

# *Modern Origins, Language and Languages*

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## **Abstract**

Mitochondrial and nuclear genetic variation in humans is much lower than in extant apes (Gagneux 1999; Fischer *et al.* 2006). The effective population size of extant humans is slightly >10,000. In contrast, the effective population size of the common ancestor of chimpanzees and humans is estimated at four to seven times larger (Wall, 2003). Comparable estimates for the effective population size of the common chimpanzees or orang-utans ancestors have been obtained. These data are usually interpreted as resulting from a much longer history for the different species of apes than for our own species and/or from the existence of one or several bottlenecks at the origin of modern humans. Genetic evidence is presented primarily in support of the "Out-of-Africa" model for the origin of modern humans. According to this model, which has become prevalent, no biological continuity existed between archaic and modern populations outside of Africa. All modern humans have a recent (ca. 150,000 BP) African origin and non-African archaic populations were essentially replaced after ca. 50,000 BP by immigrants originating in a relatively limited group of individuals. However, paleogenetic evidence indicates that Neandertal mtDNA also displays low variability, comparable to that of a large modern population (Serre *et al.* 2004). This has been interpreted as resulting from successive bottlenecks in relation with dramatic environmental oscillations in the middle latitudes (Hublin 1998). Further, the recent sequencing of 1,000,000 base-pairs of Neandertal nuclear DNA (Green *et al.*, 2006) has allowed the computation of the effective population size of the common ancestor of Neandertals and modern humans. This effective population size is estimated to be around 3,000 for a split time between *Homo sapiens* and *Homo neanderthalensis* around 400,000 BP, with a confidence interval ranging from 0 to 12,000, taking into account methodological uncertainties. This result suggests that what we observed with modern human origins might not be an exceptional event in the course of modern human evolution, but rather a regular pattern in human evolution along the late Middle and Upper Pleistocene. This pattern is clearly distinct from what we observe in closely related species of apes. This paper will entertain the hypothesis that group selection is more likely to be effective in humans than in apes in relation with the importance of cultural adaptation in humans and with the increasing cultural differentiation since the Middle Pleistocene. Although stabilizing selection would have been more effective in apes, in humans drift would have been prevalent (Weaver *et al.*, in press), explaining the rapid phenetical divergence observed in *Homo sapiens* and *Homo neanderthalensis* lineages. The most recent species of humans, although they diverged very recently, display phenetical differences at least as marked as sister groups of apes such as common chimpanzees and bonobos, who diverged more than 2 million years ago (Harvati *et al.*, 2004). Complex language and, perhaps more importantly, separated languages acting as cultural markers are likely to have played a key role in these processes, and specifically, in the emergence and spread of modern humans.