Abstract of Presentation

Note: This paper should be typed in "Times New Roman" of 12pt.

Presentation Title(Should be no more than 20 words):

Analysis of genomic diversity in Mexican Mestizos to develop genomic medicine in Mexico

Abstract :

The extensive study of genetic diversity and linkage disequilibrium (LD) structure of different populations, have made possible the development of tagging and imputation strategies to comprehensively assess common genetic variation in association studies of complex traits and diseases. Nevertheless, these approaches may be somehow limited when populations being analyzed have ancestral contributions not comprehensively represented in public databases. It has been shown that efficient application of these strategies in recently admixed populations such as Mexican Mestizos and other Latinos, rely on the use of a higher number of markers to achieve the same relative power compared to Asians and Europeans. The large size and diversity of Latino populations pose several challenges for genetic studies but also represent a powerful resource for analyzing the genetic bases of complex traits and diseases, and their interaction with environmental factors such as diet, infectious agents and others. In the past five years, Mexico has made a serious commitment to the development of human and technological infrastructure for Genomics. This situation, together with a population of over 105 million inhabitants, including more than 60 Amerindian groups and with a complex history of admixture, makes Mexico an ideal country in which to perform research in genomics. As an initial effort to develop genomic medicine in Mexico, we have assessed the potential benefit of a Mexican haplotype map for a better design of genetic association studies. For this, we have extensively analyzed genome-wide data of Mexicans Mestizos from regions with different history of admixture and particular population dynamics. Mestizos ancestry was evaluated by including Amerindian as well as HapMap data. Our results give further evidence of genetic differences between Mexican subpopulations that should be considered in the design and analysis of association studies in complex trait and diseases; pharmacogenomics and nutrigenomics. We have evidence that a haplotype map for Mexicans is feasible and could be useful to optimize association studies in this population. Our study is one the first genome-wide genotyping efforts of a recently admixed Latin American population available in the public domain.