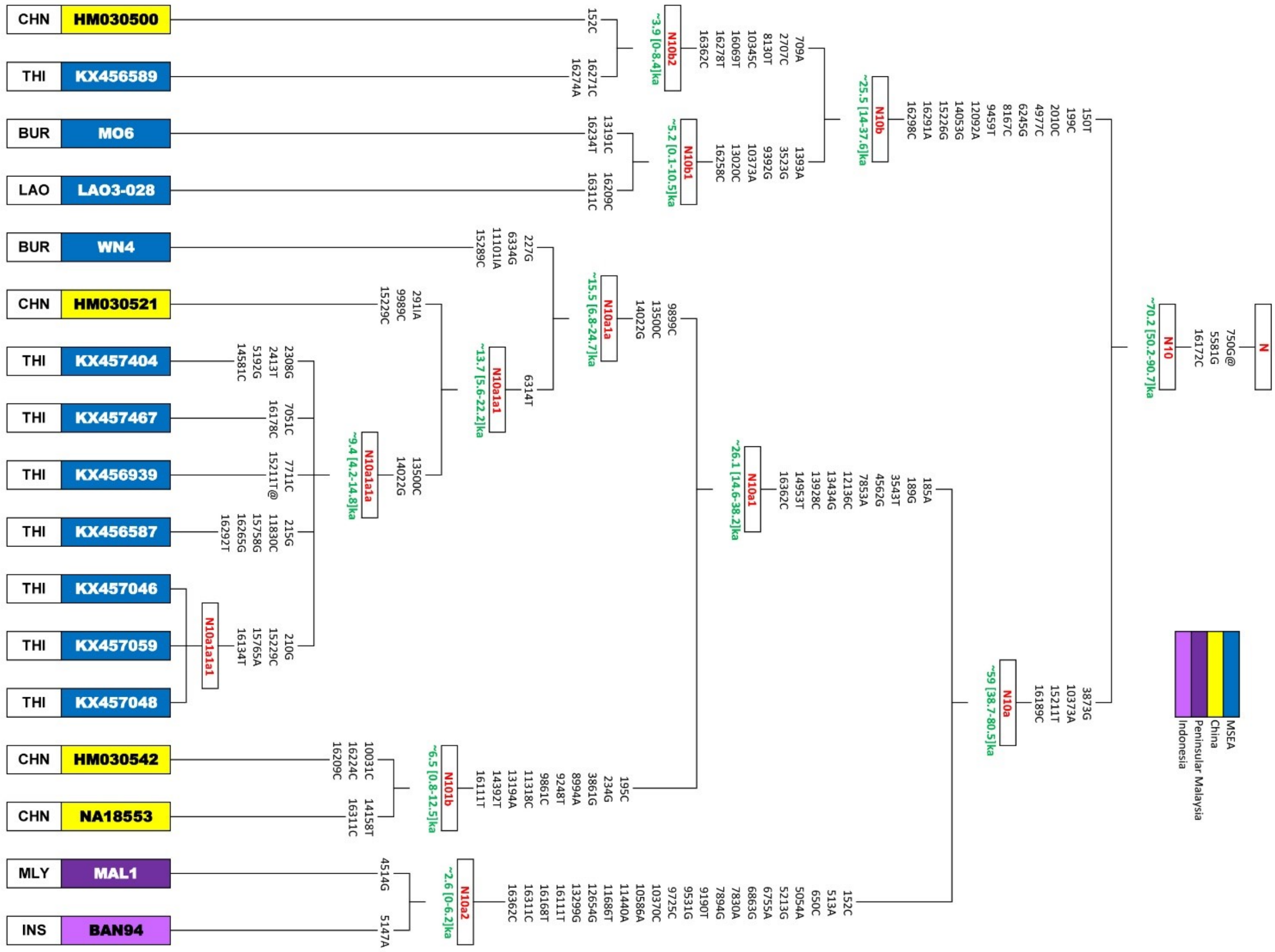


Figure 77. The tree of haplogroup N10 Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand, INS – Indonesia, MLY – Malaysia).

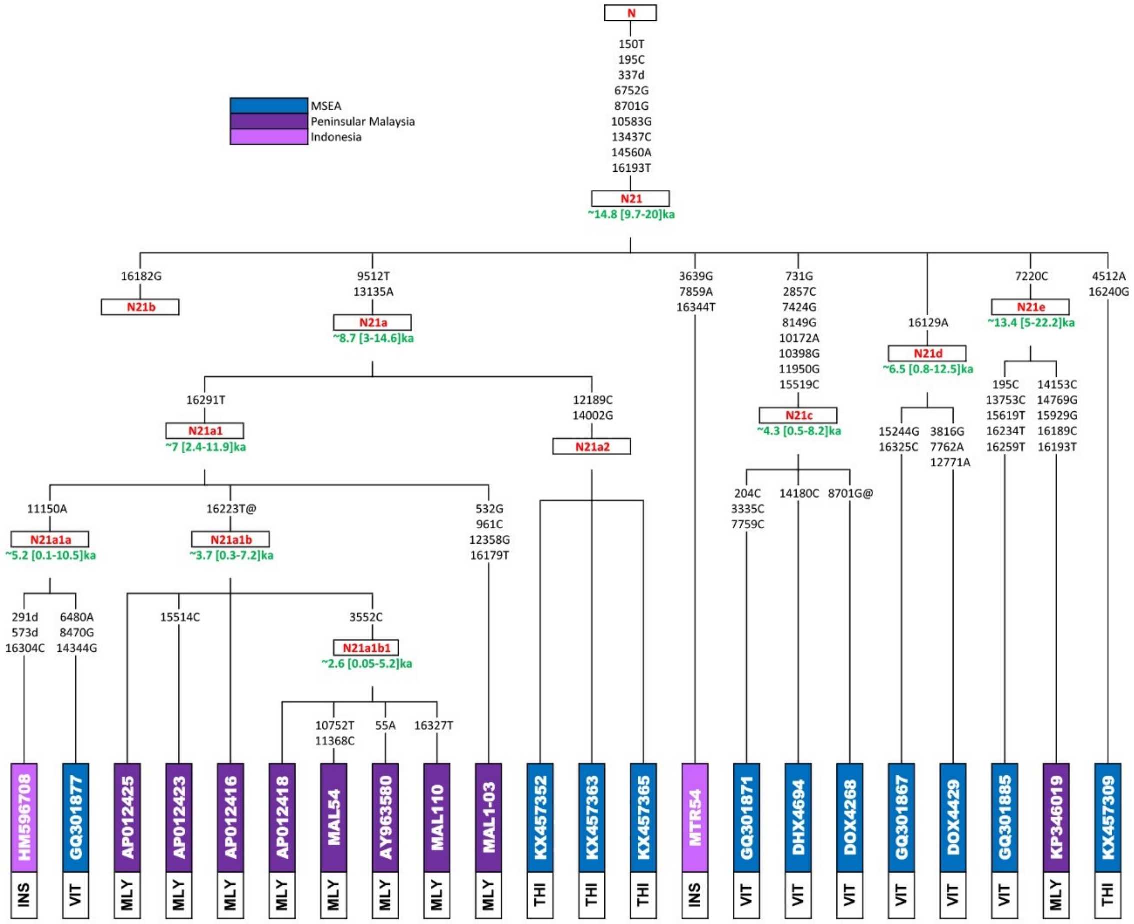


Figure 78. The tree of haplogroup N21. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (THI – Thailand, VIT – Vietnam, MLY – Malaysia, INS – Indonesia).

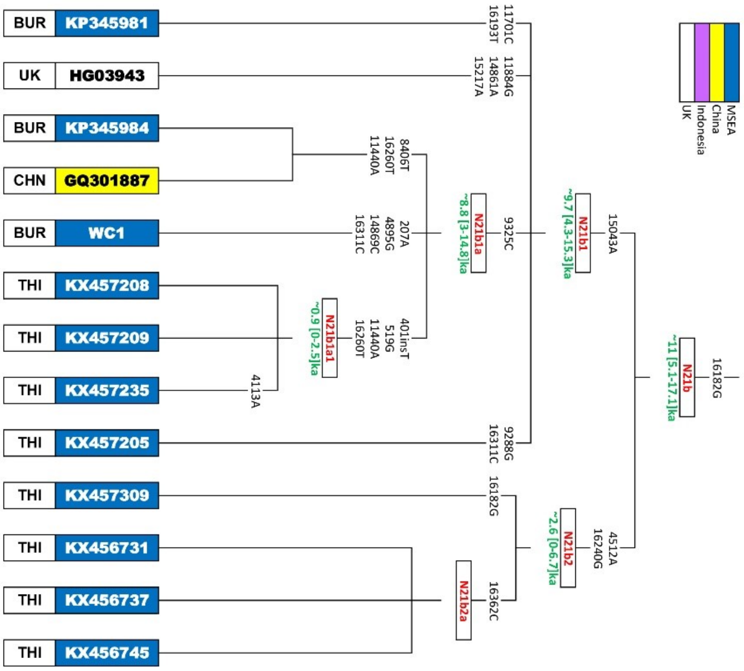


Figure 79. The tree of haplogroup N21b. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand, VIT – Vietnam, MLY – Malaysia, INS – Indonesia, BUR – Myanmar, UK – United Kingdom).

4.3.6 Haplogroup N22

N22 is a basal haplogroup within N, and is characterized by transitions at nps 150, 942, 7158, 9254 and 11365 in the coding region and 16168 and 16249 in the control region (Macaulay et al., 2005). It dates to ~19 ka and the tree (Figure 80), like N8, indicates it is a deep Sundaic haplogroup, since it is found across Peninsular Malaysia, MSEA and ISEA regions. N22 divided into subclades N22a and N22b.

The MSEA samples were found branching from the N22b1 node, which assuming an ISEA source suggests a founder age of ~3.4 ka with the *f1* criterion (table 11). This could suggest a migration event into MSEA during the Neolithic expansion in Southeast Asia.

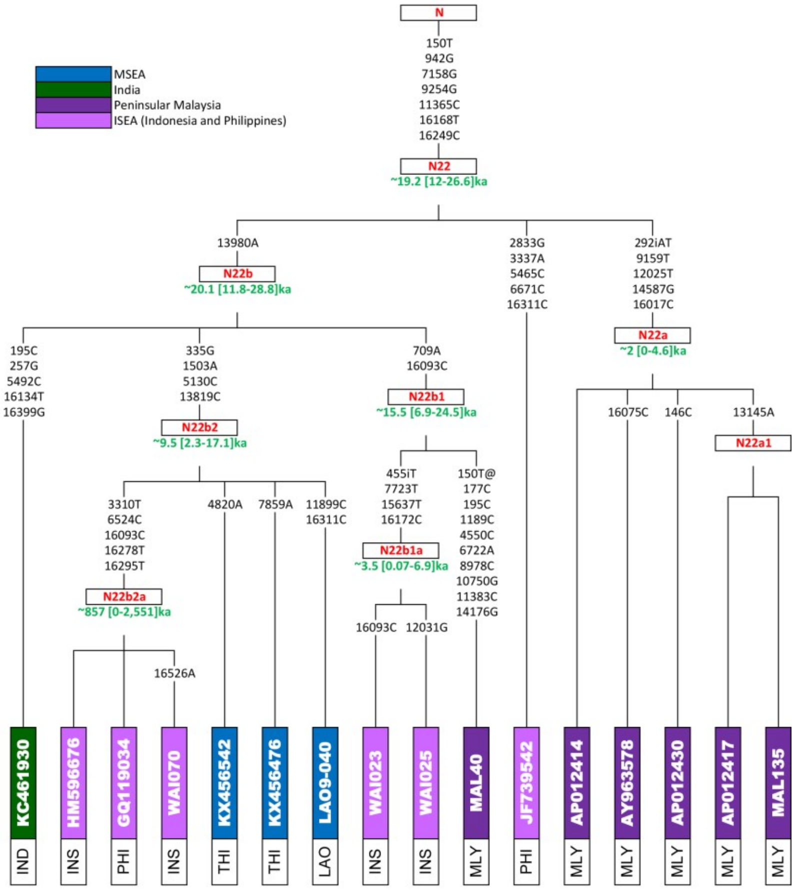


Figure 80. The tree of haplogroup N22. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (PHI – Philippines, MLY - Malaysia, INS – Indonesia, LAO – Laos and IND – India).

4.4 Haplogroup R

Haplogroup R dates close to the age of M and N and is globally the third main Eurasian founder, branching from the root of N. It is defined by transitions at np 12705 in the coding region and np 16223 in the control region. The R sub-haplogroups found in MSEA include B4'5, R11’B6, R22 and R9.

4.4.1 Haplogroup B

B is a basal haplogroup within R, defined by a transition at np 16189 in the control region. It can be divided into two main haplogroups B4’5 and R11’B6. B4’5 is one of the most common haplogroups in Southeast Asia and is characterized by a 9 base-pair deletion (np 8281- 8289d) in the coding region, uniting haplogroups B4 and B5 (Hartmann et al., 2009; Kong et al., 2010; P. Soares et al., 2011). The much less common haplogroup R11’B6 is defined by a transition at np 12950 in the coding region, and sub-divided into R11 and B6, where R11 is mainly distributed in China, and B6 is widely found in Southeast Asia.

The phylogenetic tree of B4 is reconstructed from 2031 complete mtDNA sequences: B4a (1460), B4b (220), B4c (212), B4g (39), B4d (32), B4e (29), B4k (11), B4i (8), B4f (6), B4m (5), B4h (5), B4j (2) and B4* (2). The haplogroup B4 are commonly found in East Asia and Southeast Asia, with more recent dispersals into the Pacific islands (Kivisild et al., 2002; Y.-G. Yao & Zhang, 2002). A MSEA component is found within the following B4 sub-clades; B4a1e, B4a1c4, B4g, B4h, B4e, B4b1a2 and B4c2. While there are some sub-clades, such as B4a1c2, found in north Eurasia, both B4a1a1a and B4a1a1b are commonly seen in Near Oceania. But overall, the pattern of haplogroup B4 suggests that the ancient ancestry of this haplogroup is in East Asia and it then dispersed into SEA after the LGM (P. Soares et al., 2011).

4.4.2 Haplogroup B4

B4 is defined by a transition np 16217 in the control region, dates to ~35 ka, and includes four main sub-haplogroups; B4+16261T, B4b'd'e'j, B4c and B4f. The B4+16261T sub-haplogroup is dated to ~30 ka, and contains all the major B4 sub-clades; B4a, B4g, B4h, B4i, B4k and B4m. The B4b'd'e'j sub-haplogroup is dated to ~35.5 ka, and contains four main sub-clades; B4b, B4d, B4e and B4j.

B4a is dated to ~24.6 ka and is divided into five main sub-clades: B4a1, B4a2, B4a3, B4a4 and B4a5. B4a1 is dated to ~21.9 ka, and has five main sub-clades, B4a1a, B4a1+16311C (including B4a1b), B4a1c, B4a1d and B4a1e. B4a1a is dated to ~10.8 ka and the basal branches of this sub-clade are found throughout Southeast Asia, including the Pacific islands, Papua New Guinea (Duggan et al., 2014; Pierson et al., 2006), Taiwan (Ko et al., 2014; Loo et al., 2014), Philippines, Indonesia (Gunnarsdottir et al., 2011; Soares et al., 2011) and Peninsular Malaysia (Eng, 2014; Wong et al., 2013) (Eng, 2014; Wong et al 2013). This latter pattern shows a dramatic expansion across the Pacific region, through ISEA, in the early Holocene, similar to this pattern seen in haplogroup E (Soares et al., 2008). The B4a1a has seven major sub-clades: B4a1a1, B4a1a2, B4a1a3, B4a1a4, B4a1a5, B4a1a6 and B4a1a7. B4a1b dates to ~14.6 ka, with a nested sub-clade B4a1b1, dating to ~4 ka, and is seen mainly in Japan (Tanaka et al., 2004). B4a1c has three main sub-clades, B4a1c1, B4a1c3 and B4a1c+146, and is dated to ~15.4 ka. B4a1c+146C includes three main sub-clades B4a1c2, B4a1c4 and B4a1c5, dates to ~12 ka. Both B4a1c2 and B4a1c5 are dated to the Neolithic age (~4 ka), and are commonly found in South China (Zheng et al. 2011) and Taiwan (Loo et al., 2012). Meanwhile, the B4a1c4 (Figure 81) is dated to the middle Holocene age ~8.5 ka, and is mainly found in Thailand and Vietnam in MSEA.

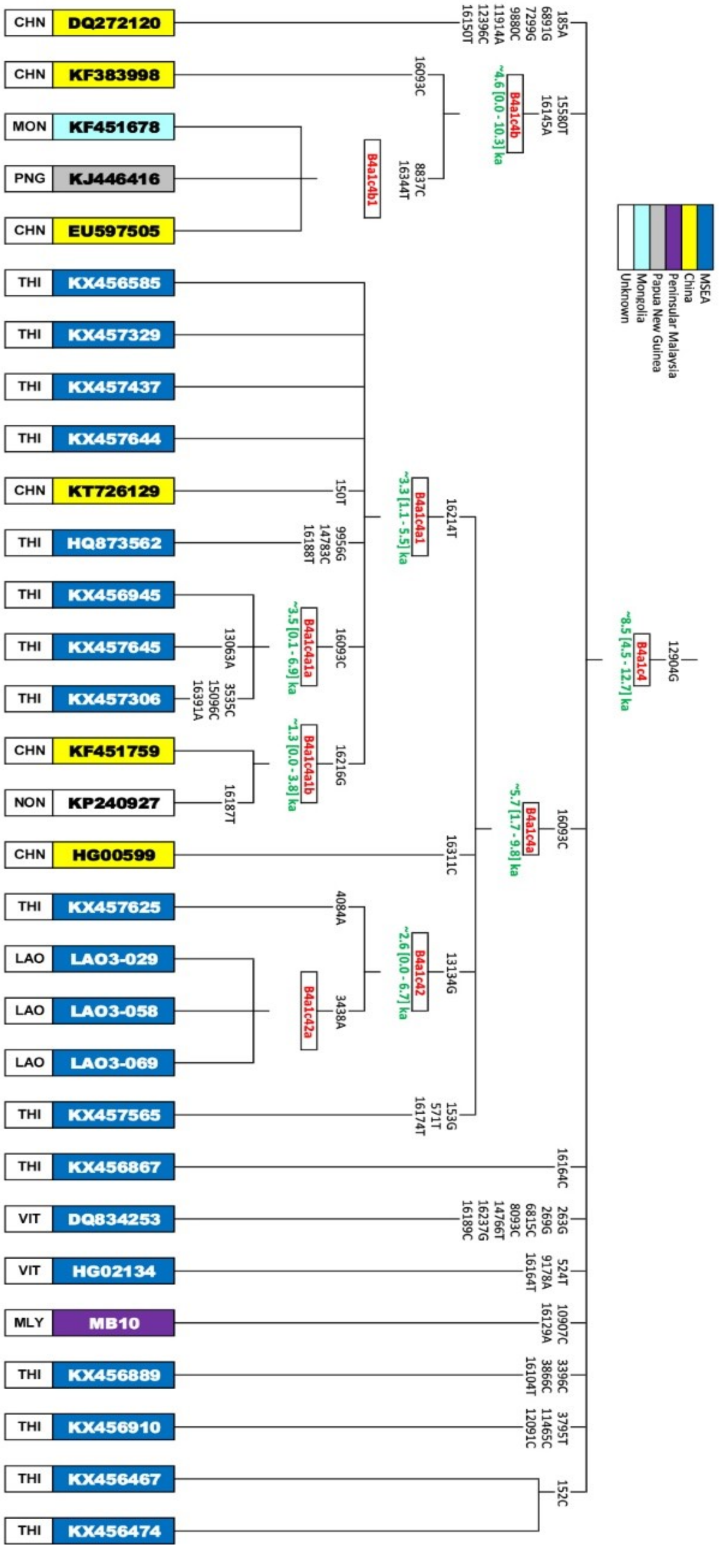


Figure 81. The tree of haplogroup B4a1c4. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, MLY - Malaysia, THI – Thailand, LAO – Laos, MON – Mongolia, PNG – Papua New Guinea and NON - Unknown).

B4a1d (Figure 82) is restricted just to Vietnam (this study; Soares et al., 2011), and dates to the middle Holocene age ~7.2 ka, while B4a1e sub-clade (Figure 83) is dated to the late Pleistocene/early Holocene age ~12 ka, and is found in Laos (this study) and Thailand (Kuantan et al., 2017) in MSEA, Taiwan (Ko et al., 2014) and China (Bi et al 2011; Jiang et al., 2014).

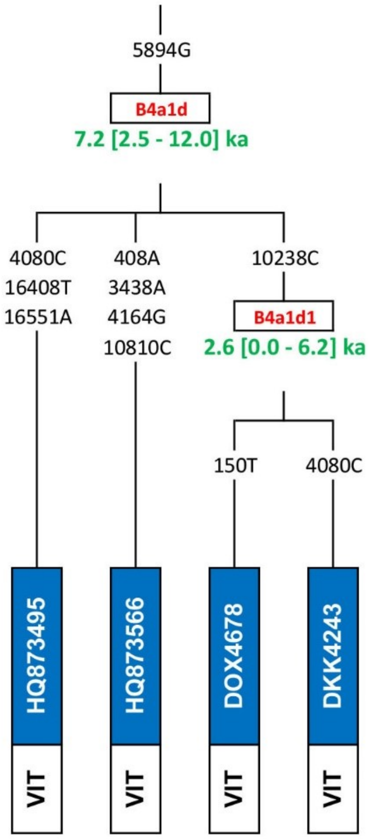


Figure 82. The tree of haplogroup B4a1d. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (VIT - Vietnam).

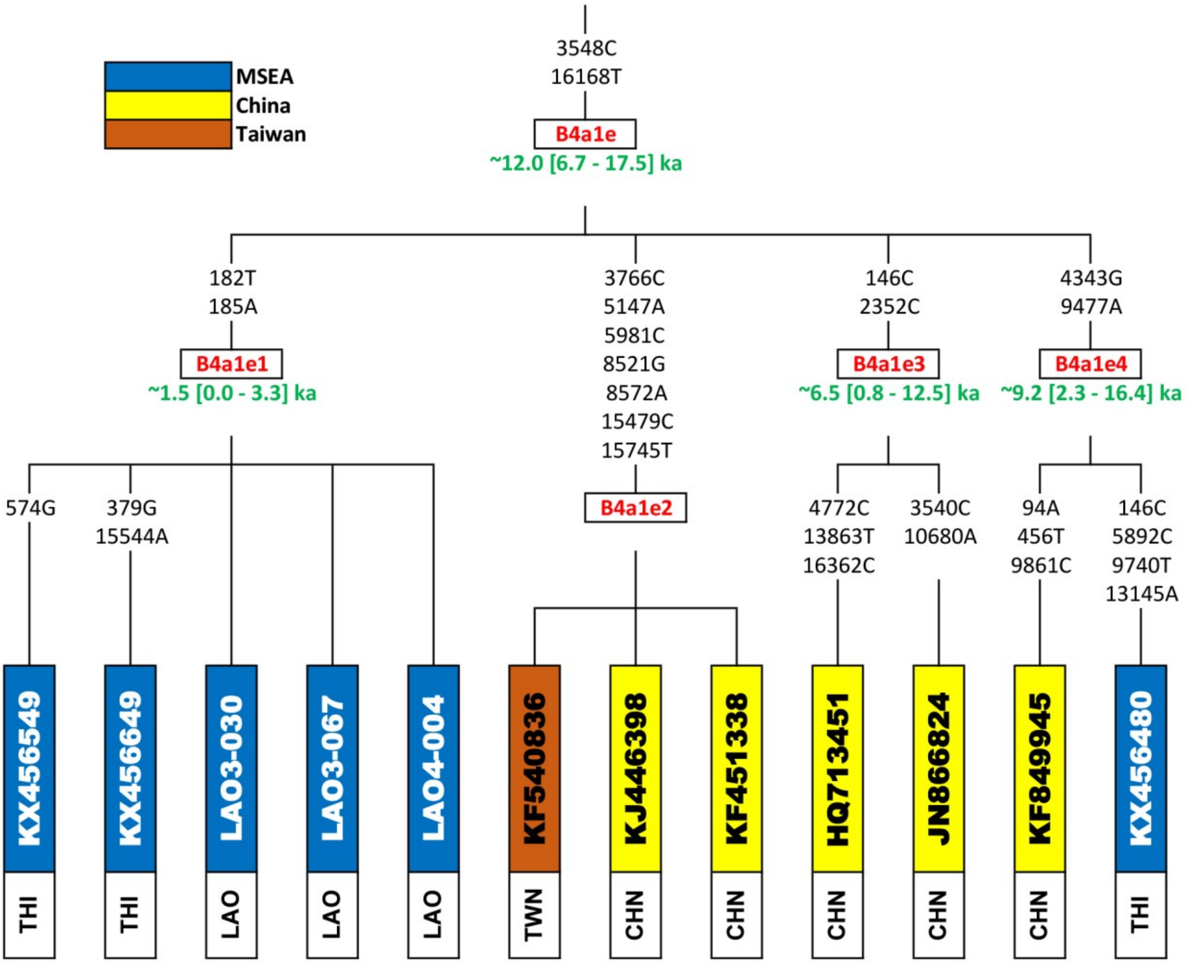


Figure 83. The tree of haplogroup B4a1e. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, TWN - Taiwan, THI – Thailand and LAO – Laos).

B4g sub-clade (Figure 84) is dated about 20 ka, divided into; B4g1 and B4g2, and it is commonly found in MSEA; Laos (This study), Thailand (Behar et al., 2012; Kutanan et al., 2017) and Vietnam (this study). Although few complete sequences represent the Chinese component (Am et al., 2003; Bi et al., 2011; Zheng et al., 2011), the HVS-I database confirms that this sub-clade is found widely across South China, Laos, Thailand and Vietnam. The B4g1 sub-clade is defined by a transition np 7789 in the coding region, and is dated to the Late Glacial period (~16 ka), while B4g2 (Figure 85) is defined by four transitions at nps 61 and 62 in the control region and 2378 and 6482 in the coding region, and is dated to the early Holocene age (~10.6 ka).

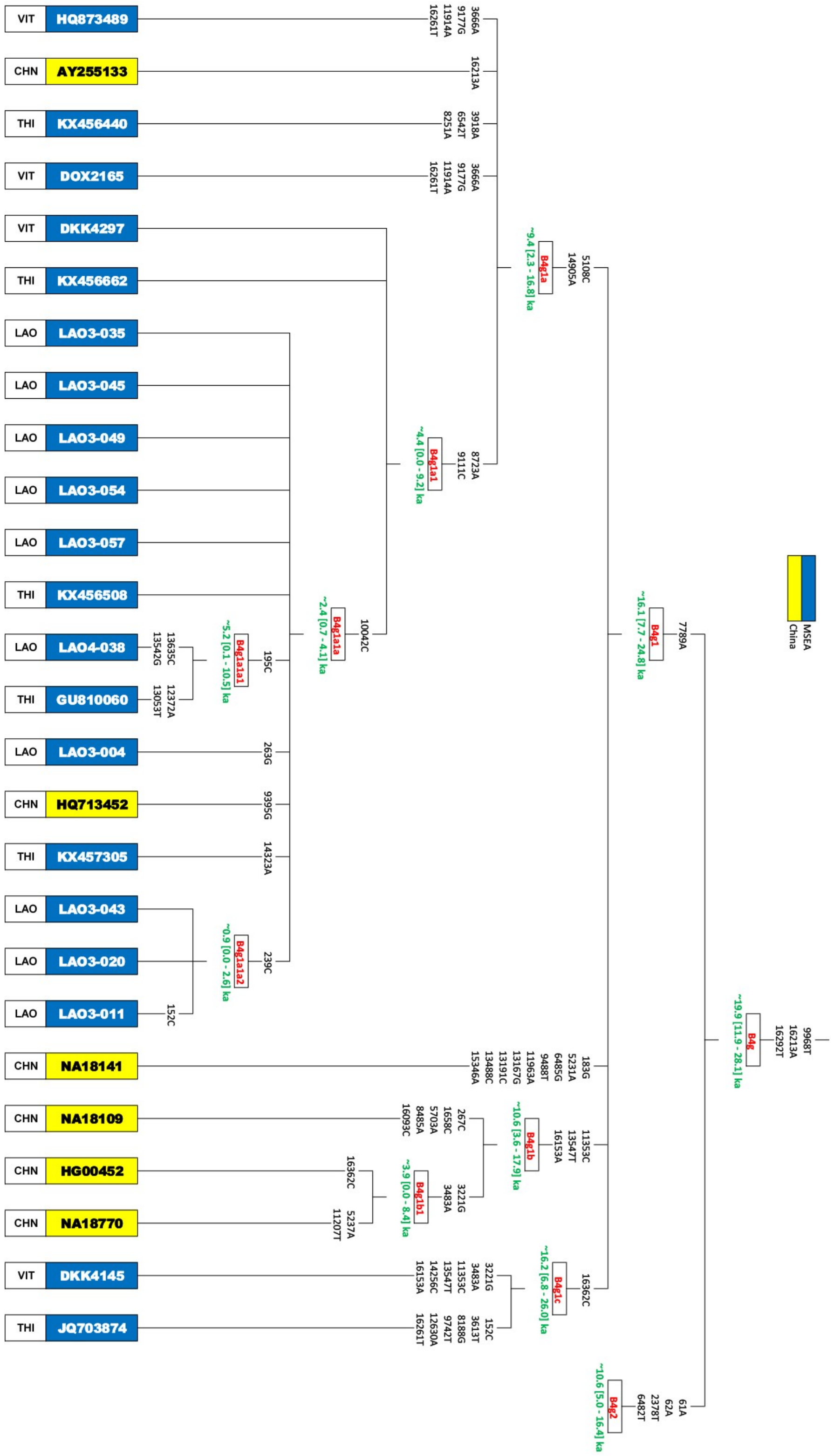


Figure 84. The tree of haplogroup B4g. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, THI – Thailand and LAO – Laos).

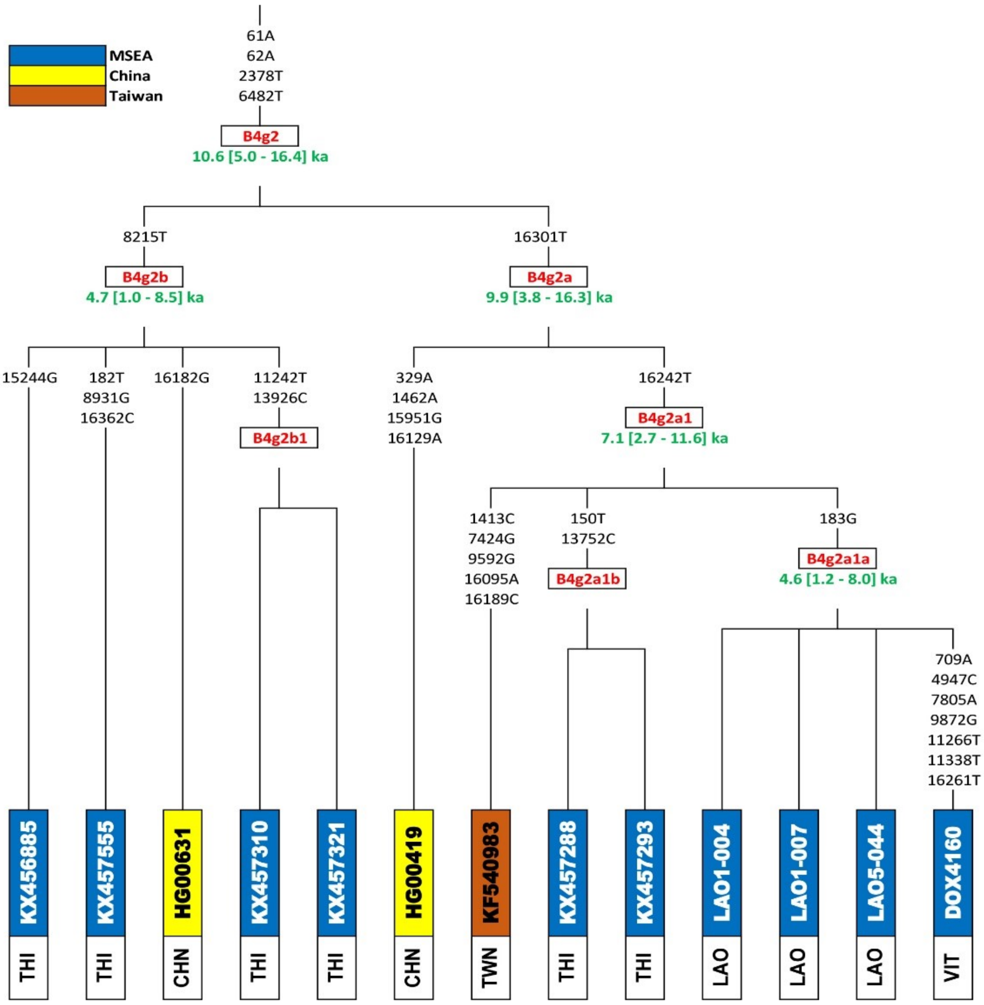


Figure 85. The tree of haplogroup B4g2. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, THI – Thailand, LAO – Laos and TWN – Taiwan).

The B4+16261T sub-haplogroup with transitions at nps 5093, 13269 and 16129 defines the B4h sub-clade (Figure 86), it dates to ~16.5 ka and is seen mainly in Laos (this study) with basal ancestry mainly in South China (Soares et al., 2011; Zheng et al., 2011; Lippold et al 2014). B4h is divided in this study into five sub-clades; B4h1, B4h2, B4h3, B4h4 and B4h5. The youngest sub-clades are B4h2 and B4h5, dating to the early Holocene age (~10.4 ka and 12 ka respectively). B4h2 is restricted to north Laos, except for on basal Chinese lineage (this study), while most of the other sub-clades seem to have originated in South China during the last glacial age.

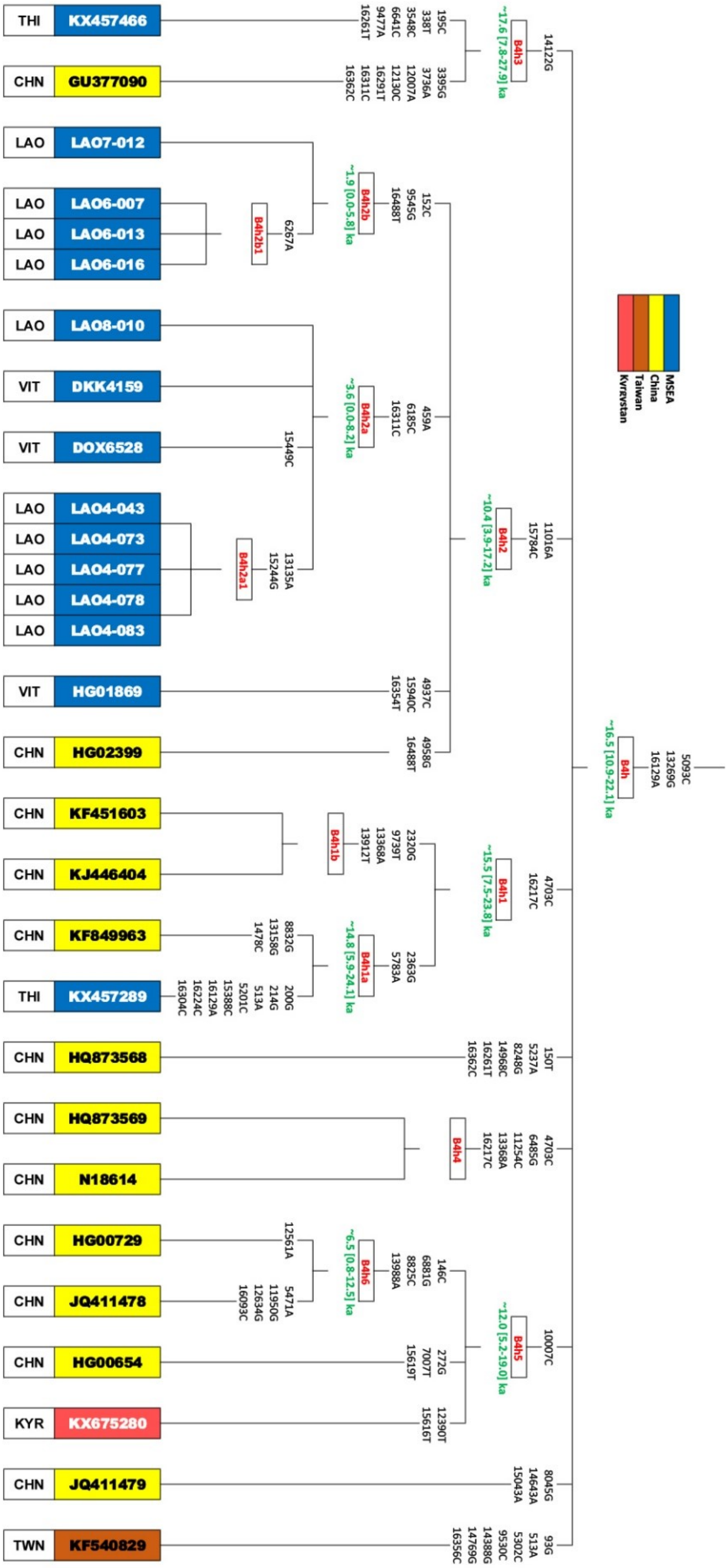


Figure 86. The tree of haplogroup B4h. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, THI – Thailand, LAO – Laos KYR- Kyrgyzstan and TWN – Taiwan).

Within the **B4b’d’e’j** haplogroup, the **B4b** sub-clade is dated to ~27 ka and within it a transition at np 16136 in the control region defines B4b1. B4b1 is dated to the LGM ~24 ka, and it is divided into two main sub-clades B4b1a and B4b1b'c (including B4b1b and B4b1c). B4b1a dates to ~18.4 ka with a basal lineage seen in Vietnam (1000 Genomes Project, 1KGP), China (Li et al., 2016) and south Siberia in Russia (Starikovskaya et al., 2005). A further transition at np 207 in the control region, dating to ~15.5 ka, defines the MRCA for the three main B4b1a sub-clades (B4b1a1, B4b1a2 and B4b1a3).

B4b1a1 is restricted to Japan only (Tanaka et al., 2004; Zheng et al., 2011), and dated to the Neolithic age, ~4.9 ka. It includes the sub-clades B4b1a1a, B4b1a1b, B4b1a1c and B4b1a1d, and they are dated to ~2.6, ~4.3, ~3.5, and ~3.9 ka respectively.

B4b1a2 dates to the early-to-middle Holocene age between 7.2 to 13.3 ka, and basal lineages are mainly seen in the Philippines (Delfin et al., 2014) with two more basal linages in South China and Indonesia. Overall, this pattern of distribution suggests Southeast Asia as the place of origin for this sub-clade. B4b1a2 is divided into B4b1a2a, B4b1a2b, B4b1a2c, B4b1a2d, B4b1a2e, B4b1a2i, B4b1a2h, B4b1a2f and B4b1a2g, of which the latter three are all restricted to Taiwan (Ko et al., 2014; Loo et al., 2014), and both B4b1a2f and B4b1a2g are dated to the Neolithic age ~4 ka, while B4b1a2h is very recent (~400 years ago).

B4b1a2a (Figure 87) dates to the early Holocene age, ~13.3 ka, and is mainly seen in Vietnam (this study) and Thailand (Kutanan et al., 2017). The rest of the B4b1a2 sub-clades, B4b1a2b, B4b1a2c, B4b1a2d and B4b1a2e, are restricted to the Philippines and dated to ~7.9, ~1.7, ~0.6 ka respectively, while B4b1a2e and B4b1a2i are both dated to the middle Holocene age about ~8 ka, but found in two different locations, south China and the Remote Pacific Islands (Duggan et al., 2014) respectively.

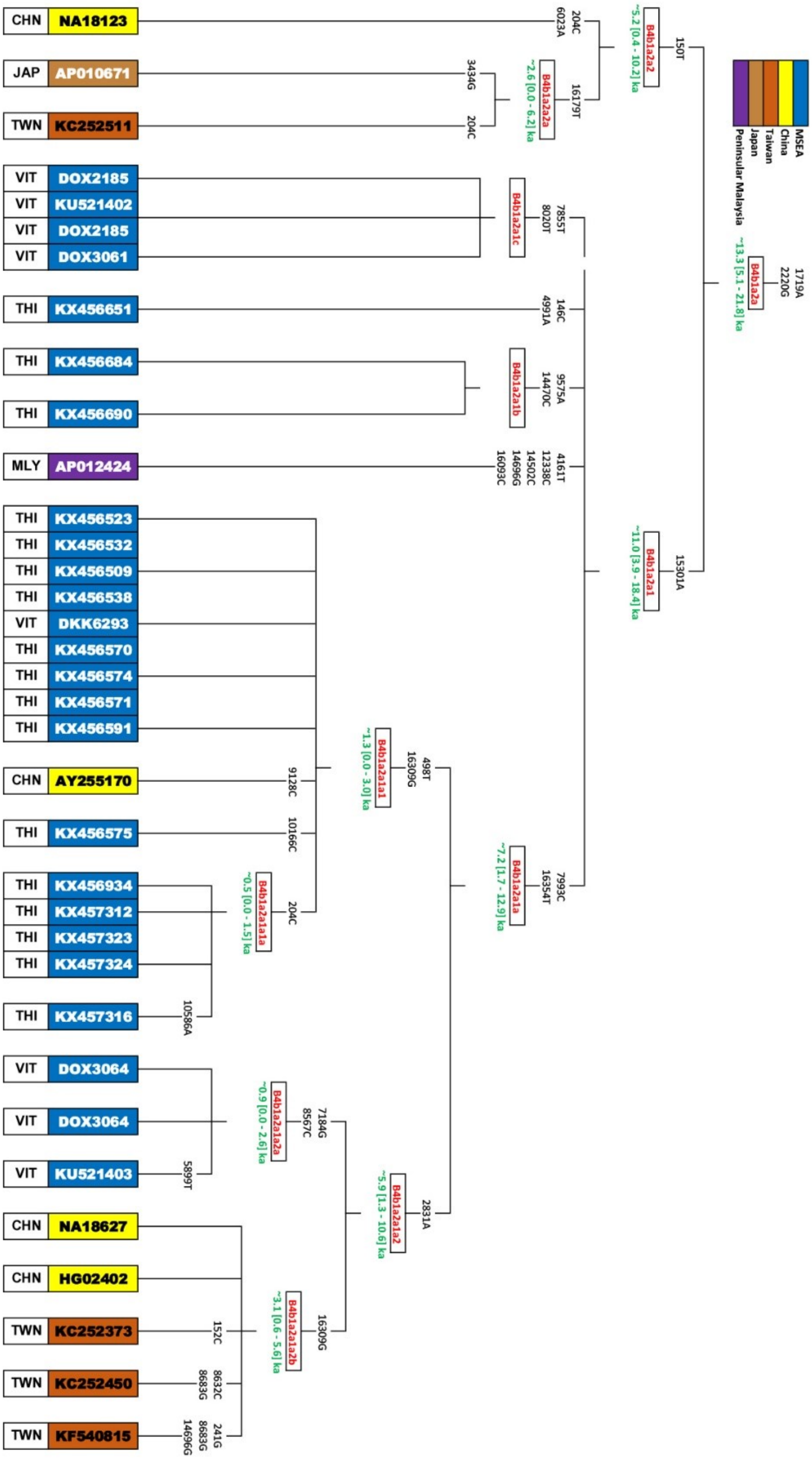


Figure 87. The tree of haplogroup B4b1a2a. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, THI – Thailand, MLY- Malaysia, JAP – Japan and TWN – Taiwan).

4.4.3 Haplogroup B4c

B4c dates to ~33 ka and it is divided into two sub-clades, B4c1 and B4c2. B4c1, dated to ~31.9 ka, is common across East Asia, in Japan (Guo et al., 2005), Taiwan (Ko et al., 2014) and the Sundaic region particularly in Peninsular Malaysia, Borneo (Archaeogenetics Research Group, Huddersfield) and the Philippines (Gunnarsdóttir et al., 2011). B4c1 also includes many sub-lineages, found in North Asia (B4c1a2) in Siberia (Derenko et al., 2012), with few lineages in South China and MSEA (Kong et al. 2003; Wang et al., 2007; Zheng et al., 2011). The latter sub-clade distribution could suggest that the initial spread might have taken place along the East Asia and the Sundaic eastern coastlines towards Borneo, ultimately reaching the Philippines rather than via Taiwan.

B4c2 is dated to the early Holocene age ~12.4 ka, and is divided into two sub-clades, B4c2a and B4c2b (Figure 88). Overall, B4c2 is found mainly in Vietnam, Laos (this study), Thailand (Kutanan et al 2017) and South China (Lippold et al 2014; Zheng et al 2014), with the latter mainly restricted to the nested sub-clade B4c2a2. This could suggest that B4c2 has an origin in MSEA during the late Pleistocene age. B4c2b is defined by transitions nps 6221 and 6815, restricted to Vietnam and is dated 600 years of age, while the B4c2a is defined by a transition np at 16235 at the control region and dated to the early Holocene age, ~10.5 ka. In this study, B4c2a is divided into three main sub-clades (Figure 89), B4c2a1, B4c2a2 and B4c2a3, dating between the middle Holocene and the Neolithic age: ~8.9, ~2.8 and ~6.5 ka respectively.

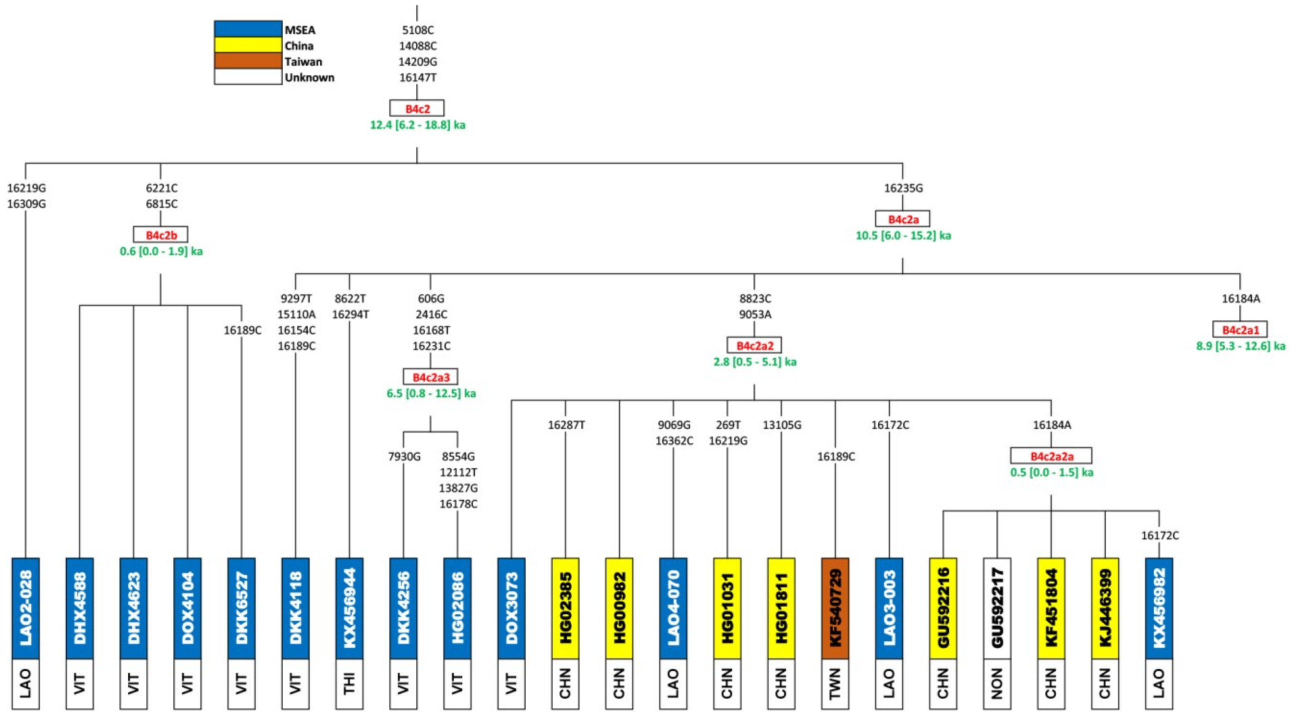


Figure 88. The tree of haplogroup B4c2. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, THI – Thailand, LAO – Laos and TWN – Taiwan).

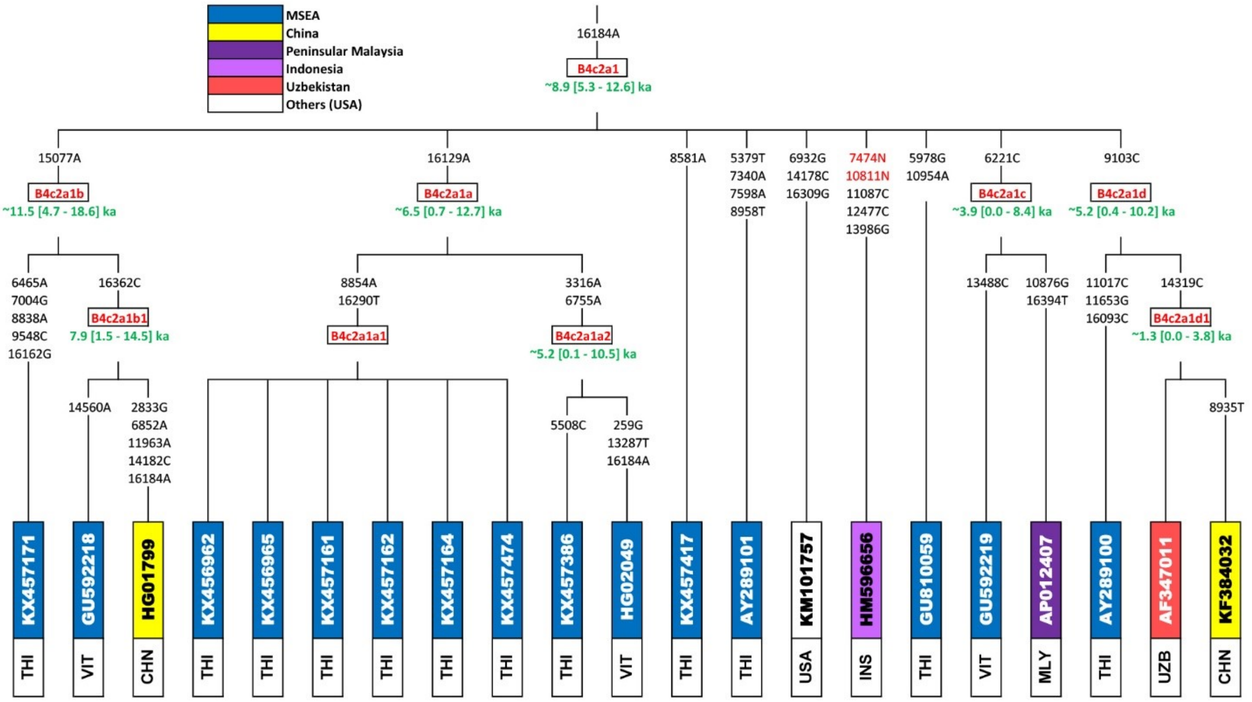


Figure 89. The tree of haplogroup B4c2a1. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, MLY- Malaysia, THI – Thailand, USA – United State and UZB – Uzbekistan).

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4.4.4 Haplogroup B5

Along with B4, haplogroup B5 (Appendix B) is one of the major branches of B, dating to ~40.6 ka, and is commonly seen in MSEA and South China, with sub-clades that are found in Japan, Taiwan and the Sundaic region. This could suggest that this haplogroup may have a southern origin in MSEA or South China and then spread into East and Island Southeast Asia, as shown particularly in sub-clades B5a1a1, B5a2a1+16129, B5a2a2a, B5b1a2, B5b1c, B5b3 and B5b2a1. The B5 haplogroup in this study was reconstructed using 599 complete sequences, representing the two sub-clades, 455 B5a and 144 B5b.

4.4.5 Haplogroup B5a

Haplogroup B5a is estimated to date to the LGM ~21 ka (Appendix B) and it has four sub-clades, B5a1, B5a2, B5a3 and B5a4. B5a1 is dated to the end of LGM about 15.6 ka and can be divided into B5a1a, B5a1c, B5a1b, B5a1e, B5a1d, B5a1f and B5a1g. B5a1a and B5a1d are dated to the middle Holocene ~8 ka and it is commonly seen in Sunda/MSEA, including Thailand (Pradutkanchana & Kimura, 2010), Cambodia (Lippold et al 2014), Peninsular Malaysia (Eng, 2014), Sumatra in Indonesia (Greenspan 2013, Gunnarsdóttir et al., 2011), Vietnam and the Nicobar Island (Thangaraj et al., 2005). B5a1a1 is only seen in the Austro-Asiatic-speakers of the Nicobar Island and it dates to ~2.6 ka.

Sub-clades B5a1f and B5a1g are mainly found in Vietnam and Laos (this study) and Thailand (Kutanan et al., 2017), and they are dated to ~8.4 ka and 16.2 respectively. B5a1c is typically seen in MSEA and South China and dated to the early Holocene age ~12.5 ka. Sub-clade B5a1c1 is restricted to Laos (this study) and South China (1KGP) and it is dated to the Neolithic age ~4.5 ka. B5a1a and its sub-clades spread across a large area of Southeast Asia; MSEA, the Malaysian Peninsula and the Nicobar Islands, which could support the “Coastal Neolithic” expansions suggested by Higham (2004) and Bulbeck (2008) (Bulbeck, 2008; Charles Higham, 2004).

B5a2 is commonly found in Taiwan and Japan in East Asia, is dated to before the LGM ~26.2 ka, and its basal lineages are found in South China. It has two main sub-clades; B5a2a1 and B5a2a2. B5a2a1 is dated to ~13.5 ka, nesting a Taiwanese lineage (Pierson et al., 2006; Loo et al., 2014), while the B5a2a2 is dated to ~15 ka which in turn nests only a Japanese lineage (Tanaka et al., 2004). B5a3 is dated to ~12.3 ka and it mainly found in south China, MSEA and Taiwan. B5a4 is restricted mainly to Laos and Vietnam (this study), and it is defined by a transition and reversion at np 16266, and it is date to early Holocene ~10 ka. This pattern could suggest a dispersal from Southeast Asia into East Asia during the early Holocene.

4.4.6 Haplogroup B5b

B5b is not very common in MSEA, but is mainly found in South China, East Asia (Japan and Taiwan), Peninsular Malaysia and the Philippines, with some lineages in south Siberia. This haplogroup is divided into four sub-clades B5b1, B5b2, B5b3 and B5b4, dating to ~33.4 ka. B5b1 and B5b2 are dated to pre-LGM ~24.5 ka and 23 ka respectively, and most of their basal lineages are found in South China (Zheng et al., 2011). The sub-clades of B5b1 and B5b2 are seen in Japan (Tanaka et al., 2004; Bilal et al. 2008), the Philippines (Delfin et al. 2014), and Peninsular Malaysia (Eng 2014), with some basal lineages found in south Siberia (Starikovskay et al., 2005, Derenko et al., 2012), and these sub-clades are dated to the late Pleistocene to middle Holocene age, between ~7 ka and ~13 ka. This could suggest that the B5b1 and B5b2 are more likely to have an origin in South China, dispersing into North and Southeast Asia during this period.

B5b3 is restricted to Japan (Tanaka et al., 2004; Zheng et al., 2011) and dated to the late Pleistocene ~13.4 ka, which could indicate a dispersal from South China to Japan during the Holocene age. B5b4 is found in South China (Jiang et al., 2014) and south Siberia (Derenko et al., 2012), dating to the Late Glacial, ~16 ka, suggesting a northern dispersal from South China to south Siberia after the LGM in Asia.

4.4.7 Haplogroup R11‟B6

Haplogroup R11’B6 seems to have an origin in South China/MSEA and is dated to ~45.7 ka, and it branches into two haplogroups; B6 and R11 (Figure 90). This haplogroup is defined by the fast transition at np 16189 in the control region (along with B4’5, although it is unlikely that they form a true clade since 16189 evolves very rapidly: Soares et al., 2009), and np 12950. Oddly, like B4’5, B6 also carries the 9-base pair deletion (nps 8281-8289d), but this is unlikely to be due to the same event as for B4’5, since R11 lacks it and np 12950 is a fairly stable position. This haplogroup looks very rare but is difficult to recognize using only the control region. In this study, nine complete sequences were added from Vietnam and Laos, three in B6 (one Lao and two Vietnamese) and six in R11 (three each Lao and Vietnamese). Overall, the R11’B6 is reconstructed in total from 85 complete sequences: 45 B6 and 40 R11.

4.4.8 Haplogroup B6

Haplogroup B6 (Figure 90), is seen predominantly in MSEA and it is dated (with large uncertainty) to the LGM, ~12-28 ka. It branches into B6a and B6b. B6a is dated to LGM period ~21 ka, branches into two sub-clades, B6a1 and B6a2, and is almost wholly found in MSEA. B6a is seen in Vietnam (this study) and Thailand (Kutanan et al., 2017), while the late Pleistocene component in this sub-clade is B6a2, dating to ~14 ka, and almost wholly found in Thailand and Myanmar (Summerer et al., 2014) with a basal linage from Peninsular Malaysia (Jinam et al., 2012).

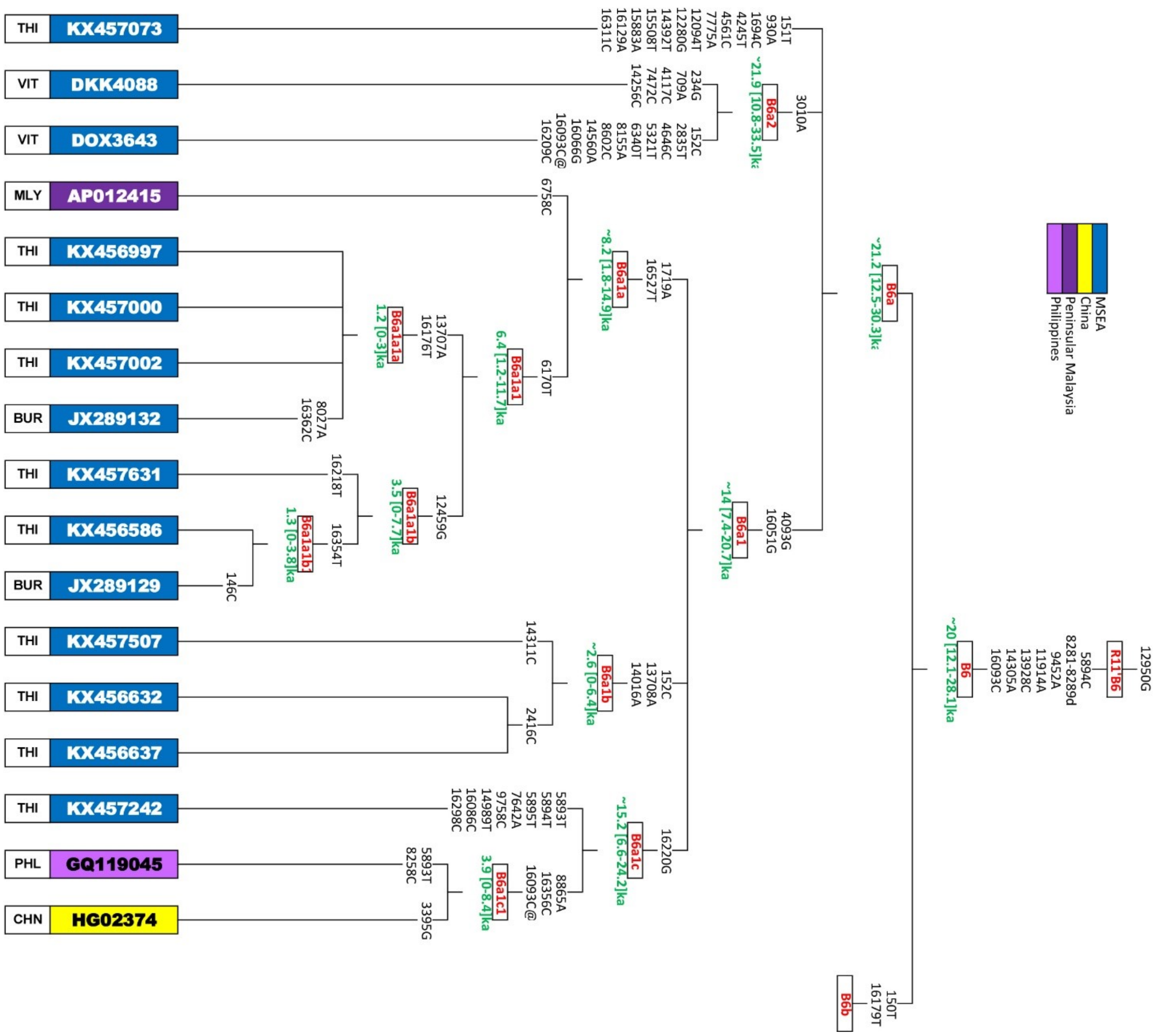

Figure 90. The tree of haplogroup B6. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT - Vietnam, MLY- Malaysia, THI – Thailand, BUR – Myanmar and PHL – Philippine).

B6b is dated to the late Pleistocene ~13.6 ka (Figure 91) and is entirely found in MSEA, in Laos (this study) and Thailand (Kutanan et al 2017), with two complete sequences from South China (1KGP; Kong et al., 2003).

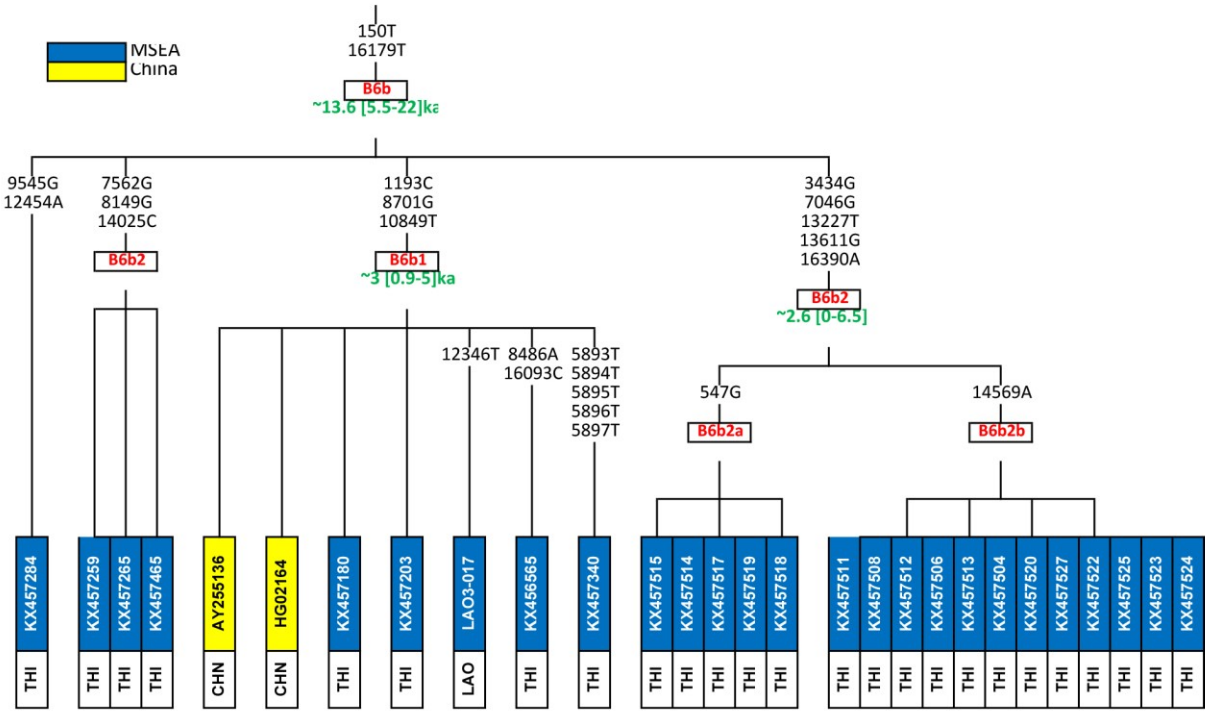

Figure 91. The tree of haplogroup B6b. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, THI – Thailand and LAO – Laos).

4.4.9 Haplogroup R9

R9 is characterized by s at nps 3970, 13928C and 16304 (Appendix B), with three main branches: R9b, R9c and F (Kong et al., 2003), and dates to ~51 ka. R9 (Appendix B) seems to have originated in MSEA/South China and expanded throughout SEA. Haplogroup R9b dates to ~35 ka and has deep branches in MSEA, commonly found in in North Laos, Thailand and South China. R9b1 is seen in Peninsular Malaysia and ISEA. R9c is an uncommon haplogroup that dates to ~24 ka, sub-divides into R9c1 and R9c2, and dispersed into Taiwan and ISEA, while R9c1b is mainly seen in South China and MSEA.

Haplogroup F dates to ~47 ka, is defined by mutations at nps 6392 and 10310, and sub-divides into four subclades, F1, F2, F3 and F4. F1 is the largest subclade within the R9 haplogroup, and sub-divides into F1a'c'f and F1+16189, which unites (probably artefactually by long-branch attraction) F1b, F1d, F1g and F1h, which are commonly found in Japan and China. F1a'c'f is seen mainly in South China and MSEA and consists of three main subclades, F1a, F1c and F1f. The latter subclades have quite different distributions: F1c dates to ~23 ka, has a deep root reported in Japan (Tanaka et al., 2004), and is seen also in North India, South China, MSEA, Peninsular Malaysia and Indonesia, while F1f dates to ~6.8 ka, and has a source in MSEA from where it dispersed into Peninsular Malaysia and Indonesia. F2 dates to ~21 ka, has deep roots in Japan and China, is found in different parts of MSEA, and is completely absent from ISEA. F3 dates to ~37 ka, and subdivides into two main subclades F3a and F3b. F3a is found mainly in South China and MSEA, while F3b is restricted to Taiwan and ISEA. F4 is dated to ~32.8 ka, and has two subclades F4a and F4b. F4a distributed through South China, Japan and MSEA, while F4b is mostly restricted to Taiwan and is also seen in South China and MSEA.

4.4.10 Haplogroup F1a

F1a is defined by a transition at np 4086 (Appendix B), dates to ~19 ka, and most of its branches are found across MSEA and South China. It can be sub-divided into four subclades: F1a1'4, F1a2, F1a3 and F1a5. F1a2 is characterized by a transition at np 16129, dates to ~10 ka, has its deepest branch in China (1 KGP), and is seen only in MSEA and South China. F1a3 dates to ~17 ka, and sub-divides into three subclades: F1a3a, F1a3b and F1a3c. The latter subclade is restricted to Northeast Thailand and South China, while F1a3a seems to have originated in Taiwan and is distributed through Japan and the Philippines. F1a5 is defined by transition at np 10604C, dates to ~9.6 ka, has deep roots in South China, and it is found in Laos, Vietnam (this study) and Taiwan (Loo et al 2014).

F1a1'4 is characterized by a transition at np 9548, dates to ~17 ka, has deep roots in South China (1 KGP), and divides into two main subclades; F1a1 and F1a4. The latter subclade dates to ~17 ka, and has a nested subclade found mainly in Taiwan and the Philippines, named F1a4a1, and dates to ~5.5 ka. The latter distribution was reported by Hill et al. (2007) as a possible marker for the Austronesian dispersal.

F1a1 is defined by a transition at np 16162 in the control region, dates to ~14 ka, and splits into four main subclades: F1a1a, F1a1c, F1a1b and F1a1d. F1a1 has deep roots in South China (Ji et al 2008) and MSEA (this study), and its subclades are widespread in MSEA, China, Taiwan, Japan and ISEA. F1a1b seems to have originated in Japan, while Taiwan and the Philippines can be seen within the subclade F1a1d, and in the HVS-I data (Figure 36), F1a1* branches are also seen in Peninsular Malaysia, Korea, Indonesia, Singapore and India. F1a1c is defined by transitions at nps 548 and 10211, dates to ~11.9 ka, and has basal lineages found in South China (1KGP), Taiwan (Ko et al 2014) and Myanmar (Mormina, 2007). F1a1c is also seen in western Thailand (Pradutkanchana et al 2010) as a separate subclade which is defined by a transition at np 16224, dates to ~10 ka, and includes a basal branch from Northwest Peninsular Malaysia (Eng 2010) where it may have originated and then dispersed into west Thailand.

F1a1a is defined by transitions at nps 8149 and 16108, dates to ~8.8 ka, is commonly found in MSEA, and its basal lineages are seen in MSEA and South China. In MSEA it is commonly found in North Laos (this study, Bodner et al 2011), northwest Thailand

(Fucharoen et al., 2001, Jin et al., 2009, Zimmermann et al., 2009), the Stieng people in southern Vietnam (this study) and the Kayin people in Myanmar (summerer et al., 2014). In Malaysia, it is mainly detected within the aboriginal Senoi people in West Malaysia (Macaulay et al., 2005), and it is also seen in western Indonesia (Hill et al., 2007). However, this haplogroup is almost absent from the northern parts of Asia, and completely absent in Japan and Korea. This could suggest that the origin of this haplogroup was in MSEA/South China, followed by migratory events into the Peninsular Malaysia and then to the ISEA. The main derived cluster, F1a1a1 is defined by a transition at np 11215, dates to ~7.8 ka, and is mainly seen in MSEA, where most of the basal lineages are found in Thailand (Pradutkanchana et al 2010; Kuntnan et al 2017), Vietnam (1 KGP), and in Peninsular Malaysia (Eng 2014). Overall the F1a1a pattern could indicate the rapid spread of the coastal Neolithic into MSEA during the early Holocene (Higham 2014).

4.4.11 Haplogroup R11

Haplogroup R11 is seen primarily in China (Kong et al., 2003, Zheng et al., 2011; Lippold et al., 2014). R11 is dated to ~21 ka, branching into R11a, R11b and R11+5105 (R11C). All three branches are dated to the Late Glacial between ~16 and 20 ka. R11a is absent from MSEA and restricted to South China with just one from Japan (Ueno et al 2009), while both R11b and R11c include some complete sequences from Laos, Vietnam (this study; Mormina 2007) and Thailand (Kutanan et al 2017). R11b is divided into two main sub-clades, R11b1 (Figure 93) and R11b2 (Figure 92), with a basal linage from China (1KGP), and both sub-clades date to the Late Glacial, ~16 ka and ~18 ka respectively. R11b1 branches into R11b1a, R11b1b, and R11b1c (nomenclature introduced here), and they all date to the late Pleistocene/early Holocene age, between ~13.4 and 8.4 ka.

Both R11b1a and R11b1b are largely restricted to South China (Kong et al 2003; Lippold et al., 2014) with just one complete sequences from south Siberia (Derenko et al., 2012). R11b1c is divided into R11b1c1 and R11b1c2; R11b1c1 is restricted to Peninsular Malaysia (Eng, 2014), and is dated to the early Holocene age ~10.6 ka and R11b1c2 is dated to the Neolithic age ~4.6 ka, and includes the major MSEA component within R11, where it represents particularly the northern side of MSEA; Tai-Kadai (specifically Tay and Nùng) speakers in north Vietnam, north Laos (this study) and northeast Thailand (Kutanan et al. 2017). The latter sub-clade pattern and its age reflects the founder analysis result (Figure 92) for MSEA (table 11), which showed the major fraction of the migration events into MSEA dated between ~4.2 and 6.9 ka (using *f1* and *f2* criteria, respectively), suggesting a Neolithic or postglacial component dispersal from South China into north MSEA.

4.4.12 Haplogroup R22

R22 is a basal haplogroup within R dating to ~41.4 ka, and within the complete sequence data it seems mainly found in MSEA. But, the HVS-I data indicate that there are many mtDNA samples from South and Southeast Asia that could belong to this haplogroup. R22 is sub-divided into three sub-clades, which are newly named her as R22a, R22b and R22c (Figure 94). In this study, the R22 tree was reconstructed from 42 complete sequences: 23 R22a, 5 R22b and 3 R22c. The latter sub-clades show high levels of genetic drift.

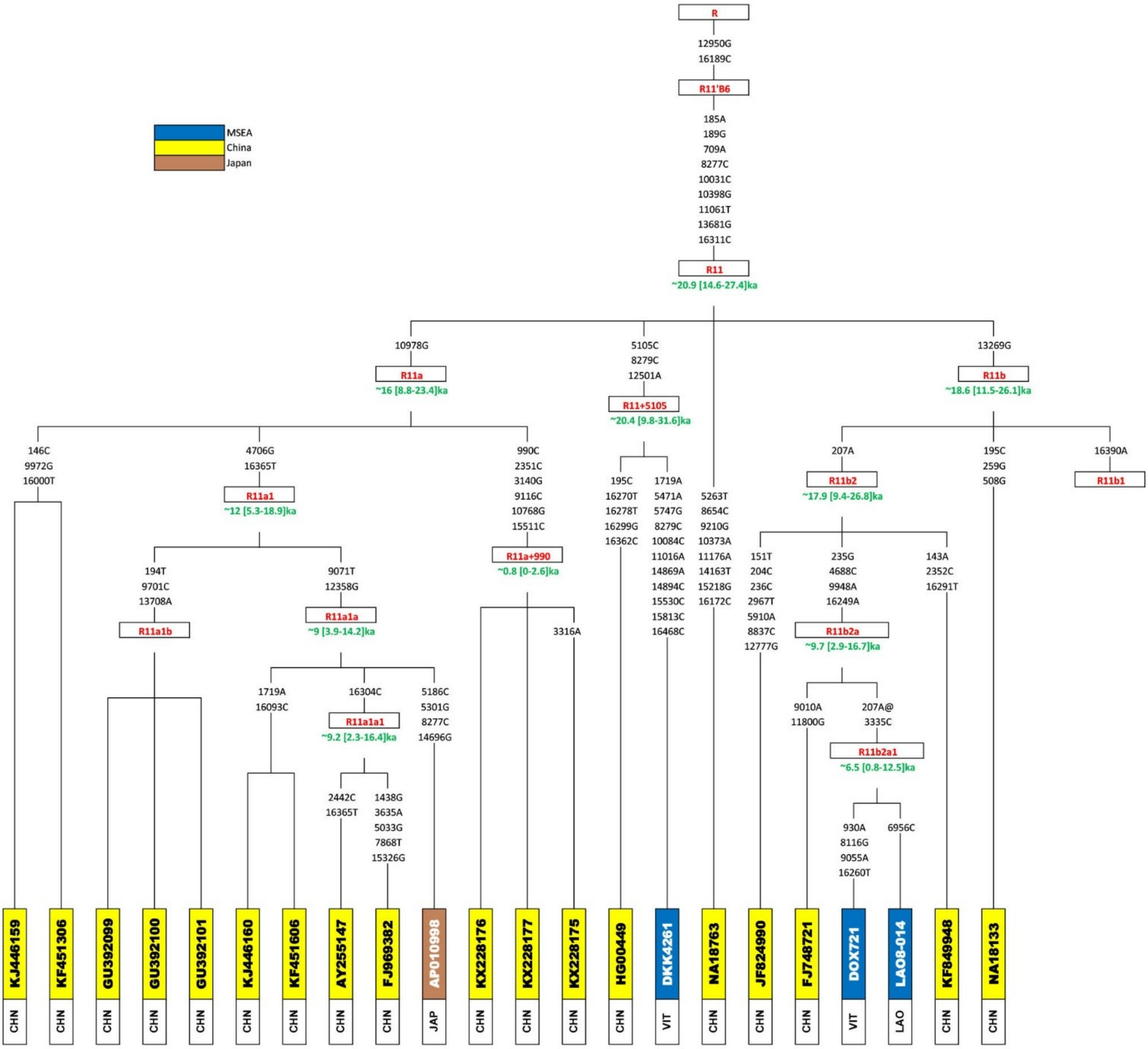

Figure 92. The tree of haplogroup R11. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, JAP – Japan, LAO – Laos).

R22a is defined by a reversion at np 152, dividing into R22a1, R22a2 and R22a3, and is dated to ~40 ka. Both R22a1 and R22a2 date to before the LGM, between ~34 and ~38 ka, while R22a3 is seen in Myanmar, Peninsular Malaysia, Indonesia (Eng, 2014) and Vietnam (1KGP) and dates to the early Holocene age ~13.4 ka. In the HVS-I data, R22a can be recognized within the R22a1a1 sub-clade (Figure 95) by the transitions at nps 16390 and 16301, which cluster many Cambodians (Zhang et al 2013) with some samples from India (Cordaux et al., 2003), the Nicobar Island (Trivedi et al., 2006), Indonesia, Malaysia (Hill et al., 2007), Thailand (Yao et al., 2002) and Vietnam (Peng et al., 2010). This pattern could suggest that R22 could be a surviving lineage from the first arrivals of the Sunda shelf region, and then it is widespread as indigenous groups.

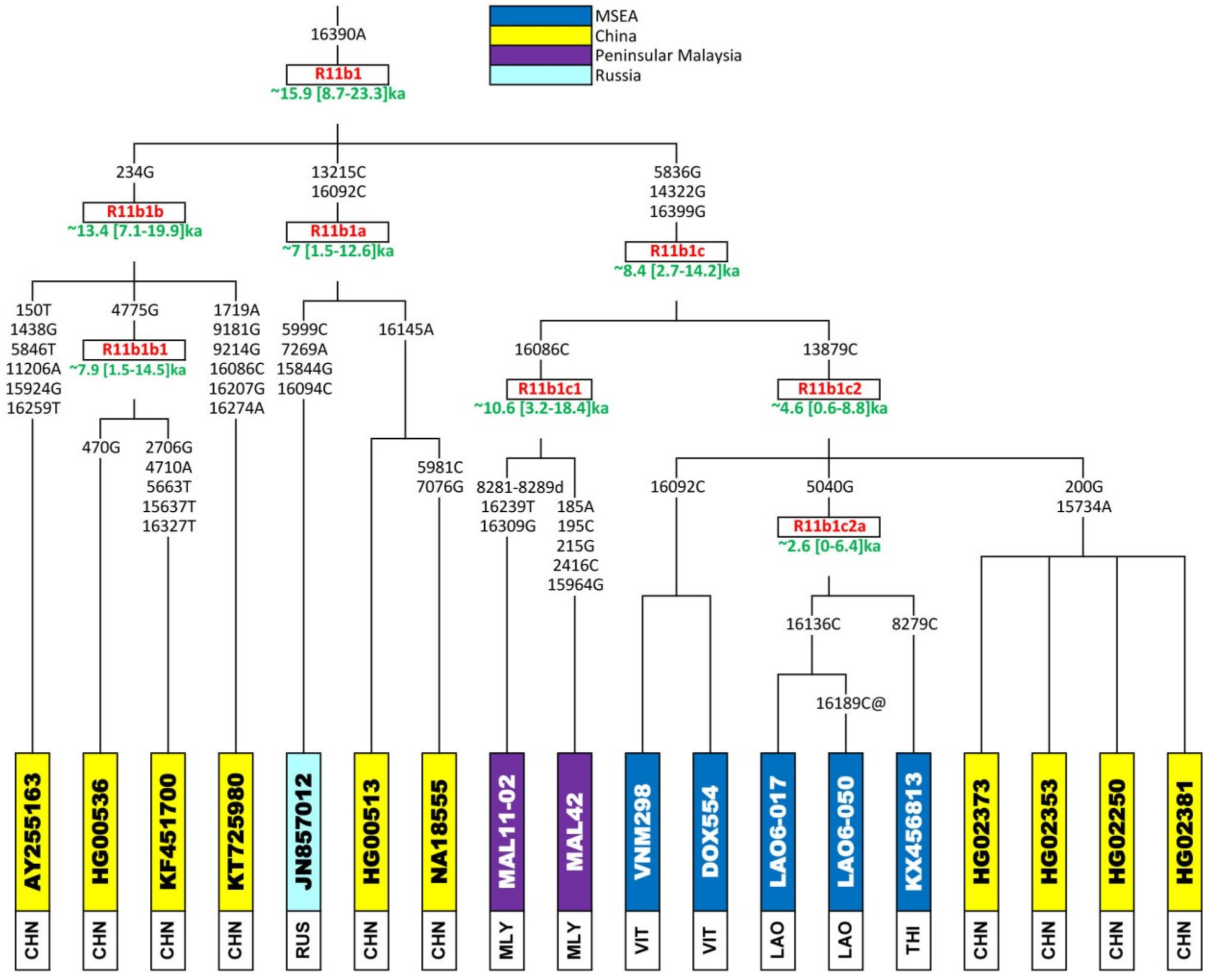

Figure 93. The tree of haplogroup R11b1. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, JAP – Japan, LAO – Laos).

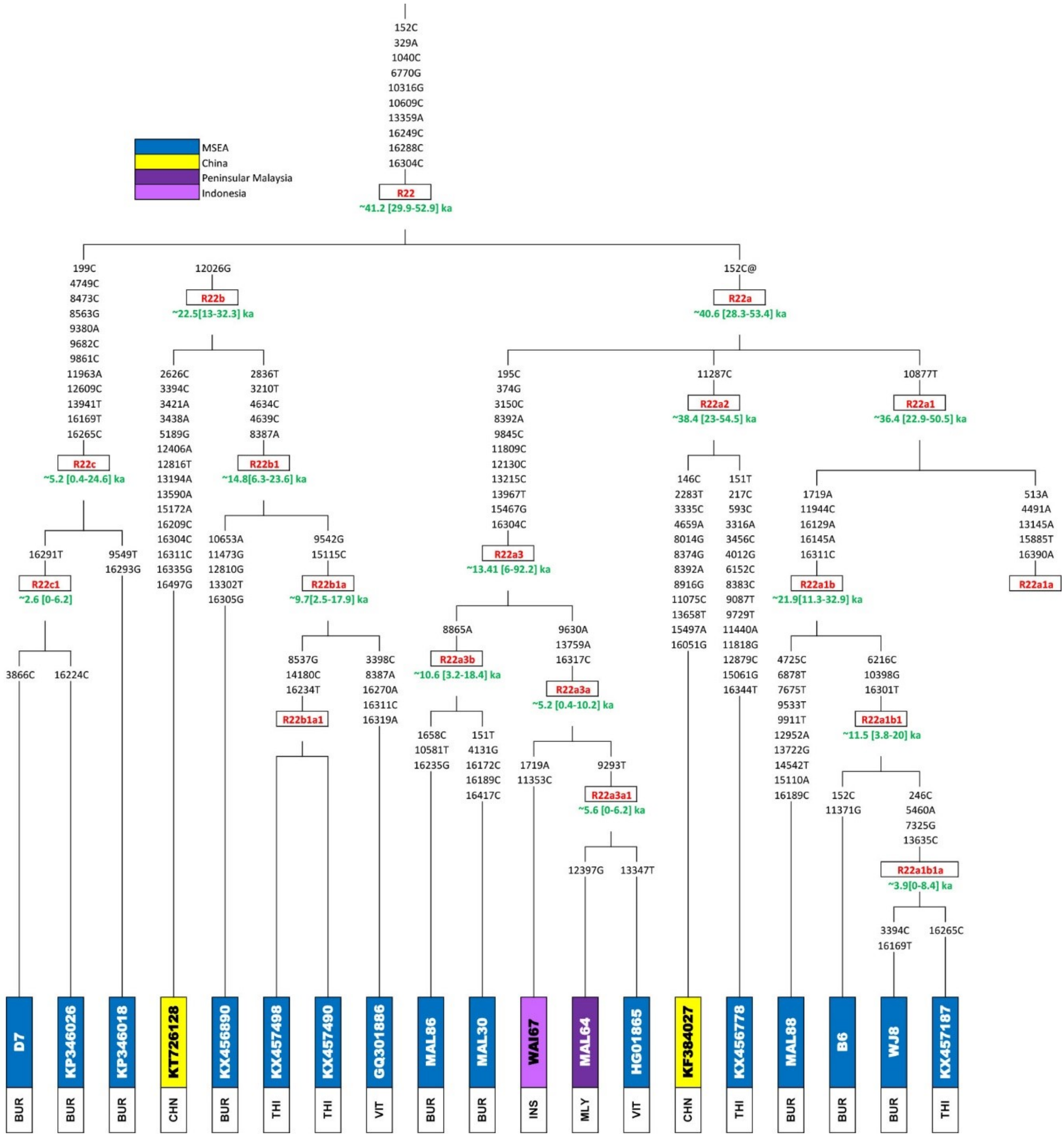

Figure 94. The tree of haplogroup R22. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, BUR – Myanmar, MLY – Malaysia, THI – Thailand and INS - Indonesia).

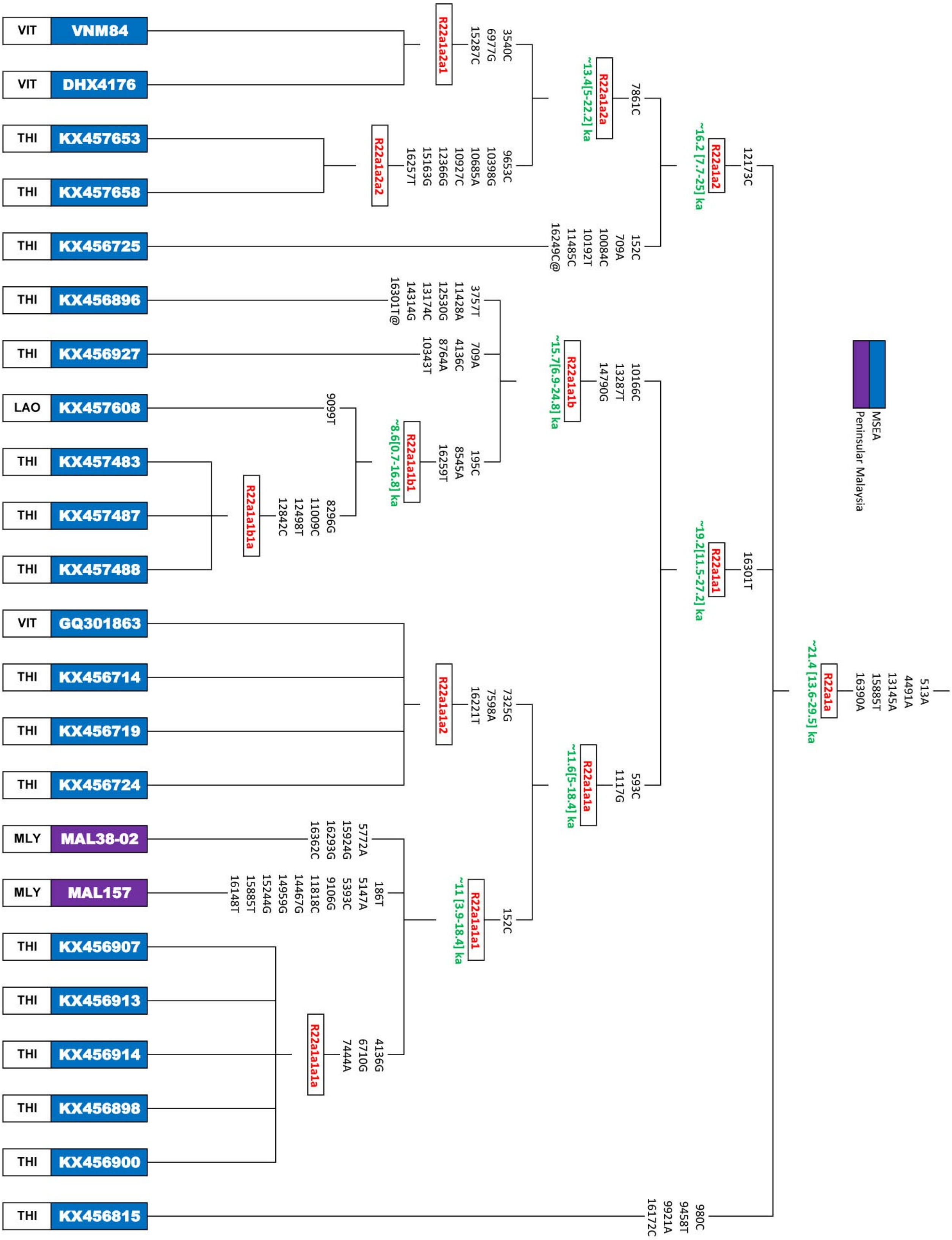

Figure 95. The tree of haplogroup R22a1a. Age estimates (in ka) displayed is an averaged distance (ρ) in green. (CHN – China, VIT – Vietnam, BUR – Myanmar, MLY – Malaysia, THI – Thailand and INS - Indonesia).

5. Result and Discussions: Founder analysis

- **Founder Analysis results.**

I used founder analysis to address the following questions for the MSEA populations:

- What fraction of modern-day lineages date to the first settlements? What fraction of lineages date to arrivals at the time of the rice Neolithic, around 3.8 ka?
- Are there signs of an important impact of postglacial climate change and sea-level rises on human population dispersals, as in ISEA?
- Are there significant dispersals from the north in the early Holocene that might be associated with the so-called "coastal Neolithic" expansion of foraging populations?
- Are there signs of either ancient or recent dispersals to the Indian Subcontinent?
- In addition, I used a modification of the founder analysis to estimate the timing of the major splits between basal ISEA and MSEA lineages, in order to estimate when the mtDNA pools of the two regions first separated after the initial out-of-Africa arrivals, and to date any further major separations.

5.1 Selecting the sink and source populations

The first important step in the founder analysis is defining the sink and source populations, meaning the regional population datasets for each lineage or haplogroup within a certain region are going to be defined as sink or source (or undefined if the datasets are not playing any role in the founder analysis).

In this study, the sink population is defined as all of the MSEA countries (Myanmar, Cambodia, Thailand, Laos and Vietnam), and in total 3,790 HVS-I sequences and 2752 complete mtDNA sequences for all the latter countries were used.

Three main source populations were selected for the founder analysis, including other parts of Southeast Asia (South China, Peninsular Malaysia and ISEA), East Asia (Japan, Korea and Taiwan) and South Asia (Nepal, Bangladesh, Bhutan, India and Sri Lanka). South China (*n* = 5058) is considered as a primary source for the rice agriculturalists in Southeast Asia (Charles Higham, 2014), but all the other parts of China were also included in this study because of the complex history of Chinese people and the need for as full a source database as possible. Additionally, since the Southeast Asian coastline saw major dispersals due to sea level rise at the end of last ice age (Jiao 2006), all other parts of Southeast Asia, *i.e.* Peninsular Malaysia (n= 916) and ISEA (n= 2386), were included in the source database as potentially carrying source lineages for MSEA. Increasing the range of the source database can only improve the analysis since if the additional data is not part of the source it will have no effect but if some further source lineages are included they will improve the accuracy of the results.

5.2 HVS-I founder analysis

I performed the founder analysis first for HVS-I data, using reduced-median networks of HVS-I data (see chapter 2.11.3). To ensure sufficient coverage of variation in the source, the founder analysis requires large datasets, selected from the tens of thousands of HVS-I datasets published. HVS-I datasets are remain very valuable in this regard.

The results are shown in Tables 10 and 11, representing the founder estimations for the *f1* and *f2* criteria for each branch within M and N haplogroups, their founder and ancestor ages and standard errors (SE). The data in Tables 10 and 11 are represented graphically by Figure 96 for the *f1* criterion and Figure 97 for the *f2* criterion. In the latter figure s, the founder types were divided into three main components: The Southeast Asian component (mainly from a South China source), the indigenous Sunda component and the South Asian (or Indian) component.

The Southeast Asian component includes the founder types within B5a, D4g2a, D5, D5a2a1, F1a, G2, M12a1a1, M20a, M21b2, M7b, M9a, N10a, R9b1, R9c1 and Z. Most of these major founder types are dated between end of LGM and the Neolithic. The older founder types are seen within M7b*, M12b, M74, N10, N21 and Z, dating to around the LGM and Late Glacial, while the most recent founder types are found within D5 and C*, and date to the last few thousand years (table 10). The most important contributors to the pre-Neolithic postglacial period (are found within F1a*, F1a1a and B5a. The latter branches are not commonly found further north, but are common in South China and MSEA. With their founder ages estimations, this could indicate to that they arrived before the rice expansion event in MSEA.

The founder age for M7b1b *(f1)* dates to 4.5 and it is seen on the eastern coast of China (Wen et al., 2004), north Laos, north Vietnam (this study) and north Thailand (Kuantan et al., 2017) but is not found in south MSEA. Therefore, it could contribute both coastal and rice Neolithic expansions. Many less common founder types within the Southeast Asian component date to the early and middle Holocene age between 11.6 and 6 ka. All these founder types, R9b1, R9c1, M12a1a1, M7b1a1a, M21b2, M9a, M20a, G2, B5a, B4g2a, B5a1d and F1a1a are seen mainly in South China, and they represent the hunting and gathering component and a deeper ancestry relationship between MSEA and South China.

B5a, F1a and M7b are the most frequent haplogroups in MSEA and the founder types in MSEA within their branches suggest several important events. Both B5a and F1a with their subclades are widely distributed in Southeast Asia, especially in South China, their ancestral ages in SEA date to ~14.5 ka, and the founder ages in MSEA mostly indicate pre-Neolithic events (except F1a1* *(f1)* which has a founder age dating to the Neolithic age ~3.5 ka). M7b* are less common in MSEA than South China and its ancestor and founder age date to the LGM age (table 6), while subclades M7b1b (with ancestor age ~6.3) and M7b1a1a (with ancestor age ~15.5 ka) are more common in MSEA and their founder ages indicate Neolithic (~5) and early Holocene (~10 ka) expansions respectively. This suggests multiple migration waves from South China to MSEA during the Holocene.

The founder types in MSEA within the Sunda and Indian components are less common and older than the South Chinese components (Figures 96 and 97). The Sunda component includes the branches B6a, M12a1b1, M12b, M17a, M51, M71, M72, N21 and R22a, which are largely confined in MSEA, ISEA and Peninsular Malaysia (Sundaland). Their founder and ancestor ages predate the sea-level rise events (from ~14.5 ka), excluding R22a which dates to ~4.2 ka This pattern suggests that the Sunda component could be surviving lineages from the first arrivals of the Sunda shelf region.

The Indian component includes the founder types within branches of N*, M3, M33a2'3, M33b1, M84 and U2e, which are commonly found in India. Most of these founder types in MSEA date to the LGM and pre-LGM, excluding U2e and M49 which date to ~3.7 ka and ~8.8 ka respectively. These results might be taken to indicate that a major

South Asian component in MSEA arrived in multiple waves during prehistoric times, but the small sample sizes for the founder clusters and consequent wide confidence intervals mean that we should treat this with some caution.

The *f1* and *f2* results are overall very similar. Overall, the data in Tables 6 and 7 suggest that, excluding minor “accidental” lineages (i.e., very recent arrivals: Richards et al. 2000), the South Asian component amounts to just 3.1% in *f1* and 3.5% in *f2*, and the indigenous Sunda component to 18-19%. By far the largest component is from the northern Southeast Asia/South China source, which amounts to 79% in *f1* and 77% in *f2*.

Table 10. HVS-I phylogenetic network of Haplogroup M, with inferred sources distinguished in red (South Asia), black (northern Southeast Asia/South China) and blue (Sunda).

Haplogroup to which founder cluster belongs			*f1/f2*	Motif	*n*	Founder (ka)		*n*	Ancestor age (ka)	
						Age	(SE)		Age	(SE)
M	M3	M3	*f1*	root	8	27.1	(± 10.0)	83	23.5	(± 5.8)
		M3	*f2*	root	8	27.1	(± 10.0)	83	23.5	(± 5.8)
	M7b	M7b1b	*f1*	+192	81	4.5	(± 1.6)	332	6.3	(± 1.4)
		M7b1a1a	*f1*	+189	34	9.8	(± 3.7)	301	15.5	(± 6.8)
		M7b	*f1*	root	16	19.8	(± 8.8)	854	28.5	(± 9.7)
		M7b1b	*f2*	+192	82	4.9	(± 1.6)	332	6.3	(± 1.4)
		M7b1a1a	*f2*	+189	35	10.0	(± 3.6)	301	15.5	(± 6.8)
		M7b	*f2*	root	16	19.8	(± 8.8)	854	28.5	(± 9.7)
	M9	M9a1b1	*f1*	+158 +234	37	4.1	(± 1.7)	136	8.6	(± 2.4)
		M9a	*f1*	234	12	8.3	(± 4.8)	408	26.8	(± 11.5)
		M9a1b1	*f2*	+158 +234	37	4.1	(± 1.7)	136	8.6	(± 2.4)
		M9a	*f2*	234	12	8.3	(± 4.8)	408	26.8	(± 11.5)
	M12	M12a1b1	*f1*	+172 +189	17	19.0	(± 12.8)	22	20.6	(± 16.2)
		M12b	*f1*	+129 +172	84	23.2	(± 12.1)	92	24.0	(± 13.2)
		M12a1a1	*f1*	362	8	10.4	(± 8.6)	31	12.0	(± 7.1)
		M12a1b1	*f2*	+172 +189	17	19.0	(± 12.8)	22	20.6	(± 16.2)
		M12b	*f2*	+129 +172	86	23.2	(± 12.1)	92	23.9	(± 12.9)
		M12a1a1	*f2*	362	10	11.7	(± 7.6)	32	12.0	(± 7.1)
	M17	M17a	*f1*	+129 +325 +209	14	13.1	(± 8.7)	27	17.3	(± 6.5)
		M17a	*f2*	+129 +325 +209	16	16.7	(± 8.2)	27	17.3	(± 6.5)
	M20	M20	*f1*	root	26	8.3	(± 4.8)	109	14.1	(± 8.3)
		M20	*f2*	root	26	8.3	(± 4.8)	109	14.1	(± 8.3)
	M21	M21b2	*f1*	+192 +291 +145 +181 +304	7	9.5	(± 5.8)	15	10.0	(± 6.9)
		M21b2	*f2*	+192 +291 +145 +181 +304	7	9.5	(± 5.8)	15	10.0	(± 6.9)
	M33	M33b1	*f1*	+259 +324 +362	9	22.2	(± 13.6)	17	22.6	(± 10.5)
		M33a2'3	*f1*	+172	4	25.0	(± 13.2)	36	26.4	(± 14.9)
		M33b1	*f2*	+259 +324 +362	10	21.7	(± 12.4)	17	22.6	(± 10.5)
		M33a2'3	*f2*	+172	4	25.0	(± 13.2)	36	26.4	(± 14.9)
	M49	M49	*f1*	root	17	8.8	(± 5.3)	174	32.2	(± 7.8)
		M49	*f2*	root	17	8.8	(± 5.3)	174	32.2	(± 7.8)
	M51	M51	*f1*	root	17	26.5	(± 17.4)	30	31.1	(± 11.9)
		M52	*f2*	root	25	28.7	(± 13.1)	30	31.1	(± 11.9)
	M71	M71	*f1*	root	37	33.8	(± 14.8)	73	33.6	(± 10.5)
		M71	*f2*	root	44	36.0	(± 13.1)	73	33.6	(± 10.5)
	M72	M72	*f1*	root	21	30.2	(± 12.5)	26	30.1	(± 11.4)
		M72	*f2*	root	21	30.2	(± 12.5)	26	30.1	(± 11.4)

	D4	D4g2a	*f1*	+274	14	6.0	(± 2.7)	35	12.9	(± 3.7)
		D4g2a	*f2*	+274	15	7.8	(± 2.9)	35	12.9	(± 3.7)
	D5	D5a2a1a	*f1*	+@172 +164 +92 +266 +172	7	1.0	(± 0.6)	44	11.8	(± 3.9)
		D5b1c1	*f1*	+92 +148	2	1.7	(± 1.2)	37	9.9	(± 4.9)
		D5	*f1*	root	11	0.8	(± 0.5)	352	47.4	(± 15.2)
		D5a2a1a	*f2*	+@172 +164 +92 +266 +172	9	1.3	(± 0.6)	44	11.8	(± 3.9)
		D5b1c1	*f2*	+92 +148	2	1.7	(± 1.2)	37	9.9	(± 4.9)
		D5	*f2*	root	11	0.8	(± 0.5)	352	47.4	(± 15.2)
	Z	Z	*f1*	root	25	15.3	(± 7.3)	249	17.1	(± 5.1)
		Z	*f2*	root	47	22.4	(± 9.9)	249	17.1	(± 5.1)
	G2	G2	*f1*	root	22	7.6	(± 5.8)	276	57.0	(± 22.0)
		G2	*f2*	root	23	8.7	(± 5.6)	276	57.0	(± 22.0)

Table 11. Founder estimates for the *f1* and *f2* criteria within haplogroup N, with inferred sources distinguished in red (South Asia), black (northern Southeast Asia/South China) and blue (Sunda).

Haplogroup to which founder cluster belongs			*f1/f2*	Motif	Founder			Ancestor		
					n	Age	(SE)	n	Age	(SE)
N	N*	N*	*f1*	root	4	37.5	(± 16.1)	35	59.6	(± 10.2)
		N*	*f2*	root	4	37.5	(± 16.1)	35	59.6	(± 10.2)
	N10	N10a	*f1*	+300	6	19.5	(± 14.4)	31	26.4	(± 12.8)
		N10a	*f2*	+300	6	19.5	(± 14.4)	31	26.4	(± 12.8)
		N10b	*f1*	+69 +278 +291A +298	3	22.2	(± 15.7)	10	15.0	(± 6.5)
		N10b	*f2*	+69 +278 +291A +298	4	20.8	(± 12.5)	10	15.0	(± 6.5)
	N21	N21	*f1*	root	5	16.7	(± 7.5)	96	24.8	(± 10.6)
		N21	*f2*	root	68	23.1	(± 11.4)	96	24.8	(± 10.6)
R	R9	R9c1	*f1*	+157	9	11.1	(± 6.9)	143	30.2	(± 16)
		R9b1	*f1*	+309 +390	3	11.1	(± 7.9)	238	35.4	(± 13.8)
		R9b2	*f1*	+362	30	7.8	(± 2.4)	33	9.1	(± 2.6)
		R9c1	*f2*	+157	9	11.1	(± 6.9)	143	30.2	(± 16)
		R9b1	*f2*	+309 +390	3	11.1	(± 7.9)	238	35.4	(± 13.8)
		R9b2	*f2*	+362	30	7.8	(± 2.4)	33	9.1	(± 2.6)
	R22	R22a	*f1*	+301 +390	67	4.2	(± 1.6)	92	7.6	(± 3)
		R22a	*f2*	+301 +390	67	4.2	(± 1.6)	92	7.6	(± 3)
	U2	U2	*f1*	root	2	-	-	284	62.0	(± 12.4)
		U2e	*f1*	+129C +189 +362	9	3.7	(± 2.6)	21	22.2	(± 6.8)
		U2	*f2*	root	10	20.0	(± 14)	284	62.0	(± 12.4)
		U2e	*f2*	+129C +189 +362	9	3.7	(± 2.6)	21	22.2	(± 6.8)
	B5	B5a1d	*f1*	+261	73	5.9	(± 2.2)	191	13.8	(± 6.8)
		B5a	*f1*	root	308	6.9	(± 2.6)	973	14.3	(± 3.9)
		B5a1d	*f2*	+261	84	8.3	(± 3)	191	13.8	(± 6.8)
		B5a	*f2*	root	348	8.7	(± 2.5)	972	14.2	(± 3.9)
	B6	B6a	*f1*	+51	35	18.6	(± 10.3)	47	20.9	(± 8.2)
		B6a	*f2*	+51	37	19.8	(± 9.8)	47	20.9	(± 8.2)
	F1a	F1a	*f1*	root	200	4.8	(± 1.8)	630	14.7	(± 5.5)
		F1a	*f2*	root	205	5.0	(± 1.8)	630	14.7	(± 5.5)
	F1a1	F1a1	*f1*	root	71	3.5	(± 1.4)	378	6.9	(± 1.6)
		F1a1	*f2*	root	82	5.7	(± 2)	378	6.9	(± 1.6)
	F1a1a	F1a1a	*f1*	root	336	5.4	(± 1.4)	668	7.7	(± 1.5)
		F1a1a	*f2*	root	457	7.8	(± 1.9)	668	7.7	(± 1.5)

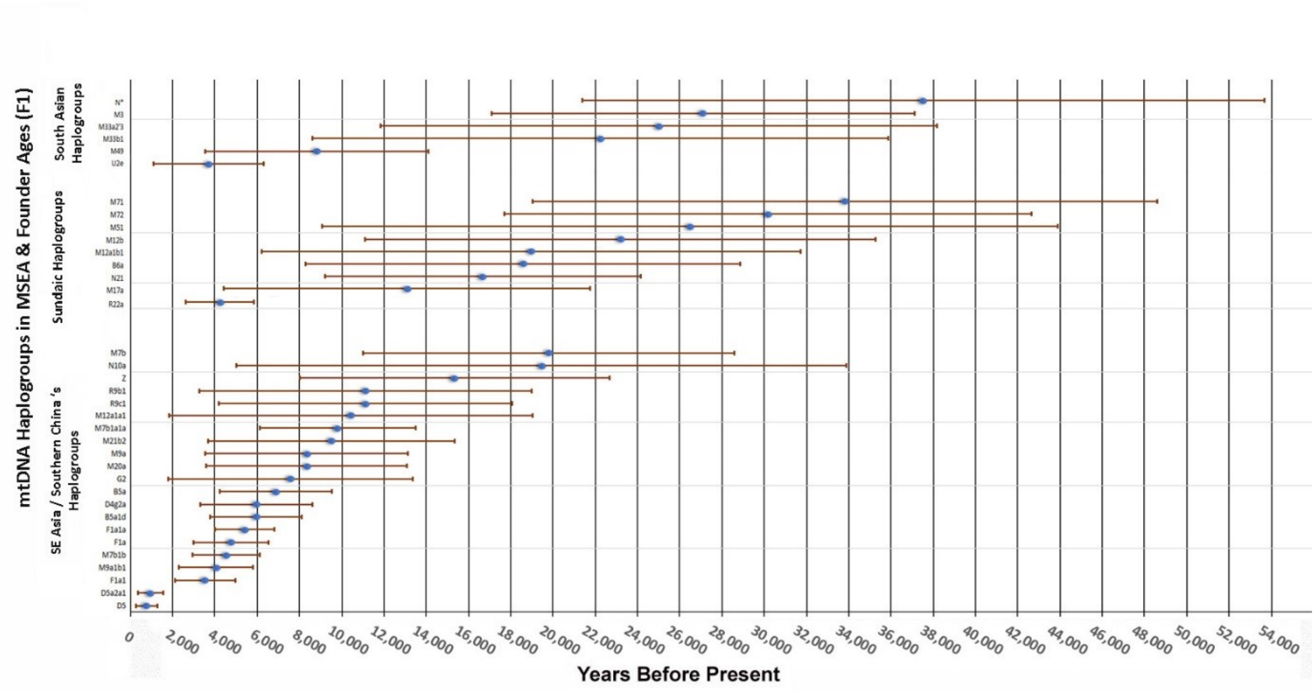

Figure 96. Founder types (f1) for MSEA with inferred sources in Southeast Asia, Sunda and South Asian lineages.

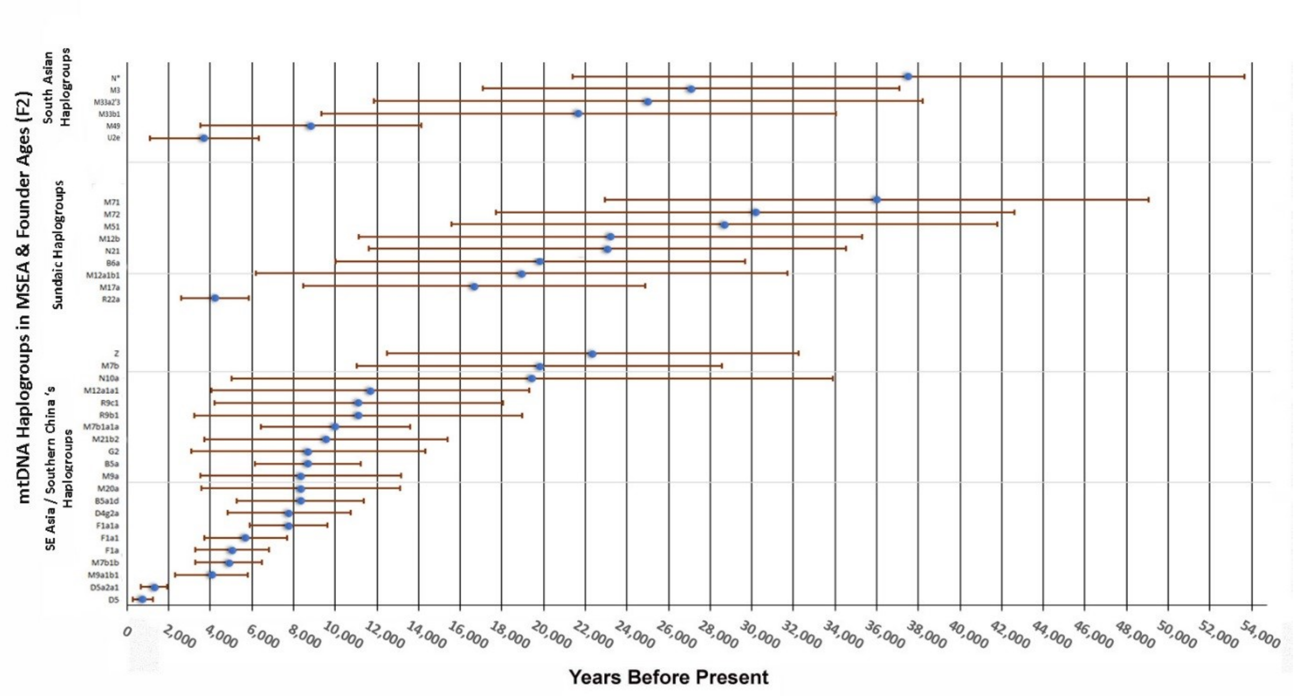

Figure 97. Founder types (f2) for MSEA with inferred sources in Southeast Asia, Sunda and South Asian lineages.

5.3 Founder analysis of complete mtDNA genome data

The increasing accessibility of next-generation sequencing during the course of this project meant that it became possible to sequence the whole mtDNA genome of around 900 samples from MSEA, at a time when the published database was also increasing rapidly. This meant that it became possible to perform a founder analysis with almost as many sink (if not source) samples as the HVS-I analysis, and substantially sharpen and refine the results of the HVS-I analysis. The development of the software (by Dr P. Soares' group, at the University of Minho) also meant that the new complete genome results could be graphically presented in several more illuminating ways.

For the complete mtDNA genome sequences, I applied the analysis using a new version of software which can partition the lineages into either inferred or assumed migration events at particular times (the “Bayesian migration partitioner” or BMP: Richards et al., 2000). A modification of this approach applies discrete migration events for each 200-year interval between 0 to 55 ka in order to perform a preliminary scan of the data for peaks of migration (*cf.* Soares et al., 2016, for ISEA).

In this analysis (Figure 98), we can see that, as for the HVS-I analysis, *f1* and *f2* give very similar results, and indeed the overall pattern is quite similar to that seen with HVS-I. There are two main peaks: the first between ~8 and 6 ka and the second ~50 ka. There are also, however, two slight humps on the left (between ~4.3 and ~3.6 ka) and right (between ~14.8 and ~13.6 ka) of the 8-6 ka peak.

The first, major mid-Holocene peak at 8-6 ka correlates with the third major rapid sea level rise in SEA and the time of the “coastal Neolithic” of foraging groups in MSEA, and the second major peak dates to the time of the first colonization, ~50 ka. The slight humps on the left and right of the first main peak may correspond with the Neolithic proper, which we can call the “rice Neolithic”, and early Holocene movements possibly associated with first major sea-level rise at ~14 ka.

The first peak represents the highest level of immigration into MSEA, during the period referred to by Vietnamese archaeologists as the “coastal Neolithic”, and comprises mainly the major F1a1a (~7.9 ka), B5a1a (~6.7 ka) and F1g (~6.4 ka) founders.

The founder types apportioned to the rice Neolithic are mainly found within M7b1a1, various lineages within F1a, B5a1c1, F3a1, B4b1a2a, B4g1a and C7a. The founder types in the second peak include the basal haplogroups within M, N and R, relating to the first colonization in MSEA.

The Bayesian migration partitioner (BMP) software uses the ρ values for each founder cluster to assign them probabilistically to specific pre-set migrations. Here, the BMP analysis was applied to a five-migration model (100, 3,800, 7,000, 14,200 and 50,000). The 100-year migration represents very recent or historical gene flow, the 3,800-year migration detects the founder types most closely associated with the rice Neolithic, for which the earliest radiocarbon dates are 3.8 ka), the 7,000-year migration (based on the age of the main peak) identifies lineages involved with postglacial expansions, the 14,200-year migration (based on the age of the earlier hump and the timing of the main phase of Late Glacial warming) assesses the impact of the first main rapid warming and sea-level rise, and the 50,000-year migration relates to the earliest peak and the approximate time of the first colonization in SEA.

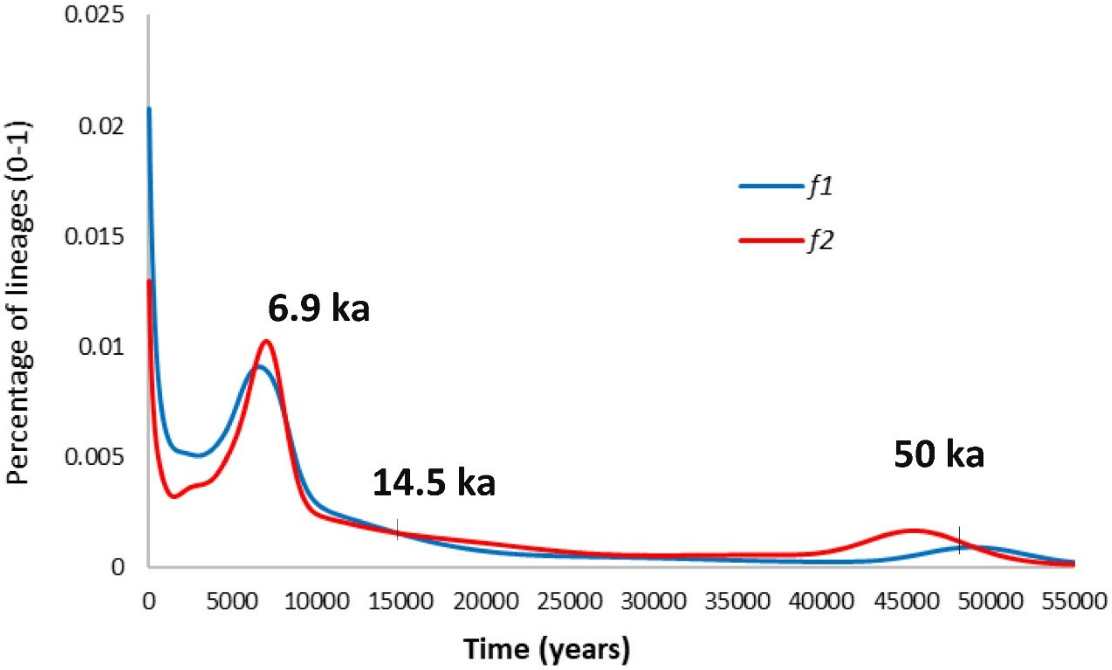

Figure 98. Founder analysis for MSEA mtDNA lineages. Probabilistic distribution of founder lineages across different migration times, with time covered at 200-year intervals from 0 to 50 ka, using f1 (blue) and f2 (red) criteria.

Table 12. Fraction of lineages from complete mtDNA genome pool of MSEA, associated with each of five putative migrations using the two criteria (*f1* and *f2*).

Migration time (ya)	*f1*	*SE*	*f2*	*SE*
100	0.1120	0.0044	0.0622	0.0034
3800	0.2448	0.0342	0.1751	0.0314
7000	0.3651	0.0364	0.3623	0.0337
14,200	0.1690	0.0159	0.2074	0.0049
50,000	0.1091	0.0068	0.1930	0.0146

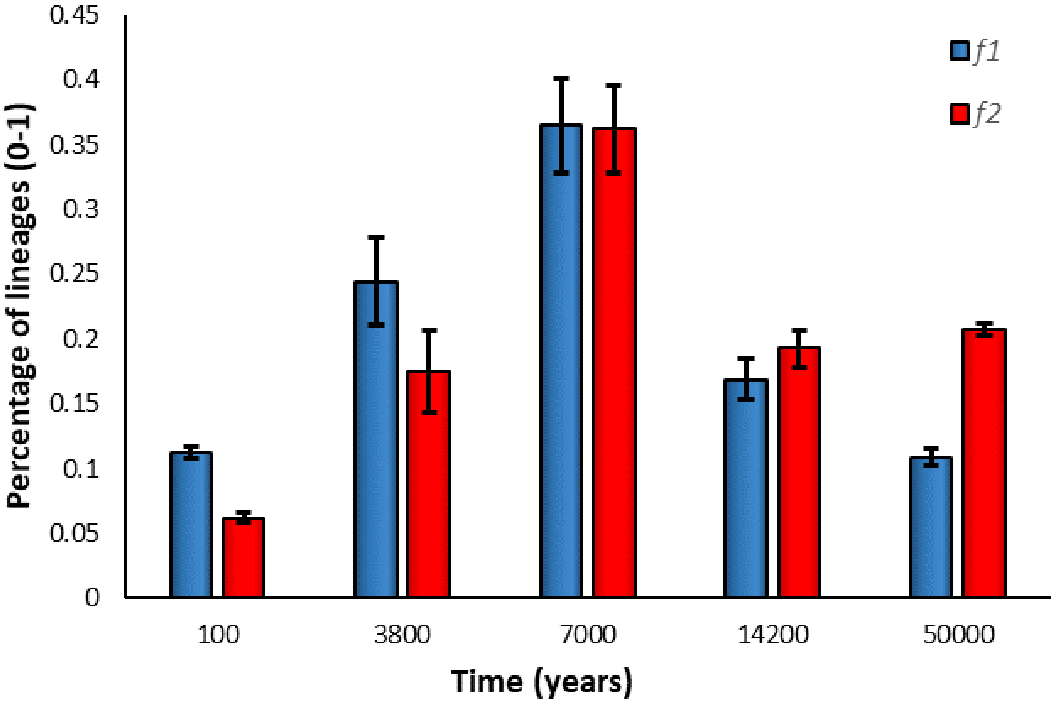

Figure 99. Percentage of lineages from complete mtDNA genome pool of MSEA, associated with each of five putative migrations using the two criteria (f1 and f2).

Table 12 and Figure 99 show the fraction of lineages of the present mtDNA gene pool that contributed to each migration into MSEA, assuming the five-migration model, and each of the main founder clusters (~80% of the total MSEA lineages) is assigned probabilistically to each of the five putative migrations in Figure 100.

The majority of the clusters are found within the Neolithic and early Holocene components which together forms about 61% *(f1)* and 54% *(f2)* of all the founder clusters, and the percentages of the end of LGM (14,200 years' migration) and first colonization components are ~28% *(f1)* and ~40% *(f2)*. The latter percentages of founder types using the *f2* criterion in particular are strikingly similar to the HVS-I analysis.

- *Recent migrations (100 years)*

Very recent gene and historical gene flow into MSEA is formed only 11.2% *(f1)* and 6.22% *(f2)* of all the founder clusters. The major recent migrations are related mainly to R9b1a2a, M7c1a and M7b1a1a3, arriving from the north.

- *Rice Neolithic (3.8 ka migration)*

The “rice Neolithic” component varies between the *f1* (24.5%) and *f2* criterion (17.5%), but the major haplogroups contributing founder lineages within the both criteria are M7b1a1, F1a, B5a, F3a1, B4b, B4g and C7a, as mentioned above. Of the most frequent, M7b1a is the most obviously intrusive primarily during this period whereas others such as especially F1a and B5a are subclades within mainly postglacial MSEA lineages. In some cases, the criteria differ in their assignment of some of these to either the 3.8 ka or 7 ka migrations. F1a1a is a particular example that remains ambiguous although overall more likely to pre-date the rice Neolithic; it is a 7 ka component at 80% probability with the *f2* criterion, but with *f1* it shows 50% probability as a rice Neolithic dispersal.

- *The “coastal Neolithic” (7 ka migration)*

For both the *f1* and *f2* criteria, this migration contributes about 36-37% of all the founder types in MSEA, and the major components include lineages within: B5a, F1a, F1f and F1g. B4a and F1a are amongst the most commonly seen haplogroups in MSEA and South China. Since these likely have an origin in South China, this indicates to a deep genetic relationship between the South China region and MSEA even before the Neolithic farming expansions, with multiple waves of southward migrations throughout prehistory.

- *The Late Glacial (14.2 ka migration)*

This migration contributes ~17% and ~19% with the *f1* and *f2* criteria respectively. Together with the first colonization migration the major components allocated to the 14,200-year migration include many basal M and N haplogroup lineages. For the *f1* criterion, the basal M and N haplogroups include M12, M71, M74b, N9a, B6b, B6a1 and M72, with other lineages including F3a1, F1a1 and B4h. The basal M and N components for the *f2* criterion also include M91a, M49, B6 and M71, with more founder types seen in R9b1a3, B4g1a, D4e1a, C7, B4h, F1a1, B5a1 and F2a. Most of the latter haplogroups are primarily found in Southeast Asia (MSEA/South China) and likely originated there, although *f2* also includes the northeast Indian lineage M49.

- *The first settlement (50 ka migration)*

The first settlement migration (~50 ka) contributes about 11% with the *f1* criterion and 19% with *f2* of the present mtDNA gene pool. The major components of this migration are the remaining paragroups of M* and N*, R22 and R9/R9b. The founder lineages with *f1* include N*, M*. M1’20’51’102’103, R22+152 and R9b; with *f2* they also include M12’G, M74, M9, M73 and M20’103 (Figures 100 and 101).

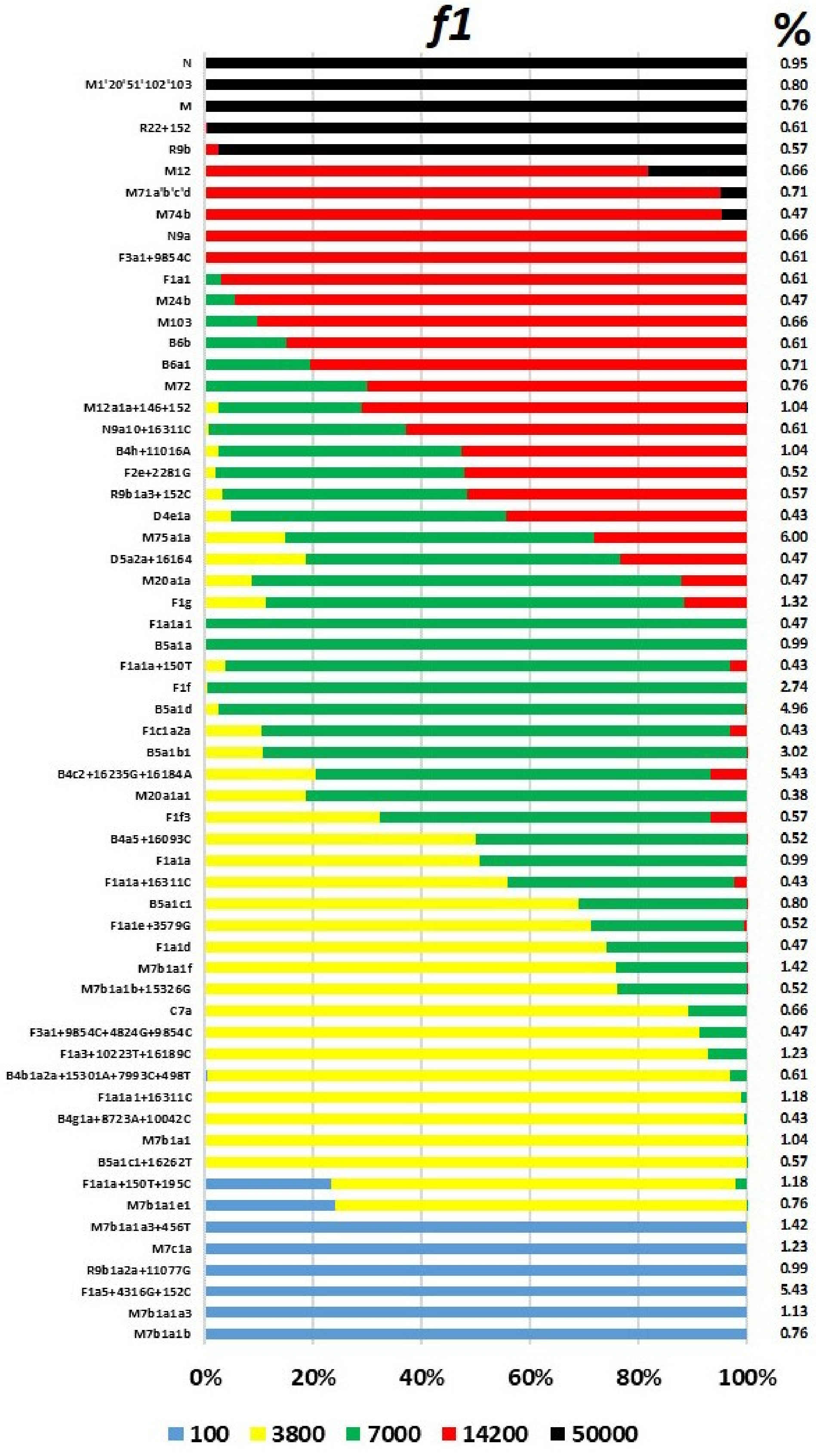

Figure 100. Percentage of each lineage from complete mtDNA genome pool of MSEA associated with each of the 5 migrations using the f1 criteria.

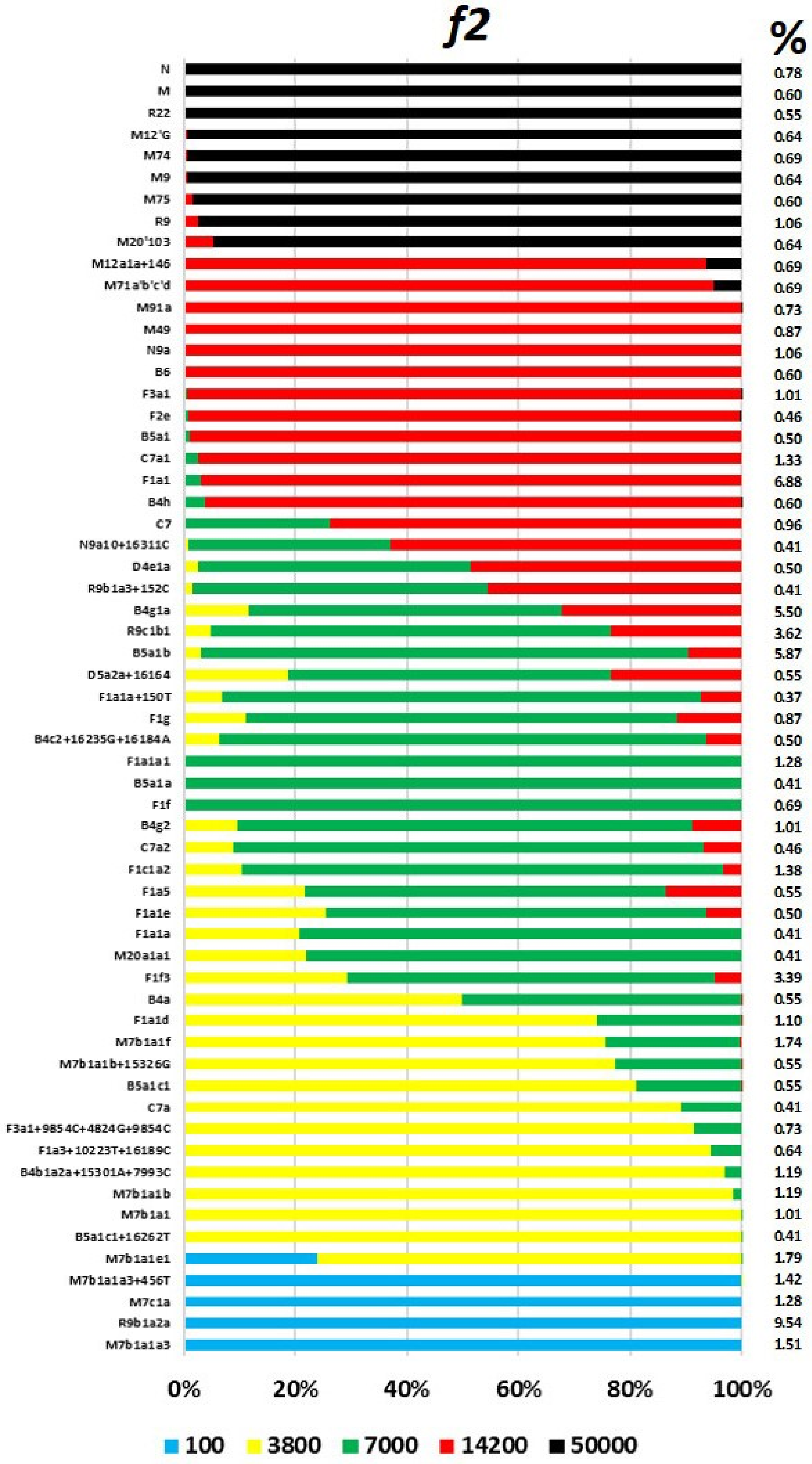

Figure 101. Percentage of each lineage from complete mtDNA genome pool of MSEA associated with each of the 5 migrations using the f2 criteria.

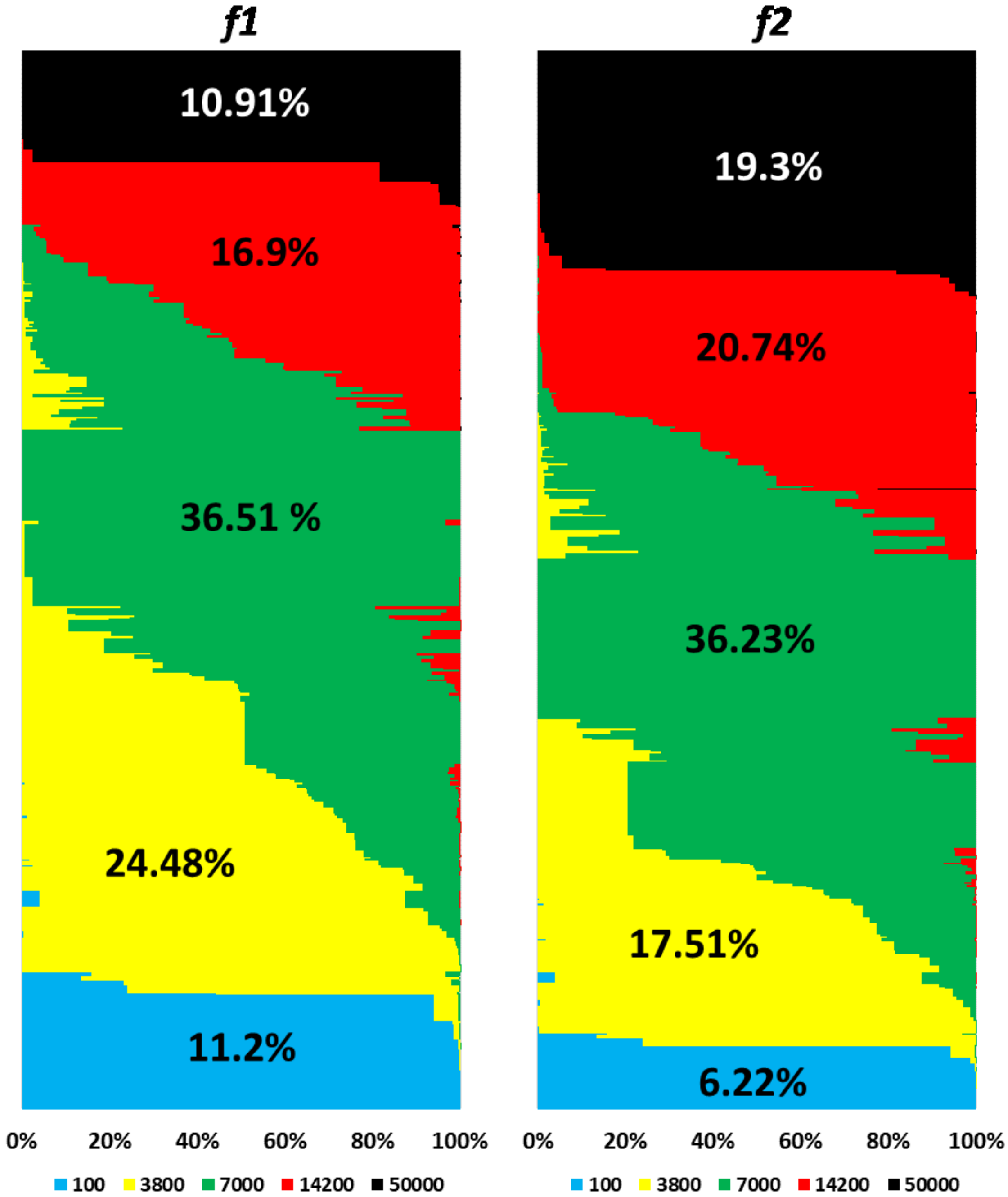

Figure 102. Total Percentages for each migration (5 migrations modal) in MSEA using the two criteria (f1 and f2).

5.3.1 Statistical splitting analysis

In this approach, the founder analysis was modified to obtain split times between the autochthonous Sunda lineages, those found only in MSEA and ISEA. These Sunda lineages have a number of the indigenous Southeast Asian Basal M, N and R haplogroups are shared between MSEA and ISEA, with some showing earlier branching in MSEA and others in ISEA. Each of the divergences into MSEA- or ISEA-specific lineages may therefore correspond to times at which gene flow between the two regions ceased.

Since a standard founder analysis considers only one population as a sink and the other one as a source, I performed the analysis reciprocally, considering in one case ISEA as source and MSEA as sink and in the second case the reverse. After using the splitting analysis, the Bayesian Migration Partitioner was used to obtain a scan of the probabilistic distribution of the age estimates at 200-year intervals from 0 to 70 ka, as before. I performed the analysis with both *f1* and *f2*, but only *f1* gave clear results and is presented here. In Figure 103, we see three major peaks: 54.1-54.8 ka (across the range for both directions), then 13.2 ka for ISEA to MSEA, and 8.4-8.5 ka for MSEA to ISEA.

The earliest major peak of ~54.4 ka is almost identical in both of directions, and this indicating the earliest separation following the first colonization of Sundaland from a common ancestral maternal pool. This would provide a lower bound estimate for the settlement time and compares with 60.8 [54.9 - 66.9] and 55.1 [50.5 - 59.7] ka for the overall age of haplogroup M lineages with ML and ρ respectively, and 64.1 [55.9 - 72.5] and 63.0 [53.4 - 72.8] for haplogroup R lineages with ML and ρ respectively (haplogroup N lineages do not readily provide a similar founder age due to the nesting of R). These estimates overlap in the rang 55-60 ka, just above the estimate for the time of the split.

Intriguingly we see a distinction between the two regions after the end of the ice age, with MSEA lineages separating in the Late Glacial ~13 ka and ISEA lineages separating later, ~8.5 ka, around the time of the final sea-level rise (Pelejero et al., 1999). The latter matches the pattern of dispersal across ISEA seen in haplogroups E and B4a1a (P. Soares et al., 2011; P. Soares et al., 2008), which similarly indicated that the final stage of sea-level rise left the clearest signature in mtDNA distributions, whilst the earlier stages may have led the widespread extinctions witnessed by very long branches due to high levels of genetic drift. Lasting impact in MSEA, where loss of territory due to encroachment by the sea was minimal, seems to have been much earlier in the process.

Between the last two events (the major flooding and first colonization for the Sundaland region) we can also see slight enigmatic humps during the glacial period, ~41 ka in ISEA and ~23 in MSEA. These were both periods of cooling, which potentially might be relevant, but the reason for them merits further investigation.

After the peak ~8.5 ka in both directions there is a slight hump ~3-4 ka that possibly could represent a slight impact of the (distinct) Neolithic expansions from one region to the other.

Overall, the plot encapsulates the major demographic episodes in the history of the Sunda continent: the first settlement by anatomically modern humans dispersing from Africa and the break-up into MSEA and the islands of Sumatra, Borneo and Java in ISEA after the end of the Ice Age.

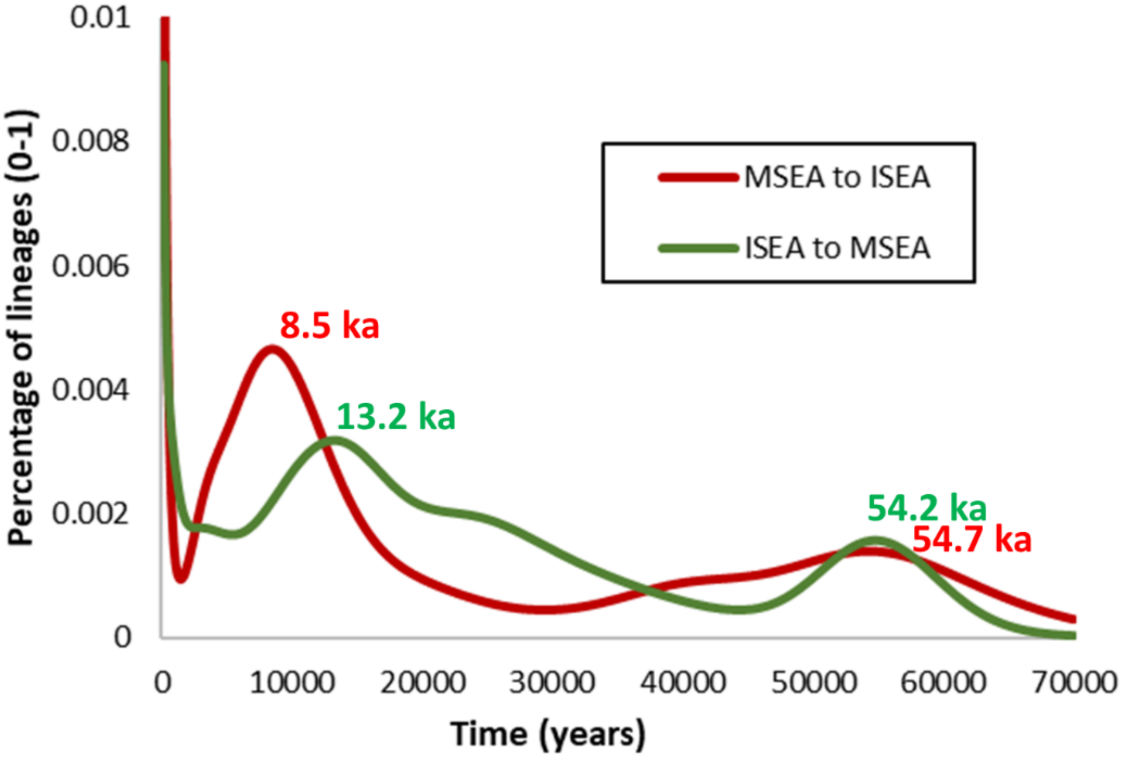

Figure 103. Probabilistic distribution of lineage splitting for the Sundaland region (MSEA and ISEA) across migration times, with time scanned at 200-year intervals from 0 to 70 ka, using migrations in two directions: MSEA to ISEA (red) and ISEA to MSEA (green).

6. Discussion and Conclusion

6.1 Discussion

In the current study, I attempted to investigate the arrival of populations in MSEA by means of screening the maternal evolutionary history of its populations. There are some limitations of using mtDNA as a genetic marker to understand the full evolutionary history of human populations. This marker can be used only to investigate the human evolution from the perspective of the maternal line of descent. Technically speaking, there are also limitations in the software that can analyse efficiently the massive mtDNA data that can be produced by the NGS platforms. Most of the bioinformatics software struggle to identify the indels (deletion/insertion variants) during mapping the NGS reads data to the reference sequence (rCRS), such as the mtDNA-server (https://mtdna-server.uibk.ac.at/index.html) and the MtoolBox (https://sourceforge.net/projects/mtoolbox/). However, all the NGS reads can be mapped using the EAGER software (see 2.8) which works more efficiently to detect the indels in the mtDNA data, and then all the samples that contain the insertion and deletion variants can be checked by using the Geneious (see 2.9).

In addition, using only modern DNA samples will not allow us to understand the full picture of the evolutionary process over time. Therefore, the availability of ancient DNA data in the same region can help to support and clarify the details of this process. In Southeast Asia, the human ancient DNA data is, however, very limited. The only ancient human genome-wide studies in the region to date are eighteen Southeast Asian individuals for five ancient sites in MSEA spanning from the Neolithic to Iron Age between ~4.1-1.7 ka (Lipson et al 2018), and a further 26 individuals from across prehistoric Southeast Asia and Japan, including Laos, Thailand and Vietnam (McColl et al. 2018). The former study in particular reported that the early farmers from Vietnam have a mixture of southern Chinese agriculturalist and eastern Eurasian hunter-gatherer ancestry, and the latter study arrived at similar conclusions from its broader prehistoric dataset (although there were few early Neolithic samples). These ancient DNA results support and clarify further details about the rice Neolithic expansion process investigated and discussed in this study using modern mtDNA data (see 6.1.4).

MSEA lacks geographic barriers, which may be an important factor that has led to high levels of gene flow since the time of the first settlement. The screening of the maternal genome diversity shows a rich mtDNA gene pool extending over Southeast Asia and South China (especially. the adjoining provinces of Guangxi and Yunnan in coastal China). The neighbouring areas of South China and coastal China harbour the highest maternal genomic similarities with MSEA, particularly the northern parts of Vietnam, Laos and Thailand, while the East and Central China (including the Yangtze River regions) are genetically more closely related to northern Asian populations. The latter convergences were confirmed by the PCA result which showed both Yunnan and Guangxi as the most similar regions in China with Vietnam, Laos and Thailand, and the Yangtze River provinces such as Jiangsu, Hubei and Anhul are located within the northern Asian populations.

The gene flow and the varies settlements events in MSEA were likely most significant at certain times: in particular, the initial Pleistocene settlement, the end of the Last Glacial maximum and the Late Glacial warming phase, the early Holocene and the Neolithic. By using a high-resolution phylogeographic analysis with a well-estimated molecular clock (P. Soares et al., 2012; P. Soares et al., 2009), the latter events can be investigated and discussed to address the direction and timing of modern human dispersals and expansions in MSEA.

6.1.1 The first settlement of Sundaland

The ancient Sundaland region is considered to be a key area of initial settlement of the anatomically modern humans, who likely expanded along the coastal route from the Horn of Africa via Arabia and South Asia towards Australasia. During the Ice Age the Sunda shelf was exposed and the Sunda continent connected MSEA western ISEA (Java and Sumatra) and whole of the island of Borneo, but global warming after about 20 ka led to rises in sea levels which flooded a large part of the Sundaland continent.

Although beginning ~19 ka, the rises in sea level were probably not gradual but occurred in three main episodes, at ~14 ka, ~11.5 ka and ~7–8 ka (Oppenheimer 1998, Pelejero et al 1999; Bird et al 2007). The latter episode is considered the smallest, but according to our results, most likely simply because it was the most recent, it left the clearest imprint in the demographic history and population structure of Southeast Asia.

It is well known that the three non-African founder haplogroups, M, N and R, are distributed across the whole of South Asia, Southeast Asia and the ancient Sahul region (the Australian/New Guinean continent), and each region has its own subset of lineages which all branched from the roots of the three founders (Hudjashov et al., 2007; Kong et al., 2010; Macaulay et al., 2005; Mellars et al., 2013). The existence of these three founder haplogroups within the latter regions and the similar ages of M and N are an important line of evidence for the single southern coastal route expansion model of anatomically modern humans after the out-of-Africa migration (Macaulay et al., 2005). In addition, the ages of these founders indicate that the ancestral sequence of each of these lineages successfully entered and crossed each region after the Toba eruption in Sumatra ~75 ka (Macaulay et al., 2005; Mellars et al., 2013).

Between a tenth and a fifth of the mtDNA lineage in present-day MSEA date to the first settlement. The two founder main haplogroups in Southeast Asia, M and R, are dated in this study by ML to ~61 ka and ~64 ka respectively, with approximately 10 ka 95% confidence intervals, with upper bounds of ~67-73 ka. The splitting analysis (using ρ) indicates that the first signal for the separation of lineages within ancient Sundaland region is about 54.4 ka, providing a lower bound estimate for the settlement time. These results fit well with recent palaeontological and archaeological estimates for the initial settlement of Southeast Asia, especially the most recent modern human remains at Sumatra around 63-73 ka (Westaway et al., 2017) and northern Australia about 65 ka (Clarkson et al., 2017). These results suggest a rather older settlement than previous estimates from human remains found in MSEA, dated to between 46-63 ka from Tam Pa Ling Cave in northern Laos and 39-45 ka for the “Deep Skull” from Niah Cave in Sarawak, Borneo (Barker & Richards, 2013; Demeter et al., 2015).

The ages of haplogroups M and R have been recently estimated with ML to about 54 ka and 64 ka respectively in South Asia, likely due to later re-expansions reducing the age of M in particular in that region (Silva et al., 2017), but while in this study the haplogroup M seems to have an older estimation, closer to that of R, both M and R in Southeast Asia still appear younger than the Toba eruption, and none of the upper bounds for the 95% confidence intervals reach the age of the eruption (recently estimated at 73.88 ± 0.32 ka: (Storey, Roberts, & Saidin, 2012).

6.1.2 Late Glacial expansions in MSEA

The end of the last glacial period exposed the world to rapid climatic changes that dominated the Late Pleistocene. Melting of large amounts of Arctic ice led to a substantial rise in the sea level in the oceans (~120m), which affected the world shorelines of many different regions but had a particularly powerful impact on Southeast Asia. People who were adapted to coastal regions at the time would likely have been the most affected by these changes, which had a major impact on human populations, at least in ISEA (Soares et al., 2008).

The founder analysis for the complete mtDNA sequences shows ~17%-~19% of present-day variation in MSEA allocated to the 14,200-year migration, including many basal haplogroup M and R lineages that are unique to MSEA/South China.

For instance, with the *f1* criterion, the basal M and R founder haplogroups include M12, M71, M74b, N9a, B6b, B6a1 and M72 with other lineages including F3a1 and B4h. All the latter basal haplogroups are commonly found in MSEA and are frequent in Peninsular Malaysia, a reservoir for ancient genetic variation in the region (Macaulay et al., 2005; Hill et al., 2006; Hill et al., 2007), while the more derived founders, such as F3a1 and B4h, are found in northern MSEA and South China (coastal China), suggesting intensive gene flow between these two regions. For instance, the local subclade of N9a, N9a6, is restricted to Sundaland with a coalescence age of ~12.6 ka and is more common in Peninsular Malaysia (within the aboriginal *Orang Asli*) and southern Vietnam (the Stieng people). On the other hand, the N9a1 type is found in MSEA but it is more frequent in South China (coastal China).

According to the archaeological evidence the best-unknown arrivals to coastal habitats during the end of the last glacial age is the Hunting-gathering groups Hoabinhian. The Hoabinhian is found at many different sites in Southeast Asia (mainly in MSEA) including South China Vietnam, Myanmar, Thailand and Peninsular Malaysia, but also Sumatra, an even New Guinea and Australia (Bowdler, 2006). Although they have been dated recently to ~43.5 ka old in Yunnan, South China (Ji et al., 2016), they found in north Vietnam from at least ~20,000 years old in northern Vietnam (Seonbok et al., 2008), and between 20,000 and 5,000 years old across many regions of MSEA (Bowdler, 2006). Since the Hoabinhian stone tools are found across a wide region in Southeast Asia during the Late Pleistocene to Early Holocene transitions (Marwick, 2013, Patole-Edoumba et al., 2015) they support the existence of hunting and gathering inhabitants throughout this period, who seem likely to have left significant traces in the modern mtDNA genetic pool.

The indication of a surge of dispersal at ~14 ka not only confirms the impact of the sea-level rise on the population history of MSEA, but casts a different light on the process to what has previously been learned from ISEA. The major signature in ISEA appears to be during the early Holocene, as indeed is confirmed here in the major split of ISEA mtDNA lineages from MSEA at ~8.5 ka, around the time of expansion of haplogroup E within ISEA (Soares et al., 2008). However, the major peak in the splitting analysis for MSEA occurs much earlier, in the Late Glacial period at ~13 ka. This difference may be due to the lesser direct impact of sea-level rise in MSEA, where loss of land was much less, and the survival of hunter-gatherer groups whose contemporaries may have perished in much greater numbers in ISEA where the loss of and must have had a huge impact, possibly witnessed in the lng branches suggesting high extinction and genetic drift in haplogroups in ISEA such as B4a1a, E1 and E2 (Soares et al. 2008; Soares et al. 2011), compared with lineages that spread later in the Holocene, such as M7 (Soares et al. 2016).

6.1.3 Early Holocene and “coastal Neolithic” expansions

The early postglacial period, in the early Holocene between ~11.5 ka to ~6 ka, can be seen to have been pivotal in forming the current genetic structure of both MSEA and ISEA. In the founder analysis, migrations in this period, centring around 7 ka, contribute about 36-37% of all lineages in MSEA – the single largest fraction. These founder lineages arrived from the north and major components include major northern MSEA/South China lineages such as B5a, B4a, F1a, F1f and F1g. B5a and F1a are the most common haplogroups in MSEA. The diversity of both decreases towards north Asia and towards southern MSEA, suggesting dispersals in both directions from South China.

This time period corresponds to the period that Vietnamese archaeologists classify as middle Neolithic, or “coastal” Neolithic. They are regarded as Neolithic due to the presence of polished stone tools and ceramics, and for the first time the sites appear along the coastline. They may also have practiced horticultural and arboriculture activities lifestyles, possibly with small amounts of rice (Nguyen et al. 2004, Bulbeck 2011; Higham 2014), rather than using the rice agriculture which appeared later, and which is known locally as the late Neolithic or which we can call (for clarity) the “rice Neolithic”.

The mtDNA results indicate that these groups originated in the north, and dispersed southwards down the coasts during the early to mid-Holocene. They also emphasize the significant changes in the geography and populations structures (Oppenheimer

1998), leading to the reduction of some groups and disappearance of others, whilst perhaps some of those who relied on maritime lifestyle (Solheim, Bulbeck, & Flavel, 2006).

Since the lineages most likely had an origin in South China, this indicates a deep genetic relationship and high level of gene flow between the South China region and MSEA, long before the Neolithic rice-farming expansions, with multiple waves of southward migrations from at least the end of the LGM onwards. This pattern of multiple Late Glacial, postglacial and Neolithic dispersals in the mtDNA record is similar to that seen between the eastern side of the Fertile Crescent (Iran/Afghanistan) and South Asia (Pakistan/India) (Silva et al., 2017).

6.1.4 Rice Neolithic expansions

After the early Holocene age, more sophisticated technology appeared in the region, linked to the agriculture expansion during the Neolithic age, beginning about 3.8 ka. There are two main alternative theories concerning the beginning of rice (and millet) agriculture in MSEA. The first argues that farming expanded via the offspring of hunter-gatherers who adopted food cultivation, a view that has received support from some physical anthropologists (Pietrusewsky, 2010). The alternative theory argues that the relocation of early rice farmers into MSEA from centres of domestication in South China resulted in the expansion of farming – the “farming-language dispersal hypothesis” that has also been discussed for ISEA, sub-Saharan Africa and Europe (Bellwood, 1997; Bellwood & Dizon, 2005). According to the latter expansion model, the earlier settlers were replaced in the last ~4 ka by Neolithic rice agriculturalists from South China. By this time, MSEA and ISEA were already separated by water.

This is proposed to have led to two distinct Neolithic expansions, accompanied by two languages family dispersals, those of the Austronesian family in ISEA (and the Pacific) and Austroasiatic in MSEA (Bellwood 1997, Diamond and Bellwood 2003, Bellwood 2007). According to Bellwood and Higham's proposals (Bellwood 2002; Higham 2002) the first farmers in MSEA were Austroasiatic speakers, and the homeland of proto-Austroasiatic, like rice agriculture, was the Yangtze river region in central China (Bellwood et al., 2013). An intermediate model has been proposed by Higham, who has argued that the rice Neolithic may not have been defined by a large-scale migration of Austroasiatic farmers from China but rather that small groups may have arrived from China carrying new agricultural techniques that they passed on to the local MSEA population (Higham 2014). The latter intermediate model has recently been supported by ancient mtDNA and genome-wide data (Lipson et al., 2018; McColl et al., 2018) which linked the group of Austro-Asiatic-speaking migrants in MSEA with South China, congruently with the modern mtDNA findings in the current study. In the founder analysis results (figure 102), the rice Neolithic component ~3.8 ka was estimated to between 24.5% (with *f1*) and 17.5% (with *f2*). Of the mtDNA gene pool in the current MSEA population, the major subclades for both criteria were M7b1a1, F1a1, B5a1, F3a1, B4b, B4g and C7a, where the first three respectively are the clearest markers for the Neolithic period. These subclades, such as M7b1a1, F1a1d and B5a1c1 (Appendix B), have deep roots in South China (Appendix B), which supports the Southern Chinese origin for the early farmers in MSEA during that time. The ancient genome studies can be considered as a significant supporting evidence for the current findings, in addition to providing more detailed understanding of the agriculture expansion in the MSEA during the Neolithic age.

Strikingly, the overall distribution of the founder lineages using the HVS-I seems very close to that from the complete sequences, but the results with the complete sequences are sharper and much better defined.

6.1.5 Evidence of recent gene flow

By using the founder analysis, there is a signal of very recent gene flow into MSEA comprising only 11.2% (*f1*) and 6.22% (*f2*) of all the founder clusters. The major recent migrations are related mainly to R9b1a2a, M7c1a and M7b1a1a3, probably from China.

6.2 Conclusions

This study provides a one of the largest single data sets of complete mtDNA genomes from one region yet assembled, helping to provide insight into the history of MSEA. Recent technological advances in next-generation DNA enables us to dramatically increase the number of samples that can be analysed by reducing the time and the cost – the Illumina sequencing performed here was carried out for only a tenth of the cost of Sanger sequencing. This means that the limitations are no longer sequencing costs but sample availability and computational labour.

The high phylogenetic resolution of the complete mtDNA genome from MSEA has improved our understanding of the detail of the maternal relationship between the modern MSEA populations and surrounding regions, throughout South, Southeast and East Asia, and even with western Pacific islands, revealing the complexity of the history of settlement and migrations in the region. They confirm that climatological changes played the main role in forming the demographic structure of Sundaland's population, especially during the periods of sea-level rise due to the global warming at the end of the last Ice Age. However, as might be expected, the impact of the climate change was very different from in ISEA, especially during the early Holocene period during which time we detect the largest expansion components for MSEA lineages (more than a third of the present-day lineages) according to the founder analysis.

The archaeological evidence describes the lifestyle of the early Holocene age in MSEA as hunting and gathering/fishing activities linked initially to the Hoabinhian people who occupied a vast region from South China and Vietnam, Laos, the Peninsular Malaysia, western Indonesia, possibly even reaching Australasia. Yet a major wave of new populations spread south from China during this period, with coastal rather than inland riverine adaptations, and possibly being the first to practice some kind of food management, including arboriculture and horticulture. They and their rice-using successor eventually assimilated the early Hoabinhian foragers. As for other parts of the world, the details of this process over time will only be fully accessible if and when ancient DNA studies become a reality in the region, and mtDNA from different time periods is able to test the predictions of the founder analysis.

More modern sampling is also needed from under-sampled regions of MSEA, especially from Myanmar and Cambodia which have the lowest number of complete mtDNA sequences. In addition, the Y-DNA and the whole-genome analysis will soon be able to give a more rounded picture of MSEA history, in order to see whether the maternal patterns are representative of the genome as a whole, and testing models of sex-specific dispersal, as in other parts of the world.

7. References

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Appendices

Appendix A. List of the Complete mtDNA genomes sequenced in this study with their coverage details.

ID	Country	mean coverage	Min. coverage	Max. coverage	Haplogroup	Variants
DHX4000-58	Vietnam	213.3	77	374	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4001-59	Vietnam	219.7	94	388	M73	73, 93, 146, 195, 263, 489, 547, 750, 1438, 2263A, 2352, 2706, 3396, 3399T, 3705, 4769, 5655, 5774G, 6446, 7028, 8701, 8860, 9540, 9548, 10364, 10398, 10400, 10873, 11719, 12346, 12405A, 12705, 13743, 14034, 14371, 14690, 14766, 14783, 15043, 15148, 15301, 15326, 16183, 16223, 16278, 16519
DHX4002-60	Vietnam	256.1	78	570	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4006-61	Vietnam	324.2	84	555	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4007-62	Vietnam	125.8	43	249	F1a1a	73, 249d, 263, 750, 1438, 2706, 3316, 3970, 4086, 4769, 6392, 6962, 7028, 7061, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4010-63	Vietnam	138.4	62	255	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4028-64	Vietnam	236.1	90	358	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4042-65	Vietnam	137.9	49	276	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519

DHX4044-66	Vietnam	145.6	31	338	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4048-67	Vietnam	120	39	231	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4059-68	Vietnam	189.4	56	423	M12a1b	73, 143, 152, 263, 489, 606, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4069-69	Vietnam	535.5	170	1093	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6491, 6605, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14530, 14766, 15226, 15235, 15326, 16140, 16189, 16261, 16266A, 16519
DHX4074-70	Vietnam	494	230	1178	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9286, 9950, 10398, 11465, 11719, 12193, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DHX4095-71	Vietnam	209.2	50	496	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16189, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4105-72	Vietnam	224.4	88	461	M72a	73, 263, 489, 750, 1438, 1872, 2706, 4058, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16124, 16166d, 16175, 16214, 16223, 16519
DHX4106-73	Vietnam	445.7	144	1281	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6491, 6605, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14530, 14766, 15226, 15235, 15326, 16140, 16183C, 16189, 16261, 16266A, 16519
DHX4107-74	Vietnam	153.8	35	325	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353,

						11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16311, 16519
DHX4117-75	Vietnam	260.8	47	572	M72a	73, 263, 489, 750, 1438, 1872, 2706, 4058, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16124, 16166d, 16175, 16214, 16223, 16390, 16519
DHX4119-76	Vietnam	174.3	43	394	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16311, 16519
DHX4122-77	Vietnam	426.2	137	745	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4123-78	Vietnam	172.8	71	400	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14581, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4137-79	Vietnam	229.5	53	464	M59	73, 249, 263, 489, 750, 1438, 2706, 4021, 4769, 4901, 7028, 8701, 8860, 8970, 9380, 9540, 10256, 10398, 10400, 10873, 11140, 11719, 12171, 12705, 13708, 14040, 14766, 14783, 15043, 15301, 15326, 16140, 16172, 16189, 16223
DHX4138-80	Vietnam	212.8	49	418	M59	73, 249, 263, 489, 750, 1438, 2706, 4021, 4769, 4901, 7028, 8701, 8860, 8970, 9230, 9380, 9540, 10256, 10398, 10400, 10873, 11140, 11719, 12171, 12705, 13708, 14040, 14766, 14783, 15043, 15301, 15326, 15774, 16140, 16172, 16189, 16223
DHX4139-81	Vietnam	214.8	67	514	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4152-82	Vietnam	198.2	51	416	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 6233, 7028, 7270, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519

DHX4166-83	Vietnam	262.4	89	494	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1284, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4176-84	Vietnam	245.6	72	410	R22	73, 263, 329, 513, 750, 1040, 1438, 2706, 3540, 4491, 4769, 6770, 6977, 7028, 7861, 8860, 10316, 10609, 10877, 11719, 12173, 13145, 13359, 14766, 15287, 15326, 15885, 16249, 16288, 16304, 16390, 16519
DHX4178-291	Vietnam	270.3	63	612	F2	73, 249d, 263, 750, 1005, 1438, 1824, 2706, 3010, 3970, 4769, 6392, 7028, 7337, 7828, 8264, 8860, 10310, 10535, 10586, 11719, 12338, 13708, 13928C, 14766, 14875, 15326, 16299, 16304
DHX4183-85	Vietnam	209.8	21	400	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12030, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4188-86	Vietnam	204.1	80	387	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4189-87	Vietnam	621.5	230	1743	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 5460, 5821, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16189, 16207, 16266A, 16311, 16362, 16519
DHX4215-88	Vietnam	331.1	92	772	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4216-89	Vietnam	127.6	35	287	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4217-90	Vietnam	557.7	212	1355	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6338, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13368, 14766, 15235,

						15326, 15784, 16127, 16140, 16189, 16266A, 16519
DHX4252-91	Vietnam	230.7	80	386	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4258-92	Vietnam	227.2	92	378	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12297, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4260-292	Vietnam	166.3	73	310	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8572, 8860, 9053, 10310, 10609, 11719, 12397, 12406, 12771, 12882, 13708, 13759, 13928C, 14766, 15326, 15930, 16129, 16172, 16189, 16295, 16304, 16519
DHX4262-93	Vietnam	185.4	49	395	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DHX4266-94	Vietnam	151.5	36	341	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DHX4272-95	Vietnam	655.1	172	1483	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16297, 16519
DHX4275-96	Vietnam	282.2	85	509	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2074, 2706, 3537, 4086, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9286, 9950, 10398, 11465, 11719, 12193, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DHX4277-97	Vietnam	1168	384	2776	M12a1b	73, 127, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4278-98	Vietnam	219.5	72	369	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053,

						9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4279-99	Vietnam	559.9	221	1117	M12a1b	73, 127, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4281-100	Vietnam	758.4	208	2167	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16297, 16519
DHX4282-101	Vietnam	187.3	53	345	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4284-102	Vietnam	738.2	274	1463	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
DHX4288-103	Vietnam	554.5	206	1308	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16297, 16519
DHX4289-104	Vietnam	275	70	517	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12297, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4291-105	Vietnam	622.3	217	1512	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16311, 16519
DHX4292-106	Vietnam	238.2	69	428	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15247, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4293-107	Vietnam	299.1	77	742	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043,

						15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4295-108	Vietnam	258.2	82	658	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16519
DHX4298-109	Vietnam	310.4	99	747	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4300-110	Vietnam	686.8	264	1591	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9286, 9950, 10398, 11465, 11719, 12193, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16275, 16519
DHX4302-111	Vietnam	225.4	70	408	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DHX4305-112	Vietnam	209.7	47	419	M72a	73, 263, 489, 750, 1438, 1872, 2706, 4058, 4769, 7028, 8584, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16124, 16166d, 16175, 16214, 16223, 16519
DHX4309-113	Vietnam	246.5	74	521	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4312-293	Vietnam	107.9	30	230	F3a	73, 195, 249d, 263, 750, 1438, 2706, 3390, 3434, 3970, 4136, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 7094, 7258, 8860, 9301, 9813, 10310, 10320, 11065, 11719, 12237, 12621, 13928C, 14766, 15326, 15924, 16093, 16209, 16298, 16355, 16362
DHX4323-115	Vietnam	169.2	36	579	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4326-116	Vietnam	785.4	267	1443	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6491, 6605, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398,

						11465, 11719, 14530, 14766, 15226, 15235, 15326, 16140, 16183C, 16189, 16261, 16266A, 16519
DHX4328-117	Vietnam	691.3	227	1523	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16297, 16519
DHX4334-118	Vietnam	222.9	92	381	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4335-119	Vietnam	230.6	67	433	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4337-120	Vietnam	455.5	176	1161	B5a1d	73, 152, 210, 263, 318, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9286, 9950, 10398, 11465, 11719, 12193, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DHX4343-121	Vietnam	222.2	99	361	F1a1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 5582, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4348-122	Vietnam	197.4	62	377	F1a1a	73, 185, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4360-123	Vietnam	697.8	230	1811	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
DHX4365-124	Vietnam	97.8	26	238	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4385-125	Vietnam	168.2	61	458	M20	73, 151, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8222, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398,

						10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4386-126	Vietnam	212.4	45	454	M68a1a	73, 152, 178, 195, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14464, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4394-127	Vietnam	232.2	82	423	F1a1a	73, 185, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4401-128	Vietnam	150	48	360	M20	73, 152, 249d, 263, 316, 489, 619, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9165, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14001, 14110, 14766, 14783, 14883, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16519
DHX4402-129	Vietnam	216.6	56	499	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4406-130	Vietnam	217.9	63	597	M20	73, 152, 249d, 263, 316, 489, 619, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9165, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14001, 14110, 14766, 14783, 14883, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16519
DHX4407-131	Vietnam	230	17	552	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DHX4411-132	Vietnam	193.6	81	343	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6359, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 15613, 16108, 16129, 16162, 16172, 16304, 16519

DHX4412-133	Vietnam	317	96	829	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4501-134	Vietnam	693.8	247	1258	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6338, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13368, 14766, 15235, 15326, 15784, 16127, 16140, 16183C, 16189, 16266A, 16519
DHX4505-135	Vietnam	693.3	249	1664	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13105, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DHX4506-136	Vietnam	208.8	63	401	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4509-137	Vietnam	268.6	85	833	M74b	73, 263, 489, 750, 1438, 1719, 2263, 2706, 4639, 4769, 5054, 6443, 6896, 7028, 8080A, 8167, 8251, 8701, 8860, 8870, 9468, 9540, 10268, 10322, 10398, 10400, 10873, 11719, 12530, 12651, 12705, 14766, 14783, 15043, 15301, 15326, 15908, 16093, 16145, 16223, 16311, 16362, 16519
DHX4512-138	Vietnam	182.4	66	353	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4514-139	Vietnam	159.4	13	436	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4520-140	Vietnam	261.7	103	454	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4522-141	Vietnam	210	58	424	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519

DHX4523-142	Vietnam	169	40	331	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4526-144	Vietnam	201.3	65	394	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4532-145	Vietnam	195	58	406	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8222, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4536-146	Vietnam	181.9	54	404	M68a1a	73, 152, 178, 195, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14464, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16391, 16519
DHX4554-147	Vietnam	253	85	483	F1a1a	73, 185, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 15908, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4573-148	Vietnam	248.8	62	612	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DHX4578-149	Vietnam	217.6	67	592	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8222, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4588-150	Vietnam	595	175	1257	B4c2b	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 6221, 6815, 7028, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16519
DHX4595-151	Vietnam	168.5	55	291	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882,

						13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4597-152	Vietnam	189.1	38	394	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4598-153	Vietnam	208.7	69	336	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4599-154	Vietnam	192.6	82	344	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7394, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4609-155	Vietnam	196.6	66	369	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4611-156	Vietnam	1390.2	245	3723	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DHX4612-157	Vietnam	411.3	32	1397	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4623-158	Vietnam	96.9	23	295	B4c2b	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 6221, 6815, 7028, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16519
DHX4628-159	Vietnam	202.5	69	369	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DHX4629-160	Vietnam	207.4	64	393	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882,

						13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4630-294	Vietnam	147.3	36	298	M7c2	73, 146, 263, 489, 750, 1438, 2706, 3912, 4071, 4769, 4850, 5378, 6340, 6455, 7028, 8701, 8860, 9449, 9540, 9824, 10398, 10400, 10873, 10897, 11665, 11719, 11923, 11932, 12091, 12705, 14053, 14766, 14783, 15043, 15301, 15326, 15338, 16172, 16223, 16311, 16519
DHX4634-161	Vietnam	176.2	74	279	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4636-162	Vietnam	224.4	91	419	M72a	73, 263, 489, 750, 1438, 1872, 2706, 3320, 4058, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16124, 16166d, 16175, 16214, 16223, 16519
DHX4637-163	Vietnam	137.1	46	249	M12a1b	73, 127, 143, 152, 204, 207, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4639-164	Vietnam	181.4	71	353	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8222, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DHX4639-173	Vietnam	148.9	28	400	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16519
DHX4642-165	Vietnam	238.7	78	468	R9b2	73, 263, 750, 1438, 1541, 2706, 3666, 3970, 4769, 6647, 7028, 8724, 8860, 9821, 11299, 11422, 11719, 13191, 13722, 13928C, 14684, 14766, 15314, 15326, 15883, 16270, 16304, 16362, 16519
DHX4659-166	Vietnam	214.9	72	530	M72a	73, 263, 489, 750, 1438, 1872, 2706, 4058, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16124, 16166d, 16175, 16214, 16223, 16519
DHX4663-167	Vietnam	195.6	61	343	F1a1a	73, 200, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860,

						9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16274, 16304, 16391, 16519
DHX4667-168	Vietnam	192.8	76	447	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DHX4668-169	Vietnam	168.9	50	309	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6164, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4671-170	Vietnam	182.6	59	327	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6164, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4673-171	Vietnam	187.5	66	378	M12a1b	73, 127, 143, 152, 263, 489, 750, 1438, 2706, 4170, 4769, 5492, 5580, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11353, 11361, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16172, 16189, 16223, 16234, 16249, 16290, 16519
DHX4675-172	Vietnam	243.9	68	437	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13722, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DHX4684-174	Vietnam	218.1	81	373	F1a1a	73, 200, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16274, 16304, 16391, 16519
DHX4685-175	Vietnam	244.1	112	410	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13722, 13759, 13928C, 14635, 14766, 14950, 15148, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DHX4694-176	Vietnam	68.1	25	136	N21	73, 150, 195, 263, 337d, 731, 750, 1438, 2706, 2857, 4769, 6752, 7028, 7424, 8149, 8701, 8860, 10172, 10398, 10583, 11719, 11950, 12705, 13437, 14180, 14560, 14766, 15326, 15519, 16193, 16223, 16519
DHX4701-177	Vietnam	203.5	72	358	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12297, 12406,

						12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4702-295	Vietnam	314.7	116	580	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
DHX4703-178	Vietnam	246.2	90	475	M51b	73, 150, 152, 228, 263, 489, 750, 1438, 2706, 2833, 3915, 4221, 4697, 4769, 4973, 6455, 7028, 7372, 8701, 8860, 9156, 9470, 9509, 9540, 10128, 10398, 10400, 10873, 11719, 12705, 13515, 13722, 14020A, 14110, 14356, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16168, 16189, 16223, 16278
DHX4705-179	Vietnam	237.6	53	520	M73	73, 150, 204, 249d, 263, 489, 709, 750, 1438, 2263A, 2352, 2706, 3010, 3396, 3399T, 3594, 4769, 5655, 7028, 7281, 8251, 8701, 8860, 9064, 9540, 10398, 10400, 10873, 11563, 11708, 11719, 12612, 12705, 14034, 14766, 14783, 15043, 15299, 15301, 15326, 15663, 15894, 16223, 16278, 16519
DHX4706-180	Vietnam	240.9	87	412	F1a1a	73, 249d, 263, 750, 1438, 2706, 3438, 3970, 4086, 4769, 6392, 6962, 7028, 8020, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4708--181	Vietnam	77.5	28	124	N9a6	73, 150, 263, 709, 750, 1438, 2706, 4769, 4856, 5231, 5417, 7028, 8860, 10226, 11719, 12358, 12372, 12705, 13707, 14766, 15080, 15326, 16189, 16223, 16257A, 16261, 16292, 16519
DHX4711-182	Vietnam	178.8	48	354	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DHX4712-183	Vietnam	188.9	55	344	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13722, 13759, 13928C, 14635, 14766, 14950, 15148, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DHX6481	Vietnam	153.6	42	278	F1a1a1	73, 195, 217, 249d, 263, 750, 1438, 2706, 3337, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12400, 12406, 12882, 13759, 13928C, 14311, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK352-359	Vietnam	170.7	29	372	M59	73, 249, 263, 489, 750, 1438, 1719, 2706, 3531, 4021, 4769, 4901, 6026T, 7028, 7289, 8701, 8750, 8860, 8970, 9380, 9540, 10256, 10398, 10400, 10873, 11140, 11719, 12705, 13708, 14040, 14766, 14783, 15043, 15301,

						15326, 16129, 16140, 16172, 16189, 16223, 16278
DKK353-360	Vietnam	148.7	45	646	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16183C, 16189, 16266A, 16519
DKK370-361	Vietnam	136.3	29	388	G2a1	73, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 5601, 6531, 7028, 7148, 7600, 8701, 8860, 9377, 9540, 9575, 10398, 10400, 10873, 11719, 12510, 12705, 13563, 14200, 14569, 14766, 14783, 15043, 15301, 15326, 16223, 16227, 16278, 16362
DKK3728-365	Vietnam	166.1	77	257	M7c1a	73, 114, 146, 152, 199, 263, 489, 745, 750, 1438, 1809, 2706, 3316, 3882, 4071, 4634, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11152, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15301, 15326, 16075, 16223, 16274, 16293T, 16295, 16296, 16519
DKK3729-366	Vietnam	193.9	65	443	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 2833, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297, 16526
DKK3739-368	Vietnam	71.6	23	122	D4	73, 184, 195, 263, 489, 750, 1438, 2706, 3010, 4769, 4883, 5178A, 7028, 8414, 8701, 8860, 9540, 9856, 10398, 10400, 10873, 11002, 11719, 11914, 12115, 12705, 14668, 14766, 14783, 15043, 15301, 15326, 15519, 16192, 16222, 16223, 16311, 16316, 16362
DKK3788-367	Vietnam	200.6	70	522	G2a1	73, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 5601, 6531, 7028, 7148, 7600, 8701, 8860, 9377, 9540, 9575, 10398, 10400, 10873, 11719, 12510, 12705, 13563, 14200, 14569, 14766, 14783, 15043, 15301, 15326, 16093, 16223, 16227, 16278, 16362
DKK394-362	Vietnam	227.9	61	433	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7934, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12561, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK4005-1	Vietnam	137.7	43	269	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DKK4018-2	Vietnam	189.5	54	612	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924,

						16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DKK4039-4	Vietnam	215.2	58	431	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
DKK4050-5	Vietnam	195.6	69	328	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DKK4054-6	Vietnam	258.4	68	480	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DKK4057-184	Vietnam	216.6	30	756	M7b1a1f	73, 150, 199, 263, 332, 489, 709, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 5773, 6455, 6680, 7028, 7684, 7853, 8110, 8251, 8701, 8860, 9024, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14128, 14766, 14783, 15043, 15235, 15301, 15326, 16129, 16192, 16223, 16297, 16324
DKK4059-185	Vietnam	214.2	74	357	B4a	73, 146, 263, 750, 1438, 2706, 4769, 5465, 5899.1C, 7028, 8281-8289d, 8860, 9123, 11719, 12634, 14766, 15326, 16183C, 16189, 16217, 16219, 16261, 16286, 16355, 16519
DKK4063-186	Vietnam	217.7	79	354	M7c1a	73, 146, 199, 263, 489, 750, 1438, 2706, 3882, 4071, 4769, 4850, 5442, 6455, 7028, 7746, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12535, 12705, 13434, 14766, 14783, 15043, 15175, 15289, 15301, 15326, 16223, 16295, 16519
DKK4065-187	Vietnam	190.1	66	306	D4a	73, 152, 263, 489, 750, 1438, 2706, 3010, 3206, 4769, 4883, 5178A, 7028, 8410, 8414, 8473, 8701, 8860, 9540, 9845, 10398, 10400, 10873, 11719, 12705, 13650, 13966, 14668, 14766, 14783, 14979, 15043, 15301, 15326, 15889, 16129, 16223, 16263, 16362, 16519
DKK4069-189	Vietnam	191.1	40	387	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9141, 9540, 9824, 9957, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 13145, 14053, 14766, 14783, 15043, 15301, 16223, 16297
DKK4071-190	Vietnam	225.7	74	391	F1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759,

						13928C, 14063, 14259, 14766, 15326, 16129, 16172, 16304, 16519
DKK4075-191	Vietnam	253.4	105	464	F1f	73, 249d, 263, 750, 1393, 1438, 2706, 2780, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8293G, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13437, 13759, 13928C, 14323, 14766, 15326, 16129, 16172, 16294, 16304, 16519
DKK4076-192	Vietnam	155.6	50	297	F1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14063, 14766, 15326, 16129, 16172, 16304, 16519
DKK4080-194	Vietnam	152.1	44	327	F3a1	73, 249d, 263, 709, 750, 1438, 1943, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 6701, 7028, 8860, 10310, 10320, 10577, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 16260, 16298, 16355, 16362
DKK4085-196	Vietnam	279.9	92	535	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
DKK4088-197	Vietnam	180.5	76	275	B6a	73, 234, 263, 709, 750, 1438, 2706, 3010, 4117, 4769, 5894C, 7028, 7472C, 8281-8289d, 8860, 9452, 11719, 11914, 12950, 13928C, 14256, 14305, 14766, 15326, 16093, 16189
DKK4091-198	Vietnam	165.1	44	311	B4	73, 263, 523, 750, 1438, 2706, 3423, 4769, 7028, 8281-8289d, 8860, 10398, 11719, 12358, 14766, 15326, 16183C, 16189, 16217, 16261, 16294, 16519
DKK4098-369	Vietnam	178.6	73	288	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783, 14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK4103-370	Vietnam	283.2	101	480	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2232.1A, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10795T, 10873, 11719, 12405, 12705, 12811, 14512, 14766, 14783, 15043, 15301, 15326, 15604, 16129, 16192, 16223, 16297
DKK410-363	Vietnam	113.9	31	183	M7c1a	73, 114, 146, 152, 199, 263, 489, 745, 750, 1438, 1809, 2706, 3316, 3882, 4071, 4634, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11152, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15301, 15326, 16075, 16223, 16274, 16293T, 16295, 16296, 16519
DKK411-364	Vietnam	199.8	55	406	M10	73, 263, 489, 709, 750, 953, 1438, 2706, 3172.1C, 4140, 4769, 4823, 7028, 8701,

						8793, 8860, 9540, 9644, 9729, 10398, 10400, 10873, 11719, 12549, 12705, 12976, 13152, 14502, 14766, 14783, 15040, 15043, 15071, 15301, 15326, 16223, 16256, 16299, 16311
DKK4114-371	Vietnam	152.4	47	294	M7c1a	73, 114, 146, 152, 199, 263, 489, 745, 750, 1438, 1809, 2706, 3316, 3882, 4071, 4634, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11152, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15301, 15326, 16075, 16223, 16274, 16293T, 16295, 16296, 16519
DKK4115-372	Vietnam	175.9	59	291	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783, 14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK4116-373	Vietnam	162.9	47	270	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783, 14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK4118-7	Vietnam	61.9	13	121	B4c2	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 7028, 8281-8289d, 8860, 9297, 11719, 14088, 14209, 14766, 15110, 15326, 15346, 16147, 16154, 16217, 16235, 16519
DKK4121-199	Vietnam	156.6	64	254	C7a	73, 150, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11506, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327
DKK4124-374	Vietnam	269.8	83	519	F1a4a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 5102, 5985, 6392, 6962, 7028, 7897, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13422, 13759, 13928C, 14766, 15326, 15445, 16129, 16172, 16294, 16304, 16362, 16519
DKK4125-375	Vietnam	135.7	48	224	D4b2b2a	73, 150, 194, 263, 489, 750, 1382C, 1438, 2706, 3010, 3666, 4769, 4883, 5178A, 7028, 8020, 8414, 8701, 8860, 8964, 9296, 9540, 9824A, 10398, 10400, 10873, 11719, 12358, 12705, 14668, 14766, 14783, 15043, 15301, 15326, 15754, 16093, 16223, 16362, 16519
DKK4133-376	Vietnam	362.8	145	711	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783,

						14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK4141-377	Vietnam	281.6	110	508	D4a	73, 152, 263, 489, 750, 1438, 2706, 3010, 3206, 4769, 4883, 5178A, 5582, 7028, 8414, 8473, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 14668, 14766, 14783, 14979, 15043, 15301, 15326, 15596, 16129, 16223, 16362
DKK4144-378	Vietnam	248	67	463	M74a	63, 64, 66, 73, 215, 263, 489, 750, 1438, 2706, 4769, 5054, 6185, 6575, 7028, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12705, 12850, 14311, 14766, 14783, 15043, 15301, 15326, 15565, 16093, 16223, 16286, 16294, 16311, 16362, 16381
DKK4145-379	Vietnam	127.4	30	264	B4g1b	73, 263, 750, 1438, 2706, 3221, 3483, 4769, 7028, 7789, 8281-8289d, 8860, 9968, 11353, 11719, 13547, 14256, 14766, 15326, 16153, 16189, 16213, 16217, 16261, 16292, 16362, 16519
DKK4146-380	Vietnam	257	81	476	M10	73, 263, 489, 709, 750, 953, 1438, 2706, 3172.1C, 4140, 4769, 4823, 7028, 8701, 8793, 8860, 9540, 9644, 9729, 10398, 10400, 10873, 11719, 12549, 12705, 12976, 13152, 14502, 14766, 14783, 15040, 15043, 15071, 15301, 15326, 16223, 16256, 16299, 16311
DKK4149-381	Vietnam	130.9	62	229	D5b	73, 150, 194, 263, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 4092, 4769, 4883, 5153, 5178A, 5301, 7028, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 14094, 14766, 14783, 15043, 15301, 15326, 15724, 16183C, 16189, 16223, 16234, 16362
DKK4150-382	Vietnam	246.8	64	425	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783, 14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK4152-383	Vietnam	423	130	841	C7a	73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16092, 16189, 16223, 16298, 16327, 16355, 16519
DKK4159-384	Vietnam	109.7	38	189	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
DKK4160-200	Vietnam	284.9	69	644	M12a1a1	73, 125, 127, 128, 263, 318, 489, 750, 1438, 2706, 4048, 4170, 4769, 5580, 7028, 7403, 8412, 8701, 8860, 9490, 9540, 10398, 10400, 10873, 11719, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010,

						15043, 15301, 15326, 15463, 15651, 16223, 16234, 16290, 16362
DKK4172-8	Vietnam	214.3	52	416	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DKK4176-9	Vietnam	232.4	77	447	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DKK4208-10	Vietnam	215.9	60	464	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DKK4227-201	Vietnam	177.2	18	509	M7b1a1	73, 146, 150, 199, 234, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 5480, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 13879, 14766, 14783, 15043, 15301, 15326, 16129, 16182, 16223, 16297, 16356
DKK4229-202	Vietnam	140.2	39	247	M7c1c2	73, 146A, 199, 263, 489, 750, 1438, 2706, 3606, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8790, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15236, 15301, 15326, 16311, 16356, 16519
DKK4232-203	Vietnam	290.3	85	463	M7b1a1f	73, 150, 189, 199, 263, 332, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8110, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16192, 16223, 16297
DKK4240-204	Vietnam	193.6	63	382	F1a1a1	73, 150, 185, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 5512, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14596, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK4241-205	Vietnam	272.4	63	611	M73	73, 93, 146, 195, 263, 489, 547, 750, 1438, 2263A, 2352, 2706, 3396, 3399T, 3705, 4769, 5655, 5774G, 6446, 7028, 8701, 8860, 9540, 9548, 10364, 10398, 10400, 10873, 11719, 12346, 12405A, 12705, 13743, 14034, 14371, 14690, 14766, 14783, 15043, 15148, 15301, 15326, 16183, 16223, 16278, 16519

DKK4243-206	Vietnam	143.5	36	278	B4a1d	73, 263, 750, 1438, 2706, 4080, 4769, 5465, 5894, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 14766, 15326, 16189, 16217, 16261, 16519
DKK4251-207	Vietnam	208.7	96	363	F1a1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4131, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16261, 16304, 16398, 16519
DKK4256-208	Vietnam	285	109	563	B4c2	73, 263, 606, 750, 1119, 1438, 2416, 2706, 4769, 5108, 7028, 7930, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16168, 16189, 16217, 16231, 16235, 16519
DKK4258-209	Vietnam	168.9	65	398	B4a	73, 146, 263, 750, 1438, 2706, 4769, 5465, 5899.1C, 7028, 8281-8289d, 8860, 9123, 11719, 12634, 14766, 15326, 16183C, 16189, 16217, 16219, 16261, 16286, 16355, 16519
DKK4259-210	Vietnam	148.9	43	343	B4	73, 152, 183, 244, 263, 374, 750, 1313, 1438, 2361, 2706, 3948, 4769, 4961, 7028, 7389, 8027, 8281-8289d, 8860, 11527, 11719, 12975, 13896, 14319, 14766, 14857, 15153, 15326, 15748, 15928, 16092, 16183C, 16189, 16217, 16274, 16289, 16301, 16519
DKK4261-211	Vietnam	168.2	43	330	R11	73, 185, 189, 263, 709, 750, 1438, 1719, 2706, 4769, 5105, 5471, 5747, 7028, 8277, 8279, 8860, 10031, 10084, 10398, 11016, 11061, 11719, 12501, 12950, 13681, 14766, 14869, 14894, 15326, 15530, 15813, 16189, 16311, 16468, 16519
DKK4263-212	Vietnam	240.7	89	432	F1a1	73, 152, 183, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 7853, 8860, 9053, 9548, 10310, 10420, 10609, 10972, 11719, 12406, 12882, 12963, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16292, 16304, 16519
DKK4264-213	Vietnam	204.7	74	404	M73	73, 93, 146, 195, 263, 489, 547, 750, 1438, 2263A, 2352, 2706, 3396, 3399T, 3705, 4769, 5655, 5774G, 6446, 7028, 8701, 8860, 9540, 9548, 10364, 10398, 10400, 10873, 11719, 12346, 12405A, 12705, 13743, 14034, 14371, 14690, 14766, 14783, 15043, 15148, 15301, 15326, 16183, 16223, 16278, 16519
DKK4267-215	Vietnam	245.8	94	487	F1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9205, 9548, 9806, 10310, 10420, 10609, 10972, 11719, 12406, 12882, 12963, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16292, 16304, 16519
DKK4276-216	Vietnam	261.4	84	499	N9a6	73, 150, 263, 750, 961, 1438, 2706, 4769, 4856, 5231, 5417, 7028, 8860, 11017, 11719, 12358, 12372, 12705, 14766, 15326,

						16189, 16223, 16257A, 16261, 16292, 16519
DKK4282-217	Vietnam	276.2	66	526	M7b1a1a2	73, 150, 199, 263, 489, 750, 1438, 1694, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14052, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16223, 16227, 16297, 16519
DKK4287-218	Vietnam	302.6	102	523	R9c	73, 150, 152, 263, 750, 1438, 2706, 3970, 4769, 5324, 5794, 5951, 7028, 7861, 8860, 10403, 11002, 11719, 13928C, 14766, 15326, 15479, 16304, 16335, 16362
DKK4291-219	Vietnam	476.1	218	1072	B5a1b1	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 7852, 8281-8289d, 8584, 8860, 9950, 10398, 10754, 11719, 13928C, 14766, 14989, 15235, 15326, 15880, 16140, 16189, 16243, 16266A, 16316, 16519
DKK4292-220	Vietnam	188	65	309	F1f	73, 249d, 263, 456, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16172, 16304, 16519
DKK4295-221	Vietnam	125.1	39	217	R9c1b1	73, 151, 263, 479, 750, 1438, 1719, 2706, 3970, 4769, 7028, 7684, 7861, 8860, 11002, 11719, 12618, 13928C, 14766, 15010, 15326, 15479, 16157, 16304, 16325, 16352, 16519
DKK4297-222	Vietnam	111.7	31	223	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
DKK4351-223	Vietnam	208.3	39	422	F1a1a1	73, 195, 249d, 263, 750, 1438, 2706, 3337, 3397, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12400, 12406, 12882, 13759, 13928C, 14311, 14766, 15326, 15519, 16108, 16129, 16162, 16172, 16304, 16519
DKK4354-11	Vietnam	140.7	46	288	M21a	73, 152, 185, 263, 489, 709, 750, 1438, 2706, 3796, 4769, 7028, 8674, 8701, 8860, 9540, 9938, 10398, 10400, 10873, 11287, 11482, 11611, 11719, 11854, 11977, 12705, 14766, 14783, 15043, 15301, 15326, 15924, 16051, 16093, 16129, 16223, 16256, 16305, 16309, 16526
DKK4367-13	Vietnam	216.6	67	358	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DKK4375-14	Vietnam	228.9	70	602	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 8989, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519

DKK4389-16	Vietnam	227.7	96	547	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16145, 16223, 16278, 16311
DKK4407-224	Vietnam	189.4	46	339	M7c2a	73, 146, 263, 489, 750, 1438, 2706, 3866, 3912, 4071, 4712, 4769, 4775, 4850, 5378, 6455, 6848, 7028, 8701, 8860, 9449, 9540, 9824, 10398, 10400, 10873, 10897, 11665, 11719, 11932, 12091, 12705, 12957, 14053, 14766, 14783, 15043, 15301, 15326, 15338, 16172, 16223, 16291, 16311, 16519
DKK4412-225	Vietnam	426.3	114	955	G2	73, 146, 210, 263, 328, 489, 709, 750, 1438, 2706, 4769, 4833, 4928, 5108, 5581, 5601, 5960, 7028, 8701, 8860, 9339, 9540, 10398, 10400, 10873, 11443, 11719, 12067, 12705, 13563, 14569, 14766, 14783, 15043, 15301, 15326, 16223, 16362
DKK4413-226	Vietnam	233.3	61	452	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10326, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 13962, 14766, 15326, 16108, 16129, 16162, 16172, 16218, 16304, 16519
DKK4418-227	Vietnam	180	84	277	M7c2	73, 146, 263, 489, 750, 1438, 2706, 3912, 4071, 4769, 4850, 5174, 5378, 6455, 6713, 7028, 8701, 8860, 9000, 9449, 9540, 9824, 10398, 10400, 10873, 10897, 11084, 11665, 11719, 11932, 12091, 12705, 14053, 14766, 14783, 15043, 15301, 15326, 15338, 16172, 16223, 16311, 16519
DKK4423-228	Vietnam	444.8	171	730	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6566, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16305, 16519
DKK4424-229	Vietnam	139.4	52	249	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 3438, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12738, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
DKK4426-230	Vietnam	95.4	47	168	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 8896, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16189, 16266A, 16304, 16519
DKK4427-17	Vietnam	223.6	41	470	M74b	73, 263, 489, 750, 1438, 1719, 2263, 2706, 4769, 5054, 6443, 6896, 7028, 8080A, 8167, 8251, 8701, 8860, 8870, 9468, 9540, 10268, 10322, 10398, 10400, 10873, 11719, 12530, 12651, 12705, 14766, 14783, 15043,

						15301, 15326, 15908, 16093, 16145, 16223, 16311, 16362, 16519
DKK4431-231	Vietnam	160.6	50	423	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 4769, 5773, 7028, 8701, 8860, 9540, 10101, 10398, 10400, 10750, 10873, 11719, 12651, 12705, 13359, 13812, 14766, 14783, 15043, 15301, 15326, 15601, 16086, 16223, 16519
DKK4435-232	Vietnam	1683.7	159	7176	F1a1a	73, 150, 249d, 263, 750, 1438, 2308, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10712, 11719, 12406, 12882, 12972C, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK4439-233	Vietnam	231.9	71	447	F1a1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8433, 8860, 9053, 9548, 10310, 10609, 11002, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16357, 16380, 16519
DKK4440-234	Vietnam	213.2	49	400	M7b1a1a2	73, 150, 199, 263, 489, 593, 750, 1438, 1694, 2706, 4048, 4071, 4137, 4164, 4769, 5351, 5460, 6253, 6455, 6680, 7028, 7684, 7853, 8281-8289d, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16132, 16189, 16192, 16223, 16297, 16519
DKK4443-235	Vietnam	122.1	56	182	M9a4a1	73, 153, 263, 489, 750, 1120, 1438, 2706, 3394, 4491, 4592, 4769, 6284, 6366, 7028, 8152, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 14308, 14766, 14783, 15043, 15301, 15326, 16223, 16234, 16271, 16362
DKK4449-236	Vietnam	298.3	86	513	F1a1	73, 150, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8676, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15236, 15326, 15928, 16129, 16162, 16172, 16243, 16292, 16304, 16311, 16519
DKK4457-237	Vietnam	168.2	38	307	M7c1c2	73, 146A, 263, 489, 750, 1438, 2706, 3606, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9007, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 13368, 14766, 14783, 15043, 15236, 15301, 15326, 16519
DKK4459-238	Vietnam	114.1	31	261	F2	73, 249d, 263, 750, 1005, 1438, 1824, 2706, 3970, 4769, 5752d, 6392, 7028, 7076, 7828, 8860, 10310, 10535, 10586, 10810, 11719, 12338, 13708, 13928C, 14766, 15151, 15203, 15326, 16167, 16203, 16304, 16318, 16519
DKK4460-239	Vietnam	69.5	25	131	Z4a1a	73, 152, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 5492, 5894, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 10398, 10400, 10873, 11719, 12705, 13105,

						13535, 14207, 14766, 14783, 15043, 15301, 15326, 15475, 15487T, 15784, 15944d, 16185, 16223, 16260, 16298, 16302, 16519
DKK4461-240	Vietnam	247	25	1001	F1a1a1	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12400, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK4462-241	Vietnam	174.1	62	295	Z4	73, 146, 152, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6620, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 10398, 10400, 10873, 11719, 12705, 14766, 14783, 15043, 15301, 15326, 15475, 15487T, 15603, 15784, 15940, 15944d, 16185, 16223, 16248, 16260, 16298
DKK4466-244	Vietnam	176.3	45	347	M79	60, 61, 73, 152, 263, 489, 499, 750, 1438, 2706, 3442, 3588, 3669, 3972, 4769, 5583, 7028, 8437, 8701, 8860, 9540, 9626, 10398, 10400, 10530, 10873, 11719, 12372, 12432, 12705, 14766, 14783, 15043, 15301, 15326, 16086, 16092, 16223, 16243, 16278, 16311, 16319
DKK4468-245	Vietnam	201.5	49	382	M7b1a1a2	73, 150, 199, 263, 489, 593, 750, 1438, 1694, 2706, 4048, 4071, 4137, 4164, 4769, 5004, 5351, 5460, 6455, 6632, 6680, 7028, 7684, 7853, 8281-8289d, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16192, 16223, 16297, 16519
DKK4470-246	Vietnam	276.9	106	524	R9b2	73, 263, 750, 1438, 1541, 2706, 3591, 3666, 3970, 4769, 6647, 7028, 8724, 8860, 11299, 11353, 11422, 11719, 13191, 13722, 13928C, 14766, 15314, 15326, 15883, 16304, 16362, 16519
DKK4471-247	Vietnam	131.8	45	247	N9a	73, 150, 263, 750, 1438, 2706, 3849, 4769, 4856, 5231, 5417, 6176, 7028, 8860, 11719, 12358, 12372, 12705, 14766, 15326, 16223, 16257A, 16261, 16519
DKK4475-248	Vietnam	238.7	71	609	M74b2	73, 263, 489, 750, 1438, 2706, 4248, 4769, 5054, 6755, 6884, 7028, 7775, 8080A, 8167, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 10993, 11167, 11719, 11914, 12007, 12651, 12705, 14766, 14783, 15043, 15301, 15326, 15908, 16037, 16223, 16311, 16362, 16519
DKK4479-249	Vietnam	241.4	62	454	M7c1c2	73, 146A, 199, 263, 489, 750, 1438, 2706, 3606, 4071, 4769, 4850, 5442, 6320, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11698, 11719, 12091, 12705, 14766, 14783, 15043, 15236, 15301, 15326, 16519
DKK4483-250	Vietnam	213.2	86	330	C7a	73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5565T, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540,

						9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14668, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327
DKK5347C-395	Vietnam	220.2	67	376	D5c	73, 150, 151, 152, 195, 263, 489, 750, 1107, 1438, 1524, 2706, 3396, 3720, 4200T, 4216, 4769, 4883, 5178A, 5301, 7028, 7269, 8701, 8860, 9540, 10397, 10398, 10400, 10873, 11719, 12705, 12945, 14766, 14783, 14927, 15043, 15301, 15326, 15622, 15737, 16223, 16311, 16316, 16362
DKK5368A-396	Vietnam	246.5	75	402	M61	73, 150, 152, 260, 263, 489, 750, 1193, 1342, 1438, 2706, 4769, 6253, 7028, 8269, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 11810, 12705, 12732, 13468, 14766, 14783, 14883, 15043, 15301, 15326, 16223, 16362, 16381, 16519
DKK5377A-397	Vietnam	205.5	76	460	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13105, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DKK6293-385	Vietnam	89.7	12	215	B4b1a2a	73, 207, 263, 498, 499, 750, 827, 1438, 1719, 2220, 2706, 4769, 4820, 5899.1C, 6023, 6216, 6413, 7028, 7993, 8281-8289d, 8860, 11719, 13590, 14766, 15301, 15326, 15535, 16136, 16183C, 16189, 16217, 16309, 16354, 16519
DKK6460-386	Vietnam	46.7	14	81	M9a5	73, 150, 263, 385, 489, 750, 1438, 2706, 3394, 4491, 4769, 7028, 8155, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12237, 12414, 12705, 13098, 14000A, 14308, 14766, 14783, 15043, 15301, 15326, 16093, 16223, 16234, 16362, 16519
DKK6527-387	Vietnam	412	126	720	B4c2b	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 6221, 6815, 7028, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16217, 16519
DKK7108-388	Vietnam	77	25	124	M10	73, 263, 489, 709, 750, 953, 1438, 2706, 3172.1C, 4140, 4769, 4823, 7028, 8701, 8793, 8860, 9540, 9644, 9729, 10398, 10400, 10873, 11719, 12549, 12705, 12976, 13152, 14502, 14766, 14783, 15040, 15043, 15071, 15301, 15326, 16223, 16256, 16299, 16311
DKK7109-389	Vietnam	102.1	25	186	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3150, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8347, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12820, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DKK7139-392	Vietnam	217.2	53	572	D4b2	73, 150, 152, 263, 374, 489, 750, 1382C, 1438, 2706, 3010, 4769, 4883, 5178A, 7028, 8020, 8414, 8701, 8860, 8964, 9296, 9449, 9540, 9824A, 10398, 10400, 10873,

						11719, 12705, 14668, 14766, 14783, 15043, 15301, 15326, 16172, 16223, 16362, 16519
DKK7142-393	Vietnam	71	24	147	B5a1a	73, 146, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 15926, 16140, 16183C, 16189, 16266A, 16360, 16519
DKK7143-394	Vietnam	893.6	301	1414	M74a	63, 64, 66, 73, 146, 263, 489, 750, 1438, 2706, 4769, 5054, 6185, 6575, 7028, 7861, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12705, 12850, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16311, 16362, 16381
DKX4026-3	Vietnam	143.4	42	241	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 4922, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13368, 14766, 15235, 15326, 15784, 16127, 16189, 16266A, 16519
DKX4068-188	Vietnam	254.4	88	390	B5a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6663, 7028, 7684, 8281-8289d, 8584, 8860, 9100, 9950, 10398, 11719, 12978, 14766, 15235, 15263, 15326, 15777, 16140, 16189, 16266G, 16519
DKX4077-193	Vietnam	224.4	76	497	M59	73, 249, 263, 489, 520, 750, 1438, 2706, 4021, 4322.1C, 4769, 4901, 6437, 7028, 8701, 8860, 8970, 9380, 9540, 10256, 10398, 10400, 10798T, 10873, 11140, 11719, 12705, 13145, 13708, 13862, 14040, 14766, 14783, 15043, 15301, 15326, 16140, 16172, 16189, 16278, 16290
DKX4082-195	Vietnam	228.1	87	426	F1e	73, 150, 249d, 263, 750, 1438, 1700, 2706, 3970, 4769, 5587, 6392, 6962, 7028, 8645, 8793, 8860, 9043, 10310, 10326, 10609, 11719, 12362, 12406, 12882, 13928C, 14766, 15024, 15326, 16189, 16304, 16311, 16519
DKX4360-12	Vietnam	206.1	47	366	B5a1c	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6338, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 13368, 14766, 15235, 15326, 15784, 16127, 16140, 16189, 16266A, 16519
DKX4378-15	Vietnam	189.9	63	363	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 5460, 5821, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16093, 16140, 16183C, 16189, 16207, 16266A, 16311, 16362, 16519
DKX4463-242	Vietnam	90.7	29	155	C7a2	73, 249d, 263, 319.1A, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12541, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326,

						15487T, 16183C, 16189, 16223, 16298, 16327, 16519
DKX7121-390	Vietnam	215.7	75	348	B5a1a	73, 146, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 15926, 16140, 16189, 16266A, 16360, 16519
DKX7137-391	Vietnam	247.5	67	708	B5a1a	73, 146, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 15926, 16140, 16183C, 16189, 16266A, 16360, 16519
DOX018-296	Vietnam	1756.3	223	5474	R9b2	73, 263, 709, 750, 1438, 1541, 2706, 3591, 3666, 3970, 4232, 4769, 6647, 7028, 8724, 8860, 11299, 11353, 11422, 11719, 13191, 13722, 13928C, 14766, 15314, 15326, 15883, 16304, 16362, 16519
DOX15-18	Vietnam	141.5	42	321	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 5978, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX2000-309	Vietnam	58.7	16	154	N9a6	73, 150, 263, 750, 1438, 2706, 3849, 4769, 4856, 5231, 5417, 7028, 8860, 9126, 11719, 12358, 12372, 12705, 14766, 15326, 16223, 16257A, 16261, 16292, 16519
DOX2001-310	Vietnam	229.5	83	478	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11167, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297
DOX2165-311	Vietnam	153.3	39	310	B4g1a	73, 263, 750, 1438, 2706, 3666, 4769, 5108, 7028, 7789, 8281-8289d, 8860, 9177, 9968, 11719, 11914, 14766, 14905, 15326, 16183C, 16189, 16213, 16217, 16292, 16519
DOX2169-312	Vietnam	344.3	132	534	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 3861, 4048, 4071, 4164, 4769, 5351, 5460, 5899.1C, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16172, 16189, 16223, 16248, 16297
DOX2171-313	Vietnam	254.2	76	584	M7b1a1a3	73, 95, 150, 195, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4679, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16183C, 16189, 16223, 16248, 16297, 16362
DOX2185-314	Vietnam	109.9	32	197	B4b1a2a	73, 207, 263, 499, 750, 827, 1438, 1719, 2220, 2706, 4769, 4820, 6023, 6216, 6413, 7028, 7855, 8020T, 8281-8289d, 8860,

						11719, 13590, 14766, 15301, 15326, 15535, 16136, 16183C, 16189, 16217, 16519
DOX2190-315	Vietnam	201.6	58	453	M7b1a1b	73, 150, 189, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297
DOX2192-316	Vietnam	155.9	50	299	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
DOX2193-317	Vietnam	206.1	62	376	N9a10	73, 152, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8281-8289d, 8860, 9055, 9468, 9740, 11719, 12358, 12372, 12705, 12771, 13135, 14766, 15326, 16184, 16223, 16257A, 16261, 16274
DOX2196-318	Vietnam	212	72	372	D5b	73, 150, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 4048, 4769, 4883, 5153, 5178A, 5301, 7028, 8701, 8860, 9180, 9540, 9667, 9992, 10397, 10398, 10400, 10873, 11176, 11719, 12705, 13954, 14766, 14783, 15043, 15301, 15326, 15724, 15734, 16189, 16223, 16362, 16519
DOX2198-319	Vietnam	114.5	37	191	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 3861, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14053, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16248, 16297
DOX2220-320	Vietnam	249.3	103	504	N8	73, 103, 151, 152, 260, 263, 750, 1438, 2706, 2760, 3027, 3565, 4769, 7028, 7885, 7961, 8188, 8860, 10398, 11719, 12705, 13710, 14766, 15211, 15326, 15746, 15924, 16223, 16263, 16274, 16311, 16343, 16357, 16519
DOX2221-321	Vietnam	74.9	18	145	N9a10	73, 150, 263, 750, 1041, 1438, 2706, 4386, 4769, 5231, 5417, 5585, 7028, 8860, 11719, 12358, 12372, 12705, 12771, 13461, 13488, 14766, 15094, 15326, 16223, 16257A, 16261, 16311, 16390
DOX2237-322	Vietnam	151.2	44	403	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX3041-323	Vietnam	176	35	450	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10397, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14187, 14766, 14783, 15043, 15301, 15326, 16038, 16129, 16220C, 16223, 16297, 16298, 16311

DOX3048-325	Vietnam	194.7	58	391	B4c1b2c	73, 150, 263, 709, 750, 1119, 1438, 2706, 3435, 3497, 3571, 3777, 4454, 4769, 5563, 7028, 7325, 8281-8289d, 8592, 8609, 8860, 9128, 9305, 11204, 11440, 11719, 12011, 13434, 14025, 14766, 15326, 15346, 16093, 16129, 16140, 16166, 16183C, 16189, 16217, 16274, 16519
DOX3055-326	Vietnam	164.3	44	55	M7b1a1a3	73, 95, 150, 195, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4679, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16248, 16297, 16362
DOX3059-327	Vietnam	220.5	87	443	B5a1a	73, 146, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 10915, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DOX3061-328	Vietnam	158.8	57	387	B4b1a2a	73, 207, 263, 499, 750, 827, 1438, 1719, 2220, 2706, 4769, 4820, 6023, 6216, 6413, 7028, 7855, 8020T, 8281-8289d, 8860, 11719, 13590, 14766, 15301, 15326, 15535, 16136, 16183C, 16189, 16217, 16519
DOX3062-329	Vietnam	98.5	33	160	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 7990, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16183C, 16189, 16223, 16298, 16311, 16327, 16519
DOX3064-330	Vietnam	180.6	47	333	B4b1a2a	73, 207, 263, 499, 750, 827, 1438, 1719, 2220, 2706, 2831, 4769, 4820, 6023, 6216, 6413, 7028, 7184, 7993, 8281-8289d, 8567, 8860, 11719, 13590, 14766, 15301, 15326, 15535, 16136, 16189, 16217, 16354, 16519
DOX3073-331	Vietnam	290.9	86	572	B4c2	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 7028, 8281-8289d, 8823, 8860, 9053, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16235, 16519
DOX3074-332	Vietnam	188.9	22	464	M7b1a1	73, 150, 159, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14118, 14766, 14783, 15043, 15191, 15301, 15326, 16129, 16223, 16297
DOX3601-333	Vietnam	69	19	153	D4h3	73, 152, 263, 489, 750, 1438, 2706, 3010, 3336, 3644, 4418, 4562, 4769, 4883, 5048, 5178A, 7028, 8414, 8701, 8860, 9540, 10398, 10400, 10873, 11150, 11719, 12373, 12705, 13135, 14668, 14766, 14783, 15043, 15301, 15326, 15346, 16223, 16301, 16311, 16362, 16519

DOX3610-334	Vietnam	177	54	325	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 7990, 8584, 8701, 8860, 8994, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16183C, 16189, 16223, 16298, 16311, 16327, 16519
DOX3643-335	Vietnam	313	133	516	B6a	73, 152, 263, 750, 1438, 2706, 2835, 3010, 4646, 4769, 5321, 5894C, 6340, 7028, 8155, 8281-8289d, 8602, 8860, 9452, 11719, 11914, 12950, 13928C, 14305, 14560, 14766, 15326, 16066, 16189, 16209
DOX4002-251	Vietnam	135.4	48	316	F1a2	73, 185, 249d, 263, 750, 1438, 2706, 3687, 3970, 4086, 4769, 5191, 6392, 6962, 7028, 8860, 9053, 9084, 10034, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14560, 14766, 15326, 16075, 16172, 16304, 16519
DOX4017--19	Vietnam	67.1	19	145	N9a6	73, 150, 263, 709, 750, 1438, 2706, 4769, 4856, 5231, 5417, 7028, 8860, 11719, 12358, 12372, 12705, 13707, 14766, 15080, 15326, 16189, 16223, 16257A, 16261, 16292, 16519
DOX4022-20	Vietnam	150.2	37	264	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4023-21	Vietnam	194.9	57	474	F1a1a1	73, 195, 211, 249d, 263, 750, 1438, 2706, 3861, 3970, 4086, 4769, 6392, 6962, 7028, 7299, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16300, 16304, 16519
DOX4037-22	Vietnam	245.1	75	500	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 2836, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9869, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16189, 16266A, 16274, 16519
DOX4041-252	Vietnam	155.3	52	304	M22a	73, 263, 489, 710, 750, 1438, 2706, 2772, 4639, 4769, 6071, 6710, 6776, 7028, 8701, 8860, 9316, 9540, 10256, 10398, 10400, 10586, 10653, 10873, 11719, 12634, 12705, 13917T, 14766, 14783, 15043, 15301, 15326, 16104, 16219, 16223, 16290, 16519
DOX4052-253	Vietnam	204.4	50	432	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9380, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 15395, 16129, 16145, 16192, 16223, 16297, 16335
DOX4054-254	Vietnam	252.9	69	421	B5a1	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6261, 6960, 7028, 8281-8289d, 8584,

						8856, 8860, 9950, 10398, 11641, 11719, 14766, 15043, 15235, 15326, 15885, 16092, 16140, 16189, 16209, 16266A, 16519
DOX4104-24	Vietnam	195.4	58	377	B4c2b	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 6221, 6815, 7028, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16519
DOX4106-25	Vietnam	511.2	195	1303	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4107-26	Vietnam	216.6	79	345	N9a6	73, 150, 263, 750, 1438, 2706, 4769, 4856, 5231, 5417, 6899, 7028, 8860, 9360, 11719, 12358, 12372, 12705, 14587, 14766, 15080, 15326, 16093, 16189, 16223, 16257A, 16261, 16292, 16519
DOX4110-27	Vietnam	131.8	39	374	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4115-28	Vietnam	161.7	40	323	M76	73, 263, 489, 750, 1438, 2706, 3753, 4769, 5315, 7028, 7521, 7624, 8701, 8764, 8860, 9377, 9540, 10325, 10398, 10400, 10873, 11152, 11719, 12361, 12406, 12705, 12738, 13135, 14341, 14766, 14783, 15043, 15301, 15326, 16069, 16124, 16189, 16278, 16293C, 16362
DOX4122-29	Vietnam	130.4	40	390	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4123-30	Vietnam	93.9	27	257	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8078, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12297, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DOX4133-32	Vietnam	196.3	52	421	M68a1a	73, 152, 178, 263, 291-294d, 489, 750, 1438, 2626, 2706, 3828, 4561, 4688, 4769, 4902C, 5489A, 7028, 8093, 8251, 8701, 8860, 9540, 9644, 10203, 10398, 10400, 10496, 10873, 11719, 12705, 12950, 13401, 13806, 14233, 14766, 14783, 15043, 15301, 15326, 16169, 16223, 16255, 16257, 16259, 16278, 16362, 16519
DOX4143-336	Vietnam	294.8	92	458	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8110, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 12588, 13145, 13395, 14766, 15235, 15326, 15930, 16140, 16183C, 16189, 16266A, 16519

DOX4158-337	Vietnam	134.2	40	206	M7b1a1b	73, 150, 189, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297
DOX4160-338	Vietnam	133.9	39	315	B4g	61A, 62, 73, 183, 263, 709, 750, 1438, 2378, 2706, 4769, 4947, 6482, 7028, 7805, 8281-8289d, 8860, 9872, 9968, 11266, 11338, 11719, 14766, 15326, 16181C, 16182C, 16183C, 16189, 16213, 16217, 16242, 16292, 16301, 16519
DOX4180-256	Vietnam	179	61	348	F1a1	73, 200, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 15346, 16129, 16162, 16172, 16186, 16189, 16193, 16242, 16243, 16304, 16519
DOX4255-33	Vietnam	220.2	77	372	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DOX4260-34	Vietnam	167	75	318	N9a6	73, 150, 263, 750, 1438, 2706, 4769, 4856, 5231, 5417, 6899, 7028, 8860, 9360, 11719, 12358, 12372, 12705, 14587, 14766, 15080, 15326, 16093, 16189, 16223, 16257A, 16261, 16292, 16399, 16519
DOX4263-35	Vietnam	154.4	50	299	M24a	73, 146, 152, 195, 263, 489, 750, 951, 1438, 2706, 4769, 5262, 5773, 6581, 7028, 7040, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13020, 13359, 14766, 14783, 15043, 15301, 15326, 15601, 16075, 16223, 16311, 16519
DOX4265-36	Vietnam	220.5	81	468	M24a	73, 146, 152, 195, 263, 489, 750, 951, 1438, 2706, 4769, 5262, 5773, 6581, 7028, 7040, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13020, 13359, 14766, 14783, 15043, 15301, 15326, 15601, 16075, 16223, 16311, 16519
DOX4268-37	Vietnam	322.7	116	534	N21	73, 150, 195, 263, 337d, 731, 750, 1438, 2706, 2857, 4769, 6752, 7028, 7424, 8149, 8860, 10172, 10398, 10583, 11719, 11950, 12705, 13437, 14560, 14766, 15326, 15519, 16193, 16223, 16519
DOX4274-38	Vietnam	224.5	75	359	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16297, 16519
DOX4287-39	Vietnam	167.9	18	442	M76	73, 263, 489, 750, 1438, 2706, 3753, 4769, 5315, 6965, 7028, 7521, 7624, 8701, 8764, 8860, 9377, 9540, 10325, 10398, 10400, 10873, 11152, 11719, 12361, 12406, 12705, 12738, 13135, 14341, 14766, 14783, 15043,

						15301, 15326, 16069, 16124, 16189, 16278, 16293C, 16362
DOX4293-257	Vietnam	224.9	69	713	F1a1a	73, 93, 95C, 150, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6663, 6932, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10795, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16311, 16519
DOX4294-258	Vietnam	137.1	32	231	R9c	73, 150, 152, 263, 750, 1438, 2706, 3970, 4769, 5012, 5324, 5951, 7028, 7861, 8860, 10403, 11002, 11719, 13928C, 14766, 15326, 15479, 16304, 16335, 16362
DOX4297-259	Vietnam	251.6	75	421	F2e	73, 200, 249d, 263, 750, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769, 5460, 6392, 7028, 7828, 8860, 10265, 10310, 10325, 10535, 10586, 11696, 11719, 12338, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
DOX4301-260	Vietnam	191.3	65	297	B5a1a	73, 210, 263, 709, 750, 1438, 2354, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 13933, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DOX4309-261	Vietnam	154.7	52	324	M10a1a1b	73, 146, 263, 489, 709, 750, 1438, 2706, 3172.1C, 4140, 4769, 7028, 7250, 8701, 8793, 8856, 8860, 9540, 9650, 10398, 10400, 10529, 10646, 10873, 11719, 12549, 12705, 13135, 13152, 14502, 14766, 14783, 15040, 15043, 15071, 15218, 15301, 15326, 16093, 16129, 16193, 16223, 16293C, 16311, 16357, 16497
DOX4315-262	Vietnam	175.3	62	293	M7b1a1a2	73, 150, 199, 263, 489, 593, 750, 1438, 1694, 2706, 4048, 4071, 4137, 4164, 4769, 5351, 5460, 6253, 6455, 6680, 7028, 7684, 7853, 8281-8289d, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16195, 16223, 16297, 16519
DOX4322-263	Vietnam	272.5	71	482	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4739, 4769, 6392, 6515, 6962, 7028, 8572, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13708, 13759, 13928C, 14766, 15326, 15930, 16129, 16172, 16295, 16304, 16519
DOX4324-264	Vietnam	114.7	30	194	M7c1a	73, 146, 199, 263, 489, 750, 1438, 2706, 3882, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12535, 12705, 13434, 14766, 14783, 15043, 15175, 15289, 15301, 15326, 16223, 16295, 16519
DOX4329-265	Vietnam	76.4	20	149	B4c1b2	73, 150, 195, 263, 709, 750, 1119, 1438, 2706, 3497, 3571, 3738, 4769, 5899.1C, 7028, 8200, 8257, 8281-8289d, 8860, 11719, 14766, 15326, 15346, 16140, 16189, 16217, 16274, 16305T, 16335, 16519

DOX4331-266	Vietnam	241.3	98	463	B5a1a	73, 146, 210, 263, 686, 709, 750, 1438, 2706, 3537, 4769, 5628, 6960, 7028, 7961, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16129, 16140, 16189, 16266A, 16519
DOX4338-267	Vietnam	214.7	52	423	D4a	73, 152, 263, 489, 750, 1438, 2706, 3010, 3206, 4769, 4883, 5178A, 7028, 8410, 8414, 8473, 8701, 8860, 9540, 9845, 10398, 10400, 10873, 11719, 12705, 13650, 13966, 14668, 14766, 14783, 14979, 15043, 15301, 15326, 15889, 16093, 16129, 16223, 16263, 16362, 16519
DOX4340-268	Vietnam	109	46	188	M7c1c2	73, 146A, 199, 263, 489, 750, 1438, 2706, 3606, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15236, 15301, 15326, 16311, 16356, 16519
DOX4341-269	Vietnam	181.4	45	906	F2	73, 182, 249d, 263, 750, 1005, 1438, 1824, 2706, 3970, 4769, 5752d, 6392, 7028, 7076, 7828, 8860, 10310, 10535, 10586, 10810, 11719, 12338, 13708, 13928C, 14766, 15151, 15203, 15326, 16167, 16203, 16304, 16318, 16519
DOX4350-271	Vietnam	235	74	460	M7b1a1a2	73, 150, 199, 263, 489, 593, 750, 1438, 1694, 2706, 4048, 4071, 4137, 4164, 4769, 5156, 5351, 5460, 6253, 6455, 6680, 6713, 7028, 7684, 7853, 8281-8289d, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16192, 16223, 16297, 16519
DOX4367-272	Vietnam	356.8	118	586	B5a2a2	73, 93, 210, 263, 709, 750, 1438, 1462, 2706, 3537, 4769, 7028, 7474, 8281-8289d, 8584, 8614, 8860, 9139, 9380, 9950, 9962, 10398, 10676, 11149, 11151, 11719, 14149, 14766, 15235, 15326, 15784, 16140, 16189, 16266G, 16519
DOX4368-273	Vietnam	152	54	266	B4c1b	73, 150, 263, 709, 750, 1119, 1438, 2706, 3497, 4769, 5246A, 7028, 8281-8289d, 8860, 11719, 14502, 14766, 15326, 15346, 16140, 16183C, 16189, 16217, 16274, 16304, 16310, 16311, 16519
DOX4370-274	Vietnam	270.8	75	517	M7c1a	73, 146, 152, 199, 263, 489, 750, 1236, 1438, 1809, 2706, 3316, 3882, 4071, 4769, 4850, 5063, 5442, 6392, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15301, 15326, 16075, 16223, 16278, 16293T, 16295, 16519
DOX4383-40	Vietnam	151.8	35	337	M51b1b	73, 150, 263, 489, 750, 1438, 2706, 2833, 3565, 3999, 4336, 4697, 4769, 4973, 7028, 7642, 8281-8289d, 8701, 8860, 9509, 9540, 10398, 10400, 10873, 11719, 12012, 12609, 12705, 13105, 13768, 13928C, 14110, 14356, 14417, 14687, 14766, 14783, 15043,

						15301, 15317, 15326, 16145, 16223, 16278, 16311
DOX4402-41	Vietnam	172.3	59	287	B5a1c	73, 146, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6425, 6960, 7028, 8281-8289d, 8584, 8616, 8860, 9950, 10325, 10398, 11719, 12192, 14766, 15235, 15326, 16127, 16140, 16183C, 16266A, 16519
DOX4412-42	Vietnam	440.7	178	1133	M76	73, 263, 489, 750, 1438, 2706, 3753, 4769, 5315, 7028, 7521, 7598, 7624, 8701, 8764, 8860, 9377, 9540, 10325, 10398, 10400, 10873, 11152, 11719, 12361, 12406, 12705, 12738, 13135, 14341, 14766, 14783, 15043, 15301, 15326, 16069, 16124, 16189, 16278, 16293C, 16362
DOX4420-275	Vietnam	268.3	100	430	D4g2a1	73, 185, 263, 279, 298, 489, 750, 1438, 2706, 3010, 4394, 4769, 4883, 5178A, 5231, 6905, 7028, 8414, 8701, 8860, 9052, 9540, 10398, 10400, 10750, 10873, 11059, 11674A, 11719, 12705, 13104, 13500, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16362
DOX4422-43	Vietnam	68.9	19	184	M19	73, 263, 489, 527, 750, 1438, 2392, 2706, 3828, 4769, 5046, 5250, 6620, 6896, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11167, 11503, 11719, 12397, 12465, 12705, 14766, 14783, 15043, 15301, 15326, 15935, 16189, 16223, 16249, 16362, 16519
DOX4423-44	Vietnam	58	14	189	M19	73, 263, 489, 527, 750, 1438, 2392, 2706, 3828, 4769, 5046, 5250, 6620, 6896, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11167, 11503, 11719, 12397, 12465, 12705, 14766, 14783, 15043, 15301, 15326, 15935, 16189, 16223, 16249, 16362, 16519
DOX4425-45	Vietnam	117.5	39	218	M19	73, 263, 489, 527, 750, 1438, 2392, 2706, 3828, 4769, 5046, 5250, 6620, 6896, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11167, 11503, 11719, 12397, 12465, 12705, 14766, 14783, 15043, 15301, 15326, 15935, 16189, 16223, 16249, 16362, 16519
DOX4426-46	Vietnam	285.8	57	793	M51b	73, 150, 152, 228, 263, 489, 750, 1438, 2706, 2833, 3915, 4221, 4697, 4769, 4973, 6455, 7028, 7372, 8701, 8860, 9156, 9470, 9509, 9540, 10128, 10398, 10400, 10873, 11719, 12705, 13722, 14020A, 14110, 14356, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16168, 16189, 16223, 16278
DOX4428-47	Vietnam	244.8	53	556	M51b	73, 150, 152, 228, 263, 489, 750, 1438, 2706, 2833, 3915, 4221, 4697, 4769, 4973, 6382C, 6455, 7028, 7372, 8701, 8860, 9156, 9470, 9509, 9540, 10128, 10398, 10400, 10873, 11719, 12705, 13722, 14020A, 14110, 14356, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16168, 16189, 16223, 16278
DOX4429-48	Vietnam	202.7	75	553	N21	73, 150, 195, 263, 337d, 750, 1438, 2706, 3816, 4769, 6752, 7028, 7762, 8701, 8860,

						10583, 11719, 12705, 12771, 13437, 14560, 14766, 15326, 16129, 16193, 16223, 16519
DOX4430-49	Vietnam	177.3	65	433	M51b	73, 150, 152, 228, 263, 489, 750, 1438, 2706, 2833, 3915, 4221, 4697, 4769, 4973, 6455, 7028, 7372, 8701, 8860, 9156, 9470, 9509, 9540, 10128, 10398, 10400, 10873, 11719, 12705, 13722, 14020A, 14110, 14356, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16168, 16183C, 16189, 16223, 16278
DOX4552-50	Vietnam	142	47	233	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DOX4560-51	Vietnam	178	55	407	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DOX4561-52	Vietnam	276.2	81	731	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16519
DOX4563-53	Vietnam	133.9	34	402	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DOX4568-54	Vietnam	283.9	53	1545	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16391, 16519
DOX4582-55	Vietnam	116.7	29	199	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 12651, 12940, 13145, 13395, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DOX4593-276	Vietnam	189.2	49	603	F2a	73, 249d, 263, 750, 1005, 1438, 1824, 2706, 3970, 4769, 6392, 7028, 7828, 8411, 8860, 10310, 10535, 10586, 11719, 12338, 13708, 13928C, 14766, 15326, 16093, 16189, 16203, 16291, 16304, 16519
DOX4594-56	Vietnam	167	65	508	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4595-57	Vietnam	231.4	81	586	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406,

						12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4603-277	Vietnam	122.8	46	486	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX4606-278	Vietnam	204.1	60	331	R9b1a3	73, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 11719, 12714, 13928C, 14766, 15326, 16192, 16304, 16309, 16390, 16519
DOX4661-279	Vietnam	137.7	46	236	R9b1a1a	73, 143, 183, 235, 263, 292, 750, 1438, 1541, 2392, 2706, 3970, 4769, 5063, 7028, 7849, 8389, 8860, 11719, 12714, 13074, 13928C, 14766, 15326, 16288, 16309, 16390, 16519
DOX4670-280	Vietnam	155	59	262	Z4a	73, 151, 152, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 10398, 10400, 10873, 11719, 12079, 12705, 14766, 14783, 15043, 15301, 15326, 15475, 15487T, 15784, 15944d, 16169, 16185, 16223, 16260, 16298, 16302, 16465
DOX4674-281	Vietnam	142.4	29	231	B5a1	73, 210, 263, 471, 709, 750, 1438, 2706, 3397, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 12397, 14162, 14766, 15235, 15326, 15466, 15884, 16140, 16183C, 16189, 16266A, 16311, 16519
DOX4678-282	Vietnam	108.9	27	202	B4a1d	73, 150, 263, 750, 1438, 2706, 4769, 5465, 5894, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 14766, 15326, 16189, 16217, 16261, 16519
DOX4689-283	Vietnam	124.9	38	229	F1d	73, 188, 249d, 263, 709, 750, 929, 1438, 1734, 2706, 3970, 4769, 5628, 6392, 6962, 7028, 7738, 8854, 8860, 9104, 9254, 9423, 10083, 10310, 10609, 11719, 11998C, 12406, 12545, 12882, 13359, 13388, 13899, 13928C, 14766, 15326, 15402, 15884, 16189, 16274, 16304, 16519
DOX4692-284	Vietnam	223.5	84	366	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 5899.1C, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9615, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14419, 14766, 14783, 14978, 15043, 15094, 15301, 15326, 16129, 16189, 16223, 16297
DOX4693-285	Vietnam	303.5	132	472	C7	73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16093, 16172, 16218, 16223, 16298, 16327, 16519
DOX4694-286	Vietnam	250.1	82	841	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053,

						9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 15448, 16108, 16129, 16162, 16169A, 16172, 16304, 16519
DOX4703-287	Vietnam	442.2	166	680	B5a1b1	73, 146, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 7852, 8281-8289d, 8584, 8860, 9950, 10398, 10754, 11719, 13928C, 14766, 14989, 15235, 15326, 15769, 16140, 16176, 16183C, 16189, 16243, 16266A, 16519
DOX4708-288	Vietnam	142.5	52	252	F1a	73, 249d, 263, 750, 1438, 1503, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14063, 14766, 15326, 16129, 16172, 16304, 16519
DOX4713-289	Vietnam	320.9	102	689	G3a2	73, 143, 152, 263, 489, 709, 750, 1438, 2706, 2857, 4769, 4833, 5108, 7028, 7621, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 14569, 14766, 14783, 15043, 15274, 15301, 15326, 15746, 16201, 16223, 16274
DOX4722-290	Vietnam	199.8	74	328	R9b1b	73, 263, 750, 1438, 1541, 2322A, 2706, 3970, 4769, 7028, 8860, 9126, 11719, 12358, 12372, 12705, 13928C, 14766, 15326, 16124, 16148, 16183, 16304, 16309, 16390, 16519
DOX4740-339	Vietnam	184	62	305	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 15718, 16129, 16172, 16304, 16519
DOX5123-340	Vietnam	302.1	91	853	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10397, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14187, 14766, 14783, 15043, 15301, 15326, 16038, 16129, 16220C, 16223, 16297, 16298, 16311
DOX553-297	Vietnam	84.8	21	148	Z3c	73, 152, 214, 249d, 263, 489, 709, 750, 1438, 2706, 4715, 4769, 4853, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 10208, 10398, 10400, 10667, 10873, 11719, 12705, 14766, 14783, 15043, 15301, 15326, 15487T, 15784, 16185, 16223, 16260, 16298, 16519
DOX554-298	Vietnam	119.7	40	199	R11b1	73, 185, 189, 263, 709, 750, 1438, 2706, 4769, 5836, 7028, 8277, 8279, 8860, 10031, 10398, 11061, 11719, 12950, 13269, 13681, 13879, 14322, 14766, 15326, 16092, 16189, 16311, 16390, 16399, 16519
DOX5633-342	Vietnam	135.2	41	225	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 15718, 16129, 16172, 16304, 16519

DOX6348-344	Vietnam	212.5	86	345	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 15718, 16129, 16172, 16304, 16519
DOX6353-345	Vietnam	175	48	313	M7b1a1e1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4188, 4769, 5351, 5460, 5964, 6228, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9803, 9824, 10232, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 15610, 16129, 16153, 16192, 16223, 16297
DOX6528-346	Vietnam	131.7	34	251	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13269, 14766, 15326, 15449, 15784, 16129, 16189, 16217, 16261, 16311
DOX6560-347	Vietnam	142	50	291	M12a1a1	73, 125, 127, 128, 263, 318, 489, 750, 1438, 2706, 4048, 4170, 4769, 5580, 6465, 6767, 7028, 8701, 8860, 9490, 9540, 10398, 10400, 10873, 11719, 11914, 12030, 12358, 12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 15451, 15463, 15651, 16223, 16234, 16290, 16362
DOX6562-348	Vietnam	127.5	50	263	G2a1	73, 263, 489, 709, 750, 1438, 2706, 3511, 4769, 4833, 5042, 5108, 5601, 7028, 7598, 7600, 8701, 8860, 9377, 9540, 9575, 10398, 10400, 10873, 11719, 12705, 13563, 14200, 14569, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16224, 16227, 16274, 16278, 16362
DOX6681-349	Vietnam	247.1	72	455	D5b	73, 150, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 4048, 4769, 4883, 5153, 5178A, 5301, 7028, 8701, 8860, 9180, 9540, 9667, 9992, 10397, 10398, 10400, 10873, 11176, 11719, 12705, 13954, 14766, 14783, 15043, 15301, 15326, 15724, 15734, 16189, 16223, 16362, 16519
DOX681-299	Vietnam	224.3	78	353	B4c1b2c	73, 150, 263, 709, 750, 1119, 1438, 2706, 3435, 3497, 3571, 3777, 4454, 4769, 5563, 7028, 7325, 8281-8289d, 8592, 8609, 8860, 9128, 9305, 11204, 11440, 11719, 12011, 13434, 14025, 14766, 15326, 15346, 16093, 16129, 16140, 16166, 16189, 16217, 16274, 16519
DOX692-300	Vietnam	415	133	798	B5a1a	73, 210, 263, 709, 750, 1438, 1462, 2361, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8835, 8860, 9950, 10398, 11719, 13145, 13203, 13395, 14180, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
DOX701-301	Vietnam	62.8	17	200	F3a1	73, 207, 249d, 263, 709, 750, 1438, 2120, 2706, 3434, 3970, 4769, 4824, 4991, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 10310, 10320, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15412G, 16260, 16298, 16355, 16362, 16526

DOX702-302	Vietnam	265.4	94	548	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8222, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 15784, 16140, 16183C, 16189, 16261, 16266A, 16519
DOX704-303	Vietnam	246.1	66	468	D4e3	73, 263, 489, 750, 1438, 2706, 3010, 4769, 4883, 5178A, 7028, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 13135, 14668, 14766, 14783, 14857, 15043, 15301, 15326, 16201, 16223, 16362
DOX707-304	Vietnam	136	55	237	M7b1a1b	73, 150, 189, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297
DOX708-305	Vietnam	600.6	171	1063	F3a1	73, 207, 249d, 263, 309.2C, 709, 750, 1438, 2706, 3434, 3970, 4769, 5237, 5302, 5585, 5823, 5894, 5913, 5978, 6392, 7028, 7151, 8860, 10310, 10320, 11065, 11719, 12621, 12696, 13928C, 14766, 14971, 15326, 15483, 16111, 16192, 16249, 16298, 16355, 16362, 16390
DOX711-306	Vietnam	189.1	83	308	F1f	73, 249d, 263, 275, 750, 1438, 2706, 3867, 3970, 4715, 4769, 5054, 5823, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 10688, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304
DOX721-307	Vietnam	192.1	60	306	R11b	73, 185, 189, 235, 263, 319.1T, 709, 750, 930, 1438, 2706, 3335, 4688, 4769, 7028, 8116, 8277, 8279, 8860, 9055, 9948, 10031, 10398, 11061, 11719, 12950, 13269, 13681, 14766, 15326, 16189, 16249A, 16260, 16311, 16519
DOX722-308	Vietnam	147.3	58	485	M71b	73, 151, 263, 489, 750, 1438, 2224, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
DOX7246-350	Vietnam	117.8	39	192	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 15718, 16129, 16172, 16304, 16519
DOX7247-351	Vietnam	143.6	42	235	M7b1a1e1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4188, 4769, 5351, 5460, 5964, 6228, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9803, 9824, 10232, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 15610, 16129, 16153, 16192, 16223, 16297
DOX7250-352	Vietnam	725.2	160	3844	F1a1a	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149,

						8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
DOX7447-353	Vietnam	161	32	711	F3a1	73, 207, 249d, 263, 709, 750, 1438, 2120, 2706, 3434, 3970, 4769, 4824, 4991, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 10310, 10320, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15412G, 16260, 16298, 16355, 16362, 16526
DOX7457-354	Vietnam	59	22	113	B4d1	73, 195, 263, 316, 619, 750, 827, 1438, 2706, 4769, 7028, 8281-8289d, 8860, 11719, 11914, 13942, 14766, 15038, 15326, 15535, 15930, 16037, 16114, 16172, 16189, 16214, 16217, 16519
DOX7462-355	Vietnam	155	59	246	F1f	73, 249d, 263, 275, 750, 1438, 2706, 3867, 3970, 4715, 4769, 5054, 5823, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 10688, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304
DOX7484-356	Vietnam	116.9	30	220	M7b1a1	73, 150, 194d, 199, 263, 489, 750, 1438, 2232.1A, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10795T, 10837, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
DOX7569-357	Vietnam	304.4	114	543	F1a1d	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7849, 8860, 9053, 9548, 10310, 10609, 11380, 11719, 12406, 12603, 12882, 13105, 13759, 13928C, 14766, 14783, 15326, 16129, 16162, 16172, 16189, 16304, 16399, 16519
DOX7570-358	Vietnam	184.8	38	419	B5a1b1	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4639, 4769, 6960, 7028, 7852, 8281-8289d, 8584, 8860, 9593, 9950, 10398, 10754, 11719, 14766, 14924, 14947A, 14989, 15235, 15326, 15534, 16140, 16183C, 16189, 16266A, 16519
LAO1-001	Laos	1251.3	492	2514	C7a	44.1C, 73, 214, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO1-002	Laos	2339.1	294	8000	M74a	63, 64, 66, 73, 189, 215, 263, 489, 750, 1438, 2706, 4769, 5054, 6185, 6575, 7028, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12705, 12850, 14311, 14766, 14783, 15043, 15301, 15326, 16093, 16223, 16311, 16362, 16381
LAO1-003	Laos	940	347	1722	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 7028, 8281-8289d, 8860, 9123, 9657, 11719, 14518, 14766, 15236, 15244, 15326,

						16093, 16169, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-004	Laos	973.3	317	1777	B4g	61A, 62, 73, 183, 263, 750, 1438, 2378, 2706, 4769, 6482, 7028, 8281-8289d, 8860, 9968, 11719, 14766, 15326, 16189, 16213, 16217, 16242, 16261, 16292, 16301, 16519
LAO1-005	Laos	813.8	229	1561	D4e1a3	73, 94, 146, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8119, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16362
LAO1-006	Laos	707	239	1504	B5a1c1	73, 150, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO1-007	Laos	663.2	250	1235	B4g	61A, 62, 73, 183, 263, 750, 1438, 2378, 2706, 4769, 6482, 7028, 8281-8289d, 8860, 9968, 11719, 14766, 15326, 16189, 16213, 16217, 16242, 16261, 16292, 16301, 16519
LAO1-008	Laos	471.4	159	1569	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO1-009	Laos	459.8	106	1599	B5a1c1	73, 150, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO1-010	Laos	659.2	184	2326	D4e1a3	73, 94, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8119, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16362, 16519
LAO1-011	Laos	731.8	236	1634	C7a1d	73, 146, 249d, 263, 489, 750, 1438, 2706, 2905, 3552A, 4715, 4769, 5821, 6338, 6827, 7028, 7196A, 7302, 7853, 8251, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11830, 11914, 12705, 12957, 13263, 14318, 14766, 14783, 14978, 15043, 15301, 15326, 15487T, 15670, 16086, 16223, 16242, 16256, 16298, 16327, 16390, 16519
LAO1-012	Laos	673.2	247	1401	A11	73, 152, 235, 263, 663, 750, 1438, 1736, 2706, 4248, 4769, 4824, 7028, 8794, 8860, 9650, 11719, 12705, 14766, 15326, 16223, 16290, 16293C, 16319, 16519
LAO1-013	Laos	702.7	215	1418	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519
LAO1-014	Laos	778.8	238	1478	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338,

						7028, 7196A, 7853, 8149, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10754, 10873, 11719, 11839, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16093, 16189, 16223, 16298, 16327, 16519
LAO1-015	Laos	330.5	95	649	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO1-016	Laos	719.8	274	1697	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8075, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14766, 15326, 16129, 16189, 16304, 16519
LAO1-017	Laos	1028.2	292	2205	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8075, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14766, 15326, 16129, 16189, 16304, 16519
LAO1-018	Laos	661	228	1330	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO1-019	Laos	892	210	1928	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14271, 14766, 15326, 16129, 16189, 16304, 16519
LAO1-020	Laos	910.7	289	1788	F3a1	73, 204, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13095, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO1-021	Laos	641.8	223	1148	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16262, 16266A, 16519
LAO1-022	Laos	563.3	176	1153	B4a	73, 263, 750, 1438, 2706, 3338, 4769, 5465, 5814, 7028, 8281-8289d, 8702, 8860, 9123, 10319, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-023	Laos	1491.7	520	3317	M24a	73, 146, 152, 195, 263, 489, 491, 750, 951, 1438, 2706, 4769, 5773, 7028, 7040, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13359, 13659, 14766, 14783, 15043, 15301, 15326, 15601, 16223, 16311, 16519
LAO1-024	Laos	890.8	322	1706	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8149, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10754, 10873, 11719, 11839, 11914, 12705, 13263,

						14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16093, 16189, 16223, 16298, 16327, 16519
LAO1-025	Laos	611.6	199	1486	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519
LAO1-026	Laos	465.5	141	932	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO1-027	Laos	570.8	190	1864	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO1-028	Laos	613.7	145	1476	F3a1	73, 204, 207, 249d, 263, 279, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO1-029	Laos	617	219	1214	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16186, 16189, 16262, 16266A, 16519
LAO1-030	Laos	689.2	199	1253	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 15841, 16140, 16183C, 16189, 16266A, 16519
LAO1-031	Laos	574.5	197	1015	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 15841, 16140, 16183C, 16189, 16266A, 16519
LAO1-032	Laos	670.2	264	1224	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 6528, 7028, 8281-8289d, 8860, 9123, 11719, 14518, 14766, 15236, 15244, 15326, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-033	Laos	678.6	164	1788	D4e1a3	73, 94, 146, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8119, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16362
LAO1-034	Laos	622.8	226	1386	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 13020, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519

LAO1-035	Laos	714.6	259	1245	B4a	73, 263, 750, 1438, 2706, 3338, 4769, 5465, 5814, 7028, 8281-8289d, 8702, 8860, 9123, 10319, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-036	Laos	651	216	1358	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16262, 16266A, 16519
LAO1-037	Laos	692.5	216	2013	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3209, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519
LAO1-038	Laos	727.3	179	2681	D4e1a3	73, 94, 146, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8119, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16362
LAO1-039	Laos	589.9	189	1042	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 7028, 8281-8289d, 8860, 9123, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-040	Laos	879.7	214	1837	F2b	73, 146, 249d, 263, 709, 750, 1005, 1438, 1709, 1824, 2706, 3290, 3970, 4769, 4811, 5417, 6040, 6392, 6408, 7028, 7828, 8860, 9137, 10310, 10346, 10535, 10586, 11719, 12338, 12609, 13500, 13708, 13768, 13928C, 14016, 14766, 15326, 16092, 16291, 16294, 16304
LAO1-041	Laos	913	336	1838	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16262, 16266A, 16519
LAO1-042	Laos	895.9	350	2580	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9615, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14419, 14766, 14783, 14978, 15043, 15301, 15326, 16189, 16223, 16297
LAO1-043	Laos	817.7	276	1671	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO1-044	Laos	783	309	1978	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519

LAO1-045	Laos	131	61	272	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 15841, 16140, 16189, 16266A, 16519
LAO1-046	Laos	312.8	149	628	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO1-047	Laos	567.7	218	996	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16262, 16266A, 16519
LAO1-048	Laos	616.8	31	1775	A11	73, 152, 235, 263, 663, 750, 1438, 1736, 2706, 4248, 4769, 4824, 7028, 8794, 8860, 9650, 11719, 12705, 14766, 15326, 16223, 16290, 16293C, 16319, 16519
LAO1-049	Laos	941.2	340	1806	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 7028, 8281-8289d, 8860, 9123, 9657, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16169, 16183C, 16189, 16217, 16261, 16357, 16519
LAO1-050	Laos	458.5	111	962	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519
LAO1-051	Laos	1501.3	494	2999	F1a1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 4965, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO1-052	Laos	958.3	308	2201	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14271, 14766, 15323, 15326, 16129, 16189, 16304, 16519
LAO1-053	Laos	513.1	160	1282	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO1-054	Laos	1426.8	547	2815	C5	73, 249d, 263, 489, 595.1C, 750, 1438, 2706, 3552A, 4715, 4769, 6338, 6827, 7028, 7196A, 7302, 7853, 8251, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11830, 11914, 12705, 12957, 13263, 13722, 14318, 14766, 14783, 15043, 15080, 15301, 15326, 15487T, 15884, 16223, 16288, 16300, 16327, 16519
LAO1-055	Laos	697.2	111	1709	C5	73, 249d, 263, 489, 595.1C, 750, 1438, 2706, 3552A, 4715, 4769, 7028, 7196A, 8584, 8701, 8860, 9540, 9545, 10398,

						10400, 10873, 11092, 11719, 11914, 12705, 13263, 13722, 14318, 14766, 14783, 15043, 15080, 15301, 15326, 15487T, 15884, 16223, 16288, 16300, 16327, 16519
LAO1-056	Laos	1024.5	290	2428	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16186, 16189, 16262, 16266A, 16519
LAO1-057	Laos	663.1	147	1374	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14766, 15326, 16129, 16189, 16304, 16519
LAO2-001	Laos	555.2	170	1551	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO2-002	Laos	694.5	252	1455	F1a1d	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9548, 10310, 10609, 11380, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16399, 16519
LAO2-003	Laos	708.3	235	1387	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 5894, 6815, 7028, 8860, 10581, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16239, 16304, 16309, 16390, 16519
LAO2-004	Laos	645.8	239	1297	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-005	Laos	1133.1	412	3141	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO2-006	Laos	920.2	306	1770	M71a2	73, 143, 146, 151, 263, 489, 750, 1438, 2706, 4769, 4853, 7028, 8440, 8701, 8718, 8838, 8860, 9540, 9615, 10398, 10400, 10873, 11719, 12705, 13759, 14605, 14766, 14783, 15043, 15301, 15326, 15458, 16129, 16140, 16203, 16223, 16271
LAO2-008	Laos	690.2	192	2060	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C,

						14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-009	Laos	200.9	67	400	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-010	Laos	626.3	231	1322	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-011	Laos	427.5	129	1481	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-012	Laos	57	14	117	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-013	Laos	706.5	199	1405	M8a2a1	73, 146, 263, 489, 750, 1438, 2706, 2835, 3714, 4715, 4769, 6179, 7028, 7196A, 8584, 8684, 8701, 8860, 9540, 10398, 10400, 10873, 11176, 11719, 12705, 14470, 14766, 14783, 15043, 15301, 15326, 15487T, 16184, 16189, 16223, 16298, 16311, 16319, 16390, 16468, 16470, 16471, 16473
LAO2-014	Laos	649	147	1913	D5b1c1	73, 150, 152, 185, 263, 271, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 4769, 4883, 5153, 5178A, 5301, 5899.1C, 6253, 7028, 8394, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 12544, 12666C, 12705, 14766, 14783, 15043, 15301, 15326, 15470, 16092, 16111A, 16148, 16189, 16223, 16293, 16362, 16519
LAO2-015	Laos	791.6	249	1864	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-016	Laos	772.2	211	1701	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-017	Laos	524.1	120	2320	F1a1a	73, 150, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7258,

						8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13353, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304
LAO2-018	Laos	592.2	149	2061	M71a	73, 151, 263, 489, 518, 750, 884, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16209, 16223, 16271, 16294
LAO2-019	Laos	697	246	2051	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-020	Laos	505.9	164	2732	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-021	Laos	893.8	359	2127	F1c1a	73, 152, 195, 234, 249d, 263, 750, 980, 1438, 1849, 1927, 2706, 3970, 4769, 5628, 6392, 6599, 6962, 7028, 8860, 9053, 10310, 10454, 10457, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16111, 16129, 16304, 16519
LAO2-023	Laos	703.5	145	1903	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3397, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16519
LAO2-024	Laos	396.6	63	4216	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-025	Laos	901.1	351	1888	F1c1a	73, 152, 195, 234, 249d, 263, 750, 1438, 1849, 1927, 2706, 3970, 4769, 6392, 6599, 6962, 7028, 8860, 9053, 10310, 10454, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16111, 16129, 16189, 16304, 16519
LAO2-026	Laos	958.9	318	2007	M24a	73, 146, 152, 195, 263, 489, 750, 951, 1438, 2706, 3398, 4769, 5773, 6852, 7028, 7040, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13359, 14512, 14766, 14783, 15043, 15301, 15326, 15601, 16223, 16311, 16519
LAO2-027	Laos	836.9	184	1925	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326,

						16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO2-028	Laos	687.6	253	1255	B4c2	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 7028, 8281-8289d, 8860, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16219, 16309, 16519
LAO2-029	Laos	678.7	172	1937	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-030	Laos	670.8	184	1258	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 2833, 4769, 5162, 5773, 7028, 8269, 8701, 8854, 8860, 9540, 10101, 10335, 10398, 10400, 10873, 11719, 12651, 12705, 13359, 13686, 13812, 14766, 14783, 15043, 15244, 15301, 15326, 15327, 15583, 15601, 16150, 16223, 16519
LAO2-031	Laos	1228	422	3585	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-032	Laos	816.3	248	1707	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3397, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16519
LAO2-033	Laos	1028.1	349	2809	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-034	Laos	960.6	392	1809	G2	73, 195, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 5601, 7028, 8701, 8860, 9540, 10237, 10398, 10400, 10873, 11719, 12705, 13563, 14569, 14766, 14783, 15043, 15301, 15326, 16217, 16223, 16362
LAO2-035	Laos	67	18	195	M20	73, 152, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16284, 16360, 16519
LAO2-036	Laos	570.5	180	1698	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873,

						11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297, 16299
LAO2-037	Laos	817.4	232	1862	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16189, 16223, 16266, 16311, 16362
LAO2-038	Laos	953.4	294	2152	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO2-039	Laos	955.9	198	2180	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 2833, 4769, 5162, 5773, 7028, 8269, 8701, 8854, 8860, 9540, 10101, 10335, 10398, 10400, 10873, 11719, 12651, 12705, 13359, 13686, 13812, 14766, 14783, 15043, 15244, 15301, 15326, 15327, 15583, 15601, 16150, 16223, 16519
LAO2-040	Laos	599.1	116	1610	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 5894, 6815, 7028, 8860, 10581, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16239, 16304, 16309, 16390, 16519
LAO2-041	Laos	709.6	215	1475	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO2-042	Laos	874.6	217	2280	M20	73, 152, 225, 249d, 263, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8251, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16235, 16272, 16519
LAO2-043	Laos	819.1	231	4167	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-044	Laos	709.2	253	1344	M71a2	73, 143, 146, 151, 263, 489, 750, 1438, 2706, 4769, 4853, 7028, 8440, 8701, 8718, 8838, 8860, 9540, 9615, 10398, 10400, 10873, 11719, 12705, 13759, 14605, 14766, 14783, 15043, 15301, 15326, 15458, 16129, 16140, 16203, 16223, 16271
LAO2-045	Laos	75	33	200	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769,

						5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO2-046	Laos	892	205	1840	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO2-047	Laos	690.7	203	2493	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-048	Laos	643.6	173	3543	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-049	Laos	782.3	176	2341	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-050	Laos	141.8	44	245	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-051	Laos	524.6	198	1199	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-052	Laos	746.3	264	1505	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-053	Laos	622.4	176	1807	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9300, 9548, 10310, 10609, 11215, 11719, 11809, 12241d, 12406, 12738, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-054	Laos	788.2	232.4	349	G2	73, 195, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 5601, 7028, 8701, 8860,

						9540, 10237, 10398, 10400, 10873, 11719, 12705, 13563, 14569, 14766, 14783, 15043, 15301, 15326, 16217, 16223, 16362
LAO2-055	Laos	780.1	280	1803	F1c1a	73, 152, 195, 234, 249d, 263, 750, 1438, 1849, 1927, 2706, 3970, 4769, 6392, 6599, 6962, 7028, 8860, 9053, 10310, 10454, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16111, 16129, 16189, 16304, 16519
LAO2-056	Laos	665.7	187	1799	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16189, 16223, 16266, 16311, 16362
LAO2-057	Laos	869.6	389	2676	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-058	Laos	734.4	161	4522	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO2-059	Laos	713.8	169	3219	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-060	Laos	1061	348	2480	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-061	Laos	698.7	203	1560	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-062	Laos	642.8	261	1488	R9b2	73, 263, 750, 1438, 1541, 2706, 3666, 3970, 4769, 6647, 7028, 7328, 8724, 8860, 9801, 11299, 11422, 11719, 12599, 13191, 13722, 13928C, 14766, 15314, 15326, 15883, 16189, 16304, 16362, 16519
LAO2-063	Laos	907.6	412	2080	R9b2	73, 263, 750, 1438, 1541, 2706, 3666, 3970, 4769, 6647, 7028, 7328, 8724, 8860, 9801, 11299, 11422, 11719, 12599, 13191, 13722, 13928C, 14766, 15314, 15326, 15883, 16189, 16304, 16362, 16519

LAO2-064	Laos	501.1	144	1093	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-065	Laos	3385.2	424	9627	M74a	63, 64, 66, 73, 263, 489, 750, 1438, 2706, 4769, 5054, 5981G, 6185, 6575, 7028, 7861, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10685, 10873, 11719, 12705, 12850, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16311, 16362, 16381
LAO2-066	Laos	1174	315	3097	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9300, 9548, 10310, 10609, 11215, 11719, 11809, 12241d, 12406, 12738, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-067	Laos	876.2	273	1686	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3397, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16519
LAO2-068	Laos	664.4	205	1308	F1c1a	73, 152, 195, 234, 249d, 263, 750, 1438, 1849, 1927, 2706, 3970, 4769, 6392, 6599, 6962, 7028, 8860, 9053, 10310, 10454, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16111, 16129, 16189, 16304, 16519
LAO2-069	Laos	750	259	1481	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 5894, 6815, 7028, 8860, 10581, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16239, 16304, 16309, 16390, 16519
LAO2-070	Laos	851.4	154	6214	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-071	Laos	363.1	45	3620	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-072	Laos	181.2	56	342	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 2833, 4769, 5162, 5773, 7028, 8269, 8701, 8854, 8860, 9540, 10101, 10335, 10398, 10400, 10873, 11719, 12651, 12705, 13359, 13686, 13812, 14766, 14783,

						15043, 15244, 15301, 15326, 15327, 15583, 15601, 16150, 16223, 16519
LAO2-073	Laos	646.8	189	2392	B5a1a	73, 210, 263, 709, 750, 1438, 1462, 2361, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8835, 8860, 9950, 10398, 11719, 13145, 13203, 13395, 14180, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO2-074	Laos	619.5	218	1116	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 15841, 16140, 16183C, 16189, 16266A, 16519
LAO2-075	Laos	623.1	177	2446	F1a1a	73, 150, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7258, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13353, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304
LAO2-076	Laos	1755.6	191	5811	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 3591, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16051, 16129, 16192, 16223, 16297
LAO2-077	Laos	721.3	224	2172	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO2-078	Laos	340.4	125	635	F1a1a	73, 249d, 263, 295, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-079	Laos	791.3	226	1554	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-080	Laos	815	275	2270	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO2-081	Laos	936.9	219	4740	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519

LAO2-082	Laos	1101.1	407	2894	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO2-084	Laos	1360.8	157	5049	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 3591, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16051, 16129, 16192, 16223, 16297
LAO2-085	Laos	529.7	102	1593	B5a1d	73, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11465, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16261, 16266A, 16519
LAO2-086	Laos	997	275	2778	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 2833, 4769, 5162, 5773, 7028, 8269, 8701, 8854, 8860, 9540, 10101, 10335, 10398, 10400, 10873, 11719, 12651, 12705, 13359, 13686, 13812, 14766, 14783, 15043, 15244, 15301, 15326, 15327, 15583, 15601, 16150, 16223, 16519
LAO2-087	Laos	124.3	50	203	M24b	73, 146, 195, 263, 489, 750, 951, 1438, 2140, 2706, 2833, 4769, 5162, 5773, 7028, 8269, 8701, 8854, 8860, 9540, 10101, 10335, 10398, 10400, 10873, 11719, 12651, 12705, 13359, 13686, 13812, 14766, 14783, 15043, 15244, 15301, 15326, 15327, 15583, 15601, 16150, 16223, 16519
LAO2-088	Laos	778.6	296	1654	M7c1b2b	73, 146, 152, 199, 263, 489, 750, 1438, 2706, 4071, 4769, 4850, 5442, 6455, 7028, 7337, 8029, 8701, 8860, 9540, 9824, 9957, 10118, 10398, 10400, 10861, 10873, 11337, 11665, 11719, 12091, 12561, 12705, 13590, 14766, 14783, 15043, 15301, 15315, 15326, 16223, 16295, 16519
LAO2-089	Laos	871.8	270	3412	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO2-090	Laos	563.3	193	1101	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354

LAO2-091	Laos	856.5	228	1794	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-092	Laos	111	28	216	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 5894, 6815, 7028, 8860, 10581, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16239, 16304, 16309, 16390, 16519
LAO2-093	Laos	641.7	223	1357	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6065, 6815, 7028, 8860, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16192, 16239, 16304, 16309, 16390, 16519
LAO2-095	Laos	152.2	50	289	M74a	63, 64, 66, 73, 263, 489, 750, 1438, 2706, 4769, 5054, 5981G, 6185, 6575, 7028, 7861, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10685, 10873, 11719, 12705, 12850, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16311, 16362, 16381
LAO2-099	Laos	335.1	56	701	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO2-103	Laos	260.7	71	605	R9b1a3	73, 152, 263, 750, 951, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 8998, 11719, 12714, 13477, 13928C, 14664, 14766, 15326, 16192, 16304, 16309, 16390, 16519
LAO3-001	Laos	591.6	179	1153	F1f	73, 249d, 263, 593, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16311, 16519
LAO3-002	Laos	591.8	243	1682	F2g	73, 152, 249d, 263, 747, 750, 1005, 1040, 1438, 1824, 2706, 3970, 4769, 6392, 6647, 7028, 7211, 7828, 8860, 10310, 10535, 10586, 11016, 11629, 11719, 12338, 13708, 13928C, 14766, 15326, 16291, 16304, 16311, 16519
LAO3-003	Laos	164.9	21	373	B4c2	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 7028, 8281-8289d, 8823, 8860, 9053, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16172, 16189, 16217, 16235, 16519
LAO3-004	Laos	89.8	35	169	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-005	Laos	925.7	307	1999	F1a1a1	73, 249d, 263, 750, 1438, 2581, 2706, 3565, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C,

						14766, 15326, 16108, 16129, 16162, 16172, 16209, 16304, 16311, 16519
LAO3-006	Laos	521.3	188	1079	C7	73, 195, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 13722C, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16093, 16172, 16223, 16298, 16311, 16327, 16519
LAO3-007	Laos	102.9	10	331	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-008	Laos	642.6	214	1262	M9a5	73, 150, 153, 263, 385, 489, 750, 1438, 2706, 3394, 4491, 4769, 7028, 8155, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12237, 12705, 14308, 14766, 14783, 15043, 15301, 15326, 16148, 16223, 16234, 16355, 16356, 16362
LAO3-009	Laos	157.8	49	442	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-010	Laos	726.2	288	1400	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12541, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16189, 16223, 16239, 16298, 16327, 16519
LAO3-011	Laos	656.6	286	1225	B4g1a	73, 152, 239, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-012	Laos	718.9	171	1427	F1a	73, 189, 207, 249d, 260, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8285.1C, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14684, 14766, 15262, 15326, 16129, 16172, 16304, 16519
LAO3-013	Laos	638.4	215	1178	F1a1a1	73, 249d, 263, 750, 1438, 2259, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7278, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO3-014	Laos	822.4	150	4407	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO3-016	Laos	777.8	255	1426	F1a1a1	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860,

						9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16519
LAO3-017	Laos	711.5	224	1560	B6a	73, 150, 263, 750, 1193, 1438, 2706, 4769, 5894C, 7028, 8281-8289d, 8701, 8860, 9452, 10849, 11719, 11914, 12346, 12950, 13928C, 14305, 14766, 15326, 16093, 16179, 16183C, 16189, 16519
LAO3-018	Laos	933.2	316	2550	M7b1a1d1	73, 150, 199, 263, 489, 750, 980, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6125, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-019	Laos	1152.1	308	2156	M61	73, 263, 489, 750, 1193, 1342, 1438, 2706, 4769, 5812, 6253, 7028, 7759, 8269, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 11810, 12705, 12732, 13468, 14334, 14766, 14783, 15043, 15301, 15326, 16223, 16304, 16344, 16362, 16381, 16519
LAO3-020	Laos	881.2	292	1721	B4g1a	73, 239, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16181C, 16182C, 16183C, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-021	Laos	1063.5	344	3117	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-022	Laos	262.4	118	429	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-023	Laos	965.3	255	2178	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16292A, 16304, 16519
LAO3-024	Laos	865.1	264	1681	D5b	73, 150, 263, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 3582, 4092, 4769, 4883, 5153, 5178A, 5301, 7028, 8460T, 8701, 8860, 9180, 9540, 10088, 10397, 10398, 10400, 10873, 10951, 11293, 11719, 12705, 14094, 14766, 14783, 14821G, 15043, 15301, 15326, 15724, 16160, 16183C, 16189, 16223, 16362
LAO3-025	Laos	627.4	182	194	M7b1a1a3	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9615, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14419, 14766,

						14783, 14978, 15043, 15301, 15326, 16129, 16189, 16192, 16223, 16297
LAO3-026	Laos	81.5	26	153	M7b1a1e1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6228, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10232, 10398, 10400, 10873, 11719, 12405, 12561, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297, 16302
LAO3-027	Laos	655.4	114	2312	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16223, 16297
LAO3-028	Laos	750.2	295	1777	N10b	73, 150, 199, 263, 1393, 1438, 2010, 2706, 3523, 4769, 4977, 5581, 6245, 7028, 8167, 8860, 9392, 9459, 10373, 11719, 12092A, 12705, 13020, 14053, 14766, 15226, 15326, 16172, 16209, 16223, 16258C, 16291A, 16298, 16311
LAO3-029	Laos	1062.3	300	3056	B4a1c4	73, 146, 263, 709, 750, 1438, 2706, 3438, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 12904, 13134, 14766, 15326, 16093, 16183C, 16189, 16217, 16261, 16519
LAO3-030	Laos	624.1	254	1303	B4a1e	73, 182, 185, 204, 263, 750, 1438, 2706, 3548, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 14766, 15326, 16168, 16183C, 16189, 16217, 16261, 16311, 16519
LAO3-031	Laos	737.6	194	1866	M7b1a1d1	73, 150, 199, 263, 489, 750, 980, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6125, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-032	Laos	933.3	224	3913	F1a	73, 195, 249d, 263, 750, 1438, 2706, 3474, 3970, 4086, 4769, 6392, 6962, 7028, 7091, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14063, 14766, 15326, 16129, 16172, 16304G, 16519
LAO3-033	Laos	674.7	222	1433	M7c1c2	73, 146A, 263, 489, 750, 1438, 2706, 3606, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15236, 15301, 15326, 16311, 16356, 16519
LAO3-034	Laos	750.5	279	1927	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519

LAO3-035	Laos	534.1	202	1090	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-036	Laos	867	214	3211	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO3-037	Laos	998.1	268	3409	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO3-038	Laos	784.3	287	1603	B5a1a	73, 210, 263, 319.1T, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16129, 16140, 16148, 16154, 16189, 16239, 16266A, 16519
LAO3-039	Laos	263.1	68	587	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO3-040	Laos	607.4	175	2572	F1a1a1	73, 249d, 263, 750, 1120, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO3-041	Laos	86.1	27	139	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-042	Laos	1006.5	226	6240	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO3-043	Laos	665.3	253	1286	B4g1a	73, 239, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16183C, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-045	Laos	629	202	1401	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16183C, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-046	Laos	465.5	135	848	U7a3	73, 151, 152, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519

LAO3-047	Laos	596.2	197	1572	B5a	73, 210, 263, 294, 709, 750, 1393, 1438, 2706, 3537, 4769, 7001, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 14178, 14766, 15229, 15235, 15236, 15326, 16092, 16093, 16140, 16183C, 16189, 16260, 16266G, 16519
LAO3-048	Laos	210.2	65	387	Z4a	73, 151, 152, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 10398, 10400, 10873, 11719, 12705, 14766, 14783, 15043, 15301, 15326, 15475, 15487T, 15773, 15784, 15944d, 16185, 16223, 16260, 16302
LAO3-049	Laos	142.3	10	450	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-050	Laos	353.6	107	1058	M7b1a1	73, 150, 182, 199, 263, 459d, 489, 750, 1438, 1806, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 13380, 14542A, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-052	Laos	60	23	187	C7a2	73, 489, 750, 1438, 2232.1A, 2706, 3552A, 4062, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16092, 16189, 16223, 16298, 16327, 16519
LAO3-053	Laos	294.8	36	715	D5b	73, 150, 456, 489, 681, 750, 1048, 1107, 1438, 2706, 3826, 4048, 4769, 4883, 5153, 5178A, 5301, 7028, 8602, 8701, 8860, 9180, 9540, 9667, 9992, 10397, 10398, 10400, 10873, 11176, 11719, 12705, 13954, 14766, 14783, 15043, 15301, 15326, 15724, 16189, 16213, 16223, 16362, 16519
LAO3-054	Laos	744.5	284	1398	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519
LAO3-055	Laos	101.1	24	196	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO3-056	Laos	215.5	84	355	U7a3	73, 151, 152, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519
LAO3-057	Laos	60	16	183	B4g1a	73, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 14766, 14905, 15326, 16189, 16213, 16217, 16261, 16292, 16519

LAO3-058	Laos	117.9	44	214	B4a1c4	73, 146, 263, 709, 750, 1438, 2706, 3438, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 12904, 13134, 14766, 15326, 16093, 16189, 16217, 16261, 16519
LAO3-059	Laos	229	65	433	M7b1a1	73, 150, 182, 199, 263, 459d, 489, 750, 1438, 1806, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 13380, 14542A, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-060	Laos	61	22	170	C7	73, 152, 249d, 263, 449, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 8584, 8701, 8856, 8860, 8868, 9540, 9545, 10370, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16129, 16148, 16223, 16298, 16327, 16519
LAO3-062	Laos	242.9	76	398	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8572, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13708, 13759, 13928C, 14766, 15326, 15930, 16129, 16172, 16295, 16304, 16519
LAO3-063	Laos	222.8	67	418	M7b1a1d1	73, 150, 199, 263, 489, 750, 980, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6125, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-065	Laos	167.2	36	480	M7b1a1d1	73, 150, 199, 263, 489, 750, 980, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6125, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO3-067	Laos	70.6	17	148	B4a1e	73, 182, 185, 204, 263, 750, 1438, 2706, 3548, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 14766, 15326, 16168, 16183C, 16189, 16217, 16261, 16311, 16519
LAO3-068	Laos	103.2	36	162	F1f	73, 152, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 15940, 16086, 16129, 16209, 16223, 16272, 16519
LAO3-069	Laos	67	18	180	B4a1c4	73, 146, 263, 709, 750, 1438, 2706, 3438, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 12904, 13134, 14766, 15326, 16093, 16183C, 16189, 16217, 16261, 16519

LAO3-070	Laos	145.4	25	452	F1a1a1	73, 146, 249d, 263, 750, 789, 961, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12820, 12882, 12975, 13434, 13759, 13928C, 14512, 14766, 15326, 16108, 16129, 16145, 16162, 16172, 16304, 16519
LAO3-071	Laos	101.7	37	176	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO3-072	Laos	414.8	121	799	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-001	Laos	169.3	27	461	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-002	Laos	584.4	237	1215	B5b1a	73, 103, 204, 263, 709, 750, 1438, 1598, 2706, 4769, 7028, 8108, 8281-8289d, 8584, 8784, 8829, 8860, 9950, 10398, 11146, 11719, 12361, 12840, 14470, 14766, 15223, 15326, 15508, 15662, 15851, 15927, 16140, 16189, 16243, 16519
LAO4-003	Laos	635.7	172	1407	B5a	73, 210, 263, 709, 750, 1438, 3537, 4769, 6663, 7028, 8281-8289d, 8584, 8860, 9100, 9950, 10398, 11719, 12501, 13281, 14766, 15235, 15263, 15326, 15777, 16140, 16189, 16266G, 16291, 16519
LAO4-004	Laos	652.7	277	1565	B4a1e	73, 182, 185, 204, 263, 750, 1438, 2706, 3548, 4769, 5465, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 14766, 15326, 16168, 16183C, 16189, 16217, 16261, 16311, 16519
LAO4-005	Laos	934.3	263	1864	M7b1a1a3	73, 150, 199, 204, 263, 456, 481, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5330, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16297
LAO4-006	Laos	1085.5	192	2667	M20	73, 152, 225, 249d, 263, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15226, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16362, 16519
LAO4-007	Laos	169.8	48	295	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406,

						12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-008	Laos	599.3	152	1559	M71a	73, 151, 263, 489, 518, 750, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16209, 16223, 16271, 16294
LAO4-009	Laos	586	165	1146	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO4-010	Laos	1025	312	2374	D4g2a1b	73, 263, 298, 459d, 466, 489, 750, 1438, 2706, 3010, 4394, 4769, 4883, 5081, 5178A, 5231, 6164, 7028, 8414, 8701, 8860, 9540, 10398, 10400, 10873, 11059, 11719, 12705, 13104, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16362
LAO4-011	Laos	795.1	195	2660	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-012	Laos	654.9	195	1552	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4062, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12672, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16189, 16223, 16298, 16327, 16519
LAO4-013	Laos	839.5	178	4451	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-014	Laos	768.6	271	1455	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 12501C, 13145, 13395, 14766, 15235, 15326, 16140, 16166, 16189, 16243, 16266A, 16359, 16519
LAO4-015	Laos	568.3	217	1339	M17a	73, 146, 150, 263, 489, 650, 750, 862, 930C, 1438, 2706, 4769, 7028, 8701, 8860, 8930, 9540, 10324, 10398, 10400, 10873, 11016, 11719, 11908, 12705, 12711, 12804, 12973, 14766, 14783, 15043, 15301, 15317, 15326, 15530, 15802, 15884, 16093, 16129, 16209, 16223, 16278, 16290, 16325, 16519
LAO4-016	Laos	711.6	188	3171	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-017	Laos	712.7	230	1467	M7c2	73, 146, 263, 489, 750, 1438, 2706, 3912, 4071, 4769, 4850, 5378, 6455, 7028, 8701, 8860, 9449, 9540, 9824, 10398, 10400,

						10873, 10897, 11084, 11665, 11719, 11932, 12091, 12705, 14053, 14766, 14783, 15043, 15301, 15326, 15338, 16172, 16223, 16311, 16519
LAO4-018	Laos	765.9	164	1595	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 10481, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16189, 16266A, 16519
LAO4-019	Laos	334.2	38	1072	M7b1a1	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 6719, 7028, 7684, 7853, 8557, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11503, 11719, 12405, 12705, 12811, 13834, 14128, 14766, 14783, 15043, 15301, 15326, 16129, 16145, 16192, 16297
LAO4-020	Laos	679.6	208	3218	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-021	Laos	875.9	261	3402	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-022	Laos	596.8	217	1214	F2e	73, 152, 249d, 263, 709, 750, 930, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769, 6260, 6392, 7028, 7828, 8860, 10265, 10310, 10535, 10586, 11719, 12338, 13428, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
LAO4-023	Laos	535	192	1155	B5a	73, 210, 263, 709, 750, 1438, 3537, 4769, 6663, 7028, 8281-8289d, 8584, 8860, 9100, 9950, 10398, 11719, 12501, 13281, 14766, 15235, 15263, 15326, 15777, 16140, 16189, 16266G, 16291, 16519
LAO4-024	Laos	735.9	152	3790	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-025	Laos	726.8	224	1534	F2e	73, 152, 249d, 263, 709, 750, 930, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769, 6260, 6392, 7028, 7828, 8860, 10265, 10310, 10535, 10586, 11719, 12338, 13428, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
LAO4-026	Laos	113.6	34	180	F1a1a	73, 143, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8723, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16256, 16362, 16519, 16527
LAO4-027	Laos	629.7	79	1412	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540,

						9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO4-028	Laos	1319.1	444	2030	F1a1a	73, 150, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7278, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16189, 16209, 16274, 16304, 16519
LAO4-029	Laos	1201	478	2489	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 10481, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16189, 16266A, 16519
LAO4-030	Laos	544	141	3708	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-031	Laos	557.3	49	2108	M7b1a1e1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6228, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10232, 10398, 10400, 10873, 11719, 12405, 12561, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297, 16302
LAO4-032	Laos	1044.2	296	5684	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-033	Laos	716.3	133	1486	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO4-034	Laos	660.8	196	1600	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO4-035	Laos	654	213	1836	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-036	Laos	174.8	54	343	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO4-037	Laos	655.2	255	1484	M24a	73, 146, 152, 195, 263, 489, 750, 951, 1438, 2706, 4769, 5773, 7028, 7040, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705,

						13359, 14512, 14766, 14783, 15043, 15301, 15326, 15601, 16223, 16311, 16519
LAO4-038	Laos	180.1	41	382	B4g1a	73, 195, 263, 750, 1438, 2706, 4769, 5108, 7028, 7789, 8281-8289d, 8723, 8860, 9111, 9968, 10042C, 11719, 13542, 13635, 14766, 14905, 15326, 16183C, 16189, 16213, 16217, 16261, 16292, 16519
LAO4-039	Laos	1008.7	302	2216	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-040	Laos	796.5	244	2236	M7c2	73, 146, 263, 489, 750, 1438, 2706, 3912, 4071, 4769, 4850, 5378, 6455, 7028, 8701, 8860, 9449, 9540, 9824, 10398, 10400, 10873, 10897, 11084, 11665, 11719, 11932, 12091, 12705, 14053, 14766, 14783, 15043, 15301, 15326, 15338, 16172, 16223, 16311, 16519
LAO4-041	Laos	671.9	248	1594	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 11719, 12714, 13928C, 14766, 15326, 16192, 16304, 16309, 16390, 16519
LAO4-042	Laos	886	327	2222	M7b1a1a3	73, 150, 199, 204, 263, 456, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16297
LAO4-043	Laos	568.6	171	2287	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13135, 13269, 14766, 15244, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
LAO4-044	Laos	584.2	147	1145	F2e	73, 152, 249d, 263, 709, 750, 930, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769, 6260, 6392, 7028, 7828, 8860, 10265, 10310, 10535, 10586, 11719, 12338, 13428, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
LAO4-045	Laos	632.5	285	1585	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4062, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12672, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16189, 16223, 16298, 16327, 16519
LAO4-046	Laos	806.1	247	1613	B5a1b1	73, 210, 235, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 7852, 8065, 8281-8289d, 8584, 8860, 9950, 10398, 10754, 11719, 14766, 14989, 15235, 15326, 16140, 16189, 16266A, 16325, 16519
LAO4-047	Laos	847.1	336	1933	F2e	73, 152, 249d, 263, 709, 750, 930, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769,

						6260, 6392, 7028, 7828, 8860, 10265, 10310, 10535, 10586, 11719, 12338, 13428, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
LAO4-048	Laos	743	255	1811	F4b	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4769, 5263, 6392, 6653, 7028, 8020, 8575, 8603, 8860, 10097C, 10310, 11719, 12630, 13928C, 14766, 15326, 15670, 16218, 16304, 16311
LAO4-049	Laos	704.2	253	1886	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9615, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14419, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16297
LAO4-050	Laos	206.6	44	464	D4g2a1b	73, 263, 298, 459d, 466, 489, 750, 1438, 2706, 3010, 4394, 4769, 4883, 5081, 5178A, 5231, 6164, 7028, 8414, 8701, 8860, 9540, 10398, 10400, 10873, 11059, 11719, 12705, 13104, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16362
LAO4-051	Laos	262.5	53	546	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO4-055	Laos	372	126	626	D4g2a1b	73, 263, 298, 459d, 466, 489, 750, 1438, 2706, 3010, 4394, 4769, 4883, 5081, 5178A, 5231, 6164, 7028, 8414, 8701, 8860, 9540, 10398, 10400, 10873, 11059, 11719, 12705, 13104, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16274, 16362
LAO4-057	Laos	168.4	60	278	F4a1b	73, 146, 249d, 263, 317A, 750, 1438, 2706, 2763, 3290, 3316, 3970, 4769, 5263, 6392, 7028, 8860, 10310, 10915, 11719, 12153, 12630, 13602, 13928C, 14766, 15326, 15670, 16126, 16140, 16207, 16304, 16362, 16399
LAO4-058	Laos	116.9	14	333	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO4-059	Laos	88.8	39	147	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 4913, 5351, 5460, 6455, 6680, 7028, 7079, 7278, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16223, 16297
LAO4-060	Laos	197.7	63	324	M7b1a1b	66, 73, 150, 199, 204, 252, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8699, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11266, 11719, 12405, 12705,

						12811, 14766, 14783, 15043, 15301, 15326, 16176, 16223, 16271, 16297, 16309, 16519
LAO4-062	Laos	84.1	31	133	B5b1a	73, 103, 204, 263, 709, 750, 1438, 1598, 2706, 4769, 7028, 8108, 8281-8289d, 8584, 8784, 8829, 8860, 9950, 10398, 11146, 11719, 12361, 12840, 14470, 14766, 15223, 15326, 15508, 15662, 15851, 15927, 16140, 16189, 16243, 16519
LAO4-063	Laos	119.4	48	213	B5b1a	73, 103, 204, 263, 709, 750, 1438, 1598, 2706, 4769, 7028, 8108, 8281-8289d, 8584, 8784, 8829, 8860, 9950, 10398, 11146, 11719, 12361, 12840, 14470, 14766, 15223, 15326, 15508, 15662, 15851, 15927, 16140, 16189, 16243, 16519
LAO4-064	Laos	45.7	12	98	B5a1a	73, 210, 263, 503, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO4-065	Laos	265	89	454	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO4-067	Laos	208	74	364	R9	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 7028, 8281-8289d, 8860, 9123, 10238, 11719, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-068	Laos	215.6	19	582	R9	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-069	Laos	190.8	65	389	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO4-070	Laos	86.9	12	220	B4c2	73, 263, 750, 1119, 1438, 2706, 4769, 5108, 7028, 8281-8289d, 8823, 8860, 9053, 9069, 11719, 14088, 14209, 14766, 15326, 15346, 16147, 16189, 16217, 16235, 16362, 16519
LAO4-071	Laos	55.8	20	98	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16183C, 16189, 16266A, 16519
LAO4-072	Laos	119.3	39	209	M7b1a1a3	73, 150, 199, 204, 263, 456, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 14978, 15043, 15301, 15326, 16129, 16189, 16223, 16297

LAO4-073	Laos	104.9	23	216	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13135, 13269, 14766, 15244, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
LAO4-075	Laos	170.6	68	342	M9a5	73, 150, 263, 385, 489, 750, 1438, 2706, 3394, 4491, 4769, 7028, 8155, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12237, 12414, 12705, 13098, 14308, 14766, 14783, 15043, 15301, 15326, 16223, 16234, 16362, 16519
LAO4-076	Laos	231.1	49	531	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO4-077	Laos	120.4	45	210	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13135, 13269, 14766, 15244, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
LAO4-078	Laos	59	18	188	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13135, 13269, 14766, 15244, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
LAO4-079	Laos	83	25	182	M17c	73, 146, 150, 263, 489, 709, 750, 930C, 1438, 1598, 2706, 2746, 3915, 4529, 4769, 5911, 7028, 8701, 8860, 9540, 10319, 10398, 10400, 10873, 11719, 11914, 12055, 12705, 12973, 14470, 14544, 14766, 14783, 15043, 15272, 15301, 15326, 15500, 15517, 16183C, 16189, 16209, 16223, 16519
LAO4-080	Laos	147.9	35	284	M7b1a1b	73, 150, 199, 203, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10007, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16223, 16297
LAO4-082	Laos	154.8	55	252	M7b1a1a3	73, 150, 199, 204, 207, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9615, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14419, 14766, 14783, 14978, 15043, 15301, 15326, 15497, 16111, 16129, 16189, 16192, 16223, 16297
LAO4-083	Laos	51.5	10	117	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13135, 13269, 14766, 15244, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16311
LAO4-084	Laos	204.4	68	446	R9c1b1	73, 151, 263, 479, 750, 1438, 2706, 3970, 4769, 5655, 6339, 7028, 7684, 7861, 8860, 11002, 11719, 12618, 13194, 13500, 13708, 13928C, 14560, 14766, 15326, 15479, 16157, 16278, 16304

LAO4-085	Laos	142.1	51	271	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16183C, 16189, 16266A, 16519
LAO4-088	Laos	264.4	17	968	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 14890, 15326, 16075, 16108, 16129, 16162, 16172, 16304, 16311, 16519
LAO4-089	Laos	101.9	12	264	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO4-090	Laos	324.8	86	676	M7b1a1	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 6719, 7028, 7684, 7853, 8557, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11503, 11719, 12405, 12705, 12811, 13834, 14128, 14766, 14783, 15043, 15301, 15326, 16129, 16145, 16192, 16297
LAO4-092	Laos	185	75	332	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3397, 3714, 4385T, 4769, 4772, 5300, 7028, 7433, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16086, 16129, 16209, 16223, 16272, 16519
LAO4-093	Laos	98.5	15	254	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 10481, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16189, 16266A, 16519
LAO4-094	Laos	96.7	15	251	M71a	73, 151, 263, 489, 518, 750, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16209, 16223, 16271, 16294
LAO4-095	Laos	393.8	153	581	F2e	73, 152, 249d, 263, 709, 750, 930, 1005, 1438, 1824, 2281, 2706, 3010, 3970, 4769, 6260, 6392, 7028, 7828, 8860, 10265, 10310, 10535, 10586, 11719, 12338, 13428, 13708, 13928C, 14766, 14769, 15326, 16304, 16527
LAO4-096	Laos	279.5	79	512	M7b1a1b	66, 73, 150, 199, 204, 252, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8699, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11266, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16176, 16223, 16271, 16297, 16309, 16519
LAO4-097	Laos	154	45	266	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860,

						9053, 9152, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO4-098	Laos	134.2	21	317	B5a	73, 210, 263, 709, 750, 1438, 3537, 4769, 6663, 7028, 8281-8289d, 8584, 8860, 9100, 9950, 10398, 11719, 12501, 13281, 14766, 15235, 15263, 15326, 15777, 16140, 16189, 16266G, 16291, 16519
LAO4-099	Laos	299.7	114	515	M7b1a1a	73, 146, 150, 199, 263, 489, 593, 750, 1438, 1694, 2706, 4048, 4071, 4137, 4164, 4769, 5351, 5460, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14766, 14783, 15043, 15301, 15326, 16129, 16189, 16192, 16223, 16297, 16519
LAO4-100	Laos	64.3	15	173	F4a2	73, 146, 150, 152, 249d, 263, 281, 750, 1438, 2706, 3290, 3970, 4703, 4769, 5263, 6392, 7028, 8860, 10310, 10915, 11719, 11776, 12612, 12630, 13928C, 14016, 14766, 15314, 15326, 15670, 15908, 16207, 16304, 16399
LAO4-101	Laos	109	36	198	B5a1	73, 210, 263, 709, 750, 1438, 1926, 2706, 3537, 4454, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 14587, 14766, 15235, 15326, 15900, 16140, 16189, 16266A, 16519
LAO4-102	Laos	106	34	183	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO4-103	Laos	108.7	15	263	C7	73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12483, 12705, 13263, 14226, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16093, 16172, 16223, 16298, 16327, 16519
LAO4-104	Laos	280.8	72	621	R9b1a2a	73, 183, 263, 750, 1438, 1462, 1541, 2706, 3970, 4769, 7028, 8860, 10736, 11077, 11719, 12172, 12714, 13928C, 14766, 15326, 16145, 16192, 16243, 16304, 16309, 16390, 16519
LAO4-105	Laos	283.5	97	511	R9b2	73, 263, 750, 1438, 1541, 2706, 3666, 3970, 4769, 5074, 6647, 7028, 8724, 8860, 11299, 11422, 11719, 13191, 13722, 13928C, 14766, 15314, 15326, 15883, 16304, 16362, 16519
LAO5-001	Laos	85.8	18	202	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-002	Laos	786.5	313	2005	C5	73, 195, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 7028, 7196A, 8584, 8701, 8860, 9509, 9540, 9545, 10398, 10400, 10873, 11092, 11719, 11914, 12705,

						13263, 13722, 14318, 14766, 14783, 15043, 15080, 15301, 15326, 15487T, 15884, 16223, 16288, 16298, 16300, 16327, 16519
LAO5-003	Laos	795.7	243	1393	F3a1	73, 204, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO5-004	Laos	892.9	210	1844	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 6528, 7028, 8281-8289d, 8860, 9123, 11719, 14518, 14766, 15236, 15244, 15326, 16183C, 16189, 16217, 16261, 16357, 16519
LAO5-005	Laos	156.9	17	455	F3a1	73, 152, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 7151, 8860, 10310, 10320, 10646C, 11065, 11617, 11719, 12621, 12696, 13928C, 14178, 14766, 14971, 15326, 15483, 15493, 16249, 16298, 16355, 16362, 16390
LAO5-006	Laos	148.7	57	342	F1a1a	73, 150, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7258, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13353, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304
LAO5-007	Laos	682.3	210	3020	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235C, 15326, 16140, 16189, 16262, 16266A, 16519
LAO5-009	Laos	302.5	106	611	D4e1a3	73, 94, 146, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8119, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 11215, 11719, 12705, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16362
LAO5-010	Laos	922.1	376	2130	B4a	73, 263, 750, 1438, 2706, 4769, 5465, 5814, 6123C, 7028, 8281-8289d, 8860, 9123, 11719, 14518, 14766, 15236, 15244, 15326, 16183C, 16189, 16217, 16261, 16357, 16519
LAO5-011	Laos	307.8	103	489	F3a1	73, 152, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 7151, 8860, 10310, 10320, 10646C, 11065, 11617, 11719, 12621, 12696, 13928C, 14178, 14766, 14971, 15326, 15483, 15493, 16249, 16298, 16355, 16362, 16390
LAO5-012	Laos	704.4	251	1180	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16262, 16266A, 16519

LAO5-013	Laos	769.7	77	3856	M74a	63, 64, 66, 73, 215, 263, 489, 750, 1438, 2706, 4769, 5054, 6185, 6575, 7028, 8251, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12705, 12850, 14311, 14766, 14783, 15043, 15301, 15326, 16093, 16223, 16311, 16362, 16381
LAO5-014	Laos	608.3	160	1173	B5a1c1	64, 73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16262, 16266A, 16519
LAO5-015	Laos	917.2	177	2158	B4a	73, 263, 750, 1037, 1438, 2706, 4769, 5465, 5814, 7028, 8281-8289d, 8860, 9123, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16183C, 16189, 16217, 16261, 16357, 16519
LAO5-016	Laos	556.6	209	1689	B4a	73, 263, 750, 1438, 2706, 3338, 4769, 5465, 5814, 7028, 8281-8289d, 8702, 8860, 9123, 10319, 11719, 14518, 14766, 15236, 15244, 15326, 16093, 16183C, 16189, 16217, 16261, 16357, 16519
LAO5-017	Laos	228.1	68	394	F1g1	73, 249d, 263, 750, 1438, 2389, 2706, 2889, 3398, 3621, 3970, 4769, 6392, 6962, 7028, 8860, 10310, 10609, 11719, 12406, 12882, 13928C, 14271, 14766, 15323, 15326, 16129, 16183C, 16189, 16304, 16519
LAO5-018	Laos	1021.1	321	3189	F3a1	73, 204, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13095, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO5-019	Laos	241.9	102	419	F3a1	73, 204, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13095, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO5-020	Laos	760.8	74	1721	M24a	73, 146, 152, 195, 263, 489, 491, 750, 951, 1438, 2706, 4769, 5773, 7028, 7040, 8701, 8860, 9531, 9540, 10398, 10400, 10873, 11719, 12705, 13359, 13659, 14766, 14783, 15043, 15301, 15326, 15601, 16223, 16311, 16519
LAO5-021	Laos	570.6	167	1331	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10754, 10873, 11719, 11839, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16189, 16223, 16298, 16319, 16327, 16519
LAO5-022	Laos	910.5	350	1832	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9758, 9950, 10325, 10398,

						10448, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO5-023	Laos	555.1	203	1308	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-024	Laos	473.3	148	1209	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-025	Laos	812.3	285	1552	B5a1c1	73, 146, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 5918, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16189, 16266A, 16519
LAO5-026	Laos	511.6	183	896	A	73, 152, 235, 263, 663, 750, 1438, 1736, 2706, 4248, 4769, 4824, 7028, 7705, 8794, 8860, 9033, 9545, 11719, 12705, 13707, 14766, 15326, 16223, 16290, 16311, 16319, 16362
LAO5-027	Laos	584.6	220	1315	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-028	Laos	92.5	30	190	B5a1c1	73, 210, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 5453T, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO5-029	Laos	451	74	1539	D4	73, 263, 489, 750, 1438, 2706, 3010, 4769, 4883, 5178A, 7028, 8414, 8701, 8860, 9540, 9725, 10398, 10400, 10873, 11719, 12432, 12705, 14668, 14766, 14783, 15043, 15301, 15326, 16223, 16356, 16362
LAO5-030	Laos	964.6	306	2014	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 15841, 16140, 16183C, 16189, 16266A, 16519
LAO5-031	Laos	1274	328	5364	F1a2	73, 249d, 263, 750, 1438, 2706, 3970, 4025, 4086, 4769, 5191, 6392, 6962, 7028, 7853, 8860, 9053, 10034, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16172, 16224, 16304, 16519
LAO5-032	Laos	708.6	199	199	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-034	Laos	545.6	255	1472	F3a1	73, 204, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894, 5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO5-035	Laos	509.2	243	1114	F3a1	73, 204, 207, 249d, 263, 279, 709, 750, 1438, 2706, 3434, 3970, 4769, 5585, 5894,

						5913, 5978, 6392, 7028, 8860, 9854, 10310, 10320, 10499, 11065, 11719, 12621, 13928C, 14766, 14971, 15326, 15943, 16260, 16298, 16355, 16362
LAO5-036	Laos	744.5	232	1765	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-037	Laos	491.1	127	1658	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-038	Laos	689.8	197	3536	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-039	Laos	50.9	11	108	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-040	Laos	514.2	174	1120	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO5-041	Laos	838.8	363	1731	B5a1c1	73, 210, 252, 263, 593, 709, 750, 1438, 2706, 3537, 4769, 5237, 6960, 7028, 8281-8289d, 8584, 8860, 9950, 10325, 10398, 10523, 11719, 14766, 15235, 15326, 16140, 16183C, 16189, 16266A, 16519
LAO5-042	Laos	661.8	134	3422	N9a10	73, 150, 199, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-043	Laos	683.3	244	1445	N9a10	73, 150, 199, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO5-044	Laos	696.6	237	1447	B4g	61A, 62, 73, 183, 263, 750, 1438, 2378, 2706, 4769, 6482, 7028, 8281-8289d, 8860, 9968, 11719, 14766, 15326, 16183C, 16189, 16213, 16217, 16242, 16261, 16292, 16301, 16519
LAO5-045	Laos	2522.1	451	6735	M74a	63, 64, 66, 73, 146, 215, 263, 489, 750, 1438, 2706, 4769, 5054, 6185, 6575, 7028, 8251, 8473, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12705, 12850, 14311, 14766, 14783, 15043, 15301, 15326, 16093, 16223, 16311, 16362, 16381
LAO6-001	Laos	452.5	128	789	F1a1d	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9548, 10310, 10609, 11380, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16399, 16519
LAO6-002	Laos	394.6	28	1106	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028,

						8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-003	Laos	483.4	186	847	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO6-004	Laos	473.9	94	1028	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-005	Laos	165.8	34	512	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 6455, 6680, 7028, 7364, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11659, 11719, 12405, 12705, 12811, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO6-006	Laos	356.8	39	1014	M7c1b2b	73, 146, 152, 199, 263, 489, 750, 1438, 2706, 4071, 4769, 4850, 5442, 6455, 7028, 7337, 8029, 8701, 8860, 9540, 9824, 9957, 10118, 10398, 10400, 10861, 10873, 11337, 11665, 11719, 12091, 12561, 12705, 13590, 14766, 14783, 15043, 15301, 15315, 15326, 16223, 16295, 16519
LAO6-007	Laos	201.6	55	365	B4h	73, 152, 263, 750, 1438, 2706, 4769, 5093, 6267, 7028, 8281-8289d, 8860, 9545, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16488
LAO6-009	Laos	175.3	42	334	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-010	Laos	220.9	41	524	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO6-011	Laos	238.7	74	404	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519

LAO6-012	Laos	45.5	14	88	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO6-013	Laos	158.5	46	343	B4h	73, 152, 263, 750, 1438, 2706, 4769, 5093, 6267, 7028, 8281-8289d, 8860, 9545, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16488
LAO6-014	Laos	158.5	21	260	B5a1a	73, 210, 263, 709, 750, 1438, 2706, 3537, 4769, 6960, 7028, 8251, 8281-8289d, 8584, 8860, 9950, 10398, 11719, 13145, 13395, 14467, 14766, 15235, 15326, 15569, 16140, 16183C, 16189, 16266A, 16311
LAO6-016	Laos	200.8	26	495	B4h	73, 152, 263, 750, 1438, 2706, 4769, 5093, 6267, 7028, 8281-8289d, 8860, 9545, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16488
LAO6-017	Laos	197.6	50	402	R11b1	73, 185, 189, 263, 709, 750, 1438, 2706, 4769, 5040, 5836, 7028, 8277, 8279, 8860, 10031, 10398, 11061, 11719, 12950, 13269, 13681, 13879, 14322, 14766, 15326, 16136, 16183C, 16189, 16311, 16390, 16399, 16519
LAO6-018	Laos	96.5	26	219	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO6-020	Laos	215.8	53	420	M74b1	73, 195, 263, 489, 750, 1438, 2706, 3394, 4769, 5054, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14577, 14766, 14783, 15043, 15226, 15301, 15319, 15326, 15777, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO6-021	Laos	192.9	51	386	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 7830, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16304, 16519
LAO6-022	Laos	82.8	32	192	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354

LAO6-023	Laos	320.5	105	536	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-024	Laos	79.9	28	155	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO6-025	Laos	244.3	79	411	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-026	Laos	234.9	41	556	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO6-027	Laos	199.7	46	389	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO6-028	Laos	199.1	50	419	M71a2	73, 143, 146, 151, 263, 489, 750, 1438, 2706, 4769, 4853, 7028, 8440, 8701, 8718, 8838, 8860, 9540, 9615, 10398, 10400, 10873, 11719, 12705, 13759, 14605, 14766, 14783, 15043, 15301, 15326, 15458, 16129, 16140, 16203, 16223, 16271
LAO6-029	Laos	180.2	55	341	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-030	Laos	196.2	45	391	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-031	Laos	285.6	41	722	F1a1a	63, 73, 249d, 263, 295, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-032	Laos	221.3	53	467	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028,

						8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO6-033	Laos	165.7	35	372	F1a1d	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9548, 10310, 10609, 11380, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16399, 16519
LAO6-034	Laos	182.8	71	337	F1a1a	63, 73, 249d, 263, 295, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-035	Laos	122.7	45	208	M74b1	73, 195, 263, 489, 750, 1438, 2706, 3394, 4769, 5054, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14577, 14766, 14783, 15043, 15226, 15301, 15319, 15326, 15777, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO6-036	Laos	123.2	44	213	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO6-038	Laos	504.7	164	971	F1a1a	73, 249d, 263, 750, 1438, 1462, 2706, 3970, 4086, 4092, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 9629, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16140, 16162, 16172, 16304, 16519
LAO6-040	Laos	246.8	84	538	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO6-041	Laos	133	18	402	F1a1	73, 94, 249d, 263, 750, 1438, 2706, 3970, 4086, 4755, 4769, 6392, 6962, 7028, 8860, 8973, 9053, 9548, 10310, 10609, 11719, 12406, 12715, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO6-042	Laos	164.4	27	383	F1a1	73, 94, 249d, 263, 750, 1438, 2706, 3970, 4086, 4755, 4769, 6392, 6962, 7028, 8860, 8973, 9053, 9548, 10310, 10609, 11719, 12406, 12715, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519

LAO6-043	Laos	181.8	19	479	B4c	73, 263, 750, 1119, 1438, 2706, 2884, 4769, 5585, 7028, 7783, 8281-8289d, 8860, 9024, 9030, 9151, 11719, 14766, 15010, 15055, 15326, 15346, 16189, 16217, 16362, 16519
LAO6-044	Laos	243.4	36	565	R9b1a3	73, 152, 215, 263, 750, 951, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 8998, 11719, 12714, 13477, 13928C, 14664, 14766, 15326, 16192, 16304, 16309, 16390, 16519
LAO6-045	Laos	181.8	49	352	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-046	Laos	201.2	58	403	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO6-047	Laos	182.6	72	379	F1g	73, 152, 249d, 263, 750, 1438, 2389, 2706, 3398, 3970, 4769, 6392, 6962, 7028, 8860, 10310, 10454, 10609, 11719, 12406, 12882, 13928C, 14766, 15326, 16189, 16262, 16304, 16519
LAO6-048	Laos	202.8	40	452	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3604, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 10754, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15139, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO6-049	Laos	132.6	38	261	R9b1a3	73, 152, 263, 750, 951, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 8998, 11719, 12714, 13477, 13928C, 14664, 14766, 15326, 16192, 16304, 16309, 16390, 16519
LAO6-050	Laos	95	17	286	R11b1	73, 185, 189, 263, 709, 750, 1438, 2706, 4769, 5040, 5836, 7028, 8277, 8279, 8860, 10031, 10398, 11061, 11719, 12950, 13269, 13681, 13879, 14322, 14766, 15326, 16136, 16311, 16390, 16399, 16519
LAO6-051	Laos	116.6	31	250	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 3531, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 16086, 16223, 16297
LAO7-001	Laos	225.7	60	388	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519

LAO7-002	Laos	54.6	13	651	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5147, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 13988G, 14766, 15326, 16129, 16172, 16213, 16304, 16519
LAO7-003	Laos	137.9	49	267	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-004	Laos	225.9	53	644	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-005	Laos	163.4	50	350	M74b1	73, 195, 263, 489, 750, 1438, 2706, 3394, 4769, 5054, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14577, 14766, 14783, 15043, 15226, 15301, 15319, 15326, 15777, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO7-006	Laos	359.4	93	646	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-007	Laos	210.6	28	504	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-011	Laos	362.4	118	658	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-012	Laos	151.8	54	304	B4h	73, 152, 263, 750, 1438, 2706, 4769, 5093, 7028, 8281-8289d, 8860, 9545, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16183C, 16189, 16217, 16261, 16488
LAO7-013	Laos	264.6	93	654	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-016	Laos	212.3	14	616	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719,

						12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO7-017	Laos	265.9	86	1232	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-018	Laos	248.1	55	484	F1f	73, 146, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 7738, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16213, 16304, 16519
LAO7-019	Laos	184.3	25	465	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-020	Laos	206.3	30	493	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-021	Laos	277.4	86	437	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO7-022	Laos	224.7	62	433	F1a1	73, 152, 204, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9548, 10310, 10420, 10609, 10972, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16093, 16129, 16162, 16172, 16292, 16304, 16519
LAO7-023	Laos	198.4	16	594	F1a1	73, 94, 249d, 263, 750, 1438, 2706, 3970, 4086, 4755, 4769, 6392, 6962, 7028, 8860, 8973, 9053, 9548, 10310, 10609, 11719, 12406, 12715, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO7-024	Laos	241.7	61	419	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO7-025	Laos	133.8	30	256	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-026	Laos	239.6	55	535	M71a	73, 151, 263, 489, 518, 750, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9540, 10398, 10400, 10873, 11719, 12397,

						12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16093, 16223, 16271
LAO7-029	Laos	154.2	45	275	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-030	Laos	114.5	40	222	M7c1b2b	73, 146, 152, 199, 263, 489, 750, 1438, 2706, 4071, 4769, 4850, 5442, 6455, 7028, 7337, 8029, 8701, 8860, 9540, 9824, 9957, 10118, 10398, 10400, 10861, 10873, 11337, 11665, 11719, 12091, 12561, 12705, 13590, 14766, 14783, 15043, 15301, 15315, 15326, 16223, 16295, 16352, 16519
LAO7-031	Laos	211.8	33	770	F1a1a1	73, 249d, 263, 750, 769, 1438, 2706, 3593, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9300, 9548, 10310, 10609, 11215, 11719, 11809, 12241d, 12406, 12738, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO7-032	Laos	225.7	30	597	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-033	Laos	98.7	45	167	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301, 15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-034	Laos	266	115	780	F1f	73, 195, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-035	Laos	381.2	87	817	F1f	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5147, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-036	Laos	238.7	55	497	M75	73, 146, 150, 152, 195, 263, 489, 750, 1438, 1719, 2706, 3316, 3453, 3666, 4769, 5147, 7028, 7313, 7765, 8701, 8860, 9111, 9540, 10398, 10400, 10873, 11233, 11719, 12279, 12609, 12705, 13269, 14110, 14224T, 14356, 14766, 14783, 15043, 15109, 15301,

						15326, 16068, 16093, 16126, 16183C, 16189, 16223, 16319, 16325, 16354
LAO7-040	Laos	174.6	48	377	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16362
LAO7-041	Laos	52.8	25	95	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-042	Laos	308.3	95	588	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-043	Laos	230	76	419	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-045	Laos	230.9	62	456	F1a1	73, 94, 249d, 263, 750, 1438, 2706, 3970, 4086, 4755, 4769, 6392, 6962, 7028, 8860, 8973, 9053, 9548, 10310, 10609, 11719, 12406, 12715, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519
LAO7-046	Laos	88.6	19	264	B4c1b2c	73, 150, 263, 709, 750, 961, 1119, 1438, 2706, 3435, 3497, 3571, 4769, 7028, 8281-8289d, 8860, 9128, 11440, 11719, 14766, 15247G, 15326, 15346, 16140, 16189, 16217, 16274, 16519
LAO7-047	Laos	120.3	33	220	B4c1b2c	73, 150, 263, 709, 750, 961, 1119, 1438, 2706, 3435, 3497, 3571, 4769, 7028, 8281-8289d, 8860, 9128, 11440, 11719, 14766, 15247G, 15326, 15346, 16140, 16189, 16217, 16274, 16519
LAO7-048	Laos	217.3	90	359	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9190, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO7-049	Laos	253.6	26	613	M7c1b2b	73, 146, 152, 199, 263, 489, 750, 1438, 2706, 4071, 4769, 4850, 5442, 6455, 7028, 7337, 8029, 8701, 8860, 9540, 9824, 9957, 10118, 10398, 10400, 10861, 10873, 11337, 11665, 11719, 12091, 12561, 12705, 13590, 14766, 14783, 15043, 15301, 15315, 15326, 16223, 16295, 16352, 16519
LAO7-050	Laos	122	32	254	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4769, 4772, 7028, 7433, 8701, 8853, 8860, 9127, 9512,

						9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15106, 15301, 15326, 15565, 15691, 16086, 16129, 16209, 16223, 16272, 16519
LAO7-051	Laos	139.2	34	272	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO7-052	Laos	159.8	48	336	M74b1	73, 195, 263, 489, 750, 1438, 2706, 3394, 4769, 5054, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14577, 14766, 14783, 15043, 15226, 15301, 15319, 15326, 15777, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO7-053	Laos	308.1	90	847	Z3a	73, 152, 204, 207, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 9713, 10208, 10398, 10400, 10873, 11719, 12705, 13135, 13620, 14198, 14476, 14766, 14783, 15043, 15097, 15301, 15326, 15487T, 15784, 15884, 15928, 16093, 16185, 16223, 16260, 16298
LAO7-054	Laos	243.4	61	504	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6911, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO7-055	Laos	151.1	25	357	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 5471, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO7-056	Laos	163.9	43	303	B4c	73, 263, 750, 1119, 1438, 2706, 2884, 4769, 7028, 8281-8289d, 8860, 9024, 9151, 11719, 14766, 15010, 15326, 15346, 16108, 16183C, 16189, 16217, 16362, 16519
LAO7-057	Laos	224.1	83	396	M7c1b2b	73, 146, 152, 199, 263, 489, 750, 1438, 2706, 4071, 4769, 4850, 5442, 6455, 7028, 7337, 8029, 8701, 8860, 9540, 9824, 9957, 10118, 10398, 10400, 10861, 10873, 11337, 11665, 11719, 12091, 12561, 12705, 13590, 14766, 14783, 15043, 15301, 15315, 15326, 16223, 16295, 16352, 16519
LAO8-001	Laos	714.6	181	1580	F1a1a	73, 249d, 263, 750, 1438, 2706, 3254, 3970, 4086, 4768, 4769, 6392, 6962, 7028, 7934, 8149, 8634, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12561, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16214, 16304, 16519

LAO8-002	Laos	486.6	204	1196	U7a3	73, 151, 152, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519
LAO8-003	Laos	204.9	53	432	C7a2	73, 204, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10754, 10873, 11719, 11839, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 15601, 16183C, 16189, 16223, 16298, 16327, 16519
LAO8-004	Laos	1108.8	29	2927	F1a2a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 10034, 10310, 10609, 11437, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16172, 16304, 16465, 16519
LAO8-005	Laos	258.5	95	437	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO8-008	Laos	175.4	63	448	M71a	73, 151, 263, 489, 518, 750, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16271
LAO8-009	Laos	90	25	191	C7	73, 152, 249d, 263, 449, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 8584, 8701, 8856, 8860, 9540, 9545, 10370, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16129, 16148, 16223, 16298, 16327, 16519
LAO8-010	Laos	116	32	185	B4h	73, 263, 459A, 750, 1438, 2706, 4769, 5093, 6185, 7028, 8281-8289d, 8860, 11016, 11719, 13269, 14766, 15326, 15784, 16129, 16189, 16217, 16261, 16311
LAO8-011	Laos	178.1	42	366	F1a1	73, 152, 249d, 263, 750, 1438, 2280, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9548, 10310, 10420, 10609, 10972, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16093, 16129, 16162, 16172, 16292, 16304, 16519
LAO8-012	Laos	80.2	13	185	B5a1d	73, 146, 152, 210, 263, 709, 750, 1438, 2706, 3537, 4086, 4769, 5772, 6960, 7028, 8281-8289d, 8473, 8584, 8860, 9950, 10398, 11465, 11719, 12192C, 14417, 14766, 15235, 15326, 16140, 16189, 16261, 16266A, 16519
LAO8-013	Laos	142	54	241	F1a1	73, 249d, 263, 750, 1438, 2706, 3579, 3970, 4086, 4769, 6392, 6962, 7028, 8860, 9053, 9141, 9548, 10003, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16162, 16172, 16304, 16519

LAO8-014	Laos	112.4	18	332	R11b	73, 185, 189, 235, 263, 709, 750, 1438, 2706, 3335, 4688, 4769, 6956, 7028, 8277, 8279, 8860, 9948, 10031, 10398, 11061, 11719, 12950, 13269, 13681, 14766, 15326, 16189, 16249A, 16311, 16519
LAO8-020	Laos	70	35	188	M74b1	73, 195, 263, 489, 750, 1438, 2706, 4769, 5054, 5806, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14384, 14766, 14783, 15043, 15226, 15301, 15326, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO8-021	Laos	169.1	20	425	M9a1b1	73, 150, 151, 152, 153, 263, 489, 709, 750, 1041, 1438, 2706, 3394, 4491, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12362, 12705, 14308, 14766, 14783, 15043, 15301, 15326, 15671, 16158, 16223, 16234, 16311, 16362, 16519
LAO8-025	Laos	193.4	80	438	U7a3	73, 151, 152, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519
LAO8-027	Laos	393.8	93	762	M7c1a	73, 146, 152, 199, 263, 489, 750, 1236, 1438, 1809, 2706, 3316, 3882, 4071, 4769, 4850, 5442, 6455, 7028, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11665, 11719, 12091, 12705, 14766, 14783, 15043, 15301, 15326, 16075, 16223, 16293T, 16519
LAO8-029	Laos	178	39	398	U7a3	73, 151, 152, 215, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519
LAO8-030	Laos	197.2	10	539	F1a1a	73, 249d, 263, 709, 750, 1438, 2706, 3970, 4086, 4769, 6345, 6392, 6962, 7028, 8149, 8200, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13191, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO8-031	Laos	236.7	55	512	F1c1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4769, 6392, 6599, 6962, 7028, 8567, 8860, 9053, 10310, 10454, 10609, 11719, 12406, 12882, 13681, 13759, 13928C, 14766, 15326, 16111, 16129, 16266, 16304, 16519
LAO8-035	Laos	207.5	92	343	U7a3	73, 151, 152, 263, 750, 980, 1438, 1811, 2523, 2706, 3741, 3834, 4769, 5360, 7028, 7925, 8137, 8684, 8860, 10142, 11467, 11719, 12308, 12372, 12618, 13500, 14569, 14766, 15326, 16207, 16318T, 16519
LAO8-038	Laos	112.6	29	203	M7b1a1	73, 150, 199, 263, 489, 750, 1438, 2706, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405,

						12705, 12811, 14766, 14783, 15043, 15301, 15326, 16129, 16192, 16223, 16297
LAO8-042	Laos	291.1	92	539	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6260, 6392, 6515, 6962, 7028, 8860, 9053, 9163, 10310, 10609, 11719, 11824, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519
LAO8-046	Laos	211.2	16	597	M71b	73, 151, 263, 489, 750, 1438, 2706, 3777, 4769, 7028, 7055, 8701, 8718, 8860, 9540, 9548, 10398, 10400, 10873, 11719, 12705, 13149, 13988G, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16260, 16264, 16271, 16519
LAO8-047	Laos	243.5	57	474	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6065, 6815, 7028, 8860, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16192, 16239, 16304, 16309, 16390, 16519
LAO8-050	Laos	345.4	18	1013	F1a1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 4965, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO8-052	Laos	85.1	22	183	N9a10	73, 150, 263, 750, 1438, 2706, 4769, 5231, 5417, 7028, 8433, 8860, 9738, 11719, 12358, 12372, 12705, 12771, 14766, 15326, 16086, 16223, 16257A, 16261, 16311
LAO8-056	Laos	185.6	21	492	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6815, 7028, 8860, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16192, 16239, 16304, 16390, 16519
LAO8-057	Laos	246.4	87	429	C7a2	73, 249d, 263, 489, 750, 1438, 2232.1A, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 7990, 8584, 8701, 8860, 8994, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16183C, 16189, 16223, 16298, 16311, 16327, 16519
LAO8-058	Laos	124.6	29	278	M71a	73, 151, 263, 372, 489, 518, 750, 1438, 2083, 2706, 4769, 7028, 8440, 8701, 8718, 8860, 9196, 9540, 10398, 10400, 10873, 11719, 12705, 13392, 14766, 14783, 15043, 15301, 15326, 15458, 16223, 16271
LAO8-060	Laos	180.2	17	489	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7830, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO8-061	Laos	156.5	50	256	M12a1a	73, 125, 127, 128, 146, 152, 263, 489, 750, 1438, 1819, 2706, 4170, 4769, 5580, 6293, 7028, 8701, 8860, 9064, 9540, 10235, 10398, 10400, 10873, 11719, 12030, 12358,

						12372, 12705, 14569, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 15463, 15562, 15651, 16093, 16223, 16234, 16266, 16290, 16311
LAO8-063	Laos	126.5	52	230	G2	73, 195, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 5601, 7028, 8701, 8860, 9540, 10237, 10398, 10400, 10873, 11719, 12705, 13563, 14569, 14766, 14783, 15043, 15301, 15326, 16217, 16223, 16362
LAO8-065	Laos	131.4	42	349	M7b1a1b	73, 150, 199, 204, 263, 489, 750, 1438, 2706, 3483, 4048, 4071, 4164, 4769, 5351, 5460, 6455, 6680, 7028, 7684, 7853, 8701, 8860, 9540, 9824, 10398, 10400, 10873, 11719, 12405, 12705, 12811, 14766, 14783, 15043, 15301, 15326, 16223, 16297, 16519
LAO8-067	Laos	170.1	62	317	F1a1a	73, 150, 195, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 7258, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13353, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304
LAO9-001	Laos	211.1	61	399	R9b1a2	73, 183, 204, 263, 750, 1438, 1541, 2706, 3970, 4769, 6620, 7028, 7705, 8860, 10736, 11719, 12714, 13928C, 14766, 15326, 15547, 16192, 16304, 16309, 16390, 16519
LAO9-003	Laos	291.9	47	753	F1a1a1	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO9-004	Laos	260.1	91	449	R9b1a2	73, 183, 204, 263, 750, 1438, 1541, 2706, 3970, 4769, 6620, 7028, 7705, 8860, 10736, 11719, 12714, 13928C, 14766, 15326, 15547, 16192, 16304, 16309, 16390, 16519
LAO9-009	Laos	358.9	95	637	F1f	73, 249d, 263, 750, 1438, 2706, 3342, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12414, 12771, 12882, 13759, 13928C, 14305, 14766, 15326, 16129, 16148, 16169, 16172, 16304, 16519
LAO9-010	Laos	117.8	40	195	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO9-012	Laos	134.4	33	351	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6065, 6815, 7028, 8860, 11719, 12007, 12714, 13928C, 14766, 15326, 16189, 16192, 16239, 16304, 16309, 16390, 16519
LAO9-019	Laos	222.7	56	446	R9b1a3	73, 152, 263, 750, 1438, 1541, 2706, 3204, 3316, 3970, 4769, 6065, 6815, 7028, 8860, 11719, 12007, 12714, 13928C, 14766,

						15326, 16189, 16192, 16239, 16304, 16309, 16390, 16519
LAO9-021	Laos	144	41	290	Z3a	73, 152, 204, 207, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 9713, 10208, 10398, 10400, 10873, 11719, 12705, 13135, 13620, 14198, 14476, 14766, 14783, 15043, 15097, 15301, 15326, 15487T, 15784, 15884, 15928, 16093, 16185, 16223, 16260, 16298
LAO9-024	Laos	81.7	21	163	F1f	73, 249d, 263, 750, 1438, 2706, 3342, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12414, 12771, 12882, 13759, 13928C, 14305, 14766, 15326, 16129, 16148, 16169, 16172, 16304, 16519
LAO9-025	Laos	181.8	56	322	M9a1b1	73, 150, 152, 153, 263, 489, 750, 1041, 2706, 3394, 4394, 4491, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12362, 12705, 14110, 14308, 14766, 14783, 15043, 15301, 15326, 15671, 16158, 16223, 16234, 16362, 16519
LAO9-026	Laos	175.9	58	323	Z3a	73, 152, 204, 207, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 9713, 10208, 10398, 10400, 10873, 11719, 12705, 13135, 13620, 14198, 14476, 14766, 14783, 15043, 15097, 15301, 15326, 15487T, 15784, 15884, 15928, 16093, 16185, 16223, 16260, 16298
LAO9-027	Laos	240.5	65	469	F3a1	73, 146, 207, 249d, 263, 709, 750, 1438, 2706, 3434, 3970, 4769, 4824, 4991, 5585, 5894, 5913, 5978, 6392, 7028, 8857, 8860, 10310, 10320, 11065, 11719, 12178, 12621, 13928C, 14766, 14971, 15043, 15326, 15412G, 16249, 16260, 16298, 16355, 16362
LAO9-028	Laos	183	49	392	F1a1a1	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 4965, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12882, 13759, 13928C, 14766, 15317, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO9-029	Laos	212.9	64	396	Z3a	73, 152, 204, 207, 249d, 263, 489, 750, 1438, 2706, 4715, 4769, 6752, 7028, 7196A, 8584, 8701, 8860, 9090, 9540, 9713, 10208, 10398, 10400, 10873, 11719, 12705, 13135, 13620, 14198, 14476, 14766, 14783, 15043, 15097, 15301, 15326, 15487T, 15784, 15884, 15928, 16093, 16185, 16223, 16260, 16298
LAO9-030	Laos	121.4	32	213	F1a	73, 152, 249d, 263, 750, 1438, 2706, 3970, 4086, 4316, 4769, 6392, 6962, 7028, 8701, 8860, 9053, 10310, 10604, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16129, 16172, 16304, 16519

LAO9-033	Laos	202.2	69	329	M74b1	73, 195, 263, 489, 750, 1438, 2706, 4769, 5054, 5806, 7028, 8080A, 8155, 8167, 8251, 8616, 8701, 8860, 9540, 10268, 10398, 10400, 10873, 11719, 12651, 12705, 13105, 13434, 14384, 14766, 14783, 15043, 15226, 15301, 15326, 15908, 15969A, 16223, 16246T, 16311, 16362, 16519
LAO9-034	Laos	174	43	439	M20	73, 152, 225, 249d, 263, 316, 489, 750, 1438, 2706, 3200, 3714, 4385T, 4554, 4769, 4772, 5435, 7028, 7433, 8222, 8701, 8853, 8860, 9127, 9512, 9540, 10274, 10398, 10400, 10679, 10873, 11719, 11914, 12354, 12705, 14110, 14766, 14783, 14974, 15043, 15301, 15326, 15691, 16129, 16209, 16223, 16272, 16360, 16519
LAO9-035	Laos	56.6	24	106	M9a1b1	73, 150, 152, 153, 263, 489, 750, 1041, 2706, 3394, 4394, 4491, 4769, 7028, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12362, 12705, 14110, 14308, 14766, 14783, 15043, 15301, 15326, 15671, 16158, 16223, 16234, 16362, 16519
LAO9-036	Laos	250.9	53	513	F1a1a	73, 249d, 263, 709, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16093, 16108, 16129, 16162, 16172, 16304, 16519
LAO9-038	Laos	133.1	13	498	F1a1a1	73, 249d, 263, 750, 1120, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11215, 11719, 12406, 12771, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO9-039	Laos	72	14	198	G1a2	73, 146, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 7028, 7674, 7867, 8200, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12040, 12172, 12705, 14569, 14766, 14783, 15043, 15301, 15323, 15326, 15497, 16184, 16223, 16267, 16290, 16362, 16519
LAO9-040	Laos	145.9	56	229	N22	73, 150, 263, 335, 750, 942, 1438, 1503, 2706, 4769, 5130, 7028, 7158, 8860, 9254, 11365, 11719, 11899, 12705, 13819, 13980, 14766, 15326, 16168, 16223, 16249, 16311
LAO9-041	Laos	78.7	19	303	F1f	73, 249d, 263, 750, 1438, 2706, 3342, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12414, 12771, 12882, 13759, 13928C, 13988G, 14305, 14766, 15326, 16129, 16148, 16169, 16172, 16304, 16519
LAO9-042	Laos	194.2	68	317	G1a2	73, 146, 263, 489, 709, 750, 1438, 2706, 4769, 4833, 5108, 7028, 7674, 7867, 8200, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12040, 12172, 12705, 14569, 14766, 14783, 15043, 15301, 15323, 15326, 15497, 16184, 16223, 16267, 16290, 16362, 16519

LAO9-043	Laos	259.8	66	1389	C7a	44.1C, 73, 214, 249d, 263, 489, 750, 1438, 2056, 2706, 3552A, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
LAO9-044	Laos	211.4	60	366	F1a1a	73, 249d, 263, 709, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
LAO9-045	Laos	59	18	231	C7a	44.1C, 73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4233, 4715, 4769, 5821, 6338, 7028, 7196A, 7853, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 12705, 13263, 13928C, 13988G, 14318, 14766, 14783, 15043, 15301, 15326, 15487T, 16223, 16298, 16327, 16519
TK001	Burma	665.4	212	1113	F1f	73, 249d, 263, 750, 1438, 2706, 3970, 4715, 4769, 6392, 6515, 6962, 7028, 8860, 9053, 10310, 10609, 11719, 12406, 12495, 12771, 12882, 13759, 13928C, 14766, 15326, 16129, 16169, 16172, 16304, 16519
TK002	Burma	361.1	103	632	C4d	73, 249d, 263, 489, 750, 1438, 2706, 3552A, 4715, 4769, 6026, 7028, 7100, 7196A, 8584, 8701, 8860, 9540, 9545, 10398, 10400, 10873, 11719, 11914, 11969, 12705, 12780, 12996T, 13263, 14318, 14766, 14783, 15043, 15204, 15236, 15301, 15326, 15487T, 16093, 16223, 16298, 16311, 16327, 16519
TK003	Burma	619.2	203	1123	M12a1b	73, 125, 127, 128, 146, 152, 195, 263, 489, 750, 1438, 2706, 3316, 3621, 4170, 4562, 4769, 5492, 5563, 5580, 7028, 8701, 8860, 9540, 9755, 10398, 10400, 10873, 11353, 11719, 12030, 12358, 12372, 12705, 13966, 14569, 14687, 14727, 14766, 14783, 15010, 15043, 15301, 15326, 16129, 16172, 16183C, 16189, 16223, 16234, 16290, 16519
TK004	Burma	559.8	174	939	M49e1	73, 263, 489, 750, 1438, 2263A, 2706, 3780, 4735A, 4769, 5471, 6515, 7028, 8701, 8723, 8860, 9540, 9708, 10398, 10400, 10700, 10873, 11061, 11719, 12705, 14766, 14783, 15043, 15301, 15326, 15944d, 16223, 16234, 16519
TK005	Burma	385.4	116	738	F1b1	73, 146, 204, 249d, 263, 750, 1438, 2706, 3970, 4732, 4769, 5147, 6366, 6392, 6629, 6962, 7028, 7444, 8860, 10310, 10609, 10976, 11719, 12406, 12633, 12876, 12882, 13928C, 14476, 14766, 15326, 15924, 16189, 16232A, 16249, 16304, 16311, 16519
TK006	Burma	458.3	122	824	B4b1c	73, 251, 263, 499, 750, 827, 1438, 2706, 4769, 4820, 7028, 8281-8289d, 8343, 8860,

						11719, 12398, 13590, 14587, 14766, 15326, 15535, 16051, 16136, 16183C, 16189, 16217, 16218, 16519
TK007	Burma	777.3	338	1345	M72a	73, 263, 489, 750, 1438, 1872, 2706, 3531, 4769, 6611, 7028, 7852, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12705, 12753, 13135, 14233, 14766, 14783, 15043, 15301, 15326, 15644, 15820, 15932, 16166d, 16214, 16223
TK008	Burma	152.7	30	347	M51b	73, 150, 152, 153, 228, 263, 489, 750, 1438, 2706, 2833, 3915, 4221, 4697, 4769, 4973, 6455, 7028, 7080, 7372, 8701, 8860, 9156, 9470, 9509, 9540, 10128, 10398, 10400, 10873, 11719, 12705, 13722, 14020A, 14110, 14356, 14687, 14766, 14783, 15043, 15301, 15317, 15326, 16168, 16189, 16223, 16278
TK009	Burma	579.8	165	1528	D5a2a	73, 150, 263, 489, 750, 752, 1107, 2706, 3894, 4769, 4883, 5178A, 5301, 7028, 7269, 7299, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16164, 16172, 16183C, 16189, 16223, 16266, 16311, 16362
TK010	Burma	707.7	278	1193	R9b1a1a	73, 143, 183, 259, 263, 750, 1438, 1541, 2706, 3970, 4017, 4769, 7028, 7849, 8860, 11719, 12714, 13928C, 14766, 15326, 16288, 16304, 16309, 16390, 16519
TK011	Burma	417.4	126	736	D4e1a2	73, 94, 214, 263, 489, 750, 1438, 2706, 3010, 3316, 4769, 4883, 5178A, 5964, 7028, 8414, 8701, 8860, 9536, 9540, 10398, 10400, 10873, 10915, 11215, 11719, 12705, 12879, 14470, 14668, 14766, 14783, 15043, 15301, 15326, 15924, 16092, 16223, 16311, 16362
TK012	Burma	667	187	1189	D5a2a1	73, 150, 263, 489, 493, 750, 752, 1107, 2706, 3336, 4225, 4769, 4883, 5178A, 5301, 7028, 8701, 8860, 9180, 9540, 9966, 10397, 10398, 10400, 10873, 11719, 11944, 12026, 12705, 14142, 14766, 14783, 15043, 15301, 15326, 16038, 16086, 16092, 16164, 16186, 16189, 16223, 16266, 16362
TK013	Burma	220.4	53	415	D5a2	73, 150, 263, 489, 750, 752, 1107, 1719, 2706, 4769, 4883, 5178A, 5301, 7028, 8701, 8860, 9180, 9540, 10397, 10398, 10400, 10873, 11152, 11719, 11944, 12026, 12705, 14766, 14783, 15043, 15301, 15326, 16162, 16164, 16172, 16183C, 16189, 16223, 16278, 16362
TK014	Burma	142.9	46	227	F1a1a	73, 249d, 263, 750, 1438, 2706, 3970, 4086, 4769, 6392, 6962, 7028, 8149, 8860, 9053, 9425, 9548, 10310, 10609, 11719, 12406, 12882, 13759, 13928C, 14766, 15326, 16108, 16129, 16162, 16172, 16304, 16519
TK015	Burma	184.4	67	318	M46	73, 94, 146, 195, 263, 489, 750, 961, 1438, 2706, 3588, 4769, 5048, 5147, 5499, 5894T,

						6253, 7028, 7521, 8227, 8701, 8860, 9540, 10398, 10400, 10873, 11719, 12366, 12705, 13681, 14766, 14783, 15043, 15301, 15326, 15355, 16223, 16224, 16311, 16319, 16362, 16380, 16519
TK192	Burma	91.7	22	151	M37	73, 152, 235, 263, 489, 750, 1438, 2706, 4769, 6040, 6044, 6266, 7028, 7301, 7759, 8251, 8701, 8860, 9540, 9663, 10398, 10400, 10556, 10873, 11719, 12007, 12372, 12705, 13064, 13392, 14766, 14783, 15043, 15301, 15326, 15607, 16037, 16129, 16223, 16261, 16362, 16519

Appendix B. The phylogenies haplogroups B5, M7 and R9 (including F1a) are uploaded on a CD.