Anthropological and Medical Implications of Genetic Admixture in the Mexican Mestizo Population

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Introduction. Common complex diseases like cardiovascular disorders, cancer, asthma, diabetes, high blood pressure, schizophrenia, cleft lip and palate, etc. are the main focus of current genomic and epidemiological research. For most of these illnesses, the ethnic background is suspected to play an important ethiopathogenic role. Genomewide association studies (GWAS) have been conducted to find genetic sequences or genes associated to several of these multifactorial disorders, but most of them have found a small effect size and low heritability to be valuable for genetic probability testing. It is clear than in a near future; better planning of translational-focused genomics research and better bioinformatic approaches will improve our knowledge on gene-gene and gene-environment interactions, and genome tests will find their value to predict clinical outcomes. Most of these genomes analyzes have been conducted in subjects from particular ethnic groups, mainly Caucasians, Africans, and East Asians for whom specific and defined panel of polymorphic markers have been developed after the conclusion of the HapMap project, but conducting these studies in populations with ethnic admixture represent a challenge, as well an opportunity to understand the genetic contributions to mixed racial phenotypes. Because of their recent history, the admixed population of Latin America constitutes an interesting case-study for clinical genomics research. Initial works on the genetic structure of the Mexican population, based on blood groups, polymorphic proteins, hemoglobin variants, HLA and DNA markers, where crucial to define the inter-racial variability, mainly among the Caucasian, Native American, and African components from diverse Mexican communities; but along the time, the issue of the ethnic admixture in the Mestizo started to generate interest among the scholars. An intriguing question for population geneticists concerns about the homogeneity of the Mexican population, or more precisely, the Mestizo Mexican population. The appropriate answer to this question is fundamental for the design of genome-based population studies, GWAS for complex disease, and pharmacogenomics, among others, because there is always the risk of structure subestimation.

Methods. To develop the topic of genetic homogeneity in the Mexican population, this study will focus on reports of open population genetic studies, preferable on those carried out with anonymous genetic markers, to avoid confounding factors associated to possible genetic markers associated with prevalent complex diseases or particular premorbid life styles. I also discarded studies performed with non-randomly selected subjects, as university students, groups with defined income, religious communities, etc. I also will follow a historic perspective of the described contributions in order to correlate results with the advancements in the methodologies for genetic marker screening applied to population studies.

Results. Figure 1. Contributions from parental populations to four Mestizo populations using blood groups, and polymorphic erythrocyte enzymes and plasma proteins as genetic markers.

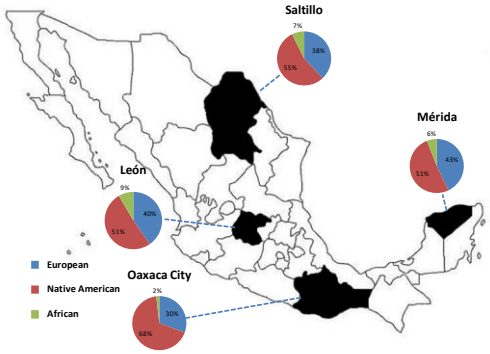


Figure 2. Contributions from parental populations to three Mestizo populations using 13 STR markers.

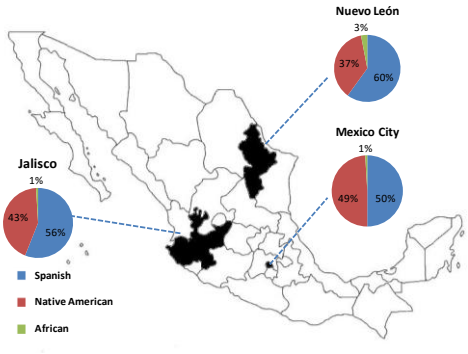
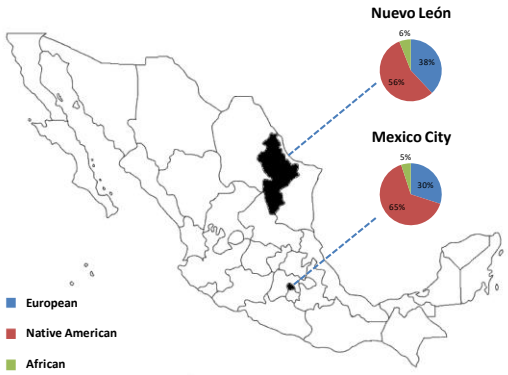


Figure 3. Contributions from parental populations to three Mestizo populations using 54 admixture informative markers.



Conclusions. Although no perfect, the word "Mestizo" describes the current predominant population more appropriately than "Hispanic". The genetic pool of the current Mestizo population of Mexico is mainly made of parental contributions from Native Americans, Spaniards, and in a lesser extent, from Africans. There is a North-South gradient in the European contribution, and inversely, a South-North gradient of Native American contribution, but admixture homogeneity is observed in most Mestizo subpopulations. Although there is not a defined panel of markers for Mexican Mestizo studies yet, recent progresses in the methodologies for Admixture Mapping, a powerful technology to discover genes associated to complex traits and diseases, will allow for ascertaining genes causing some of the most prevalent chronic diseases, like cardiovascular disorders, diabetes, and cancer. In this sense, our Mestizo population has an interesting advantage over their parental ethnic groups.

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References

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