

MITOCHONDRIAL HAPLOTYPES IN THE BASQUE POPULATION OF SOUTHERN IDAHO

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The phenomenon of continued migration and settlement of the Basque people to various countries around the world, including the United States, affords an opportunity to study the population genetics of such migrations. The Basque diaspora offers the researcher a genetically well-characterized original population, an extensively documented migration, and relatively easy designation of and access to the founder population. This study addresses the role of genetic drift (and specifically the founder effect) as it affects genetic variation and haplotype frequency in a specific sub-population, the immigrant Basques of southern Idaho. It is often assumed that via migration and settlement of human populations, the regional pattern of genetic profiles can be explained as a randomly sampled, genetically less diverse subset of the populations from which immigration took place. Although theoretically well-founded, and empirically studied for many populations of various species, the exact character of such population genetic events will vary from population to population.- Basque immigration to the America's has a long history, starting with fishing settlements in New Foundland in the 1500's, and continuing into the 20th century, for various economic and political reasons. In southern Idaho, the majority of the Basque population traces its roots back to the province of Viscaya, where approximately 98% of families originate. To collect samples for this study, individuals of Basque heritage from Idaho volunteered a buccal swab, from which mtDNA was extracted using the Qiagen Mini-Amp DNA kit. To ensure samples were from people who were of maternal Basque heritage, a questionnaire protocol was followed: a questionnaire was filled out by each volunteer, and the maiden names and birthplaces of their mother and their mother's mother was recorded. Only samples that have a recognizably Basque maiden name for their maternal grandmother were considered for this study. The specific objectives of this study are as follows: 1) determine the frequency of specific HV-1 and HV-2 mtDNA haplotypes of the Basque population residing in southern Idaho, 2) compare haplotypes of Idahoan Basque to those found in the Basque country, especially the region of Viscaya, and 3) to gain an understanding of how Basque migration patterns have had an effect on the haplotype distribution in the Idaho population.