



Standing Committee for the Humanities

OMLL: The Origin of Man, Language and Languages

A EUROCORES (European Science Foundation Collaborative Research) programme

Language and genes of the greater Himalayan Region (CRP 01-JA03)

- Guido Barbujani, Dipartimento di Biologia, Università di Ferrara, Italy
- Peter de Knijff, Department of Human Genetics, Leiden University, the Netherlands
- Mark Jobling, Department of Genetics, University of Leicester, United Kingdom

Abstract

Inferring past demographic changes from patterns of DNA diversity

Isolation is crucial to both biological and linguistic change. Populations that are separated by barriers tend to diverge genetically because of genetic drift, and to independently undergo linguistic change, resulting in often parallel patterns of genetic and cultural differentiation (“Language and genes”). Geographical as well as cultural barriers reduce population contacts, thus increasing isolation between populations. However, both biological and linguistic change are influenced by the size of the population. Hence the importance of collecting reliable information on past human demography (“Language Evolution and Computer Modelling: Evaluation of population size between 100,000 and 10,000 years ago”).

The greater Himalayan region is the ethno-linguistically most complex area of Eurasia. Besides including the highest land barrier on the planet, this region is inhabited by speakers of six language families (Tibeto-Burman, Indo-European, Austro-Asiatic, Dravidian, Daic and Altaic) plus two language isolates, Burushaski and Kusunda. We sampled about 1000 individuals from Nepal and 1000 from Bhutan, representing 35-40 different groups identified on the basis of language and/or geography or caste. Typing of polymorphisms of the Y chromosome and of the mtDNA genome in these samples will allow us to compare and test alternative models of the peopling of Eurasia based on linguistic and archaeological evidence.

In the initial phase of the project we analysed a broad genetic dataset in populations from all continents. Theory shows that past demographic expansions leave recognizable marks in the patterns of genetic diversity. Whereas mitochondrial data suggest rapid expansions for all populations, except those that did not practise agriculture, Y-chromosome diversity is compatible with constant population sizes through much of our evolutionary history. One (but not the only) way to reconcile these results is to take them as evidence that polygyny was the rule in humans up to a recent past, possibly until the Neolithic shift from mobile to sedentary communities.