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# Ancient Admixture in Human History

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## Abstract

Population mixture is an important process in biology. We present a suite of methods for learning about population mixtures, implemented in a software package called ADMIXTOOLS, that support formal tests for whether mixture occurred and make it possible to infer proportions and dates of mixture. We also describe the development of a new single nucleotide polymorphism (SNP) array consisting of 629,433 sites with clearly documented ascertainment that was specifically designed for population genetic analyses and that we genotyped in 934 individuals from 53 diverse populations. To illustrate the methods, we give a number of examples that provide new insights about the history of human admixture. The most striking finding is a clear signal of admixture into northern Europe, with one ancestral population related to present-day Basques and Sardinians and the other related to present-day populations of northeast Asia and the Americas. This likely reflects a history of admixture between Neolithic migrants and the indigenous Mesolithic population of Europe, consistent with recent analyses of ancient bones from Sweden and the sequencing of the genome of the Tyrolean "Iceman."



Keywords: human admixture, admixture proportions, SNP array, population structure, Neolithic migration, Basque



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