原始瑶语声母及瑶汉关系研
刘文
山东大学

摘要
本研究基于若干瑶语方言点的材料构建了原始瑶语的声母系统。与前人研究相比，本文首先通过建立方言间的严格语音对应（普通话对应和完全语音对应）来消除偶然相似造成的对应，进而采用历史比较法的原则构建了原始瑶语的声母系统。值得注意的是，本文根据语音对应的高度区分了原始形式的层次，这一点对于检验原始形式的时间深度以及语音对应对原始形式的支撑力度来说是十分必要的。基于这一构建系统，文章讨论了若干引人注目的话题，例如，原始瑶语鼻冠音声母的发展，响音的三分，原始瑶语和原始闭语中的六套塞音声母，以及瑶语与汉语的语流关系。

关键词
瑶语 语音对应 声母系统 构拟 汉语

THE ANCESTRY OF THE CHINESE PEOPLE BASED ON LANGUAGE AND GENES
George van Driem
Institut für Sprachwissenschaft, Universität Bern

ABSTRACT
Mandarin Chinese and the other Sinitic languages together comprise one out of many branches of the Trans-Himalayan language family. China is also home to languages of the Austroasiatic, Austro-Tai, Altaic and Hmong-Mien families. Twenty years ago, the father tongue correlation was recognised as a principle in the founding dispersals of linguistic phyla based on the ubiquity of the correlation of Y chromosomal markers with the geographical distribution of language families. The geographical distribution and the relative chronology of branching and spread of the Austroasiatic, Austro-Tai, Trans-Himalayan and Hmong-Mien language families correlate with four distinct paternal lineages that are subclades of the Y chromosomal haplogroup O.

KEYWORDS
Trans-Himalayan language family Population genetics Prehistory Historical linguistics Source of language

1. SINITIC AND TRANS-HIMALAYAN
Mandarin, Cantonese, Hakka, Xiàng, Hokkien, Teochew, Pinghuá, Gàn, Jìn, Wè and a number of other languages and dialects together comprise the Sinitic branch of the Trans-Himalayan language family. These
languages all collectively descend from a prehistorical Sinitic language, the earliest reconstructible form of which was called Archaic Chinese by Bernard Karlgren and is currently referred to in the anglophone literature as Old Chinese. Today, Sinitic linguistic diversity is under threat by the advance of Mandarin as a standard language throughout China because Mandarin is gradually taking over domains of language use that were originally conducted primarily in the local Sinitic languages. China is a demographic giant, and, within China, the speakers of Mandarin and other Sinitic languages together comprise the overwhelming majority of the population. As a consequence, the Trans-Himalayan family, to which Chinese belongs, is the second most populous family of languages in the world in terms of numbers of speakers.

This language family was first identified by Julius von Klaproth in 1823, who defined the family as consisting of Tibetan, Chinese, Burmese, Garo and all demonstrably related languages. This language family was originally called Tibeto-Burman in the British Isles, e.g., Hodgson (1857), Cusin (1878), Forbes (1878), Houghton (1896). Most speakers of Trans-Himalayan languages live to the north and east of the Himalayas (Figure 1), whereas most of the over three hundred different languages and three fourths of the major Trans-Himalayan linguistic subgroups are located to the south of the Himalayan divide (Figure 2). Since 2004, the name Trans-Himalayan has increasingly come into use because over time the original term “Tibeto-Burman” had come to be used in two opposing senses: both in its original meaning, but also in an historically and linguistically incorrect sense. The reason behind the neutral geographical name Trans-Himalayan is that the language family is spread across the Himalayas, both to the south and to the north of this greatest land barrier on our planet.

The use of the term “Tibeto-Burman” in two contradictory senses originated when a rival phylogenetic model named “Indo-Chinese” gained in popularity. This other theory of linguistic relationship differed from von Klaproth’s well-informed Tibeto-Burman language family in that the Indo-Chinese construct contained all the languages of Asia and Oceania as far as Japan, Polynesia and Papua New Guinea. The theory was dreamt up by a Scotsman named John Caspar Leyden, who made a meteoric career as a British civil servant in Asia during the Napoleonic wars but then died at the age of 35 soon after he reached Java. The idea that all Asian and Oceanic languages shared some “common mixed origin” appealed to British colonial authorities, who were persuaded that they would be better able to rule over Asian peoples if a programme of linguistic research to understand Indo-Chinese language could be effectuated.

Over time, the hypothetical Indo-Chinese language family was whittled down in size, but the model also came to be tinged with racist overtones. Chinese has been a written language for millennia, during which the language served as the vehicle for an advanced civilisation. However, the eccentric and isolated position to which Chinese was relegated within the Indo-Chinese family tree was not based on any appreciation of the sophistication of Chinese culture, but on a racist appraisal of the Chinese language and people that arose amongst a particular breed of Western scholar at the time of the Opium Wars. The rebranding of the Indo-Chinese theory as “Sino-Tibetan” in 1924 helped to disguise these earlier racist underpinnings, but the model continued to treat Sinitic as a phylogenetic oddity.

Linguistically, the Sino-Tibetan model consisted of two branches, one of which was “Sino-Daic”, and so represented a false family tree. When the Kradai languages were removed from “Sino-Tibetan”, the reduced tree still represented a false phylogeny by sleight of relegating all non-Sinitic languages to a single subgroup, which Sino-Tibetanists misleadingly labelled “Tibeto-Burman”. No linguist has yet added any historical linguistic evidence that could unite this supposedly subordinate taxon into a single branch within the family tree. The Indo-Chinese or Sino-Tibetan model was assailed by scholars who proposed other models, e.g., Sino-Burman (Ramstedt 1957), Sino-Himalayan (Bodman 1973, 1980) and Sino-Kiranti (Starostin 1994).

Matisoff, who inherited the epistemologically flawed tree model from his mentor Benedict in the 1960s and championed this unsupported phylogeny for half a century, has at times retreated from face-saving denial and publicly recanted Sino-Tibetan on three occasions. This episode in linguistic history has already been recounted in greater detail elsewhere (van Driem 2014a). Yet today the model continues to mislead students and some scholars. Dispelling myths is an arduous task because of
the tenacity with which such narratives take hold of the human mind. The default model was already presented by von Klapproth in 1823 in the form of his original Tibeto-Burman linguistic family, augmented by all the constituent linguistic subgroups which have since been recognised, some of which still remain to be properly validated (Figure 3).

Most of the speakers of Trans-Himalayan languages live within China, but most of the individual Trans-Himalayan languages are spoken exclusively outside of China. On the basis of evidence adduced by Schrorer (2016), the Dura language of central Nepal has now been subsumed into the Magaric group, reducing the number of subgroups in the family from an erstwhile 42 to 41 branches. A total of 28 out of the 41 Trans-Himalayan subgroups are found either exclusively or predominantly south of the Himalayan divide within the Indian subcontinent, viz. Tamangic, Newaric, Kiranti, Lepcha, Diginish, Lhokpa, Midzish, Chepangic, Magaric, Tani, Siangic, Rai-Raute, Kho-Bwa, Ao, Zeme, Angami-Pochuri, Karbi, Mru, Brahmaputra, Gongduk, Hrusish, Black Mountain, Dhimalis, Tangkhal, Meithei, Pyu, Karenic and Kukish.

Sinic languages are not the only Trans-Himalayan languages spoken inside China. In addition to Sinitic, six other Trans-Himalayan linguistic subgroups are found to the north and east of the Himalayas, viz. Bái, Tǔjiǎ, Ḳyǎorzongic, Qiāngic, Ėrsūnǐ and Nàncī. Six branches of the Trans-Himalayan family are represented by language communities distributed both on the north side and on the south flank of the Himalayas, viz. Tshangla, Bodish, Nungish, Lolo-Burmese, West Himalayish and Kachinich. Linguistic diversity south of the Himalayas may be even greater than shown in Figure 2. Ghola and Kake together probably constitute a distinct linguistic subgroup, separate from Tamangic. Similarly, the diagram shown in Figure 3 subsumes the Northern Naga languages within Kachinich, a conjecture which still remains to be validated.

2. OTHER LANGUAGE FAMILIES OF CHINA

In 1827, von Klapproth recognised that Mon did not belong in the same phylum as Thai, Malay, Burmese, Chinese and Japanese, but that the Mon language, with respect to the other languages then documented, was in a phylum by itself. Francis Mason, born in York in 1799, emigrated across the Atlantic to Massachusetts in 1818, became a preacher in
and archaeological evidence suggested that the colonisation of Madagascar
by the Malagasy took place between 400 and 700 AD (Dahl 1951, Dewar
1996, Adelaar 1996), but the earliest radiocarbon dates for human settle-
ments in Madagascar only date from the beginning of the 8th century, af-
after Indian influence had begun to make itself felt in insular Southeast
Asia. A population genetic study has now lent support to this late histori-
cal date for the first human settlement of Madagascar or even for a later
initial settlement than previously thought (Pierron et al. 2017).

Jacob le Maire travelled throughout the Indo-Pacific for the Dutch
East India Company during his circumnavigation of the earth in the years
1615 and 1616. He observed that the languages of Polynesia were related
to Malay and the languages of the Indonesian archipelago. On the basis of
the observations and materials provided by de Houtman and le Maire,
Adriaan van Reeland (Relandus 1708, 55–139) established the genetic
affinity between Malagasy, Malay and the Polynesian languages and
identified Malayo-Polynesian as a language family.

In 1624, on the southwestern coast of Formosa, the Dutch estab-
lished Fort Zeelandia on a sandy islet that bore the name Taiouan in the
now extinct local Formosan language Siraya. This Siraya toponym was
recorded in Dutch sources variously as Taiouan, Teyouvan, Teioun, Tai-
ouan, Taiyouuan and Taiyouan. Shifting sands soon joined the islet of
Taiouan to the Formosan coast, forming an isthmus. On the basis of the
catechisms and linguistic materials produced by the missionary Daniel
Gravius on Tâi-wân between 1647 to 1651, von Klapproth (1822) included
the Formosan languages in the Malayo-Polynesian family, a year before
he published his influential Asia Polyglotta. In 1904, the Austrian priest
Wilhelm Schmidt renamed the language family Austronesian, and Blust
(2009) furnished what is currently the authoritative phylogenetic model
of the Austronesian family tree (Figure 6).

Languages of the Kra-dai family are also spoken in China, where
the distinctness of these languages from Chinese has always been appreci-
cated and where the family is today called Zhuang-Dong in Mandarin.
On the basis of root etymology, von Klapproth (1823, 326, 364–365) recognised
that Thai was not related to Sinitic, once the obvious Chinese loan words
had been sifted out of the lexicon. Kra-dai previously went by Shafer’s
(1941) name Daic or Benedict’s (1942) coinage Tai-Kadai, but in Thai

1 Benedict initially coined the term “Kadai stock” to cover four languages,
i.e., “Li dialects of the island of Hainan, the Kelao language of southeaster-
China, and the Laoqua and Lati languages of the China-Tonkin border region”
(1942, 576), but on a later occasion he claimed, perhaps facetiously, that he
had actually intended the term “Kadai”—or had later come to use the term—
for the entire Daic language family, but that “some people”, making a head
gesture in the direction of one of the conference participants (cf. Matsuoff
1991), had popularised the jingle “Tai-Kadai” for the family because they
liked the ring of it (Benedict, personal communication at the XXIVth Inter-
national Conference on Sino-Tibetan Languages and Linguistics, Ramkham-
haeng University at Bangkok, 7 October 1991). Soon thereafter, Weera
Ostapirat (2000) changed the name of the Daic or “Tai-Kadai” family to
“Kra-Dai”, now “Kradai”, a term that had already entered into use in Thai.
Altaic and reserves the term “Altaic” for the higher-order subgroup comprising just Turkic, Mongolic and Tungusic.

Hmong-Mien is traditionally called Miao-Yao in Mandarin and has long been recognised as a distinct family of languages in China. André-Georges Haudricourt (1954) wrote the first historical phonology of Hmong-Mien. Kun Chang (1972, 1976) wrote a reconstruction of the Hmong-Mien tonal system and of the Proto-Hmong inventory of initials, representing the culmination of many years of work reflected in his earlier publications. A reconstruction of Hmong-Mien was written by Purnell (1970), followed by the reconstructions of Wáng Fúshí (1994) and Wáng Fúshí and Máo Zòngwǔ (1995), which have all been superseded by Ratliff’s (2010) Hmong-Mien reconstruction. In terms of its restricted internal diversity, the Hmong-Mien language family looked to Stanley Starosta like a vestigial branch of what once may have been a greater linguistic phylum, which Starosta (2005) called “Yangtzean” in recognition of the historical distribution of Hmong-Mien peoples along and the Yangtze and south of the Yangtze (Figure 8).

Just as Ostapirat united the Kradaï and Austronesian families into an Austro-Tai linguistic phylum, others have sought to unite recognised language families into larger linguistic phyla. Wilhelm Schmidt (1906) and Lawrence Reid (1994, 2005) sought to unite Austrosiatic and Austronesian into an Austro macrofamily, but the historical evidence does not yet hold up to scrutiny (cf. Difflloth 1994). Similarly, August Conrady (1916, 1922) and later Kurt Wulff (1934, 1942) proposed unifying Austrosiatic, Austronesian, Kradaï and Tibeto-Burman, whereas Paul Benedict (1942), Robert Bhat (1996) and Iïa Peires (1998) proposed a linguistic phylum comprising Austrosiatic, Austronesian, Kradaï and possibly Hmong-Mien.

Quite unlike Ostapirat’s Austro-Tai, no methodologically rigorous study has been conducted adding solid evidence for any of these proposals. Finally, Stanley Starosta (2005) proposed unifying the Austrosiatic, Austronesian, Kradaï, Tibeto-Burman and Hmong-Mien language families into an East Asian linguistic phylum. The shared morphological vestiges adduced by Starosta in support of his East Asian linguistic phylum comprised the agentive prefix *<s->, the patient suffix *<n->, what he called the instrumental prefix *<n-> and what he termed the perfective prefix *<n->.

Other than Ostapirat, all these scholars have ventured beyond the epistemological constraints of what I call the “linguistic event horizon”, representing the maximal time depth accessible through methodologically sound linguistic reconstruction and the boundary beyond which any reconstructions are at one point reduced to sheer speculation. Therefore, a discussion of the merits of the evidence advanced by Starosta for the East Asian linguistic phylum strikes me as being of little utility, since I consider the phylum to lie at the linguistic event horizon and therefore doubt whether this issue can ever be conclusively resolved on the basis of firmly reconstructible linguistic evidence. Rather, Starosta proposed that the “potential utility” of his hypothesis lay “in helping to focus scholars’ efforts on particular specific questions, resulting in the replacement of parts of this hypothesis with better supported arguments” (2005, 194). A tweaked version of Starosta’s East Asian family tree is the 2012 in Benares recension (van Driem 2014b), shown in Figure 9.

3. THE FATHER TONGUE CORRELATION

We ought not to lose sight of the fact that a proto-language can be reconstructed solely on the basis of linguistic evidence and that the linguistic ancestors of any modern language community were not necessarily the same people as the community’s biological forebears. Although these points have long been reiterated from the time of Julius von Klaproth (1823) and Max Müller (1872), these lessons are often lost on some audiences. By the same token, each of us has countless ancestors via numerous lineages. There is no such thing as a pure race. In fact, in molecular genetic terms there is no such thing as race (Cavalli-Sforza, Menozzi and Piazza 1994).

We are all members of one large human family. Moreover, even when languages and genes happen to exhibit a correlation, such a marker relationship should not be confused with identity. The correlation of a particular chromosomal marker with the distribution of a certain language family must not be simplistically equated with populations speaking languages of a particular linguistic phylum. Rather, molecular markers on
the Y chromosome serve as proxies or tracers for the movements of paternal ancestors.

When studying the distribution of maternally inherited markers in the mitochondrial DNA and paternally inherited markers on the Y chromosome, a Swiss-Italian team of population geneticists soon found that it was easier to find statistically relevant correlations between the language of a particular community and the paternally inherited markers prevalent in that community than between the language and the most salient maternally inherited markers found in that speech community. This Father Tongue correlation was first described by Poloni et al. (1997, 2000).

On the basis of this finding, it was inferred that paternally inherited polymorphisms may serve as markers for linguistic dispersals in the past, and that a correlation of Y chromosomal markers with language may point towards male-biased linguistic intrusions. The Father Tongue correlation is ubiquitous but not universal. Its preponderance allows us to deduce that a mother teaching her children their father’s tongue must have been a prevalent and recurrent pattern in linguistic prehistory.

There are a number of reasons why we might expect this outcome. Palaeolithic populations were small, and the effective founder population sizes of the major modern paternal subclades must have been quite small, whilst new populations arise from the small surviving subsets that have passed through bottlenecks. In fact, molecular evidence indicates that the Y chromosome underwent a global bottleneck towards the end of the last ice age, when certain paternal clades started eradicating or out-competing other clades (Karmin et al. 2015). The founding dispersals of many major language families appear to be related to the robust spread and reproductive success of the bearers of a subset of Y chromosomal haplogroups that survived such bottlenecks.

As a consequence, the global phylogeography of Y chromosomal haplogroups is shallower in terms of time depth than the worldwide mitochondrial landscape. The initial human colonisation of any virgin part of the planet must have involved both sexes in order for a population of progeny to establish itself. Once a population is in place, however, subsequent migrations could have been heavily gender-biased. Subsequently, male intruders could impose their language whilst availing themselves of the womenfolk already in place. In this regard, population geneticist Toomas Kivisild (2014) has wryly characterised warfare as a sex-specific pathology linked to the Y chromosome.

Whereas the landscape of paternal lineages often appears to correlate with language at the comparatively shallower time depth of the linguistically reconstructable past, correlations between paternal lineages and linguistic phylogeography discerned to date have been underwhelming. The Father Tongue hypothesis suggests that linguistic dispersals were, at least in most parts of the world, posterior to initial human colonisation and that many linguistic dispersals were predominantly later male-biased intrusions. Such patterns are observed worldwide.

The resolution of the Y chromosomal tree is constantly being enhanced. Haplogroup labels are updated to reflect our improved understanding of phylogeny. Mutations numbers tend to remain unchanged, provided that the markers in question prove to be reliable in defining haplogroups. Conventional haplogroup labels of the Y Chromosome Consortium are still widely in use, but have been replaced here with the newer labels of the International Society of Genetic Genealogy, reflecting refinements incorporated up to the 12th of May 2017.

Long before the linguistically reconstructable past, at a time that lay well beyond the linguistic event horizon, the paternal haplogroup K (M9) was centred in the area between South Asia and Southeast Asia, where the ancestral *K appears to have been situated. This clade spawned many successful paternal lineages, some of which moved into insular Southeast Asia, i.e., the haplogroups S (M69) and M (M304), whereas other clades moved back westward into South Asia and beyond, viz., the haplogroups Q (M242), R (M201), T (M89) and L (M429) (Karaft et al. 2015). The geographical locus of yet another descendant subclade lay in the Eastern Himalaya, i.e., the ancestral haplogroup NO (M214).

Millennia after the two paternal lineages N and O had split up, the bearers of haplogroup N set out for East Asia just after the last glacial maximum, braving ice and tundra, and—in a grand counterclockwise sweep—migrated across northern Eurasia as far as west as Lappland, whilst the ancestral form *N appears to have been situated in northern Burma, Yunnan and Sichuan (Rootsi et al. 2007; Derenko et al. 2007, Mirabal et al. 2009; Ilumäe et al. 2016).
In previous publications (van Driem 2014b, 2016, 2017b), I identified the clade N (M231) with the paternal spread of Fortescue’s Uralo-Siberian linguistic phylum. Fortescue (1998, 2011, 2017) adduced evidence for an ancient circumpolar Uralo-Siberian linguistic phylum comprising Uralic, Yukagir, Eskimo-Aleut, Nivkh and Chukoko-Kamchatkan, an ancient linguistic relationship at the very horizon of the linguistically reconstructable past that is rendered more discernible when the known cases of language shift in the circumpolar region are carefully taken into account.

4. THE EAST ASIAN DISPERSAL

The molecular marker M175 defining the paternal clade O is overwhelmingly shared by the linguistic ancestors of what Starosta called the East Asian linguistic phylum, as observed in the cited studies, where it was proposed that the four major East Asian language families, i.e., Austroasiatic, Trans-Himalayan, Hmong-Mien and Austro-Tai, had resulted from prehistoric bottlenecks correlated with specific paternal lineages. The non-random correlation of the subclades of this particular Y chromosomal haplogroup with the four recognised language families enables us to infer the following sequence of events.

Millennia before the end of the last glacial maximum, the paternal lineage O (M175) split into the subclades O2 (M122) and O1 (F265, M1354), as shown in Figure 10. The two subclades can be putatively assigned to two geographical loci, with the haplogroup O1 (F265, M1354) moving eastward into East Asia south of the Yangtze, whilst bearers of the O2 (M122) haplogroup settled in the general region of the Eastern Himalaya. Subsequently, over the course of time, as temperature and humidity increased after the last glacial maximum, haplogroup O split further into the paternal lineages that serve as tracers for the spread of Trans-Himalayan, Hmong-Mien, Austroasiatic and Austro-Tai.

The O1 (F265, M1354) lineage south of the Yangtze split into the subclades O1b (M268) and O1a (M119), with the latter moving eastward to the Fújián hill tracts and across the strait to settle on Formosa, which so became the Urheimat of the Austroasiatics (cf. Abdulla et al. 2009). The founding dispersal of the Austro-Tai language family can be traced through a correlation of the current geographical range of Austro-Tai lan-

guages with the chronology and spread of the molecular proxies defining the paternal haplogroups O1b (M268) and O1a (M119).

Subsequently, the paternal subclade O1b (M268) gave rise to the subclades O1b2 (M176) and O1b1a1a (M95). The bearers of haplogroup O1b1a1a (M95) became the progenitors of the Austroasiatics (van Driem 2007). The Austroasiatics spread throughout the Salween drainage and thence to southern Yunnán, northern Thailand and western Laos. In time, the Austroasiatics would spread as far as the Mekong delta, the Malay peninsula and the Nicobars, and their paternal lineage would also spread deep into insular Southeast Asia. However, the prominent paternal lineage O1b2 (M176), which I have previously referred to as "para-Austroasiatic", does not appear to be correlated with any extant linguistic group today.

Secondarily, bands of male Austroasiatics introduced their language and their paternal lineage, O1b1a1a (M95), to the indigenous peoples of the Chotá Nágpúr. Chauhey et al. (2010) showed that the Munda branch of Austroasiatic had arisen as the result of a sexually biased linguistic intrusion into the Indian subcontinent from the region to the north of the Bay of Bengal (Figure 11). As a consequence of the comparatively younger date and the nearly absolute gender asymmetry of this linguistic intrusion, it appears that the deepest division within the Khäsi-Asian trunk of Austroasiatic, i.e., the split between Khäsi-Pakanic and Mon-Khmer, might be more indicative of the geographical location of the Austroasiatic homeland than the split between Munda and Khäsi-Asian. If we accept this line of reasoning, then the point of dispersal for Khäsi-Asian would appear to have lain in the area between South Asia proper and mainland Southeast Asia proper.

The spread of haplogroup O1 (F265, M1354) reflects the paternal founding dispersals of both Austro-Tai and Austroasiatic as well as the geographical spread of a para-Austroasiatic paternal subclade that evidently left no modern linguistic descendants. Our data from the Himalayan region and the data from populations elsewhere in Asia indicate that the geographical range and the chronology of spread of haplogroup O2a2b1 (M134) traces the founding dispersal of the Trans-Himalayan language family, whereas the paternal lineage O2a2a1a2 (M7) serves as a molecular proxy for the founding and spread of Hmong-Mien.
About twelve thousand years ago, at the dawn of the Holocene, in the southeastern Himalayas and eastern slopes of the Tibetan Plateau, haplogroup O2 (M122) gave rise to the ancestral Trans-Himalayan paternal lineage O2a2b1 (M134) and the “Yangtzean” or Hmong-Mien paternal lineage O2a2a1a2 (M7), as shown in Figure 12. It is a reasonable conjecture that the bearers of the polymorphism O2a2b1 (M134) at first remained in the Eastern Himalayas, which today also continues to represent the centre of phylogenetic diversity of the Trans-Himalayan language family based on the geographical distribution of primary linguistic subgroups. After the bearers of the O2a2a1a2 (M7) lineage migrated eastward to settle in the areas south of the Yangtze, they were followed by early Trans-Himalayan language communities that spread from northeastern India into southeastern Tibet and northern Burma.

On their way, the early Hmong-Mien encountered the ancient Austroasiatics, from whom they adopted rice agriculture. Three principal populations of cultivated rice Oryza sativa are distinguished, comprising the families of cultivars known as *ahu*, *indica* and *japonica* rice. Earlier population genetic research on the genome of wild and cultivated varieties of rice supported the hypothesis that Asian rice was domesticated twice (Kovach et al. 2007, Sweeney and McCouch 2007, Kovach et al. 2009), but molecular evidence added in subsequent work demonstrated that the three principal cultivars represent three independent domestication processes, and that the introgression of domesticated traits occurred not just unidirectionally from *japonica* into *ahu* and *indica* rice, but multidirectionally from *ahu* and *indica* into *japonica* as well (Londo et al. 2006, McNally et al. 2009, Civerá et al. 2015).

In previous studies (van Driem 2011, 2012, 2017c), evidence from linguistic palaeontology, rice genetics and human population genetics enabled the ethnohistorical identification of the domesticators of Asian rice with the early Yangtzeans, the ancient Austroasiatics and the bearers of para-Austroasiatic haplogroup O1b1a (M176). The latter para-Austroasiatic paternal lineage advanced as far as the Korean peninsula and also represents a major wave of immigration recorded in the Japanese genome, representing the probable lineage of the Yayoi people, who introduced rice agriculture to Japan, as early as the second millennium BC, during the final phase of the Jomon period.

The intimate interaction between ancient Austroasiatics and the ancestral Hmong-Mien not only involved the sharing of knowledge about rice agriculture, but also left a genetic trace in the high frequencies of haplogroup O1b1a1a (M95) in today’s Hmong-Mien language communities and of haplogroup O2a2a1a2 (M7) in today’s Austroasiatic populations. In an earlier study on Y chromosomal haplogroups, Cai et al. (2011, 8) once ventured to speculate about “a Mon-Khmer origin of Hmong-Mien populations”. Instead, the incidence of haplogroup O2a2a1a2 (M7) in Austroasiatic language communities of Southeast Asia evinces a significant Hmong-Mien paternal contribution to early Austroasiatic populations, whereas the incidence of haplogroup O1b1a1a (M95) amongst the Hmong-Mien indicates a comparatively lower Austroasiatic paternal contribution to Hmong-Mien populations. As the Hmong-Mien moved eastward, the bearers of para-Austroasiatic paternal lineage O1b2 (M176) likewise continued to move east.

Meanwhile, the bearers of Y chromosomal haplogroup O2a2b1 (M134) in the eastern Himalayan region expanded eastward throughout Sichuan and Yunnan, north and northwest across the Tibetan plateau as well as further westward across the Himalayas and southward into the Indo-Burmese borderlands. On the Brahmaputra plain, the early Trans-Himalayans encountered the Austroasiatics, who had preceded them. The relative frequencies of the Y chromosomal haplogroup O1b1a1a (M95) in Trans-Himalayan speaking populations of the Indian subcontinent (Sahoo et al. 2006, Reddy et al. 2007) suggest that a subset of the paternal ancestors of some Trans-Himalayan populations in northeastern India, e.g., certain Bodo-Koch communities, may originally have been Austroasiatic speakers who were linguistically assimilated by Trans-Himalayans.

Finally, the ancestral Trans-Himalayan paternal lineage O2a2b1 (M134) spread further northeast to the North China plain. The complex history of Sinitic populations featured successive constellations of dynastic empires governed from geographically ever shifting capitals, whereby subjugated and neighbouring populations as well as immigrants were absorbed. Not surprisingly therefore, Han Chinese populations tend to represent an amalgam of East Asian paternal lineages. Yet even in modern Han Chinese populations, the molecular marker associated with the spread of a Trans-Himalayan father tongue from the eastern Himalayan
region, i.e., haplogroup O2a2b1 (M134), taken together with its subclade O2a2b1a1 (M117), occurs in a much higher frequency than any other O haplogroup subclade, and approximately twice as frequently as the next most frequent fraternal subclade O2a1c (002611) (Yan et al. 2011, Wang et al. 2013, Yao et al. 2017).

On the grand time scale of the present narrative, China as a cultural and linguistic entity represents only a rather recent phenomenon, and Kwang-chih Chang (1986, 242) cautioned us against anachronisms that arise from applying the label “Chinese” to archaeological cultural assemblages or to peoples of the distant past. Likewise, in his valuable pioneering interdisciplinary studies, Bill Wang (1998) stressed the distinctness of the “three windows on the past” afforded by archaeology, linguistics and genetics.

Only at a much shallower time depth did the Trans-Himalayan paternal lineage O2a2b1 (M134) spread in tandem with early Sinitic speaking populations southward from the Yellow River basin into southern China during the Qin dynasty in the third century BC (Mountin et al. 1992, Wen et al. 2004). The martial and male-biased historical spread of Hán Chinese during the gradual cultural sinification of the region south of the Yangtze involved both the spread of language and the introduction of paternal lineages and is historically documented in the Chinese chronicles. The paternal lineage O2a2b1 (M134) is also intrusively present in the Korean peninsula and beyond.

Not only do the geographical distribution of Trans-Himalayan linguistic subgroups and the chronology and spread of Y chromosomal haplogroups take us back to an eastern Himalayan homeland, basic facts of geography in light of our ultimate African origins prompt us to direct our gaze back to the Himalayas. The sub-Himalayan hill tracts offered a rich corridor replete with lush habitats for early human populations at a time that our ancestors still practised hunting and foraging as their principal subsistence strategies. The presence of Y chromosomal haplogroup D and other molecular markers in the Himalayas likewise attest to numerous older waves of peopling that passed through this region.
Figure 3 The 41 major Trans-Himalayan linguistic subgroups or “fallen leaves” of the Trans-Himalayan language family. At variance with previous depictions, the diagram shows just 41 subgroups instead of 42. Schorrer (2016) has shown Dura to be Magaric, thereby reducing the number of subgroups by one. Linguistic diversity south of the Himalayas is likely to be greater than shown here. Ghale and Kaisie probably make up a linguistic subgroup distinct from Tamangic. Here the Northern Naga languages have been expediently subsumed within Kachinic, but this conjecture still remains to be validated. The number and arrangement of subgroups in this heuristic diagram will necessarily change over time as advances in historical linguistics are made and the structure of the family tree is discovered.

Figure 4 Geographical distribution of Austroasiatic languages (reproduced from van Driem 2015, Fig. 11.12, with the gracious permission of Colin Pendry and Georg Miehe).

Figure 5 The family tree of Austroasiatic (Diffloth 2012). Unlike the Khasi-Aslian branch, the internal phylogeny of the Munda branch has not been established.
**APPENDIX (continued)**

**Figure 6** Geographical distribution of Austronesian (reproduced from van Driem 2015, Fig. 14.9, with the gracious permission of Colin Pindry and Georg Miehe). The abbreviations CMP and SHWNG stand for the linguistic subgroups Central Malayo-Polynesian and South Halmahera West New Guinea respectively. Formosan on Taiwan comprises at least nine primary branches of the language family, whilst all other groups shown represent the later geographical dispersal of the single-branch Malayo-Polynesian, which branched into West Malayo-Polynesian and Central East Malayo-Polynesian. Subsequently, Central East split into Central and East. Finally, East Malayo-Polynesian branched into the subgroups South Halmahera West New Guinea and Oceanic.

**Figure 7** Geographical distribution of Khatki languages (reproduced from van Driem 2015, Fig. 14.6, with the gracious permission of Colin Pindry and Georg Miehe). The historical times Austronesian languages of the Malayo-Polynesian group were still spoken in the Philippines, and some remnants of the Dangiren kingdom that flourished in what today is central Thailand until the 13th century.
Figure 8 Geographical distribution of Hmong-Mien languages (reproduced from van Driem 2015, Fig. 14.11, with the gracious permission of Colin Fendrey and Georg Michal). The Hmong-Mien migrated into mainland Southeast Asia relatively recently. Historically, Hmong-Mien peoples live along and south of the Yangtze.

Figure 9 The 2012 Benares recension of Stanley Starosta’s East Asian linguistic phylum presented at Périgueux in 2001 (Starosta 2005, van Driem 2014b)

Figure 10 After the last glacial maximum, the Y chromosomal haplogroup O (M175) split into the subclades O1 (F265, M1354) and O2 (M122).

Figure 11 A male-biased linguistic intrusion introduced both Austroasiatic language and a paternal lineage, haplogroup Olbala (M95), into the indigenous population of the Chotâ Nagpur
Figure 12 At a more recent time depth, paternal lineages branched into new subclades, and each event involved a linguistic bottleneck leading to language families that today are reconstructible as distinct linguistic phyla. The O1 (F265, M1354) lineage gave rise to the O1a (M119) and O1b (M268) subclades. The former moved eastward to the Fujian hill tracts and across the strait to Formosa, which so became the Urheimat of the Austroasiatics. Bearers of the paternal lineage O1b (M268) domesticated Asian rice and spawned the paternal subclades O1b1a1a (M95) and O1b2 (M176). Haplogroup O1b1a1a (M95) is the Proto-Austroasiatic paternal lineage, whereas the para-Austroasiatic fraternal clade O1b2 (M176) spread eastward, sowing seed along the way. The haplogroup O2 (M122) gave rise to the paternal subclades O2a2b1 (M134) and O2a2a1a2 (M7). The spread of the molecular marker O2a2b1 (M134) from the Eastern Himalayas serves as a tracer for the dissemination of people speaking languages of the Trans-Himalayan family, whereas the paternal lineage O2a2a1a2 (M7) serves as a tracer for the spread of people speaking languages of the Hmong-Mien family.

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THE ANCESTRY OF THE CHINESE PEOPLE  121

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