

Older glacial advances have not been dated so far and the existence, timing and extension of older glaciations remain uncertain. Obviously older yet undated morainic deposits were described from the Thakkhola above Thini and the upper Mayangdi Khola (Kuhle, 1982).

4. Because glacier mass balances are sensitive to both temperature and precipitation and cold periods generally coincide with a weakening of the Indian summer monsoon, it has been difficult to develop a general concept of timing and nature of the glaciations of the Himalayas (Mix *et al.*, 2001; Peltier and Fairbanks, 2006; Finkel *et al.*, 2003; Owen *et al.*, 2002; Owen *et al.*, 2008; Wei *et al.*, 2006). Given higher temperature sensitivities in humid areas, glaciers in the strongly monsoon-influenced southern slopes probably advanced in line with global temperature minima as during the LGM. This seems to be the case for the valley glaciations of the south side of the Annapurna and Manaslu Himal, whereas the signal is ambiguous for the Bhoté Koshi below Nyalam and the Khumbu Himal (Fig. 14.7). Other valley glaciations like that of the Langtang seem to be more precipitation-sensitive and reached their maximum length when monsoonal circulation was strong, such as during MIS 3 when increased insolation triggered strengthening of the Indian summer monsoon and its deeper penetration into the Inner Valleys. Increased snowfall at high altitudes leads to glacier advance, but glacial advances did not occur synchronously across Nepal. The lowest terminal moraines described so far reach down the main valleys between 650 and 1,500 m (W. Zech *et al.*, 2001; R. Zech *et al.*, 2009; Jacobsen, 1990; Kuhle, 1982; Fort, 1995; Meiners, 1999; König 2003) and the snowline was lowered to around 1,300 m.

The glaciers completely removed all life from the valley floors, but this effect was very limited in steep transverse gorges like the Kali Gandaki Valley below Ghasa. In the broad Inner Valleys like the Thakkhola and Manangbhot (Fig. 15.6) such effects extended across far larger areas (Chapter 6). The huge, unstable moraines created by those valley glaciations continue to be the source of slope failures and rockfall, especially after heavy monsoon rainfall.

14.3 The Himalayas as a prehistoric corridor for the peopling of E and SE Asia

Recent phylogeographic studies (Stewart and Stringer, 2012; Parducci *et al.*, 2012) have suggested that southern Tibet and the southeastern Himalayas could have been an ice age refuge

for various organisms. The prevalence of private haplotypes restricted to single populations that could not all have evolved locally in just 14,000 years appears to reflect the fragmentation of previously more widespread haplotypes before their isolation in refugia on the Tibetan Plateau and in the Himalayas during the LGM. The use of private haplotypes of scattered juniper groves (Opgenoorth *et al.*, 2010) and endemic edaphous beetles (Schmidt *et al.*, 2011) as a proxy for moderately lower LGM summer temperatures in southern Tibet is corroborated by studies of endemic flowering plants of the alpine steppe (Miehe *et al.*, 2011), the Tibetan Plateau pika (Ci *et al.*, 2009) and *Aconitum* (L. Wang *et al.*, 2009).

As outlined below, 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 at that time a large palaeo-lake amidst verdant mountains. 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 lowlands (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 Himalayas and the lowlands of the Gangetic and Brahmaputran plains must have played a role in shaping population prehistory and thus the human environment.

What do linguistics and human population genetic studies have to tell us about the prehistory of migrations affecting the greater Himalayan region? In the Himalayas, human genetic data correspond with the linguistic evidence more closely than in most other parts of the world with more diffuse gradients of biological markers across deep linguistic boundaries. By contrast, in the Himalayas the genetic and linguistic patterns correspond closely (van Driem, 2008). Nepal, at the centre of the Himalayan Arc, is a promising test site to link linguistic research with population genetic studies in high-altitude environments, and so to understand the making of alpine human environments.

Historical linguistics and human population genetics present two distinct windows on the past. The time frame accessible to historical linguistics is an order of magnitude shallower than that accessible to genetics. Language families represent the maximal time depth accessible to historical linguists because the



Fig. 14.8: Geographical distribution of the Kradai languages. Modified from van Driem (2013).

relatedness of languages belonging to a recognised linguistic phylum represents the limit of what can be demonstrated by the comparative method. Although languages and genes are independent, the basis for 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 generally, but not invariably, inherited by offspring from either or both of their parents.

Population geneticists often find molecular corroboration for patterns which linguists and ethnographers have been claiming for centuries. Whilst molecular genetic findings shed light on both ethnolinguistic prehistory and its unrecorded sociolinguistic dimensions, correlations should not be confused with identity. The correlation of a particular genetic marker with the distribution of a certain language family cannot be simplistically equated with populations speaking languages of a particular

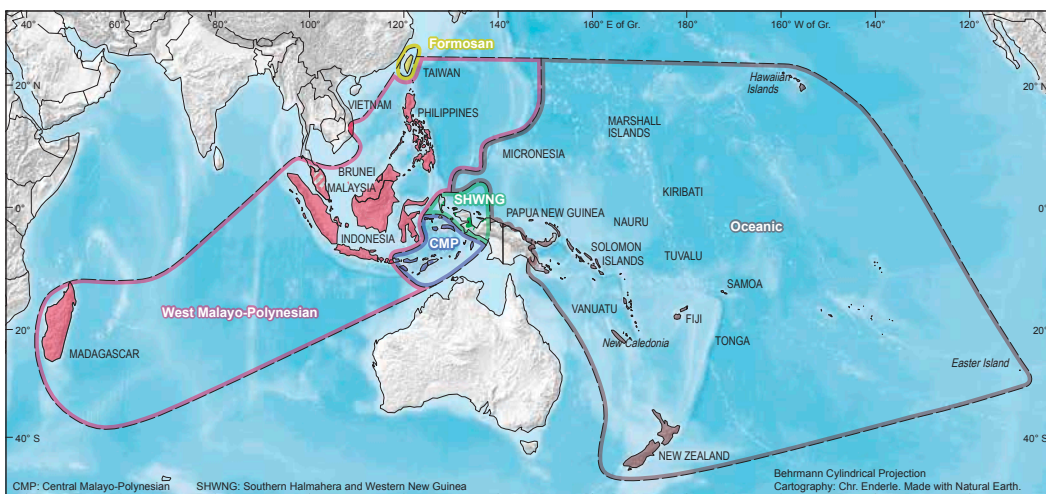


Fig. 14.9: Geographical distribution of the Austronesian languages. Modified from van Driem (2013).



Fig. 14.10: Geographical distribution of the Trans-Himalayan (Tibeto-Burman) languages. Modified from van Driem (2013).

Fig. 14.11: Geographical distribution of the Hmong-Mien languages. Modified from van Driem (2013).



linguistic phylum. With all these caveats in place it is unrealistic to attempt to summarise all of Himalayan ethnolinguistic phylogeography within this brief sub-chapter. A more detailed argumentation and exposition of the evidence with the necessary provisos and qualifications is given in van Driem (2012a, 2013).

A polymorphism may serve as a marker for a linguistic dispersal in the past, and a correlation of a Y chromosomal marker with language may point towards a male-biased linguistic intrusion. The father tongue correlation (Poloni *et al.*, 1997, 2000) 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, and it is reasonable to infer that some mechanisms of language change may be inherent to this pathway of transmission. This outcome might have been anticipated. Initial human colonisation 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 gender-biased, for example if male intruders imposed their language after reproducing with the indigenous population.

Studies of human genetics suggest that the paternal lineages N and O may have split in East Asia between 30,000 and 20,000 years ago according to the molecular clock based on calculations of coalescence times (Xue *et al.*, 2008). The Y chromosomal haplogroup N appears to be a marker for the linguistic ancestors of what Fortescue (1998) calls the Uralo-Siberian linguistic phylum, comprising Uralic, Yukagir, Eskimo-Aleut and Chukotko-Kamchatkan. The bearers of the paternal lineage N must have moved north from East Asia after the LGM, ultimately colonising the circumpolar regions.

The brother clade O appears to be a marker for the linguistic ancestors of what Starosta (2005) called the East Asian linguistic phylum, comprising Kra-dai (Fig. 14.8), Austronesian (Fig. 14.9), Tibeto-Burman (Fig. 14.10), Hmong-Mien (Fig. 14.11) and Austroasiatic (Fig. 14.12). The evidence for refugia in southeastern Tibet as outlined above 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 included refugia hospitable to human habitation during the LGM, the entire southeastern and eastern slopes of High Asia furnish numerous possible points of origin for paternal haplogroup O. The schematic reconstruction of the dispersal of Y chromosomal haplogroup O subclades based on the father tongue hypothesis and the so-



called 2012 Benares recension of East Asian phylogeny (van Driem, 2012a, 2013) can be briefly summarised here.

As temperature and humidity increased after the LGM, the Y chromosomal haplogroup O (M175) can be envisaged as dividing into the subclades O1 (M119), O2 (M268) and O3 (M122). The three subclades can be putatively assigned to three geographical loci, with the haplogroup O1 (M119) having moved to the drainage of the Pearl River and its tributaries in what today is Guangdong, and the bearers of haplogroup O2 (M268) to southern Yunnan, 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 (Fig. 14.13).

The O2 (M268) clade split into O2a (M95) and O2b (M176) just before the linguistic event horizon, i.e. the maximal time depth accessible through methodologically sound linguistic reconstruction and the boundary beyond which any reconstructions are pure speculation. It

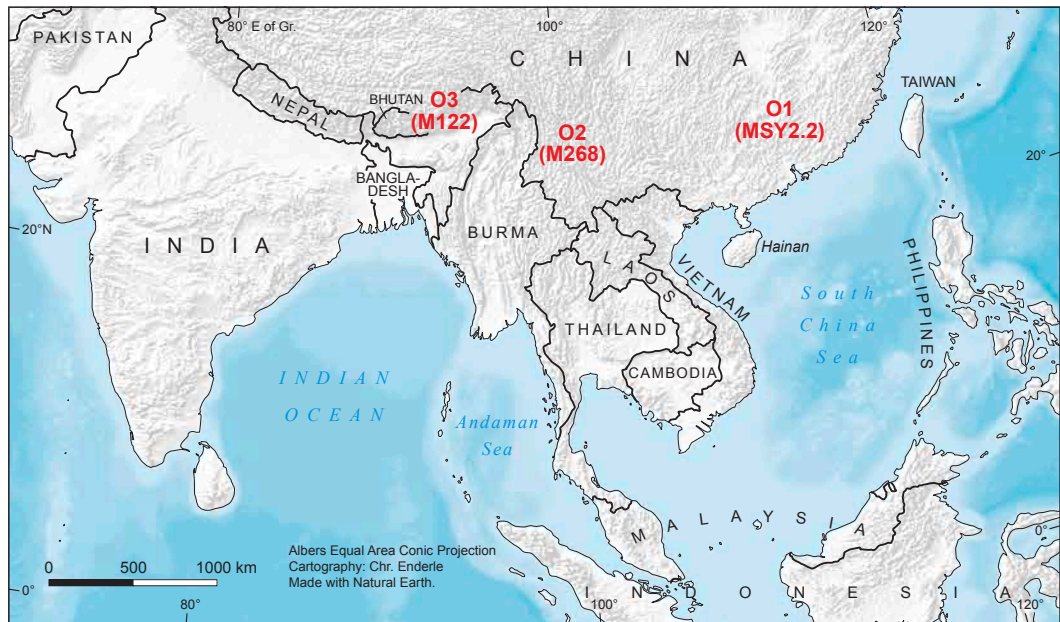
should also be borne in mind that the discrete linguistic phyla recognised by linguists could themselves represent the result of bottlenecks in linguistic prehistory.

Asian rice, perhaps both the *japonica* and the *indica* varieties, may have been domesticated roughly in the area hypothetically imputed to O2 (M268), which would have included southern Yunnan (van Driem, 2012b; Fig. 14.14). The bearers of the subclade O2a (M95) haplogroup became the progenitors 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 thence to 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 introduced both their language and their paternal lineage to indigenous peoples of the subcontinent (Fig. 14.15).

The other derivative paternal subclade O2b (M176) spread eastward, where they

Fig. 14.12: Geographical distribution of the Austroasiatic languages. Modified from van Driem (2013).

Fig. 14.13: After the Last Glacial Maximum, the Y chromosomal haplogroup O (M175) split into the subclasses O1 (M119), O2 (M268) and O3 (M122). Bearers of the O2 (M268) paternal lineage are likely to have been the first domesticators of Asian rice. Modified from van Driem (2013).

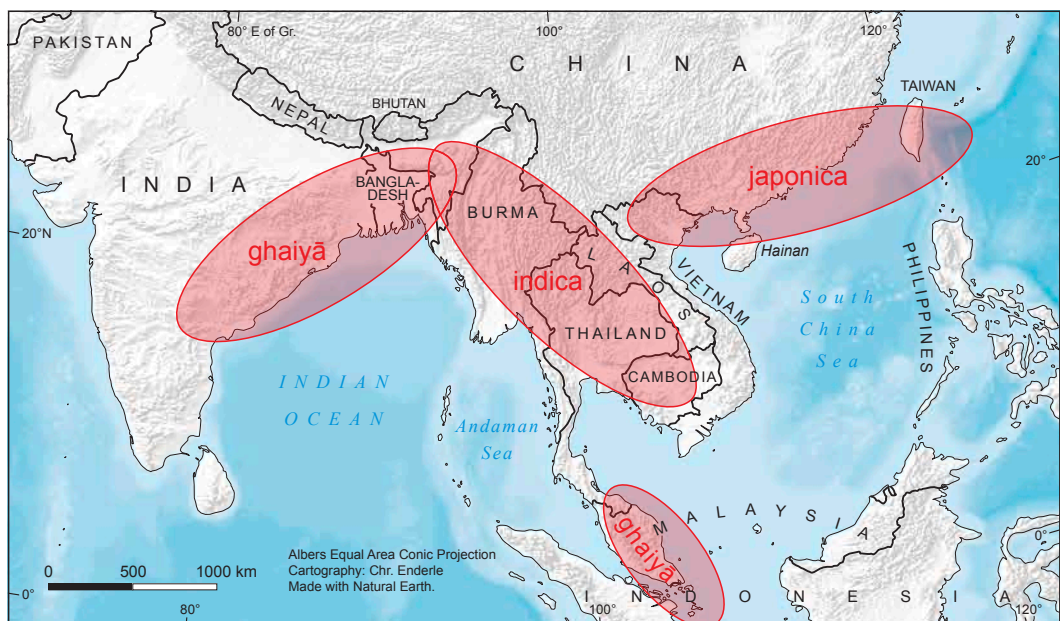


introduced rice agriculture to the areas south of the Yangtze. Though the genetic influence of the eastward migration of the bearers of the O2b (M176) can be followed, they left scant linguistic traces, except maybe an Austroasiatic name for the Yangtze (Pulleyblank, 1983), reflected as the toponym borrowed by Old Chinese as 江 *k^hroŋ (jiāng). This para-Austroasiatic paternal lineage advanced as far as the Korean peninsula and represents the second wave of immigration recorded in the Japanese genome. Whilst the maternal lineage represented by mitochondrial subclade D4 indicates an immediate provenance on the East Asian mainland, the Y chromosomal haplogroup tells a more specific story.

We can identify the O2b (M176) lineage with the Yayoi people, who introduced rice

agriculture to Japan, as early as the second millennium BC, during the final phase of the Jōmon period. The Yayoi appear also to have introduced other crops of continental origin to Japan such as millet, wheat and melons. The gracile Yayoi immigrants soon outnumbered the more robust and less populous Jōmon, who were the first anatomically modern humans to populate Japan. The Jōmon bore the mitochondrial haplogroup R30 and the Y chromosomal haplogroup D2. The paternal subclade D2 is specific to Japan but derived from early D lineages, which represent an ancient wave of anatomically modern humans which passed through the eastern Himalayas, across the Tibetan Plateau and through southern China, giving rise to the offspring clades D1 (M15), D2 (M55) and D3 (p47).

Fig. 14.14: Modelled geographical ranges for the domestication of *ghaiyā* or upland rice, wet *indica* rice and the *japonica* cultivar, based on the geographical distribution of genetic markers in the wild precursor *Oryza rufipogon*. Modified from Londo *et al.* (2007).



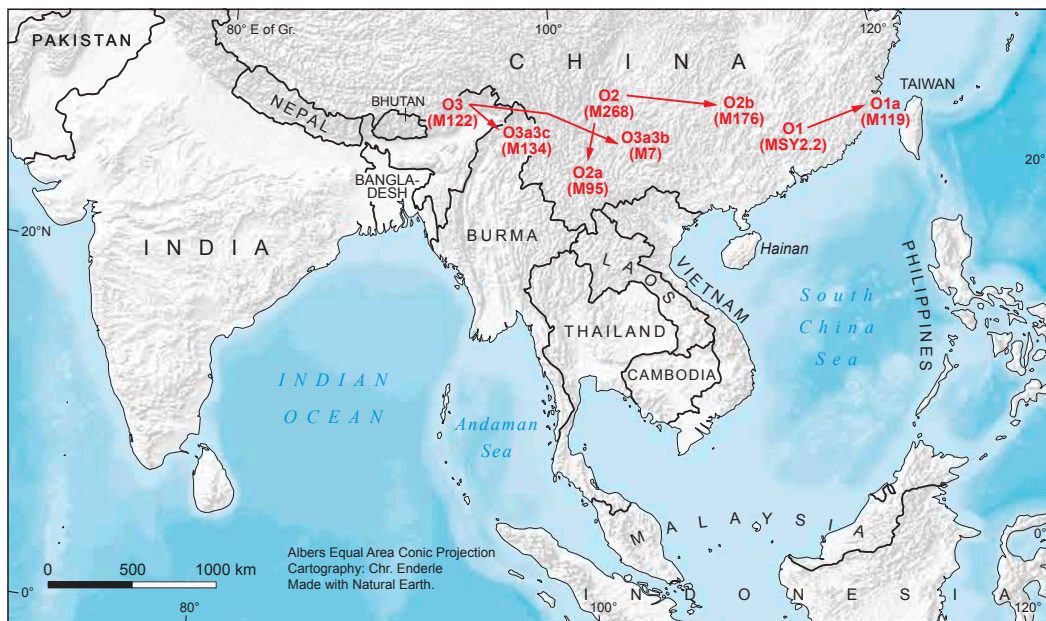


Fig. 14.15: Paternal lineages branching into new subclades. Each event involved a linguistic bottleneck leading to language families that today are reconstructible as distinct linguistic phyla. The O1 (MSY2.2) lineage in the the Pearl River drainage gave rise to the O1a (M119) subclade, which moved eastwards to the Fujian hill tracts and across the strait to Taiwan, which thus became the *Urheimat* of the Austronesians. Bearers of O3a3b (M7) became the Proto-Hmong-Mien, who migrated eastwards 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 eastwards, introducing rice cultivation and leaving behind an old toponym for the Yangtze, later borrowed by Old Chinese as 江 *kʰroŋ. Modified from van Driem (2013).

This ancient transit through the Himalayan corridor took place at a time long before the linguistically reconstructible past (Xue *et al.*, 2006; H. Shi *et al.*, 2008). Paternal D lineages are preserved on the Andaman Islands and throughout the eastern Himalayas and on the Tibetan Plateau, at frequencies that diminish eastwards through the Himalayas. Both the mitochondrial lineage R30 and the Y chromosomal haplogroup D2 indicate that the Indian subcontinent was the ultimate origin of the first wave of the colonisation of Japan, perhaps 25,000 years ago.

Twelve thousand years ago at the dawn of the Holocene, in the southeastern Himalayas and the eastern slopes 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) remained in the area comprising northeastern India, southeastern Tibet and northern Burma, whilst the bearers of the O3a3b (M7) lineage migrated eastward 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. The incidence of Y chromosomal haplogroup O2a amongst the Hmong-Mien appears to indicate a slightly lower 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



Fig. 14.16: Geographical distribution of the Dravidian languages. Modified from van Driem (2013).

drainage in the hill tracts of Fujian and across the strait to Taiwan, which consequently became the original homeland of the Austronesians. In the eastern Himalayas, the bearers of Y chromosomal haplogroup O3a3c (M134) expanded eastward into Sichuan and Yunnan, 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.

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. Median-joining network analyses of haplogroup O2a (M95) microsatellites have suggested a division in the Indian subcontinent between Tibeto-Burmans vs Austroasiatic and Dravidian (Fig. 14.16) 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).

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. At a later, shallower time depth, the Tibeto-Burman paternal lineage O3a3c (M134) spread from the Huang He Basin into southern China, beginning with the Han expansion southward during the Qin 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 firmly rooted in the eastern Himalayas, with outliers trailing off towards the loess plains of the Huang He 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.

South of the High Himalayas, the paternal haplogroup H appears to be associated with the indigenous populations of the Indian subcontinent, and this paternal lineage predominates in today's tribal populations, 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. It has likewise been proposed that the Y chromosomal lineage L, which shows a great diversity of subclades in the Iranian highlands, can be identified as the possible marker of patrilineal dispersal of Elamo-Dravidian emanating from a region which encompassed the Bactria and Margiana of later prehistory (van Driem, 2012a). One of these Y chromosomal L subclades appears to be correlated with the patrilineal spread of Dravidian languages from the Indus Valley into south India.

The Beluch have haplogroup L at greater frequencies 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 relationships and extensive bilingualism which have historically characterised the Brahui-Baluchi commensality

were documented and described by Bray (1909, 1934), Emeneau (1962) 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.

It has been 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). The Burushaski of northern Pakistan may have retained a Greater Yeniseian language but lost the presumed paternal lineage. Typological parallels between Kusunda and Greater Yeniseian have suggested that Kusunda might be the remnant of an ancient Greater Yeniseian migration into the Himalayan foothills (Watters, 2006).

In this context, it should be noted that Vajda's (2010) recent proposal of connecting Athabaskan-Eyak-Tlingit aka Na-Dené with Greater Yeniseian corresponds well with the dissemination of the paternal lineage Q to the Americas. However in his methodologically rigorous appraisal, Gerber (2013) challenges the idea that a linguistic relationship can ever be reconstructed at the putative time for such a distant genetic relationship. In other words, an entity such as Greater Yeniseian may very well lie beyond the linguistic event horizon. Gerber's 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 will tell us an illuminating story of immediate relevance to the Greater Yeniseian hypothesis.

This brief synopsis and discussion of prehistoric migrations through the Himalayas using evidence from historical ethnolinguistics and population genetics illuminate many previously poorly understood phases of migration. This is an important background to the increasing impact of humans through their use of fire and the development of agriculture.

14.4 Environmental changes during the Holocene

Pollen diagrams which cover early human impact on the Himalayan environment are all located at altitudes of approximately 3,500 m. Lake Rukche (Schlütz and Zech, 2004) on the southern slopes of the Manaslu Himal covers 18,000 years, and thus includes the Late Glacial, when there was supposedly little or no human impact, and the later stages which clearly indicate the presence of humans. Langtang 1 (Beug and Miehe, 1999) in the eastern Inner Valleys covers only the last 600 years and Jharkot (Miehe *et al.*, 2002) in the dry northern borderlands of the Inner Valleys bordering on the Arid Zone covers the last 5,500 years. All three pollen diagrams are subject to the above-mentioned constraints in reconstructing the influence of humans on a Himalayan environment.

14.4.1 Lake Rukche

Site description: Lake Rukche (28°18'N/84°46'E) is a freshwater lake at 3,500 m in the southeast of the Manaslu Himal (Fig. 14.17). It belongs to the Buri Gandaki catchment, drains into the Macha Kholā and is framed by moraines of Late Pleistocene age. Although it is located within the upper cloud forest belt, its original *Abies-Betula* forests have largely been replaced by open woodlands used as summer pasture for cattle. The dominant species are Ericaceae (*Lyonia ovalifolia*, *Pieris formosa*, *Rhododendron arboreum* v. *roseum*, *R. lepidotum*), *Daphne* spp., Berberidaceae (*Mahonia nepalensis*, *Berberis* spp.), *Piptanthus nepalensis*, *Cotoneaster* spp., *Lonicera* spp., *Viburnum* spp., *Elsholtzia fruticosa* and *Rubus* spp. Bamboos have mostly been eliminated by cutting and browsing. During the monsoon cattle resting places around seasonal settlements have luxuriant tall forbs of *Rumex nepalensis*, *Sambucus adnata*, *Senecio diversifolia*, *Iris clarkei*, *Artemisia* spp., *Impatiens* spp., *Aconitum* spp. and several tall Apiaceae species. Muddy open soils around the lake are colonised with *Koenigia* spp. Swampy lake shores have a closed carpet of *Potentilla contigua* with *Taraxacum* spp., *Anemone* spp. and stands of *Primula* spp. The less humid south-facing slopes have degraded pastures and scattered shrubs of *Rhododendron lepidotum*, *Berberis* spp. and *Cotoneaster microphyllus* with *Euphorbia sikkimensis*, *Cyananthus* spp., *Bistorta* spp., *Thalictrum* spp., *Halenia elliptica* and *Anaphalis* spp. Recently burned sites have tall forbs of *Meconopsis* spp., *Acanthocalyx nepalensis*, *Epilobium angustifolium* and carpets of the moss *Bryum argenteum*.