

The Father Tongue Hypothesis

Sexually dimorphic dispersals in prehistory

George van Driem
Leiden University

Studies of the non-recombinant portion of the human genome yield two different versions of population prehistory. Mitochondrial DNA reflects the maternal lineage, whereas the Y chromosome reflects the paternal lineage. A correlation of the linguistic mosaic of South Asian, Southeast Asian and Oceanic populations (van Driem 2001) with the findings of genome research reveals patterns of sexual dimorphism in prehistoric linguistic intrusions. More particularly, the Y chromosome and mitochondrial DNA pattern differently within the linguistic mosaic of speech communities in South and Southeast Asia and Oceania. The findings of a number of population geneticists, e.g. Poloni *et al.* (1997, 2000), Zerjal *et al.* (1997), Passarino *et al.* (1998), support what I call the Father Tongue Hypothesis, instances where Y chromosome markers correlate better with the linguistic affinities of populations than do mitochondrial DNA markers. On the other hand, Rosser *et al.* (2000) have argued that both language and Y chromosome diversity are functions of geography and that there is no significant correlation between the genetics of the Y chromosome and language. Newer population genetic studies provide an increasingly detailed view of both paternal lineages, e.g. Underhill *et al.* (2001), Qamar *et al.* (2002), and maternal lineages in the region, e.g. Kivisild *et al.* (1999a, 1999b, 2001). A closer, linguistically informed assessment of the genomic findings makes possible a more differentiated view of prehistoric linguistic intrusions. The groups of speakers who introduced languages and language stocks into different parts of South Asia, Southeast Asia and Oceania were of differing sexual composition. The Indian subcontinent will be compared with other areas. The Father Tongue Hypothesis will be shown to be valid in some areas, but not in others. A more detailed view of our past is currently emerging through the careful correlation of genomic and comparative linguistic findings.