



partitioned and were genetically distinct prior to the onset of the Neolithic, then different models may be taken to predict different genetic patterns.

The first model is classic "migrationism" and would involve genetic replacement, so that the sink region (Europe) should be genetically indistinguishable from the source (the Near East), except for any differentiation that had taken place within the last 8000 years. Model (7) would involve no movement of genes whatsoever – Ammerman's "indigenism" (Ammerman 1989). This would include both cultural diffusion (Dennell 1983; Barker 1985; Whittle 1996) and separate dev<sup>ara</sup>

The conclusions of Ammerman and Cavalli-Sforza and their colleagues were supported by Sokal and colleagues (Sokal et al. 1989; 1991), using spatial autocorrelation

These developments have led to the development of what has been termed the "phylogeographic" approach (Richards et al. 1997; Bandelt et al. 2002). Phylogeography is a heuristic tool for interpreting complex population-genetic data that tries to make maximum use of reconstructed trees of descent, along with the geographic distribution and diversity of genealogical lineages; it is effectively the mapping of gene genealogies in time and space (Avice 2000.3). The process of testing phylogeographic hypotheses always entails making assumptions, and inevitably has to be carried out within a model or framework based on external information (such as from archaeology). Even so, the assumptions themselves can often be susceptible to empirical investigation, and may often be less unrealistic than those of more traditional population-genetics approaches (Richards et al. 2000).

#### MITOCHONDRIAL DNA

The first major application of phylogeographic procedures to the question of European genetic variation was an analysis of mitochondrial DNA (mtDNA) (Richards et al. 1996). This work made use of a new phylogenetic-network approach to tree reconstruction, developing new phylogeographic approaches, such as founder analysis, to the study of migration and colonization.

Founder analysis works by comparing the genetic variation in a region that has been settled by a small group of individuals (founders) to the genetic variation in a region that has been settled by a large group of individuals (ancestral population). The founder analysis is based on the fact that the genetic variation in a region that has been settled by a small group of individuals is expected to be lower than the genetic variation in a region that has been settled by a large group of individuals. The founder analysis is based on the fact that the genetic variation in a region that has been settled by a small group of individuals is expected to be lower than the genetic variation in a region that has been settled by a large group of individuals.



ment (Semino et al. 1996). However, Semino et al. (2000) teased out some of the more detailed patterns for the first time, providing some interesting parallels with the mtDNA work. They identified several potentially Neolithic markers that implied a Near Eastern Neolithic contribution to Europe as a whole of less than 25%. There have been recent criticisms of their interpretation by Chikhi et al. (2002), on the grounds that an admixture approach suggests a much higher putative Neolithic contribution than the crude estimates. However, their arguments are unconvincing, since an admixture approach seems quite inappropriate in the context of the questions under consideration, and suffers from some of the weaknesses of the classical approach (such as lack of dating).

It is noticeable, though, that the putative Neolithic lineages are markedly more common along the Mediterranean than in central Europe, which contrasts somewhat with the mtDNA picture described above. Without a founder analysis, such as has been done for mtDNA, it is certainly likely that earlier and later processes may be conflated: the palimpsest problem again. The question is to what extent. King and Underhill (2002) have argued that the high correlation between the distribution of painted pottery and anthropomorphic clay figurines and some of the putatively Neolithic Y chromosomes indicates that indeed at least some of the latter do represent early Neolithic settlement. This implies that, on the male side, intrusive lineages from the Near East only spread through the first burst of Neolithic settlement in Europe around the eastern Mediterranean basin, but were not carried to an appreciable extent into central Europe with the LBK. This in turn supports the view that high levels of acculturation took place in the Balkans prior to the LBK expansion (Gronenborn 1999; 2003). The Near Eastern lineages that spread through the eastern and central Mediterranean in the early Neolithic would have been subsequently overlaid by later Near Eastern dispersals. It

East (Gronenborn 1999). Archaeological evidence is now emerging from both ceramics and lithics for the assimilation of Mesolithic groups into LBK settlements (cf. Gronenborn 2003).

There is some evidence for further colonization from the LBK zone into the northwest, including the British Isles, whereas the pattern in Scandinavia might be explained by frontier exchange. The Atlantic west seems also to have experienced distinct, presumably maritime leapfrog colonization events from the direction of the west Mediterranean coastline. The movements into the northwest seem either not to

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