

## The genetic history of Italy: a male perspective

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My research interests are related to the processes influencing the distribution of genetic variation across human populations. This has led my investigation across a number of different fields, from history to anthropology, using research tools offered by genetics. I am particularly interested in Y-chromosome markers to investigate population genetic history in order to provide new prospective and test alternative hypotheses. As part of my research I have also been involved in the molecular analysis of fossil remains and forensic genetics. Current projects focus on the correlation between culture and genetics, the genetic history of the Italian peninsula and the peopling of the European continent and Mediterranean.

The geographical position of the Italian peninsula, within the heart of the European continent offers a unique opportunity to investigate both the continental and Mediterranean historical demographic events. It follows that the dissection of the events that lead to the peopling of the Italian peninsula not only offer insights within the history of this specific region, but can also shed light on the dynamics occurring at continental level. However, the knowledge concerning the pattern of colonisation of the area is little known and different scenarios have been put forward by scholars in different disciplines to explain the current distribution of genetic variation (Semino *et al.*, 2000; Cunliffe, 2001).

In a recent work Capelli *et al.*, (2007) propose a model where the original inhabitants of the peninsula, possibly dating back to the late Palaeolithic-Mesolithic (40,000-12,000 year ago) did not disappear due to replacement by incoming farmers from Anatolia on the wave of the demographic expansions associated with the Near East agricultural revolution (8,000 years ago). This view is sustained by data simulations (Ammerman & Cavalli-Sforza, 1984) showing that the observed data could be explained by massive population migration from the Anatolian region. The data gathered by Capelli *et al.*, (2007), using Y-chromosome genetic variation, suggest that there was admixture between the two groups, but that the process did not happen homogenously across the peninsula. Southern Italy and the Adriatic, in fact, were the areas mostly influenced by the newcomers, while the Northern and Thyrrenic regions tended to preserve a larger proportion of "autochthons" genes. Along the peninsula, it is possible to highlight a series of clinal distributions of Y types associated with the Near East populations, indicating a gradual dilution of the farmers' genes moving North, as a result of admixture

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with the populations already present there. Similar processes have been paralled in other regions of the world in association with the agricultural revolution: the expansion of Bantu speaking farmers in Africa and the colonisation of the Polynesian islands in the Pacific, among the others (Diamond & Bellwoood, 2003). The current set of data also indicates that previous indications of significant Greek contribution to current Southern Italian populations has been overestimated (Piazza *et al.*, 1988), and the similarity between Southern Regions to Mediterranean populations is the result of the Neolithic introgression more than any Greek contribution. In fact, genetic comparison between southern Italian samples and Anatolian and Greek populations showed a closer affinity to Anatolia compared to Greece. This would suggest that there might be some discontinuity between cultural and genetic legacy, a sort of cultural dominant *elite* where autochthons people assimilated cultural innovations imported by a relatively low number of newcomers.

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