

**TITLE**  
**Allelic frequency of genes associated with type 2 diabetes**

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**Introduction.** Type 2 diabetes (T2D) is a complex disease characterized by insulin resistance and beta cell dysfunction. T2D accounts for 90-95% of diabetes cases, and is an important public health concern throughout the World. The study of T2D susceptibility with the approach of GWAS have been realized predominantly in populations of European ancestry. The GWAS performed in populations from other ancestry groups have provided initial evidence of overlap in T2D susceptibility loci between ancestry groups, as well as for coincident risk alleles at lead SNPs across diverse populations. The underlying causal variants at many of these loci are shared across ancestry groups and thus arose before migration of the human population out of Africa. However, there are also low frequency variants in Mexico and other ethnic groups.

**Methods.** A GWAS was performed in 3097 individuals living in Mexico City, of these 1865 were subjects with T2D (1200 females and 665 males) and 1232 were normoglycaemic controls (528 female and 704 males). For the association analysis, several softwares were used and an associated allele was considered when the P value was less than  $10^{-8}$ .

**Results.** The average proportions of Native American, European and West African admixture were estimated as 63.6, 33.6, and 2.8 %, respectively.

Some variants were association in European and Mexican population. Other common variants were modest effect but are homogeneous across ancestry groups.

**Conclusions.** We report the results of a GWA study of type 2 diabetes in an admixed sample from Mexico City and of a trans-ethnic meta-analysis. It is critical to carry out additional GWA studies in our populations, which have a high prevalence of type 2 diabetes. Most of the recent advances in our knowledge of the genetic architecture of type 2 diabetes have been driven primarily by GWA studies in European populations, which have sampled tens of thousands of individuals. The meta-analysis showed some variants are associated in both populations.

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