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George van Driem

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香港科技大學中國語言學研究中心

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George van Driem

University of Berne

A polyphyletic understanding of Asian linguistic diversity was first propagated in 1823. Since 1901, various scholars have proposed larger linguistic phyla uniting two or more recognised Asian language families. The most recent proposal in this tradition, Starosta's 2001 East Asian phylum, comprising the Trans-Himalayan, Hmong-Mien, Austroasiatic, Austronesian and Kradai language families, is reassessed in light of linguistic and non-linguistic evidence. Ethnolinguistically informed inferences based on Asian Y chromosomal phylogeography lead to a reconstruction of various episodes of ethnolinguistic prehistory which lie beyond the linguistic event horizon, i.e. at a time depth empirically inaccessible to historical linguistics. The Father Tongue correlation in population genetics, the evidence for refugia during the Last Glacial Maximum and the hypothesis of language families having arisen as the result of demographic bottlenecks in prehistory are shown to be crucial to an understanding of the ethnogenesis of East Asian linguistic phyla. The prehistory of several neighbouring Asian language families is discussed, and the Centripetal Migration model is opposed to the Farming Language Dispersal theory.

Keywords: Historical linguistics, prehistory, population genetics, ethnolinguistic phylogeography, refugia, bottlenecks, ethnogenesis, East Asian linguistic phylum, Trans-Himalayan, Tibeto-Burman, Hmong-Mien, Austroasiatic, Austronesian, Kradai, Father Tongue correlation, Centripetal Migration model, Farming Language Dispersal theory

1. East Asian and the linguistic event horizon

The East Asian linguistic hypothesis was proposed by Stanley Starosta in Périgueux in 2001, a year before he died of congestive heart failure in Hawai'i. Starosta conceived East Asian as an ancient linguistic phylum encompassing Kradai, Austronesian, Tibeto-Burman, Hmong-Mien and Austroasiatic. Starosta was not the first to conceive of an East Asian superfamily. Once a polyphyletic view of numerous distinct Asian language families had been propounded by Julius von Klaproth (1823), scholars began to advance proposals that might link some of these linguistic phyla

together in the form of larger genetic constructs. Gustave Schlegel (1901, 1902) agreed with Klaproth in assessing Kradai to be unrelated to Sinitic, merely replete with Sinitic loans, and argued instead that Kradai was related to Austronesian. Schlegel's old theory was taken up by Benedict (1942, 1976, 1990) under the guise of "Austro-Tai", though this putative genetic link always constituted an ingredient in grander proposals such as Austric or "Japanese/Austro-Tai".

Weera Ostapirat (2005, 2013) was the first to present methodologically sound and cogent historical comparative evidence that Kradai and Austronesian represent coordinate branches of an Austro-Tai family. The coordinate branches of Ostapirat's Austro-Tai represent an ancient migration from what today is southern China across the Taiwan Strait to Formosa, where the Austronesian linguistic phylum established itself, whilst the proto-language ancestral to today's Kradai language communities remained behind on the mainland. Much later, the Formosan exodus led to the spread of the Malayo-Polynesian branch throughout the Philippines, the Malay peninsula, the Indonesian Archipelago, Madagascar and Oceania. Transgressing the linguistic event horizon, Conrady (1916, 1922) and Wulff (1934, 1942) each proposed a superfamily consisting of Austroasiatic, Austronesian, Kradai and Tibeto-Burman. Other than the neglect of Hmong-Mien, the mega-Austric superfamily envisaged by Conrady and Wulff already comprised all the constituents of Starosta's East Asian. Benedict (1942), Blust (1996) and Peiros (1998) proposed an Austric superfamily comprising Austroasiatic, Austronesian, Kradai and Hmong-Mien.¹

¹ Sino-Austronesian, staunchly and solely defended by Sagart (1993, 2005), stands in stark contrast to these superfamilies. This highly restricted superfamily unites Sinitic and Austronesian and, more recently, "Sino-Tibetan" and Austronesian into a single phylum. Blust (2009:707) writes: "The Sino-Austronesian hypothesis is the product of an *idée fixe*". Sagart's phylogeny of Formosan languages is rejected by Blust (2009), Winter (2010) and Teng and Ross (2010). Sagart misanalysed the Puyuma data in an attempt to assail the Nuclear Austronesian hypothesis proposed by Ross (2009). Nuclear Austronesian comprises all Austronesian languages other than Puyuma, Rukai and Tsou, the latter each representing primary branches of Austronesian. Winter (2010) argues that the empirical basis for Sagart's hierarchical grouping of Formosan languages is flimsy and leads to an overly simplistic model of prehistoric migrations on Formosa. As an idea, Sino-Austronesian has evolved since Sagart first explained his theory to me at the University of Hawai'i in August 1989. After abandoning his pre-1994 position that Sinitic was unrelated to Tibeto-Burman, Sagart was compelled to adhere to the outdated and empirically unsupported Sino-Tibetan family tree model, which he requires as an ingredient for his model. Sagart identifies the Middle Yǎngsháo culture in the 5th and 4th millennia BC as the Sino-Austronesian homeland based on "regular correspondences" in the four words for pig, rice, net and millet, one of which is not reflected in Sinitic. The kindest assessment of Sagart's theory in print (van Driem 2005)

Starosta's evidence is meagre, yet primarily morphological in nature. Languages change so fast that traces of a genetic relationship between two languages are either obliterated or obscured beyond recognition after about a dozen millennia, give or take a few thousand years. Regular phonological correspondences and a common morphological system are the most compelling types of evidence for a genetic relationship between languages. When the time depth of a linguistic phylum is very great, morphological correspondences may be the only remaining vestige that evinces a genetic relationship. Despite a scarcity of lexical correspondences between Itelmen a.k.a. Kamchadal and Chukchi-Koryak, the inclusion of Itelmen within a Luoravetlan a.k.a. Chukotko-Kamchatkan family is based on formal and semantic similarities in a small number of flecional morphemes. Yet such morphological evidence would necessarily be lacking altogether if the proto-language of a given family just happened to have been typologically analytical, like Mandarin is today. Most historical linguists modestly resign themselves to a maximal time depth beyond which the comparative method is unable to distinguish between correspondence and coincidence and therefore unable to establish a genetic relationship between languages. Yet a few linguists strive to gaze beyond the linguistic event horizon.

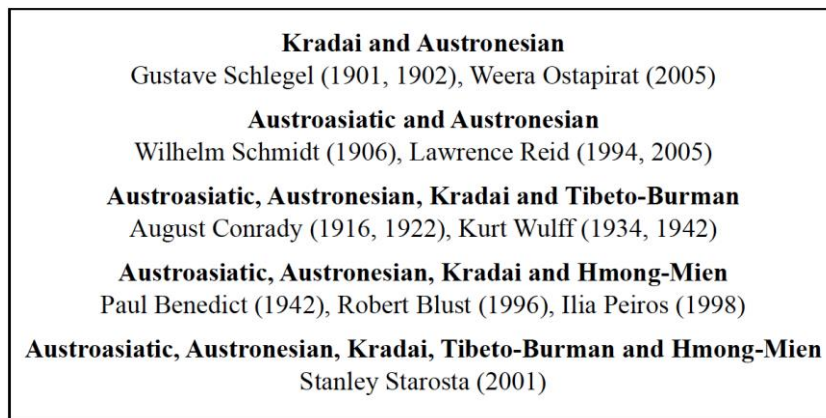


Diagram 1: Some historical antecedents leading up to the East Asian hypothesis

evaluates his evidence as failing to meet the conventional standards of proof. Sino-Austronesian does not merit serious consideration as a hypothesis about linguistic phylogeny.

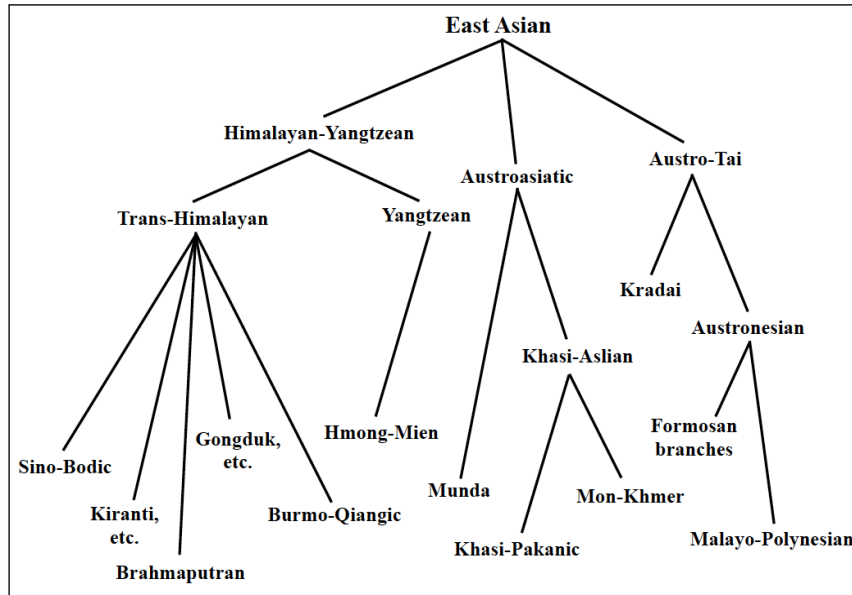


Diagram 2: The 2012 Benares Recension: A revised East Asian phylogeny

Nichols (1986, 1992, 1995, 1998) attempts to salvage empirical evidence for deep genetic relationships between linguistic phyla and to detect the vestiges of ancient substrate influence exerted by one language phylum on another in the form of typological diagnostics. She argues that languages which are distant on a morphosyntactic spectrum ranging from wholly head-marking to wholly dependent-marking are unlikely to be genetically related. Nichols' diagnostics embolden her to speculate about ancient linguistic spread zones and bottlenecks. However, many of the world's languages exhibit both head-marking and dependent-marking morphology and are thus situated somewhere in the middle of the spectrum. In modern East Asia, many languages, such as Vietnamese, Thai, Cantonese, Mandarin, show little to no morphology and so do not occupy any place in this two-dimensional spectrum, but lie instead on a third typological axis, discerned by Friedrich von Schlegel (1808), ranging from synthetic, i.e. agglutinative or flexional, to purely analytical and devoid of morphology. This widespread attrition of older morphology limits the scope for reconstructing the historical morphology of languages and linguistic subgroups which have come to be caught up in the maelstrom of what historically became the East Asian linguistic area.

Fortescue (1998, 2011) advanced the theory of an ancient circumpolar Uralo-Siberian linguistic phylum comprising Uralic, Yukagir, Eskimo-Aleut, Nivkh and Chukotko-Kamchatkan, which he associates with Neolithic assemblages appearing

across Siberia and circumpolar North America between 5000 and 3000 BC during the thermal maximum following the last Ice Age, several millennia after the land bridge across the Bering Strait had disappeared. Fortescue first pushes the comparative method as far as he can take it before introducing the notion of a “mesh”. Fortescue’s mesh not only denotes language families which derive from a single putative linguistic phylum at a time depth which lies beyond what is, strictly speaking, historically reconstructible, Fortescue’s mesh also represents a complex picture of language shift. Beyond the many known cases of language shift in the circumpolar region, Fortescue has sought typological traits which can be identified as the residue of language shifts in more distant prehistory. The mesh notion is invoked because the time depth of the relationship and the complexity of language shifts which took place have left so little evidence intact that a genetic relationship is no longer demonstrable by conventional comparative means.

One of the predecessors of East Asian, Schmidt’s (1906) Austric macrofamily, uniting Austroasiatic and Austronesian, was likewise based on morphological evidence drawn especially from Nicobarese. Today lexical evidence for Austric remains scarce (Diffloth 1994). The arguments are still primarily morphological in nature, with Nicobarese still playing a star role. Reid (1994) relates the Proto-Austroasiatic causative morphemes *⟨pa- ~ -ap-⟩ and *⟨ka-⟩ to the Proto-Austronesian causative prefixes *⟨pa-⟩, *⟨ka-⟩ and *⟨paka-⟩, the Proto-Austroasiatic agentive marker *⟨ma- ~ -am-⟩ with the Proto-Austronesian agentive *⟨mu- ~ -um-⟩, the Proto-Austroasiatic instrumental infixes *⟨-an-⟩ and *⟨-in-⟩ with the Malayo-Polynesian instrumental prefix *⟨paN-⟩, Proto-Austronesian instrumental morpheme *⟨ni- ~ -in-⟩ and a Nancowry Nicobarese nominaliser suffix ⟨-a⟩ with a Proto-Austronesian “objective” suffix *⟨-a⟩.

The morphological evidence and its interpretation remain controversial due to the widespread nature and complexity of morphological processes involving infixation and discontinuous morphemes in Austroasiatic, including Nicobarese. By comparison with Austroasiatic, greater progress has been made in understanding the historical grammar of Austronesian, which may be both a function of the paucity of historical linguists working on Austroasiatic as well as the greater intractability and complexity of the linguistic problems confronting scholars of Austroasiatic historical grammar. Progress on the Austronesian side is in no small measure due to the contributions of Reid himself, e.g. Reid (2006, 2007, 2009a, 2009b, 2010). Reid too envisaged an even larger macrofamily and contended that Austric “as a language family may eventually need to be abandoned in favour of a wider language family which can be shown to include both Austronesian and Austroasiatic languages but not necessarily as sisters of a common ancestor” (Reid 2005:150).

The evidence adduced by Starosta for East Asian, though meagre, is morphological in nature. The ancient morphological processes shared by the families of this phylum were an agentive prefix *<m->, a patient suffix *<n->, an instrumental prefix <s-> and a perfective prefix *<n->. The East Asian word was ostensibly disyllabic and exhibited the canonical structure CVCVC. By contrast, the structure of his family tree comprising Kradai, Austronesian, Tibeto-Burman,² Hmong-Mien and Austroasiatic was based on sheer impressionism. Starosta wrote 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). At the 18th Himalayan Languages Symposium, held at Benares Hindu University in 2012, I presented the revised East Asian family tree depicted in Diagram 2. The revised phylogeny is based on historical linguistic intuitions and other types of information about population prehistory.

2. Trans-Himalayan and other East Asian families

Trans-Himalayan 泛喜馬拉雅語系 is the world’s second most populous language family. Most speakers of Trans-Himalayan languages today live north of the Himalayas (Map 1), but most of the over 300 different languages and three fourths of the major Trans-Himalayan subgroups are located south of the Himalayan divide (Map 2). The Trans-Himalayan linguistic phylum was first recognised by Julius von Klaproth in 1823, who identified the family as consisting of Tibetan, Chinese, Burmese and related languages. This linguistic phylum was called Tibeto-Burman by scholars in the British Isles, e.g. Hodgson (1857), Cust (1878), Forbes (1878), Houghton (1896). Yet confusingly, adherents of the Indo-Chinese tradition use the term “Tibeto-Burman” in the sense of non-Sinitic, a putative taxon within the Indo-Chinese tree for which Sino-Tibetanists have perennially failed to adduce evidence.³

² Starosta accepted the Sino-Bodic hypothesis and rejected the Sino-Tibetan model. Due to an editorial error, the label “Sino-Tibetan” appears in the posthumous version of Starosta’s East Asian phylogeny (Starosta 2005:183). Starosta’s East Asian phylogeny, as presented at Périgueux in 2001, is reproduced correctly in van Driem (2005:322), rectifying the editorial misrepresentation. It remains a matter of conjecture whether the subordinate extra-Formosan status of Kradai in Starosta’s diagram might not also be a posthumous editorial enhancement, since this idea has chiefly been championed by one of the editors since Périgueux.

³ In 1807, the Scots amateur John Leyden proposed his exuberant but poorly informed Indo-Chinese theory to George Barlow, Governor General of India at Fort William, in which he claimed a *priori* that all the languages in Asia and Oceania shared a “common mixed origin”. Leyden died at the age of 35 after making a short but dazzling career in the British colonial

The Sino-Tibetanists' tree was assailed by scholars who proposed other models, e.g. Sino-Burman (Ramstedt 1957), Sino-Himalayan (Bodman 1976, 1980) and Sino-Kiranti (Starostin 1994). An historical account of scholarly thinking on Trans-Himalayan languages and their genetic relationships has been provided elsewhere (van Driem 2013).



Map 1: Geographical distribution of Trans-Himalayan languages

The neutral geographical name Trans-Himalayan obviates the terminological confusion which arises from some scholars using the term “Tibeto-Burman” in its original sense to denote the language family as a whole, whilst the Sino-Tibetanists use the term “Tibeto-Burman” to denote a non-existent taxon in their empirically unsupported family tree. More Trans-Himalayan languages are known today than were recognised in Klaproth’s day. Today 42 subgroups can be identified, as shown in the updated Fallen Leaves model in Diagram 3. Geographical distribution provides one

administration in Asia during the Napoleonic wars, but his hypothesis outlived him. In 1924, Indo-Chinese was renamed Sino-Tibetan by Jean Przyluski. By Przyluski’s time, Austroasiatic had been removed, but Sino-Tibetan then still comprised Sino-Daic, Tibeto-Burman and Hmong-Mien. This typologically and, in part, racially inspired theory played a large role in American academics after the Great Depression and in China after the Cultural Revolution (van Driem 2013).

key to unravelling ethnolinguistic phylogeography. The geographical centre of gravity on the basis of the distribution of major Trans-Himalayan subgroups is more indicative of the location of the linguistic homeland for the phylum than the modern distribution of speech communities.⁴

Vast swathes of what today is China are covered by Sinitic languages. Yet Manchuria was only sinicised after the Second World War, and much of southern China was only sinicised during the Qín dynasty beginning in the 3rd century BC. The global spread of English must be viewed in light of the fact that even an ancestral form of the language was not spoken on the British Isles until the fifth century AD. Viewed in terms of the distribution of other Trans-Himalayan subgroups, Sinitic represents a northeastward expansion toward the Yellow River basin. Tǔjiā and Báí most probably represent ethnolinguistic vestiges of the same ancient expansion. The internal phylogeny of Sinitic itself may also reflect this route of migration. The Cǎijiā 蔡家 language is spoken in the northwestern corner of Guizhōu province (Bó 2004). Zhèngzhāng (2010) considers Cǎijiā to be a member of the same subgroup as Báí, whereas Sagart believes that both Cǎijiā and the Wǎxiāng 瓦鄉 dialect of western Húnán could represent the first sub-branches of the Sinitic subgroup to have split off from Proto-Sinitic, even before the splitting off of the Mǐn dialects (de Sousa 2012).

The idea of an Altaic substrate influence on Sinitic, and on Mandarin in particular, has been in the air for quite some time, e.g. Poppe (1965), Ch'en (1976). In terms of its salient typological features, Mantarō Hashimoto (1976a, 1976b, 1980, 1986) argued that Sinitic could be thought of as an ancient Tibeto-Burman language which underwent pidginisation in the mouths of an Altaic population in the northeast. Hashimoto adopted William Ballard's (1979) metaphor, which depicts Sinitic as a mosaic of structural features representing a typological halfway house between Southeast and Northeast Asia. Some have responded critically, e.g. Li (1995), whereas others have received the idea favourably, e.g. Norman (1982), Wadley (1996).⁵ In terms of gross syntactic element order, Sinitic is not unique. Mru in the Chittagong and Karen in the Tenasserim are likewise not verb-final. Did Sinitic undergo an actual process of creolisation, or was the language just subject to successive phases of extreme contact influence over the millennia as a *lingua franca* shifting its centre periodically from one capital to another? Starostin (2008, posthumous) argued that the lexical items shared between Proto-Altaic and Proto-Sinitic, but not with other Tibeto-

⁴ The idea that the Tibeto-Burman homeland lay in the sub-Himalayan region was possibly first expressed by Peiros (1998:217).

⁵ Wadley disbelieves the existence of a Manchu-Mandarin pidgin during the Qīng dynasty (1644-1911), but he is receptive to Hashimoto's and Ballard's central thesis regarding profound substrate influence on the formation of Sinitic at a greater time depth.

Burman languages, indicated a not always friendly ancient contact situation which arose only after Sinitic had split off and migrated northeast to the lower Yellow River basin. Hashimoto's and Ballard's theory of Sinitic having arisen from a Tibeto-Burman creole has recently also been taken up by Comrie (2008) and DeLancey (2011).

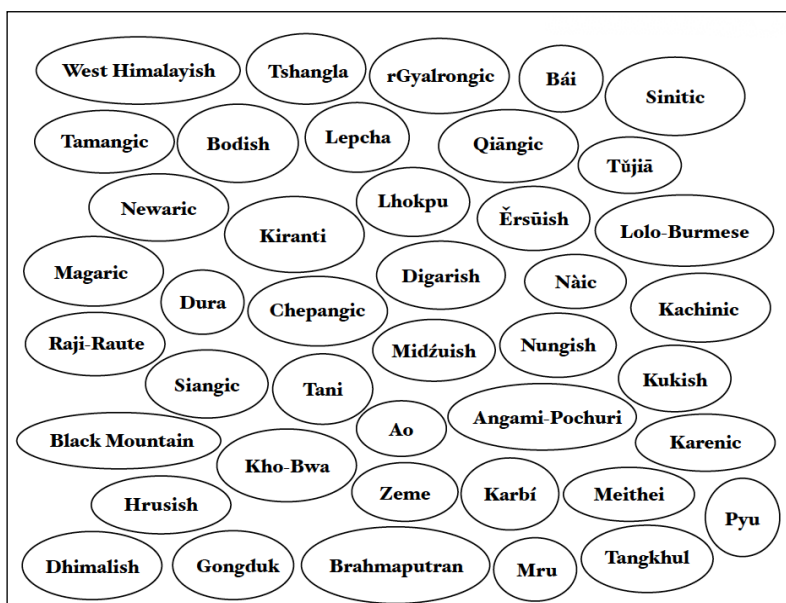


Diagram 3: Fallen Leaves. Thirty out of forty-two subgroups lie south of the Himalayan divide, seven to the north and east, and five (Tshangla, Bodish, Nungish, Lolo-Burmese and Kachinic) straddle both flanks of the Himalayas.

The ancient eastward expansion of Tibeto-Burman to the North China Plain is likely also to have brought the Trans-Himalayan group ancestral to Sinitic into contact with ancient Proto-Austronesians on the eastern seaboard.⁶ If ancient Hmong-Mien were once a predominant group in what today is southern China, then future linguistic research could evaluate the hypothesis of ancient language contact between Hmong-Mien and Kra-dai in the vast hybrid zone south of the Yangtze, where these two

⁶ I have suggested that Sagart's purported "Sino-Austronesian" correspondences, if not just representing chance resemblances, could be a residue of such an early contact between Austronesian and Sinitic in the Lóngshān interaction sphere in the fourth and third millennia BC (van Driem 1998, 2005).

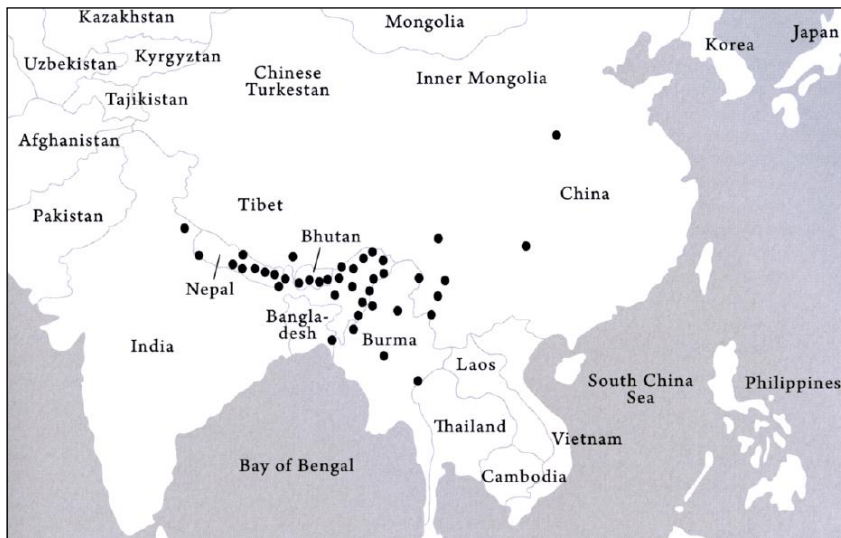
linguistically distinct sets of populations interacted. In a later epoch, a new episode of language contact arose between Tibeto-Burman and the ancient Hmong-Mien and Kra-dai when Sinitic expanded southward. Ballard (1979, 1984) argued that the Wú dialects arose from the expansion of Sinitic onto a Hmong-Mien substrate, and Haggège and Haudricourt (1978:163) proposed that Hakka likewise arose on a Hmong-Mien substrate and that Cantonese arose from the adoption of Sinitic by Kra-dai-speaking populations.

The Austronesian family is the geographically most widespread language phylum on the face of the planet, if we disregard the spread of Indo-European in the aftermath of European colonial expansion since Henry the Navigator. Linguistic, population genetic and archaeological evidence supports the theory that the linguistic homeland of modern Austronesian language communities (Map 3) lay on Formosa.⁷ The maritime expansion of Austronesian took place in spurts. The First Long Pause is a lull in the archaeological record, which suggests that there was little movement between 4300 and 3300 BC, before the agricultural colonisation of Taiwan began with the Dàpènkēng Neolithic. The colonisation of the Philippines was initiated ca. 2200 BC on the Batanes Islands and in northern Luzon (Bellwood and Dizon 2005). The Second Long Pause, from 1200 to 200 BC, is a lull between the Lapita colonisation of western Polynesia and the colonisation of eastern Polynesia.

As in the case of Trans-Himalayan and Austronesian, an assessment of the geographical distribution of other East Asian linguistic phyla such as Hmong-Mien (Map 4) and Kra-dai (Map 5) must likewise be informed by an historical linguistic understanding of these language families. The expansion of the Southwestern Tai languages into mainland Southeast Asia from the areas south of the Yangtze is an historically comparatively recent phenomenon. The expansion of Hmong-Mien groups into Southeast Asia constitutes an even more recent process. In the case of Austroasiatic (Map 6), the spread of Vietnamese southward along the mainland Southeast Asian littoral from Tonkin, where its closest linguistic relatives Mùròng, Maleng, Chút, Arem, Aheu, Krìi, Thỏ and Nguồn are still spoken, is also an historically comparatively recent phenomenon. Similarly, Khmer is believed to have spread at the expense of Pearic languages across the area that today is Cambodia during the Angkorian period and perhaps earlier. The deepest division within the Austroasiatic family lies between the Munda languages of India and the Khasi-Aslian

⁷ Lemaréchal (2010) gingerly challenges the currently prevalent theory that Formosa and the Formosan languages represent the cradle of Austronesian phylum. Peiros (2008) assails the Formosan homeland theory, claiming that Formosan subgroups collectively represent a single branch of Austronesian, and that the Austronesian *Urheimat* lay on the East Asian mainland, whence only one branch settled on Formosa.

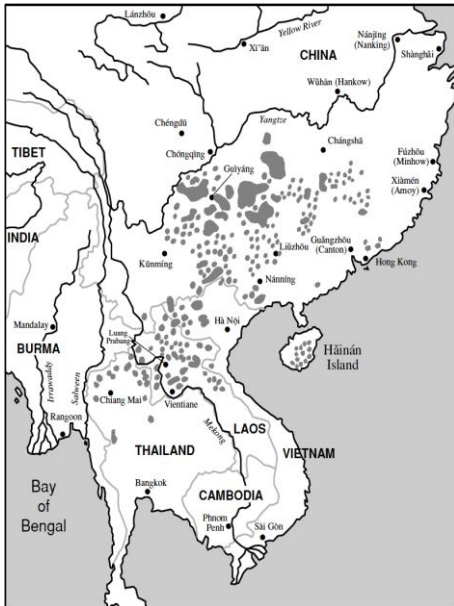
languages of Southeast Asia (Diffloth 2009). Within Khasi-Aslian, Mon-Khmer is coordinate with Khasi-Pakanic. Diffloth (2012) has presented evidence that Pearic is a sister clade of Khmuic within Khasi-Pakanic, and is not “une espèce de vieux khmèr”, as has sometimes been thought (Diagram 4). Pearic and Khmuic exclusively share the etymon *klɔŋ “cooked rice” and other features. Pearic represents the older population of most of what today is Cambodia.



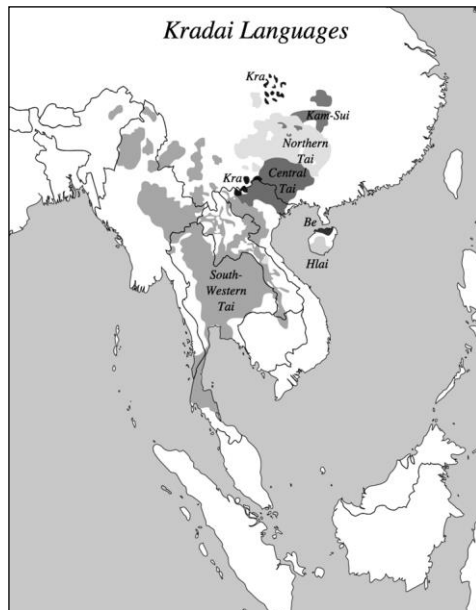
Map 2: Geographical distribution of the major Trans-Himalayan subgroups. Each dot represents not just one language, but the putative historical geographical centre of each of 42 major linguistic subgroups.



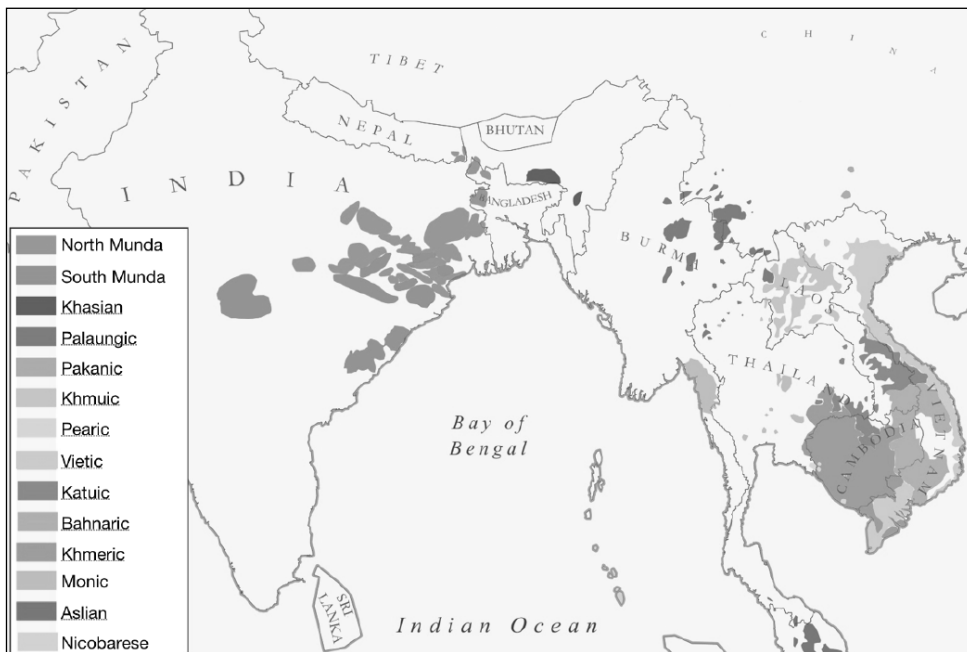
Map 3: Geographical distribution of Austronesian



Map 4: Geographical distribution of Hmong-Mien



Map 5: Geographical distribution of Kra-dai



Map 6: Geographical distribution of Austroasiatic

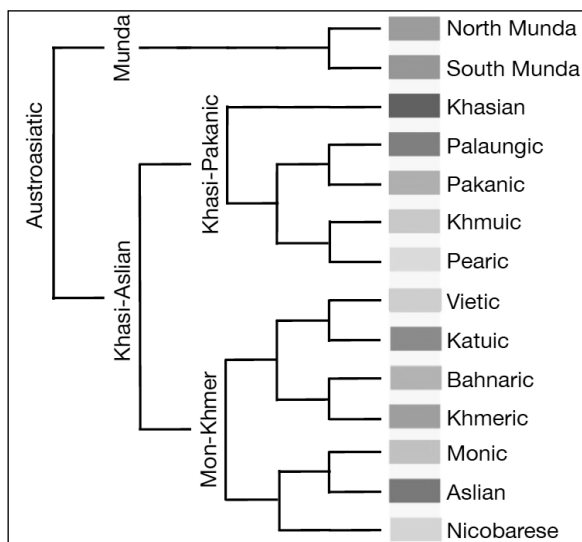


Diagram 4: Phylogeny of Austroasiatic (Diffloth 2009, 2012)

In the following sections, a new reconstruction of the prehistory of the East Asian phylum will be outlined on the basis of population genetic findings and other data and inferences about the past. Beforehand, for the sake of reference and in tribute to Starosta, his reconstruction will be briefly recapitulated, though it differs from the view which will be presented here. Starosta envisaged the Proto-East-Asian “linkage” or dialect continuum as having lain in the region laced by the Hàn, the Wèi and the central portion of the Yellow River in the period from 6500 to 6000 BC. He identified the Péilígǎng and Císhān Neolithic assemblages with East Asian, and he envisaged the linguistic ancestors of the Austronesians as the first group to have split off. He saw the Proto-Austronesians spreading to the coast and then down the eastern seaboard to establish the Hémǔdù and Dàwènkǒu Neolithic cultures of 5000 BC, ultimately to cross over to Formosa.

One migration from Formosa gave rise to the Malayo-Polynesian expansion into insular Southeast Asia, Oceania and parts of peninsular Southeast Asia, whereas another migration led back to the South China mainland, where it gave rise to Kradai or Daic.⁸ On the North China Plain, a second group, the “Yangtzeans”, split off and moved south and settle along the Yangtze, where they shifted from millet to rice agriculture. The Yangtzeans in turn later split up into the first Austroasiatic language communities, reflected in the Kūnmíng Neolithic of 4000 BC, and the Hmong-Mien, who appear in recorded history in what today is Húběi and northern Húnán as the Chǔ

⁸ See footnote 2.

polity (770-223 BC) which challenged the Eastern Zhōu. Finally, somewhere in the central Yellow River basin, a third descendant group of East Asian remained. This third family was Tibeto-Burman. In Starosta's conception, Tibeto-Burman split into Sino-Bodic, which he associated with the Yǎngsháo Neolithic of 5800 BC, and Himalayo-Burman, which he associated with the Dàdìwān Neolithic in Gānsù 6500 BC.

3. Father tongues and paternal ancestry

When studying the distribution of maternally inherited markers in the mitochondrial DNA and paternally inherited markers on the Y chromosome, 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 spoken and the most salient maternally inherited markers found in that speech community. This Father Tongue correlation was already described by Poloni *et al.* (1997, 2000) before the appearance of the seminal articles on Y chromosomal phylogeography by Underhill *et al.* (2000, 2001). The inference was made 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. It is reasonable to infer that some mechanisms of language change may be inherent to this pathway of transmission. Phylogenies of autosomal single nucleotide polymorphisms in whole genome studies are making headway (Li *et al.* 2008), but it is still too early to tell to what extent correlations of autosomal markers with language phyla will be identified that are as salient as the currently observed Father Tongue correlations.

There are a number of reasons why we might expect this outcome. Initial human colonisation of any 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. Theoretically, tribes of Amazons could have spread in a similar fashion. If so, then the tell-tale correspondences between mitochondrial lineages and the distribution of linguistic phyla would presumably have been detected by now, but correlations between maternal 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 correlations are observed worldwide.

The correlation of Niger-Congo languages with Y chromosomal haplogroups is a striking example (Wood *et al.* 2005). Likewise, the martial and male-biased historical spread of Hân Chinese during the sinification of southern China, recounted in detail in the Chinese chronicles, is just as faithfully reflected in the genetic evidence (Wen *et al.* 2004). A recent common ancestry between native Americans and indigenous Altaians is also based preponderantly on the shared Y chromosomal heritage and is not quite as well reflected in the mitochondrial lineages (Dulik *et al.* 2012). The saliency of Y chromosomal haplogroups in tribal and caste populations in India contrasts with the comparatively featureless nature and antiquity of the mitochondrial landscape (Thanseem *et al.* 2006, Thangaraj *et al.* 2006d). Previously, I have proposed that the subclades of the Y chromosomal haplogroup R (M207) are connected with the dispersal of the ancient Indo-Europeans, haplogroup O2a (M95) with the spread of Austroasiatic and O3a3c (M134) with Trans-Himalayan a.k.a. Tibeto-Burman (van Driem 2002, 2007, 2012b). Molecular genetic findings shed light both on ethnolinguistic prehistory and its unrecorded sociolinguistic dimensions, and often population geneticists find molecular corroboration of what linguists and ethnographers have been claiming for centuries. Yet correlations should not be confused with identity. The correlation of a particular genetic marker with the distribution of a certain language family should not be simplistically equated with populations speaking languages of a particular linguistic phylum.

Historical linguistics and human population genetics present two distinct windows on the past. The time depth accessible to historical linguistics is an order of magnitude shallower than the time depth accessible to genetics. Language families represent the maximal time depth accessible to historical linguists because the relatedness of languages belonging to a recognised linguistic phylum represents the limit of what can be demonstrated by the comparative method. This epistemological barrier represents the linguistic event horizon. Languages and genes are independent. Yet the probabilistic basis for possible correlations between the genetic markers and the language of a speech community lies in the fact that genes are invariably inherited by offspring from their parents, whereas languages are in most cases, but not invariably, inherited by offspring from either or both of their parents.

The potential skewing effects of natural selection, gene surfing, recurrent bottlenecks during range expansion and the sexually asymmetrical introgression of resident genes into incursive populations have been discussed elsewhere (van Driem 2012b). Factors such as ancient population structure and possible ancient Y chromosomal introgression could also affect inferences and interpretations based on

any single Y chromosomal locus when attempting to reconstruct migrations and elucidate the geographical origins of populations (Mendez *et al.* 2013). Even with all these caveats in place, we must be especially aware of all provisos and qualifications included in our inferences and working hypotheses when attempting to understand East Asian ethnolinguistic phylogeography. Yet, though paternal ancestry only represents a very small segment of our ancestry, emerging autosomal findings appear, at least in part, to corroborate the reconstruction presented here for meridional East Asia (Chaubey *et al.* 2010, Jinam *et al.* 2013).

Whilst father tongues may predominate globally, mother tongues certainly do exist in the sense that there are areas on the planet where the linguistic affinity of a community appears to correspond to the maternally transmitted mitochondrial lineage which the speakers share with other linguistically related communities. In this sense, in the north of today's Pakistan, the Balti speak a Tibetic mother tongue but profess a paternal religion that was first propagated in this area as early as the 8th century by men who came from the Near East, although the wholesale conversion of Baltistan to Islam is held to have begun only in the 14th century. The most prevalent mitochondrial DNA lineages amongst the Baltis are shared with other Tibetan communities, whereas the prevalent Y chromosomal haplogroups probably entered Baltistan during the introduction of Islam (Zerjal *et al.* 1997, Quintana-Murci *et al.* 2001, Qamar *et al.* 2002).⁹

At the same time, a disconnect is sometimes observed between a highly salient genetic marker and the linguistic affinity of a community's language. Hungarians lack the TatC deletion defining the Y chromosomal haplogroup N3 (Tat) notwithstanding the prevalence of this marker amongst Uralic language communities (Lì *et al.* 1999), suggesting that those who introduced the Hungarian language to Pannonia left no prominent genetic signature. This lineage died out, or a resident population adopted the language of newcomers without undergoing a replacement of their paternal lineages. In fact, the ancestrally preponderant Hungarian paternal lineage may already have been lost or greatly diluted by the time that the Hungarians reached Pannonia, for the case of the Hungarian language is geographically analogous to that of Ossetian. Hungarian forms the easternmost Uralic clade together with the closely related languages Khanti and Mansi, formerly known as Ostyak and Vogul. Yet in terms of its geographical position Hungarian is the most southwestern Uralic language, just as

⁹ Has female irony on the part of generations of Balti mothers been preserved in the Balti practice of calling their language བཤམ་ཅེ་ *phaskat* “father tongue” (Roland Bielemeier, personal communication, 10 September 2012), their homeland བཤམ་ཅེ་ལྗོངས་ *phayul* “father-realm” and their birthplace བཤམ་ཅེ་ལྗོངས་ *phasa* “fatherland” (Sprigg 2002:127)?

Ossetian, the westernmost Iranian language, is phylogenetically a member of the Eastern Iranian subgroup.

Such cases underscore the fact that the linguistic ancestors of a language community are not precisely the same set of people as the biological ancestors of that community. Moreover, the wave of anatomically modern humans who introduced the proto-languages that were later to give rise to today's Asian linguistic phyla and language isolates can be dated to between 25,000 to 38,000 years ago (Rasmussen *et al.* 2011). The antiquity of Y chromosomal haplogroups such as O1 or O2 has been estimated to be greater than 10,000 years old (Yan *et al.* 2011). Yet historical linguists generally estimate the linguistically reconstructible past to be shallower than 10,000 years, and this temporal gap must temper and inform all speculations regarding correlations between linguistic and genetic affinity.

4. Beyond the linguistic event horizon

Early human populations outside of Africa no doubt must have interacted with each other in parapatric or sympatric modes at various junctures in their long prehistory. There were numerous waves, and the genetic evidence is compatible with sustained and multiple migrations out of Africa through the Levant over time. Evidence has been adduced of gene flow from the now extinct Denisovans into the ancestors of the people who ultimately settled Melanesia (Reich *et al.* 2010), and Neanderthals evidently introduced a minor paternal contribution into the ancestors of all non-Africans at the time that these populations had emerged from Africa but before Eurasian groups had diverged from each other, whilst modern humans have retained no Neanderthal maternal lineages (Green *et al.* 2010, Rasmussen *et al.* 2011, Currat and Excoffier 2011). Despite this paternal contribution, it has been suggested that our Cro-Magnon ancestors may have outcompeted the Neanderthals because of a more finely honed language aptitude, or because religious belief systems and a wrathful God may have made Cro-Magnon the more hostile adversary (van Driem 2001).

All Australian Y chromosomal lineages belong to either haplogroups C and F, both of which left Africa between 75,000 to 62,000 years ago. All Australian mitochondrial DNA lineages fall within the founder branches M and N. A study of M42 coding region sequences in the mitochondrial lineage of Indian and Australian aboriginal populations supported the colonisation of Australia via a southern littoral route at this time depth (Kumar *et al.* 2007, Hudjashov *et al.* 2007, Stanyon *et al.* 2009, Rasmussen *et al.* 2011). Australian maternal lineages are most closely related to those of New Guinea and Melanesia and reflect the same Palaeolithic colonisation event some 50,000 years ago. It comes as no surprise that the deep branching of both the

maternal and the paternal lineages of Australian populations vis-à-vis other populations around the Indian Ocean shows long-term isolation after initial settlement. Genomic evidence has also been detected for some secondary gene flow at the time of the Sahul land bridge between New Guinea and Australia some 8,000 years ago. Huxley (1870) once proposed a link between populations of India and the “Australoid type”. However, the impressionism of early physical anthropology based on the phenotypical observations contrasts somewhat with the lack of uniquely shared haplogroups between India and Australia. Does the linguistic picture record for us where the maritime migration of the first Australians made landfall? Seven-eighths of the continent is covered by Pama-Nyungan languages, whilst the northwestern region of Australia shows a diversity of language families.

The set of ancestral Y chromosomal haplogroups CT (M168) encompasses a myriad of modern paternal lineages which first emerged from Africa in Palaeolithic times, first branching into the paternal lineages DE (YAP) and CF (P143). The paternal lineage DE (YAP) split into haplogroups D and E. The paternal lineage D may have originated in the Himalayan region, where this haplogroup is still represented in the highest diversity, particularly in Nepal and Tibet. This paternal lineage migrated southward to the Andamans and eastward from the eastern Himalayas across the Tibetan plateau through what today is southern China, giving rise to the offspring clades D1 (M15), D2 (M55) and D3 (P47), and ultimately reaching the Japanese archipelago, where this paternal lineage is represented by the D2 (M55) subclade (Xue *et al.* 2006, Shi *et al.* 2008). The mtDNA clades M31 and M32, specific to the Andaman Islands, also suggest a rapid Pleistocene dispersal along the Indian littoral with maritime expansion to the Andamans (Thangaraj *et al.* 2005, 2006b, 2006c, Tamang and Thangaraj 2012). By contrast, the fraternal clade E remained principally in Africa, though this lineage also occurs at a very low frequency in western Eurasia as far as east as India and Central Asia.¹⁰

The other early Out of Africa lineage CF (P143) gave rise to Y chromosomal haplogroup C (RPS4Y711) and a myriad of other haplogroups characterised by the shared innovation M89, i.e. the paternal lineages F through T. The paternal lineage C first entered the Indian subcontinent, where the lineage C5 (M356) may have branched off. The spread of the paternal lineage C may to some extent have moved in tandem with the spread of the paternal lineage D. Ancient populations bearing the Y chromosomal haplogroup C colonised Australia and New Guinea, where the lineages C2 (M38), C4 (P309, M347) and C6 (P55) are found, and moved into northeast Asia and the Americas, where the lineages C1 (P122) and C3 (P44, M217) are found. Both

¹⁰ Such ancient African signatures must be distinguished from recent small migrations from Africa to the Indian subcontinent, such as the case of the Siddis (Shah *et al.* 2011).

the paternal haplogroups C (RPS4Y711) and D (M174) represent paternal lineages which colonised East Asia before the Ice Age, which lasted from 21,000 to 18,000 years ago. These ancient populations underwent a Palaeolithic expansion between 34,000 and 22,000 years ago and are therefore believed to have exploited the megafauna of Siberia and East Asia as a food source.

At a later time depth, but still in a time inaccessible to historical linguistics, the first anatomically modern humans to populate Japan bore the mitochondrial haplogroup R30 and the Y chromosomal haplogroup D2 to the archipelago. The paternal subclade D2 is specific to Japan, but immediately related to this clade are the ancient D lineages preserved on the Andaman Islands and in the Himalayan region. The highest frequency of D is retained in Japan amongst the Ainu and the Ryūkyūan populations (Hammer *et al.* 2006), and this paternal lineage accounts for over a third of Japanese paternal lineages. Both the mitochondrial lineage R30 and the Y chromosomal haplogroup D2 indicate that this first wave of peopling of Japan originated in the Indian subcontinent at a time depth of perhaps 25,000 years ago. The paternal haplogroup C is represented as a minor lineage in Japan in a frequency of over 8%. These ancient lineages appear to represent the first wave of peopling of Japan, and the culture of their bearers later surfaced in the archaeological record from the tenth millennium BC onward as the mesolithic Jōmon. The Jōmon people were adept ancient potters who subsisted on hunting and coastal foraging and may have practised rudimentary forms of plant husbandry. The Ainu language probably represents a linguistic legacy of the original Jōmon population. The paternal lineages C and D, representing vestiges of this early wave of Palaeolithic hunter-gatherers, have also been preserved on the Korean peninsula (Jin *et al.* 2009)

The distinct waves of peopling reaching Japan are equally reflected in the maternal lineages. Mitochondrial haplogroup M7 characteristically has a southern distribution in East Asia, especially in the Yellow Sea littoral. Its daughter groups M7a and M7b2, specific to Japanese and Korean populations, attest to an ancient contribution to the modern Japanese mitochondrial DNA pool. The estimated coalescence times for the subclades M7a, M7b and M7c range between 6,000 and 18,000 years. This date suggests either that these star-like clades reflect a resettlement process around the Sea of Japan from the south after the Last Glacial Maximum, contemporary with the spread of microblades of the Suyanggae type before the onset of the Jōmon culture, or that M7a and M7b entered Japan during initial settlement over 30,000 years ago and underwent a genetic bottleneck at the time of the Last Glacial Maximum. By contrast, the mitochondrial haplogroups A5, B5, C, F1a, N9a and Z, which are shared between Koreans and Japanese and virtually absent in Ryūkyūans and in the Ainu, testify to later migrations through the Korean peninsula to Japan,

probably during the Yayoi agricultural intrusion 2,300 years ago. The presence of the mitochondrial lineage Y1 amongst the Ainu testifies to the migration of Siberian populations to the Japanese archipelago from the north (Kivisild *et al.* 2002, Tanaka *et al.* 2004).

5. Bottlenecks and refugia

The many paternal lineages from haplogroup F to T, which share the innovation M89, contain subclades whose time of divergence begins to come closer to the linguistically reconstructible past. Whilst the linguistic event horizon is an epistemological boundary beyond which historical linguistics by the comparative method is not equipped to venture, the discrete linguistic phyla recognised by linguists could themselves represent the result of bottlenecks in linguistic prehistory. Not only were Palaeolithic human populations small in size, but the effective population size of any new paternal clade must have been smaller yet. Related and relevant to the phenomenon of bottlenecks, whether linguistic or genetic, is the phenomenon of Ice Age refugia. Perhaps the earliest attestation of the term “refugium” used in the sense of an isolated non-glacial habitat during the Ice Age was by Canadian palynologist Heusser (1955).

Recent phylogeographic studies (Stewart and Stringer 2012, Parducci *et al.* 2012) suggest that southern Tibet and the southeastern Himalayas could have harboured refuge areas for various organisms during the Last Glacial Maximum. Recent genetic studies on endemic species show that the prevalence of private haplotypes restricted to single populations could not all have evolved locally in just 14,000 years. Rather, the observed genetic diversity appears to reflect the fragmentation of once more widespread haplotypes before their isolation in refugia on the Tibetan plateau and in the Himalayas during the Last Glacial Maximum. Studies of private haplotypes of scattered juniper groves (Opgenoorth *et al.* 2010) and endemic edaphous beetles (Schmidt *et al.* 2011) as proxies for assessing moderately lower summer temperatures during the Last Glacial Maximum in southern Tibet are corroborated by studies involving endemic flowering plants of the alpine steppe (Miehe *et al.* 2009, 2012), the Tibetan plateau pika (Ci *et al.* 2009), yaks (Qi *et al.* 2008) and monkshood (Wang *et al.* 2009). Barley genotyping suggests that the Tibetan plateau may even represent the site of an alpine domestication of barley, involving the selective breeding for endurance to cold and drought and independent of the domestication which took place in the Fertile Crescent (Dai *et al.* 2012).

The geological and palaeontological evidence suggests that the Tibetan plateau might not yet have been entirely in the rain shadow at the time that anatomically

modern humans spread across Asia, whilst the Kathmandu valley was a large palaeolake amidst verdant mountains 32,000 years ago until as recently as 15,000 years ago. The Himalayan region may very well have harboured suitable habitats for our hunter-gatherer ancestors. It has long been proposed that populations adapted to high altitude environments may not have suffered the diseases and parasites endemic to the jungles of the balmy plains (McNeill 1976). Epidemiology may to a large extent have determined which ancient migrations were able to leave traces in today's genome and which did not. The ecological barrier between the highlands of the eastern Himalayan region and the lowlands of the Gangetic and Brahmaputran plains must have played a role in shaping population prehistory and thus the human environment.

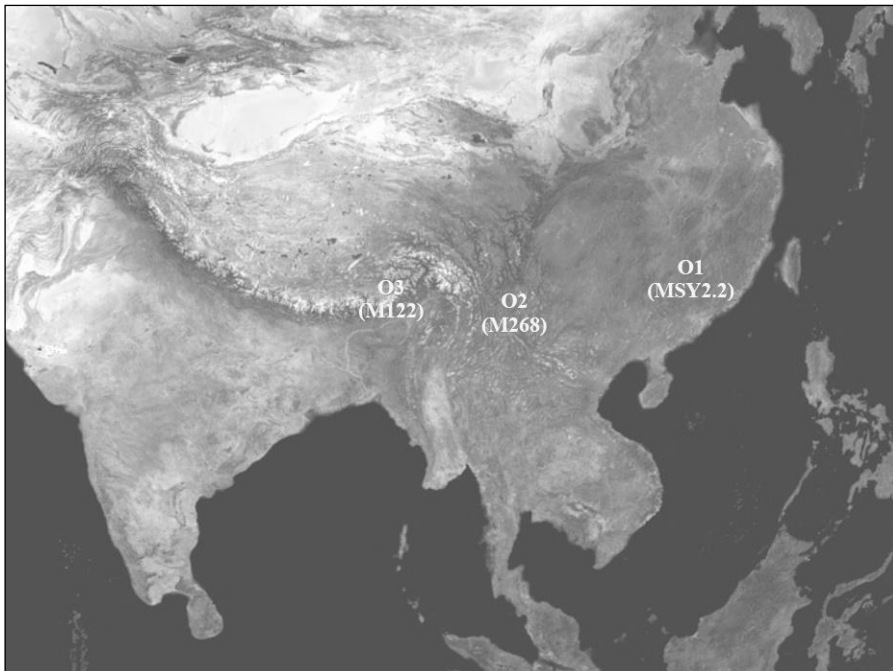
Today's limited palaeontological survey data already clearly indicate that populations of hunter-gatherers were present on the Tibetan plateau in Palaeolithic times even though the Palaeolithic of this region is still virtually unknown (Madsen *et al.* 2006, Brantingham *et al.* 2007). Genetic adaptations to the cold and to high altitude in populations of the Tibetan plateau are of a physiological sophistication suggestive of a long gradual evolution (Zhao *et al.* 2009, Yi *et al.* 2010, Xu *et al.* 2011, Wang *et al.* 2011, Peng *et al.* 2011, Qi *et al.* 2013). At the same time, the ancient paternal lineage D, which is widespread in Tibet and throughout the central and eastern Himalayas attests to an ancient wave of peopling which passed through the Himalayan corridor (Qian 2000). These findings have been construed as support for the existence of cryptic refugia at high elevations during the Last Glacial Maximum.

6. The population genetics of East Asian language families

The two paternal lineages N and O may have split up in the greater eastern Himalayan region. The highest frequency of the ancestral N* (M231) is still found in northern Burma, Yúnnán and Sichuān, whilst the brother clade O appears to be a marker for the linguistic ancestors of the hypothetical East Asian linguistic phylum, comprising Kradai, Austronesian, Tibeto-Burman, Hmong-Mien and Austroasiatic. The evidence for refugia in southeastern Tibet suggests a possible putative point of origin for the expansion of the paternal lineage O. Whilst it remains a matter of speculation at this point whether or not the Tibetan plateau could have harboured refugia hospitable to human habitation during the Last Glacial Maximum, the entire southeastern and eastern declivity of High Asia furnishes numerous possible points of origin for paternal haplogroup O. Populations bearing the Y chromosomal O haplogroups colonised southeastern Eurasia, probably beginning from a locus in the eastern Himalayas. Xue *et al.* (2006) speculate that the population expansion involved feeding on tubers as the climate warmed, but the early domestication of crops no doubt

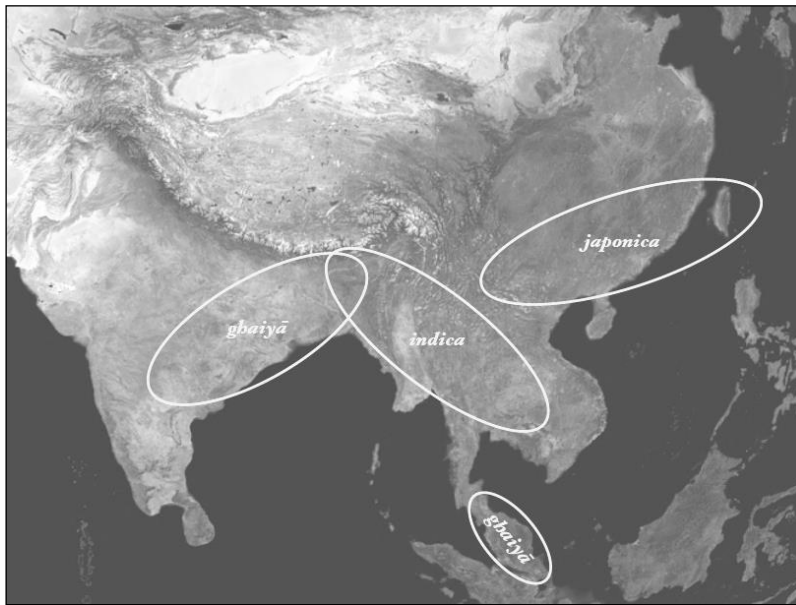
played a role for some subset of these ancient populations.

As temperature and humidity increased after the Last Glacial Maximum, the Y chromosomal haplogroup O (M175) split up into the subclades O1 (M119), O2 (M268) and O3 (M122). The three subclades can be putatively assigned to three geographical loci along an east-west axis for the sake of argument and without any claim to geographical precision. Whereas the haplogroup O1 (M119) moved to the drainage of the Pearl River and its tributaries in what today is Guǎngdōng, the bearers of haplogroup O2 (M268) moved to southern Yúnnán, whilst bearers of the O3 (M122) haplogroup remained in the southeastern Himalayas, expanding their range initially only into adjacent parts of northeastern India and northern Burma (Map 7). The O2 (M268) clade split into O2a (M95) and O2b (M176), an event which took place just before the linguistic event horizon.

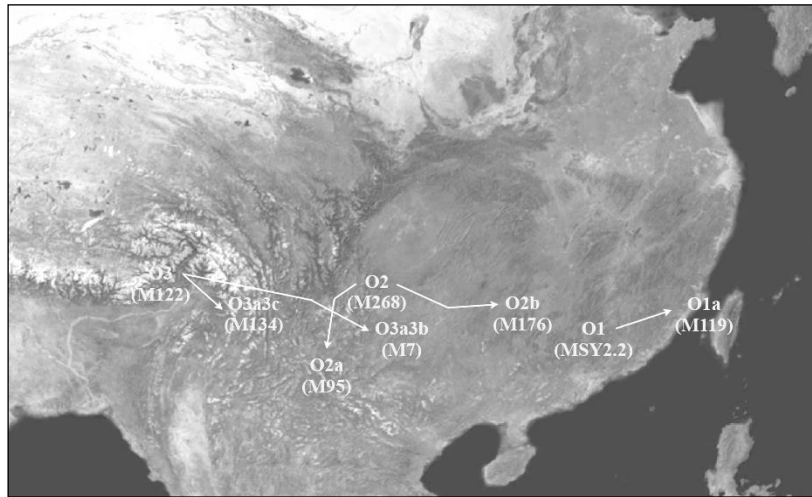


Map 7: After the Last Glacial Maximum, the Y chromosomal haplogroup O (M175) split into the subclades O1 (M119), O2 (M268) and O3 (M122). Bearers of the O2 (M268) paternal lineage domesticated Asian rice.

Asian rice, perhaps both *japonica* and *indica* rice, may have first been domesticated roughly in the area hypothetically imputed to O2 (M268), which would have included southern Yúnnán (van Driem 2011a, 2012a) (Map 8). The bearers of the subclade O2a (M95) became the *Stammväter* of the Austroasiatics (van Driem 2007, Chaubey *et al.* 2010). The Austroasiatics spread from this locus initially to the Salween drainage in northeastern Burma and to the area that today is northern Thailand and western Laos. In time, the Austroasiatics would spread as far as the Mekong delta, the Malay peninsula, the Nicobars and later even into eastern India, where they would introduce both their language and their paternal lineage to indigenous peoples of the subcontinent (Map 9). Despite its prevalence in Munda populations, the topology of haplogroup O2a does not support a South Asian origin for this paternal lineage (Kumar *et al.* 2007, Chaubey 2010, Chaubey *et al.* 2010). Again the mitochondrial background is of greater antiquity, and the paternal lineage appears to be the signature for the spread of the language phylum and its adoption by resident populations (Thangaraj *et al.* 2006a, Kumar *et al.* 2006)



Map 8: Geographical ranges for the possible domestication of *ghaiyā* or upland rice, *indica* rice and the *japonica* cultivar, based on the geographical distribution of genetic markers in the wild precursor *Oryza rufipogon* (based on Londo *et al.* 2006)



Map 9: Paternal lineages branching into new subclades. Each event involved a linguistic bottleneck leading to language families that today are reconstructible as distinct linguistic phyla. The O1 (MSY2.2) lineage in the the Pearl River drainage gave rise to the O1a (M119) subclade, which moved eastward to the Fújiàn hill tracts and across the strait to Formosa, which so became the *Urheimat* of the Austronesians. Bearers of O3a3b (M7) became the Proto-Hmong-Mien, who migrated eastward to areas south of the Yangtze. On their way, they adopted rice agriculture from the ancient Austroasiatics. In the eastern spurs of the Himalayas, the bearers of haplogroup O3a3c (M134) expanded and became the Trans-Himalayans. Haplogroup O2a (M95) is the Proto-Austroasiatic paternal lineage. The para-Austroasiatic fraternal clade O2b (M176) spread eastward, sowing seed along the way and leaving behind an old toponym for the Yangtze, later borrowed by Old Chinese as 江 *kʰroŋ.

Since we have associated the paternal lineage O2a (M95), which is a derivative clade of haplogroup O2 (M268), with the Austroasiatic language phylum, we might conjecture that Asian rice, perhaps both *japonica* and *indica* rice, was first domesticated roughly in the general area hypothetically imputed to O2 (M268) here.¹¹

¹¹ Ferlus (1996) proposed that one of the prominent Proto-Austroasiatic etyma for rice originally denoted taro, but this argument is refuted by Diffloth (2011), who shows that the two cultigens are reconstructible to separate roots which have been consistently distinguished throughout linguistically reconstructible Austroasiatic prehistory. The domestication of taro (Rao *et al.* 2010) is as important to understanding Austroasiatic prehistory as rice. Despite attempts by Bradley (2012), Blench's (2009) claim still holds true

Whilst the bearers of the O2a (M95) haplogroup became the *Stammväter* of the Austroasiatics, the other derivative paternal subclade O2b (M176) spread eastward, where they introduced rice agriculture to the areas south of the Yangtze. Though the bearers of the O2b (M176) haplogroup continued to sow seed as they continued to move ever further eastward, they left little or no linguistic traces, except maybe an Austroasiatic name for the Yangtze river, as proposed by Pulleyblank (1983), reflected as the toponym borrowed by Old Chinese as 江 *k^hroŋ (modern Mandarin: *jiāng*). This para-Austroasiatic paternal lineage moved as far as the Korean peninsula and represents the second wave of peopling attested in the Japanese genome (Jin *et al.* 2009, Karafet *et al.* 2009b). Whereas the maternal lineage represented by mitochondrial subclade D4 points toward an immediate provenance on the East Asian mainland, the Y chromosomal haplogroup tells this more specific story.

We can identify the O2b (M176) lineage with the Yayoi people, who introduced rice agriculture to Japan, perhaps as early as the second millennium BC, during the final phase of the Jōmon period (Tanaka *et al.* 2004, Hammer *et al.* 2006). The Yayoi appear also to have introduced other crops of continental inspiration to the Japanese archipelago such as millet, wheat and melons. Along the way followed by their ancestors northward toward the Korean peninsula, the earliest attested domestic millet dates from before 6000 BC at 興隆溝 Xīnglōnggōu near 赤峰 Chífēng, where a Neolithic culture without sickles has been described (Zhào 2005). The gracile Yayoi immigrants soon outnumbered the more robust and less populous Jōmon, who had been the first anatomically modern humans to populate Japan. The presence of Y chromosomal haplogroup O2b and other O haplogroups in Japan is more recent, but accounts for more than half of all Japanese paternal lineages, with their highest frequencies in Kyūshū. The Y chromosomal haplogroup N is present only as a marginal paternal clade in Japan. If we assume that the paternal lineage N represents a marker for Altaic, then this vestige may be the tenuous genetic trace of the population who once bore an Altaic language to the Japanese archipelago which eventually evolved into modern Japanese.

At the dawn of the Holocene in the southeastern Himalayas and the eastern declivity of the Tibetan plateau, haplogroup O3 (M122) gave rise to the ancestral Trans-Himalayan or Tibeto-Burman paternal lineage O3a3c (M134) and the original Hmong-Mien paternal lineage O3a3b (M7). The bearers of the polymorphism O3a3c (M134) stayed behind in the area comprising northeastern India, southeastern Tibet and northern Burma, whilst the bearers of the O3a3b (M7) lineage migrated eastward

that no rice agricultural terminology can be confidently reconstructed for Tibeto-Burman. As has long widely been presumed, the ancient Tibeto-Burmans probably first cultivated not rice, but foxtail millet *Setaria italica* and broomcorn millet *Panicum mileaceum*.

to settle in the areas south of the Yangtze. On their way, the early Hmong-Mien encountered the ancient Austroasiatics, from whom they adopted rice agriculture. The intimate interaction between ancient Austroasiatics and the early Hmong-Mien not only involved the sharing of knowledge about rice agriculture technology, but also left a genetic trace in the high frequencies of haplogroup O2a (M95) in today's Hmong-Mien and of haplogroup O3a3b (M7) in today's Austroasiatic populations.

On the basis of these Y chromosomal haplogroup frequencies, Cai *et al.* (2011:8) observed that Austroasiatics and Hmong-Mien “are closely related genetically” and ventured to speculate about “a Mon-Khmer origin of Hmong-Mien populations”. It would be more precise to infer that the incidence of haplogroup O3a3b (M7) in Austroasiatic language communities of Southeast Asia indicates a significant Hmong-Mien paternal contribution to the early Austroasiatic populations whose descendants settled in Southeast Asia, whereas the incidence of haplogroup O3a3b (M7) in Austroasiatic communities of the Indian subcontinent is undetectably low. On the other hand, the incidence of Y chromosomal haplogroup O2a amongst the Hmong-Mien appears to indicate a slightly more modest Austroasiatic paternal contribution to Hmong-Mien populations than vice versa.

As the Hmong-Mien moved eastward, the bearers of haplogroup O2b (M176) likewise continued to move east. Even further east, the O1 (M119) paternal lineage gave rise to the O1a (M119) subclade, which moved from the Pearl River drainage eastward to the Min river drainage in the hill tracts of Fújiàn and across the strait to Formosa, which consequently became the *Urheimat* of the Austronesians (cf. Abdulla *et al.* 2009). Back west in the eastern Himalayas, the bearers of Y chromosomal haplogroup O3a3c (M134) expanded eastward into Sichuān and Yúnnán, north and northwest across the Tibetan plateau as well as westward into the Himalayas and southward into the Indo-Burmese borderlands. In the west and south, the early Tibeto-Burmans encountered Austroasiatics, who had preceded them.

If we assume a linguistic dispersal in which languages were spread by populations in which a particular paternal lineage was dominant, as outlined in the scenario above, then the Malayo-Polynesian expansion via the Philippines into insular Southeast Asia must have entailed the introduction of Austronesian by bearers of the Y chromosomal haplogroup O1a (M119) to resident communities, in which an originally Austroasiatic paternal lineage O2a (M95) was and would remain dominant even after linguistic assimilation, and other older paternal lineages also persisted (Karafet *et al.* 2005, Li *et al.* 2008). Similarly, Malagasy is linguistically clearly Austronesian, but genetically the Malagasy trace both their maternal and paternal ancestries equally to Borneo and to the African mainland (Hurles *et al.* 2005).

The ancestral Trans-Himalayan or Tibeto-Burman paternal lineage O3a3c (M134)

spread from the eastern Himalayas in a northeasterly direction across East Asia to the North China plain. Subsequently, at a far shallower time depth, the Tibeto-Burman paternal lineage O3a3c (M134) spread from the Yellow River basin into what today is southern China, beginning with the Hàn expansion southward during the Qín dynasty in the third century BC. The ancestral Tibeto-Burman paternal lineage O3a3c (M134) is intrusively present in the Korean peninsula and beyond, although Uralo-Siberian populations such as the Evenki of course predominantly bear the paternal lineage N. The distribution map of major Trans-Himalayan linguistic subgroups shows the centre of linguistic phylogenetic diversity to be rooted squarely in the eastern Himalayas, with outliers trailing off towards the loess plains of the Yellow River basin in the northeast. This geographical projection of Trans-Himalayan linguistic diversity appears to reflect the spread of the paternal O3a3c (M134) lineage putatively associated with this linguistic dispersal.

Correlations between linguistic, archaeology and genetics must inform a chronologically layered view of ethnolinguistic prehistory (Bellwood *et al.* 2011, van Driem 2011b). Any attempt to span great stretches of time must distinguish numerous chronological layers. The post-glacial movements to the north and east that gave rise to the Trans-Himalayan, Austroasiatic, Hmong-Mien and Austronesian linguistic phyla took place long before the northeasterly spread of ancient Tibeto-Burmans to the putative early locus of Sino-Bodic. A distinct process was the incremental spread of diverse ancient Trans-Himalayan groups throughout the Himalayas, where linguistic and genetic evidence indicates the presence of pre-Tibeto-Burman populations. More recent than this was the southward spread of Sino-Bodic that brought Sino-Bodic groups into contact with the ancient Hmong-Mien, early Austroasiatics, Austronesians and with other Tibeto-Burman groups. More recent yet was the Bodic spread across the Tibetan plateau spilling over into the Himalayas, as evinced by the distribution of Bodish, East Bodish, Tamangic, West Himalayish and several other groups. The spread of Tibeto-Burman groups from Yúnnán into Southeast Asia, e.g. Karen, Pyu and later Lolo-Burmese, constitutes such a recent episode that parts of these movements are historically attested. Also historically documented is the Hàn spread, well reflected in linguistics and genetics, which assimilated both other Tibeto-Burman communities as well as non-Tibeto-Burman groups. The historically documented spread of Tibetic (i.e. Bodish) across the Tibetan plateau is even more recent.

The relative frequencies of the Y chromosomal haplogroup O2a (M95) in various Tibeto-Burman populations of the Indian subcontinent (Sahoo *et al.* 2006, Reddy *et al.* 2007) suggest that a subset of the paternal ancestors of particular Tibeto-Burman populations in northeastern India, e.g. certain Bodo-Koch communities, may originally have been Austroasiatic speakers who married into Tibeto-Burman communities or

were linguistically assimilated by ancient Tibeto-Burmans. At the same time, median-joining network analyses of haplogroup O2a (M95) microsatellites have suggested a division in the Indian subcontinent between Tibeto-Burmans vs. Austroasiatic and Dravidian language communities. Austroasiatics and Dravidians show greater Y chromosomal microsatellite diversification than Tibeto-Burman language communities, and the highest frequency of the O2a haplogroup is found in tribal populations in Orissa, Chattisgarh and Jharkhand (Sengupta *et al.* 2006).

At a shallower time depth, ancient mitochondrial DNA recovered in northeastern Thailand at the Bronze Age site Noen U-loke, dating from 1500 BC to 500 AD, and the Iron Age site Ban Lum-Khao, dating from 1200 to 400 BC, shows the closest affinity to the Chao-Bon, a modern Austroasiatic population who speak the Monic language Nyahkur. The Chao-Bon are directly descendant from the Mon of the Dvārāvati kingdom, which from the 7th to the 13th century extended from the Andaman Sea near present-day Mergui in the southern Tenasserim in the west to the alluvial plains of what today is central Thailand in the east. By contrast, the majority Thai of modern Thailand show the greatest autosomal affinity with Kradai language communities of southern China and with the Southern Chinese Hàn population, whilst the mitochondrial lineages of the Khmer show greater affinity with today's national majority Thai than do other Austroasiatic groups (Lertrit *et al.* 2008, Abdulla *et al.* 2009). At the same time, the Y chromosomal haplogroup frequencies of Hàn Píngguà dialect speakers in Guǎngxī province in a dendrogram clustering are shown to be intermediate between Hmong-Mien, Austroasiatic and Kradai language communities on one hand and Austronesian populations on the other (Wen *et al.* 2004, Gan *et al.* 2008). These findings dovetail with the late historical expansion of the Thai from southern China into Southeast Asia in the first part of the second millennium as well as with their subsequent subjugation by the Khmer.

7. Other Asian language families and models of migration

Human genetic studies suggest that the paternal lineages N and O may have split in East Asia between 30,000 and 20,000 years ago. The spatial dynamics of the two haplogroups diverged greatly after the split, and the ancient Asian populations which bore the Y chromosomal haplogroups N and O are calculated to have undergone an effective expansion between 18,000 and 12,000 years ago (Xue *et al.* 2006). Ancient bearers of the N haplogroup moved north from East Asia after the Last Glacial Maximum and, in a grand counterclockwise sweep, migrated across northern Eurasia as far as west as Lapland (Rootsi *et al.* 2007, Derenko *et al.* 2007, Mirabal *et al.* 2009). The Y chromosomal haplogroup N appears to be a marker for the linguistic ancestors

of Fortescue's Uralo-Siberian linguistic phylum, comprising Uralic, Yukagir, Eskimo-Aleut, Nivkh and Chukotko-Kamchatkan.

The absence of haplogroup N in the Americas and its prevalence throughout Siberia allow us to infer that the spread of the paternal lineage N northward must have taken place after the paternal founder lineages had already established themselves in the Americas (Rootsi *et al.* 2007, Fu *et al.* 2013). We may therefore imagine that the Greater Yeniseian paternal haplogroup Q must have expanded across Siberia and by way of Beringia colonised the Americas, where it became the predominant paternal lineage, before the Hyperborean intrusion of Y chromosomal N lineages replaced it in the sparsely populated north. The N (M231) lineages differentiated into N*, N1 (M128), N2 (P43) and N3 (Tat). The most prevalent haplogroup N3 (Tat) is widespread throughout the Uralo-Siberian area, spreading as far west as Scandinavia. The ancestral N* (M231) is still found in the highest frequency in the area encompassing northern Burma, Yúnnán and Sichuán, with N1 (M128) particularly frequent in the Altai region and to a lesser extent in Manchuria, and N2 (P43) showing an especially high frequency on both the Yamal and Tamyр peninsulas in northern Siberia.¹²

Previously I proposed that haplogroup Q, an offspring clade of Y chromosomal haplogroup P, could be a marker for the Greater Yeniseian linguistic phylum (van Driem 2008). A migration route from Central Asia across Beringia to the Americas is suggested by the phylogeny of the Y chromosomal haplogroup Q (M242). The ancestral paternal lineage of the Americans is still found in high frequency in the Yeniseians, and the movement across Siberia to Beringia must have taken place before the Y chromosomal haplogroup N moved north. The Y chromosomal haplogroup Q (M242) established itself as the predominant paternal lineage of the Americas, most probably in a single migration process, with the bottleneck of geography conditioning the resultant genetic bottleneck. The Q1a3a1 (M3) mutation specific to the Americas only arose after the initial colonisation of the New World and, as populations moved south, this new lineage overwhelmingly came to replace the ancestral lineages Q1a (MEH2) and Q1b (L275), which are still most prevalent in Central Asia and northeastern Siberia. The coalescence times for the haplogroups in question is compatible with conventional archaeological wisdom that the Americas

¹² Evidently inspired by the story of the Y chromosomal haplogroup N, Gão (2008, 2012) has sought to find a link between Sinitic and Uralic. This hypothesis suffers from some of the same difficulties as Sino-Austronesian. Could reconstructible linguistic vestiges have possibly ever survived in Sinitic and Uralic from a time beyond Uralo-Siberian and East Asian, or could linguistic contact influence of such hoary antiquity ever be plausibly demonstrated?

were uninhabited before the Clovis culture, and that men bearing the paternal lineage Q (M242) were also the bearers of the first Clovis projectile points into the heart of North America (Zegura *et al.* 2003, Seielstad *et al.* 2003, Schnurr 2004, Rootsi *et al.* 2007, Karafet *et al.* 2009a, Malyarchuk *et al.* 2011, Reguiero *et al.* 2013).

Following Toporov (1969, 1971), I adduced some additional linguistic evidence for the hypothesis that Burushaski might be distantly related to Yeniseseian (van Driem 2001), but because of a reinterpretation of the significance of the Karasuk cultural assemblage I later rejected the archaeologically inspired name Karasuk for the putative language family in favour of Greater Yeniseseian (van Driem 2008).¹³ The Burushaski may have retained a Greater Yeniseseian language but largely lost the presumed paternal lineage Q (M242). In fact, the ethnolinguistic history of the Burushaski may be a rather complex tale and is no doubt intimately tied up with the Indo-Iranian groups which surround them. At the time of the release of the new Kusunda material by Watters (2006), possible correspondences suggested by the Kusunda realis suffix <-ən ~ -n>, the Burushaski plural agent-subject suffix <-an> (except for genderless third person) and the Ket plural subject-agent suffix <-(V)n ~ -(V)ŋ>, by the Kusunda plural suffix <-da> and the Ket distributive prefix <d-> and by a number of other typological parallels between Kusunda and Greater Yeniseseian verbal agreement morphology raised the question in my mind whether Kusunda might be the remnant of the same ancient Greater Yeniseseian migration into the Himalayas.

Subsequently, evidence was adduced to argue that the Yeniseseian languages are genetically connected to the Athabaskan-Eyak-Tlingit a.k.a. Na-Dené languages of North America (Vajda 2010). Vajda called his hypothesis “Dene-Yeniseic”. I introduce the term “Dene-Yeniseseian” to refer to the putative linguistic phylum comprising Athabaskan-Eyak-Tlingit and Yeniseseian with the inclusion of Kusunda and Burushaski. Recently, in a methodologically rigorous appraisal, Gerber (2013) challenges the idea that a linguistic relationship can even ever be reconstructed at the putative time depth assumed for such a distant genetic relationship. In other words, entities such as Greater Yeniseseian or Dene-Yeniseseian may very well lie beyond the linguistic event horizon. At the same time, Gerber’s critical and detailed discussion of possible correspondences provides ample food for thought and numerous leads for further research. In this context, the Y chromosomal lineages of the Kusunda tell us an illuminating story of immediate relevance to the Greater Yeniseseian hypothesis and to Himalayan ethnolinguistic prehistory, but these data have yet to be published in the

¹³ I retain the conventional English spelling Yeniseseian, which follows the original German and Dutch sources, where the doubling of the *s* ensured a voiceless pronunciation, although a newer Russian-inspired spelling with a single *s* has recently come into use among some English speaking linguists.

population genetic literature.

South of the great Himalayan divide, the paternal haplogroup H appears to be associated with the indigenous populations of the Indian subcontinent, and this paternal lineage remains preponderant in today's tribal population, scheduled castes and the gypsies (Rai *et al.* 2012). It has previously been proposed that the spread of Y chromosomal R subclades is likely to be linked to the dispersal of Indo-European from an original homeland in the Pontic-Caspian steppe (van Driem 2007, 2012a), but the unfolding story of Y chromosomal R lineages will no doubt turn out to be complex (Underhill *et al.* 2010). I have proposed that the Y chromosomal lineage L, which shows a great diversity of subclades on the Iranian highland, can be identified as the possible marker of patrilingual dispersal of Elamo-Dravidian emanating from a region which included the Bactria and Margiana of later prehistory (van Driem 2012a). One of these Y chromosomal L subclades appears to be correlated with the patrilingual spread of Dravidian languages from the Indus Valley into south India.

The Beluch show haplogroup L at a greater frequency than any other group in Pakistan, far more so than the Brahui (Qamar *et al.* 2002, Haber *et al.* 2012). This paradoxical finding can, however, permit us to make inferences about the historical sociolinguistic situation in the aftermath of the Indo-Aryan incursion into the territory of the Indus civilisation and the Himalayas. The complex intercourse and extensive bilingualism which have historically characterised the Brahui-Baluchi commensality has been documented and described by Bray (1909, 1934), Emeneau (1962a, 1962b) and Elfenbein (1982, 1983, 1987). We may infer that, in part, the Beluch represent the *in situ* descendants of the ancient Dravidians who peopled the Indus civilisation. The ancestors of the Beluch, however, opted to assimilate linguistically to the incursive Indo-Europeans and retained the originally predominant Elamo-Dravidian haplogroup L at the highest frequency. By contrast, the Brahui retained the original Dravidian language of their ancestors and consequently also inherited the lower social status of the subjugated Indus population. Ironically, the lower status connected with the retention of a pre-Indo-Aryan ethnolinguistic identity rendered the Brahui language community more prone to male-biased genetic contributions from incursive Indo-European groups through hypergamy practised by succeeding generations of Brahui women.

Confronted with the overwhelming growing body of evidence in support of the Father Tongue hypothesis, Forster and Renfrew (2011:1391) impute the spread of language families to “emigrating agriculturalists” who “took local wives”. This interpretation is a transparent attempt to succour Bellwood and Renfrew's embattled First Farmers hypothesis, which seeks to ascribe the founding dispersals of language families to the spread of agriculture (Bellwood and Renfrew 2002). Those

collaborating with Renfrew continue to seek Y chromosomal correlates for the spread of the agricultural horizon in the Neolithic, even when the reasoning continues to be strained and the purported correlates are not manifestly evident (Arun Kumar *et al.* 2012). In order to buttress Renfrew's widely doubted hypothesis of an Indo-European homeland in Asia Minor, Forster and Renfrew propose a correlation of Indo-European with the Y chromosomal haplogroup J2a. In a similar vein, Wolff (2010) attributes the spread of the language families Tibeto-Burman, Austronesian, Kradai, Hmong-Mien and Austroasiatic all to the spread of rice cultivation, a highly simplistic view criticised by Blust (2011). In fact, it remains moot whether any part of Y chromosomal phylogeography correlates well with the spread of the Neolithic horizon.

Not every population movement led to the spread of a language phylum, and population movements are not uniform in nature. Whether during the exodus of anatomically modern humans out of Africa or at the shallow time depth of the peopling of Oceania by Austronesian populations, the colonisation of previously uninhabited lands invariably involved both sexes and the introduction of a linguistic phylum. During the Neolithic horizon, the spread of farming was necessarily a sedentary and incremental process, which likewise must mostly have involved both sexes. Early farmers might only have been able to spread their language at times of great surplus and concomitant population growth, perhaps sometimes involving the establishment of agricultural colonies elsewhere. By contrast, the modern ethnolinguistic composition of Asian populations must be understood, at least in part, as having resulted from male-biased linguistic intrusions, whether motivated by conquest, land grab or the urge to seek out new habitats.

The reasoning of Bellwood and Renfrew (2002) is therefore flawed, and the Centripetal Migration model was proposed as an alternative to their centrifugal Farming Language Dispersal theory (van Driem 2007). Bellwood and Renfrew argue that the surplus generated by an agricultural economy and the stratified social and command structure enabled by a Neolithic lifestyle drove demographic spread into many areas. They claim that the incremental spread of the Neolithic led to "the foundation dispersals" of language families with the ancient spread of linguistic phyla unfolding in the same direction as the demographic spread driven by Neolithic agriculture. The very opposite may be what actually happened in many cases. Across the Fertile Crescent, agriculture was adopted by ethnolinguistically unrelated populations, and agriculture spread effortlessly across ethnolinguistic boundaries without disrupting them in any significant way.

Sumerian pictographic script, developed ca. 3200 BC, appeared millennia after the invention of agriculture. Sumerian, Elamite, Akkadian,¹⁴ Hurrian, Hattic and other contemporaneous agricultural civilisations were in all likelihood not the first cultivators of the region. Yet even these antique agricultural language communities have left no surviving linguistic descendants. The earliest recorded and reconstructible history of the Near East bears witness to the permeability of linguistic boundaries for the dissemination of agriculture and crops. The Bronze Age of Asia Minor and Mesopotamia is characterised by a long period of incursive population movements into, rather than out of Anatolia and the Fertile Crescent, lured by the relative affluence of urban centres supported by agricultural surplus. Gutæans, Amorites, Kassites and other peoples were drawn in by the promise of the good life. Most linguistic reconstructions presume that Indo-European groups such as the Hittites and Mitanni likewise came to settle in Asia Minor and the Fertile Crescent from elsewhere. Toponymical evidence and details about the cults of certain deities have been used to argue that even the Sumerians originally migrated from an earlier northern homeland to lower Mesopotamia.

Were the motivations of migrating peoples in agricultural and pre-agricultural societies genuinely different at the Neolithic horizon than at later times? Tidings of technologically advanced urban societies may in the course of prehistory have provided ample motivation for migration, with enticing prospects of plunder and material advancement. We must consider such alternatives especially in those cases where the linguistic picture suggests a radically different view of prehistory than does the spread of material culture as reflected in the known archaeological record. The introduction of Proto-Sinitic to the Yellow River basin may have been likewise inspired. The Centripetal Migration model was named to contrast with the centrifugal reasoning of the Farming Language Dispersal proponents. In fact, ancient population movements may have unfolded both in centrifugal and centripetal directions with respect to centres of technologically advanced and later urban civilisations. The Centripetal Migration model acknowledges that the motives for migrations were diverse and that no model as simple as the Farming Language Dispersal theory could therefore account for all linguistic intrusions, even at the time of the Neolithic horizon.

With reference to Forster and Renfrew's wilful interpretation of the Y chromosomal haplogroup J2, I previously argued in the context of the Indian subcontinent that "the J2 haplogroup... appears to emanate from the Arabian Peninsula and, unlike haplogroups N and R1a, attains no high frequency in Ceylon" and "probably reflects the historically attested male-borne eastward spread of Islam"

¹⁴ Today Afroasiatic languages are spoken throughout this area, but none are descended directly from the extinct branch of the family represented by Akkadian.

and the ancient maritime trade across the Arabian Sea, whereas Y chromosomal haplogroups of the R subclades spread to the Subcontinent “from the northwest along with Indo-Aryan language across northern India and to Ceylon” (van Driem 2007:5). The spread of various Y chromosomal R subclades is likely to be linked to the dispersal of Indo-European from an original homeland in the Pontic-Caspian steppe, whilst the current geographical distribution of the Y chromosomal lineage L provides the likeliest candidate for a vestige of an earlier patrilingual dispersal of Elamo-Dravidian emanating from a region which encompassed the Bactria and Margiana of later prehistory.

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東亞民族語言學的譜系地理

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亞洲語言多樣性的譜系研究肇基於 1823 年。自 1901 年起，不同的學者先後提出將兩種或更多已確認的語族整合為更大語系的譜系方案，其中最近期的是 Starosta 2001 年的「東亞語系說」，這學說重新審視了語言學與非語言學的證據，提出了包括跨喜馬拉雅、苗瑤、南亞、南島、卡岱等多個語族的語系。本文根據亞 Y 染色體的譜系地理分佈進行民族語言學推論，試圖重建早於語言活動極限、無法依據歷史語言學法則追溯的史前民族語言在不同時期的面貌。族群遺傳學裏的「父語關聯」、前次冰順極盛時期殘留物種分佈區的證據，以及史前人口瓶頸造成語系分化的假說，都是了解亞洲語系族群演化的關鍵。本文同時探討了幾種鄰近亞洲語族的史前史，兼論及「農業－語言擴散理論」與「向心遷移模型」的對立。

關鍵詞：歷史語言學、史前史、群體遺傳學、民族語言學的譜系地理、殘留種保護區、瓶頸，族群孳衍、東亞語系、跨喜馬拉雅語族、苗瑤語族、南亞語族、南島語族、卡岱語族、父語關聯、向心遷移模型、農業－語言擴散理論