Review Article

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Genomic medicine in Mexico will be developed by analyzing the diversity of the genomes of Mexican Mestizo populations

Conrad Purcell*

Department of Interventional Pediatrics, USA

*Author for correspondence: Purcell_c33@gmail.com

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Abstract

In association studies of complex diseases, it is possible to develop tagging and imputation strategies to comprehensively analyze common genetic variation by studying the genetic diversity and linkage disequilibrium structure of various populations. A Mexican haplotype map's potential to aid in the identification of genes associated with prevalent diseases in the Mexican population was the subject of our evaluation. Genome-wide data from Mexican Mestizos from diverse regions with distinct histories of admixture and particular population dynamics served as the basis for our evaluation of genetic diversity, linkage disequilibrium patterns, and the extent of haplotype sharing. The Mexican Amerindian group and data from the Hap Map were used to assess ancestry. Our findings show that Mexican subpopulations have genetic differences that should be taken into account when conducting association studies of complex diseases. Additionally, these findings lend credence to the hypothesis that a haplotype map of the Mexican Mestizo population can reduce the number of tag SNPs required to characterize this population's common genetic variation.

Keywords: Genetic variation • Population genetics • SNP Tagging

Introduction

Similar to other Latino populations, Mexican Mestizos are a recently admixed population of African, European, and Amerindian ancestry [1]. Latino populations are a powerful resource for analyzing the genetic bases of complex diseases, despite the fact that their diversity presents several challenges to genetic studies. Mexico has committed itself to developing a human and technological infrastructure for genomics over the past five years, with a focus on the creation of a national platform for genomic medicine to improve Mexican healthcare. Mexico is an excellent location for conducting genomic analyses of common complex diseases due to its population of approximately 105 million people, which includes 60 Amerindian groups. Genome-wide association studies (GWAS) and admixture mapping (AM) is two current methods for locating genes involved in complex diseases [2]. AM relies on the availability of panels of genome-wide markers with frequency differences between parental populations, whereas GWAS rely on effective SNP tagging. Due to the need for a greater number of markers to achieve the same relative power as Asians and Europeans, as well as the lack of knowledge about population-specific linkage disequilibrium patterns, efficient tagging and imputation is limited for Latino populations, which are not fully represented in the Hap Map [3]. Additionally, individuals with ancestry differences are excluded in GWAS to reduce the number of false positives caused by population structure. This is impractical for studies involving Latinos, such as those involving Mexicans, where Mestizos make up more than 80% of the population and have known differences in ancestral proportions. Regarding AM, there are a few Latino-specific SNP panels, but there is still a lack of comprehensive genome-wide information from Mestizo and Amerindian populations. Recent research on Latin American populations has revealed distinct patterns of ancestral contribution between and within groups, which are correlated with the density of native pre-

Columbian populations and patterns of recent demographic growth [4]. Improved AM panels for Latin American populations should take into account these differences. Historically, variations in parental population densities and demographic growth have influenced admixture patterns across Mexico. Mestizos from various regions exhibit genetic heterogeneity both among themselves and between themselves. However, there is currently no publicly accessible genome-wide comparison of the various Mestizo and Amerindian populations in Mexico [5]. We created the Mexican Genome Diversity Project (MGDP) to investigate LD patterns and genomic diversity in Mexicans. Strategies for the genetic analysis of Mexican and related admixed populations, such as marker selection for optimal coverage of common genetic variation in GWA and targeted association studies, as well as the appropriate application of tagging and imputation approaches and AM in Mexicans and other Latino populations, will benefit from this [6].

Materials

Mexican Populations' Private Alleles

Mestizos shared all private alleles with ZAP, indicating their AMI ancestry. All six states had the same number of private alleles, but the proportion of variants with higher frequencies (MAF > 0.20) varied. In neither ZAC nor YUC did we find any alleles with MAFs greater than 0.30 or MAFs greater than 0.20. These findings are consistent with our observations that the subpopulations of Northern Mexico have the highest EUR ancestral contribution and the highest AMI ancestries, respectively [7]. We searched for alleles that were exclusive to each Hap Map group in comparison to the rest in order to analyze this result in the context of continental genetic contributions. We found 5,660 alleles that were exclusive to YRI, 1,533 to CEU, and 669 to CHB + JPT.

Hap Map and Mexican Mestizo Population LD Patterns

SON and ZAC populations had fewer low-frequency markers (MAF 0.05) than Hap Map populations, indicating lower homozygosis. The fact that SON and ZAC have the highest HET values is consistent with this outcome. LD decay plots of highly correlated (r2 > 0.8 and D′ > 0.8) common alleles (MAF > 15%) were compared between Mexicans and Hap Map populations to determine the potential size of haplotype blocks in Mexican subpopulations. Mexicans' LD decay was comparable to that of non-African Hap Map samples. Long-range haplotype diversity (LRHD) analysis was carried out in order to gain a deeper comprehension of the variation in Mexican genomic structure [8]. Most Mexican subpopulations were less diverse when compared to Hap Map populations, and only SON had a LRHD pattern that was similar to that of Asians. The Mestizo groups VER and GUE had the lowest levels of haplotype diversity of any group. Mexicans had 68 haplotypes per mega base, or 95% of the chromosomes, while the YRI CEU CHB, JPT, and 93, 83, 69, and 70 haplotypes were required for the same coverage [9].

Discussion

There were more ethnic groups in Central and Southern Mexico in the pre-Hispanic era, and they were more politically, religiously, and socially cohesive than those in the north. Between 1545 and 1548, epidemics led to a significant decline in the Amerindian population, which resulted in the introduction of African slaves into the region. Since then, various demographic and historical factors have influenced admixture processes in far-off regions, influencing Mexicans' genomic structure [10]. Genetic variation between and within subpopulations from various parts of Mexico has resulted from these factors. Even though the people who took part in our study came from areas that corresponded to modern political divisions, their demographic dynamics, patterns of human settlement, and densities of Amerindians were all different. Mestizo participants were recruited at state universities because of the known bias of admixture estimates caused by socioeconomic stratification in Mexicans. The majority of students at these universities come from both urban and rural areas and fall into a wide range of socioeconomic strata. According to our findings, differences in AMI and EUR contributions are the primary cause of genetic differences among Mexican Mestizos from various regions of Mexico. Samples from the central region were found to be closer to ZAP in the majority of analyses, while samples from the northern region were found to be closer to CEU. This correlation correlated with the Amerindian population density in those regions, both in modern times and prior to the arrival of the Spanish. We found people with high AFR ancestry in GUE and VER, despite our analysis showing that the mean AFR ancestry was low (10%) and mostly homogenous among subpopulations.

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