USING DNA TO CHARACTERIZE HUMAN MIGRATION PATTERNS: THE BASQUE OF THE AMERICAN NORTHWEST

Michael C. Davis
Boise State University, Boise, ID

Forensic DNA analyses primarily focus on the identification of individuals, in order to compare reference, suspect, and evidentiary samples. Calculating the relevant probabilities require the estimation of allele frequencies in the human population. These techniques and data are also used for solving cases involving not individuals, but populations. The "cases" are not crimes, but questions regarding the behavior of human populations, both contemporary and historical. Some of the "big cases" investigated using molecular population genetics include: What migration routes did our earliest ancestors take when they left Africa? Where did the ancestors of modern Europeans come from?

The Basque, a European ethnic group historically occupying the region of the Iberian Peninsula overlapping the modern borders of Spain and France, have been the subject of numerous genetic studies over several decades. The Basque, besides being famous for having a language unrelated to any other on earth, and possibly being the direct descendents of Paleolithic Europeans, have also participated in extensive exploration and settlement of the world. Since they maintain a strong ethnic identity, and often can trace their ancestry over many generations, they are excellent candidates for studying the genetic consequences of migration patterns.

How has the history of migration shaped the genetic diversity and structure in the community of self-identified Basques of Idaho and the Northwest? To answer this question, modern techniques of DNA collection, extraction, and analysis were employed in conjunction with analysis that compares population models and genetic data. We use mitochondrial DNA and microsatellite analysis to compare the Basque American (migrant) and European (source) populations. We have noted a decrease in genetic variability in immigrant Basque populations, which is consistent with a founder effect, despite historical records of multiple waves of migration and back-migration. Various methods of analysis will be discussed, such as constructing haplotype networks, diversity statistics, and relatedness coefficients. The possibility of a kinship bias in shaping the genetic structure of migration will also be discussed.