The Neolithic transition in Europe: comparing broad scale genetic and local scale isotopic evidence

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Genetic studies of modern populations are raising many interesting questions about how far the modern gene pool is owed to incoming populations during the agricultural revolution in Neolithic Europe. But, as the authors show, studies of isotopic data from cemeteries reveal a picture of increasing subtlety at local level. While early farmers may have been initially newcomers in the upper Rhine they may also have soon intermarried with contemporary hunter-gatherers in the uplands.

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Studies of how agriculture spread from the Near East into Central Europe (ca. 7000 – 5000 BC) are essential to theories explaining the origins of the languages, genes and demography of the region. These competing theories (e.g. Price 2000) range from “demic diffusion” through short, undirected migrations by farmers with ancestors in southeast Europe (Ammerman and Cavalli-Sforza, 1984), to the adoption of agriculture by indigenous hunter-gatherers of Late Mesolithic Europe (Tillmann 1993; Whittle 1996).

Recently, the geographic distribution of Y-chromosome haplotypes from modern Europeans has been presented in support of the Neolithic demic diffusion model (Chikhi et al. 2002), suggesting that colonising farmers from south-west Asia contributed 70–90% of the genes in the population of each Neolithic settlement with an average contribution of 50% across the continent. Since others have used mitochondrial (mt) DNA evidence to argue for only about 20% Neolithic genes (Richards et al. 2000), there appears to be serious disagreement. Although this apparent discrepancy is probably more a matter of different methods of data analysis than of actual differences in continent-wide prehistoric demography (Barbujani et al. 1998; Simoni et al. 2000), there are ways in which real differences could have developed on a local scale. For example, distributional differences in mtDNA, which is passed through the female line, and male-transmitted Y-chromosomes could have resulted if the colonising farmers were in small groups, with few unmarried, not-closely-related females with which to bear

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children. In such cases, groups that managed initially to intermarry with indigenous hunter-gatherer women would have reproduced most successfully.

For south-west Germany, we have found support for this hypothesis through a powerful method, recently highlighted in *Nature and Antiquity* (Diamond 2001; Price *et al.* 1998; Price *et al.* 2001), that can directly identify prehistoric migrants. By comparing the strontium isotope signatures of archaeological human skeletons with regional geochemical characteristics, we can distinguish ‘locals’ from ‘immigrants’ at a site (e.g., Ericson 1985; Price *et al.* 2002) and potentially, with suggestive archaeological evidence, mobile foragers from sedentary farmers (Bentley *et al.* 2003). Thus, it may be possible to test predictions concerning the prevalence of demic diffusion as opposed to, say, the immigration of forager females into farming communities.

Strontium isotope analyses in the skeletons of some of the first farmers in south-west Germany, ca. 5400 – 5000 BC, show a high incidence of non-local females in early Neolithic cemeteries (Bentley *et al.* 2002; Bentley *et al.* 2003, Price *et al.* 2001). Because the alluvial lowlands of the Upper Rhine Valley have lower $^{87}$Sr/$^{86}$Sr than the surrounding crystalline uplands (Tricca *et al.* 1999), the relatively higher $^{87}$Sr/$^{86}$Sr of the non-locals indicates they spent significantly more pre-adolescence time in these uplands than the locals (Price *et al.* 2001). This may reflect the difference between the diet catchments of prehistoric farmers, whose domestic plants and animals were raised within the lowlands, and contemporary foragers, who took food from the uplands as part of their mobile subsistence (Bentley *et al.* 2002; Bentley *et al.* 2003; Gregg 1988). Because many of these upland non-locals were buried differently from locals, particularly without the characteristic stone adze associated with the early farmers, the strontium isotope analysis may evidence intermarriage between forager and farming communities. However, even if these particular non-local females were from other Neolithic farming communities, this evidence for patrilocality suggests that upon first contact the brides may have been foragers, an occurrence that has often been observed ethnographically (Spielmann and Eder 1994).

Although the skeletal/isotopic evidence is not proof that the first farmers everywhere in Central Europe married its last foragers, this hypothesis for the Upper Rhine Valley is supported by archaeological evidence (Gronenborn 1999) and it is not in contradiction with recent genetic evidence. For the Y-chromosome data, the percentages presented above are averages, and the linear regression observed across Europe for Neolithic contributions is necessarily an oversimplification. Variation around the average trend is expected depending on gender and/or geography (Seilestad *et al.* 1998; Chikhi *et al.* 2002). For instance, we can plot the most probable Neolithic contribution obtained by these authors for

![Most probable Neolithic contribution](image)

*Figure 1.*
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each European sample against geographic distance from the Near East (Chikhi et al. 2002). As Figure 1 shows, the points appear to follow a gradual and then steep transition, followed by another gradual decrease. This suggests that colonisation could have predominated in the early stages in south eastern Europe, while indigenous involvement may have been substantially greater in some parts of north western Europe. This aligns with the analysis of the geographic distribution of radiocarbon dates in Europe. Gkiasta et al. (2003, this issue) argue that Neolithic Germany was colonised by farming populations who may have subsequently interacted with indigenous populations to the west. In any case, surely the demographics of the transition to farming in Central Europe was geographically much more complex than can be detected after several millennia in continent-scale genetic patterns whose interpretation has often relied upon ad hoc methods with unspecified assumptions (Goldstein and Chikhi 2002). Although recent population genetic models are rapidly improving, archaeologists and geneticists alike should not over-interpret the continent-wide patterns of genetic data in terms of archaeological patterns observed at the local scale, at least until more localised genetic samples become available.

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