

GENETIC CONTINUITY AND DISCONTINUITY IN PREHISTORIC ITALY

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Introduction. A large number of biological samples, ranging from the Middle Paleolithic to the Middle Age, is available in Italy. The genealogical ties among past and present individuals and populations are all but obvious, and certainly cannot be inferred from the archaeological record. Here I focus on two case studies, as examples of both genetic continuity and discontinuity across time.

Methods. Mitochondrial sequences (complete or partial) from two Mesolithic Sardinian samples, and from seven Etruscan populations (7th-2nd centuries BC), were compared with suitable databases of modern and ancient data. By methods of Approximate Bayesian Computation (ABC) we identified the demographic models most plausibly representing the relationships among samples, and estimated their evolutionary parameters (mutation rates, effective population sizes, patterns and rates of gene flow). For that purpose, we generated by serial coalescent simulation millions of mitochondrial sequences assuming different demographic scenarios; summary statistics calculated from simulated and observed data were compared by ABC. Models of isolation with migration were also used to infer population divergence dates.

Results. The complete Mesolithic Sardinian sequences find no match in either modern or Neolithic samples. Rather, they appear evolutionarily related with European sequences dating back to much earlier time periods, suggesting evolutionary ties with Paleolithic Europe, long-term isolation, and a limited, if any, contribution to the contemporary gene pool (Modi et al. 2017). Conversely, the Etruscan samples show evidence of genetic continuity with two, but not all, modern populations settled in the same Tuscan territory. They also show similarities with ancient samples from the Near East, but the estimated date of separation from such Near Eastern groups is remote (in the Neolithic period), not consistent with the hypothesis that the Etruscans immigrated from the East around the 8th century BC (Tassi et al. 2013).

Conclusions. If properly analyzed, DNA data allow testing of hypotheses about ancient population relationships and movements. Italian prehistory shows examples of both genetic continuity (between some Tuscan communities and the Etruscans; between a Sardinian community and Bronze-Age Sardinians: Ghiretto et al. 2010) and discontinuity (between Mesolithic Sardinians and the communities dwelling in the island in Neolithic, Bronze Age and modern times). The genealogical relationships between populations occupying the same territory at different times are never obvious, but can now be inferred empirically with good statistical confidence from genomic data.

References

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