

Ancestry-Associated Distribution of IL6, IL1B, and TNF Variants Reveals Differential Genetic Susceptibility to Inflammatory Diseases

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Abstract

Single nucleotide variants (SNVs) in *IL6* (rs1800795), *IL1B* (rs1143627), and *TNF* (rs1800629) have been associated with inflammatory disease susceptibility. However, their allele and genotype distributions remain insufficiently characterized in Mestizo and Indigenous populations. This study aimed to determine the distribution of these variants and assess their potential biomedical relevance. A cross-sectional study was run in 400 samples from Mexican Mestizo and Indigenous populations. Genotyping was performed using TaqMan assays by Real-Time PCR. Allele and genotype frequencies were compared among Mexican groups and worldwide reference populations. The proportion of previously reported risk alleles was estimated individually and in combination. Significant differences in their distributions were observed across populations ($p < 0.0001$). The European and Tarahumara populations exhibited the greatest genetic differentiation. Indigenous populations displayed a significantly higher frequency in the non-risk category than Mestizos (51.2% vs. 23.8%; $p < 0.01$). Globally, Europeans showed the highest frequency in the risk category (87.5%), while Indigenous populations had the lowest (48.8%). These findings reveal marked interpopulation genetic heterogeneity and suggest population-specific differences in genetic susceptibility, highlighting the importance of incorporating ancestry-informed approaches to inflammatory disease risk assessment for public health strategies and biomedical research.

Introduction

Mexico exhibits profound cultural and ethnic diversity, including 68 officially recognized Indigenous groups (Esparza-Romero 2021; Salas-Martínez et al. 2019), which collectively account for approximately 10% of the national population. The remaining 90% corresponds predominantly to Mestizo population whose genetic composition reflects admixture among European, African, and Indigenous ancestries after the Spanish colonization more than 500 years ago (Rangel Villalobos & Martínez Cortes 2019). Unlike other regions where European colonization led to a substantial —or in some cases total — decline of Indigenous populations, in Mexico these Native groups not only contributed significantly to the admixture process but also constitutes a significant component of the country's contemporary demographic structure (INEGI 2025; Moreno-Estrada et al. 2014).

The Mexican Mestizo population is characterized by substantial genetic heterogeneity. Population genetic studies have consistently demonstrated the presence of an ancestry gradient across the country, with European ancestry increasing towards the northern and western regions, while Indigenous ancestry predominates in central and southeastern regions of the country. This geographic distribution reflects the complex demographic and historical processes that have shaped the contemporary genetic landscape of Mexico (Moreno-Estrada et al. 2014; Rangel Villalobos & Martínez Cortes 2019; Rubi-Castellanos et al. 2009). Furthermore, several studies have reported important genetic differences between Mexican Mestizos and other worldwide populations, as well as between Mestizos and Indigenous groups within Mexico (Moreno-Estrada et al. 2014; Salas-Martínez et al. 2019).

Although the human genome is approximately 99.9% identical among individuals, the remaining fraction of genetic variation accounts for much of the observed phenotypic diversity across populations and contributes to interindividual differences in disease susceptibility. Among the various forms of genetic variation, single-nucleotide variants (SNVs) constitute the most prevalent type in the human genome. (Caratachea 2007; Lloyd-Price et al. 2016; Ortega & Meyers 2014; Zamudio-Felix et al. 2025).

Numerous SNVs have been implicated in inflammatory diseases, including those analyzed in the present study. For instance, the C allele of rs1800795 (NG_011640.1:g.4880C > G) in the *IL6* gene, and the T allele of rs1143627 (NG_008851.1:g.4970C > T) in the *IL1B* gene, have been reported as a risk factors for obesity (Bojarczuk et al. 2024; Gholami et al. 2019; Koc et al. 2023; Suzuki et al. 2009). Similarly, the A allele of rs1800629 (NG_007462.1:g.4682G > A) in the *TNF* gene has been associated with metabolic syndrome (Ghareeb et al. 2021; Yang et al. 2015). Despite their potential relevance in conditions characterized by a strong inflammatory component, the allele and genotype distributions of these proinflammatory gene variants remain poorly characterized in both Mestizo and Indigenous populations of Mexico.

In this context, the objective of the present study was to analyze the population distribution of functional genetic variants in the *IL6*, *TNF*, and *IL1B* genes among Mexican Mestizo and Indigenous populations, and to compare these distributions with those reported in worldwide populations. This analysis aims to enhance the understanding of the genetic structure of these populations and assess the potential biomedical implications of these variants, given their previously documented associations with inflammatory and metabolic diseases.

Materials and Methods

Study population

This cross-sectional study included 400 samples per genetic variant, obtained from resident unrelated subjects from six Mexican Mestizo populations of the following geographic regions: North (Chihuahua state; MxN), Northeast (Nuevo León state; MxNE), West (Jalisco state; MxW), Center (Mexico City and Puebla state; MxC), Southeast (Yucatán state; MxSE), South (Guerrero and Chiapas states; MxS). In addition, four Indigenous groups of the following geographic regions were analyzed: Tarahumaras (North; MxTar), Mayas (Southeast; MxMay), Purepechas (West; MxPur), and Nahuas (Center; MxNah). Each population consisted of 40 samples (n = 40) for each genetic variant analyzed.

For Indigenous populations, inclusion criteria required self-identification as a member of a representative Native group and documented parental origin from a community belonging to that group. All participants signed a written informed consent under approval of the Committee of Ethics and Research of the (CUCI-UdeG) (N° 33949), Mexico.

Population samples were obtained from the genomic repository of the Molecular Genetics Research Institute (IIGM), Centro Universitario de la Cienega, Universidad de Guadalajara (CUCI-UdeG), Mexico. DNA samples from subjects with first-degree kinship relationships (e.g., parent–offspring pairs) were excluded to avoid relatedness bias. DNA samples with concentrations below 15 ng/μL or with inadequate purity (260/280 nm ratio ranging from < 1.6 or > 2.0) were also excluded. This study complied with the Mexican General Health Law on research involving human subjects and adhered to the principles of the Helsinki Declaration (World Medical Association 2013).

Determination of genetic variants

DNA samples were quantified using the NanoDrop 2000™ instrument (Thermofisher Scientific) at a wavelength of 260 nm and diluted to 20 ng/μL. Genotyping was performed by Real-Time PCR (PCR) on a QuantStudio™ 5 instrument using TaqMan™ reagents and Genotyper software by the allelic discrimination method (Applied Biosystems, Thermofisher Scientific). Table 1 shows the reference sequence of the TaqMan probes used in the present study.

Table 1
TaqMan™ assays used in this study

SNV	Reference sequence	Allele	Fluorochrome
rs1800795	ACTTTTCCCCTAGTTGTGTCTTGC[C/G]ATGCTAAAGGACGTCACATTGCACA	C	VIC
		G	FAM
rs1143627	CCAGTTTCTCCCTCGCTGTTTTTAT[C/T]GCTTTCAAAGCAGAAGTAGGAGGC	C	VIC
		T	FAM
rs1800629	GAGGCAATAGGTTTTGAGGGGCATG[A/G]GGACGGGGTTCAGCCTCCAGGGTCC	A	VIC
		G	FAM
SNV: Single Nucleotide Variant; rs: Reference SNV; C: Cytosine; G: Guanine; T: Thymine; A: Adenine			

The PCR was performed under the following conditions: pre-reading at 60°C/30 seconds; activation at 95°C/5 minutes; 45 cycles of denaturation at 95°C/15 seconds; annealing/extension at 60°C/1 minute; and final extension at 60°C/30 seconds.

Statistical analysis

Allele and genotype frequencies were estimated using the GenAIEx 6.5 (Peakall & Smouse 2012). Genetic diversity parameters—including expected (H_e) and observed (H_o) heterozygosity, as well as the inbreeding coefficient (F)—were calculated for each population.

Hardy-Weinberg equilibrium (HWE) was evaluated using the Genetic Data Analysis 1.1 (GDA) (Lewis & Zaykin 2001) by means of Fisher’s exact tests on 5000 permutations. A Neighbor Joining (NJ) dendrogram using TreeView software (Roderic 2003) was generated to represent the relationship and genetic distances between the analyzed populations, incorporating comparative frequency data from the 1000 genomes project. For interpopulation analyses, pairwise comparisons were calculated to assess genetic differentiation among Mexican Mestizo and Indigenous populations, as well as between these groups and worldwide populations using fixation index (F_{st}). Bonferroni correction was applied to adjust multiple comparisons, and a corrected p -value ($0.05/n$, where n is the number of comparisons performed) was considered statistically significant.

Worldwide population groups assessment included Africa (AFR), America (AME) Europe (EUR), East Asia (EAS), and South Asia (SAS), as well as individuals of Mexican ancestry residing in Los Angeles, California (MXL), according to the 1000 Genomes Project (Marcus et al. 2025). Statistical analyses were conducted using IBM SPSS Statistics for Windows, version 27.0 (IBM Corp., Armonk, NY, USA).

Based on previous studies indicating that the C allele of rs1800795, the A allele of rs1800629, and the T allele of rs1143627 are associated with increased risk of inflammatory diseases (Bojarczuk et al. 2024; Ghareeb et al. 2021; Suzuki et al. 2009), we evaluated the predicted risk conferred by these variants in the Mexican populations analyzed. Two categories were defined according to the combination of alleles for the three SNVs: Non-risk (0 risk alleles) and Risk (≥ 1 risk alleles). Differences in the distribution of these categories between Mestizo and Indigenous populations were assessed using the chi-square test to identify groups with higher predicted genetic risk. Assuming no linkage disequilibrium among these variants due to their distinct chromosomal locations, the same risk classification was estimated for worldwide populations and subsequently compared through pairwise analyses.

Results

Allele and Genotype frequencies

The allele and genotype frequencies of the analyzed SNVs in the Mexican populations are shown in Table 2. For rs1800795 (*IL6*), the alternative allele G was the most frequent across populations, with frequencies ranging from 81.2 to 98.8%. For rs1143627 (*IL1B*), the reference C allele was predominant (52.5 to 85%), as was the reference G allele for rs1800629 (*TNF*), which ranged from 91.3 to 100%.

Regarding genotype distributions, the *IL6* variant (rs1800795) presented frequencies of 83.5% for G/G, 14.25% for C/G, and 2.25% for C/C. The Tarahumara population was monomorphic for the G allele in this locus. For the *IL1B* variant (rs1143627), genotype frequencies were 45.5% for C/T, 43% for C/C, and 11.5% for T/T. In the case of the *TNF* variant (rs1800629), genotype frequencies were 93% for G/G, 6.5% for G/A, and 0.5% for A/A; the Purépecha, Nahua, and Maya populations were monomorphic for the G allele at this locus. Genotype distribution in all Mexican populations agreed with HWE expectations.

Interpopulation analyses

F_{st} genetic distances and pairwise comparisons between Mexican and worldwide populations based on the studied variants in *IL6*, *TNF*, and *IL1B* presented in Supplementary Table 1. They provide further insight into the heterogeneity of genetic risk

for inflammatory diseases across worldwide populations.

Table 2
Allele and Genotype frequencies of the IL6 (rs1800795), IL1B (rs1143627) and TNF (rs1800629) variants in the Mexican population

SNV	Alleles and Genotypes	Mestizo populations					Indigenous populations				
		MxN	MxNE	MxW	MxC	MxS	MxSE	MxTar	MxPur	MxNah	MxMay
IL6 rs1800795	C	17.5	10.0	15.0	15.0	7.5	18.8	0.0	1.2	1.2	7.5
	G	82.5	90.0	85.0	85.0	92.5	81.2	100.0	98.8	98.8	92.5
	C/C	5.0	2.5	5.0	2.5	2.5	5.0	0.0	0.0	0.0	0.0
	C/G	25.0	15.0	20.0	25.0	10.0	27.5	0.0	2.5	2.5	15.0
	G/G	70.0	82.5	75.0	72.5	87.5	67.5	100.0	97.5	97.5	85.0
HWE p-value		0.310	0.316	0.189	0.901	0.189	0.597	1.000	0.936	0.936	0.936
IL1B rs1143627	C	52.5	68.8	55.0	57.5	62.5	63.8	85.0	70.0	70.0	72.5
	T	47.5	31.2	45.0	42.5	37.5	36.2	15.0	30.0	30.0	27.5
	C/C	25.0	45.0	30.0	40.0	32.5	37.5	72.5	45.0	52.5	50.0
	C/T	55.0	47.5	50.0	35.0	60.0	52.5	25.0	50.0	35.0	45.0
	T/T	20.0	7.5	20.0	25.0	7.5	10.0	2.5	5.0	12.5	5.0
HWE p-value		0.516	0.505	0.949	0.073	0.012	0.390	0.901	0.228	0.292	0.416
TNF rs1800629	G	91.3	92.5	92.5	97.5	97.5	95.0	96.0	100.0	100.0	100.0
	A	8.7	7.5	7.5	2.5	2.5	5.0	4.0	0.0	0.0	0.0
	G/G	82.5	87.5	85.0	95.0	95.0	92.5	92.5	100.0	100.0	100.0
	G/A	17.5	10.0	15.0	5.0	5.0	5.0	7.5	0.0	0.0	0.0
	A/A	0.0	2.5	0.0	0.0	0.0	2.5	0.0	0.0	0.0	0.0
HWE p-value		0.183	1.000	1.000	1.000	1.000	0.073	0.949	0.821	1.000	1.000
SNV: Single Nucleotide Variant; rs: Reference SNV; C: Cytosine; G: Guanine; T: Thymine; A: Adenine; IL6: Interleukin 6; IL1B: Interleukin-1 beta; TNF: Tumoral Necrosis Factor-alpha; HWE: Hardy-Weinberg equilibrium. Please check abbreviations in Study populations and Statistical analysis sections											

Among Mexican populations, Indigenous groups exhibited significant genetic differentiation relative to the remaining groups, with the Tarahumara group (MxTar) showing the highest degree of differentiation. At the global level, European (EUR) and East Asian (EAS) populations displayed the greatest genetic differentiation relative to the remaining groups. African (AFR), Admixed American (AMR), and South Asian (SAS) populations also showed significant differentiation, differing from eight, seven, and six populations, respectively.

The genetic differentiation among Mexican and worldwide populations for the studied SNVs were graphically represented in a NJ tree (Fig. 1). Most Mexican Mestizo populations clustered into the upper branch together with the Admixed American (AMR) and South Asian (SAS) groups. In contrast, MxNE and MxS populations occupied an intermediate position, clustering alongside the Indigenous groups MxPur, MxNah, and MxMay, as well as the African (AFR) populations. The most genetically differentiated cluster corresponded to European (EUR) populations, followed by the Tarahumara group (MxTar) and the East Asian (EAS) populations, which were located towards the lower end of the dendrogram.

Overall, these results underscore the presence of population substructure and highlight the variability in the distribution of proinflammatory genetic variants across populations, which may contribute to differences in genetic susceptibility to inflammatory-related conditions.

Risk alleles in Mexican and worldwide populations

We compared the proportion of risk alleles among Mexican and worldwide populations, using the combined three-locus model (Fig. 2), based on previously reported risk associated alleles. The EUR population showed the highest cumulative number of risk alleles, reaching up to six. In contrast, Admixed American (AMR), South Asian (SAS), East Asian (EAS), African (AFR), and Mexican Mestizo populations displayed a relatively homogeneous distribution, with most individuals carrying four or five risk alleles.

Mexican Indigenous populations showed a lower overall load of risk alleles, and the highest proportion of individuals without risk alleles. This pattern was most pronounced in the Tarahumara (MxTar) population, followed by the Nahua (MxNah), Purépecha (MxPur), and Maya (MxMay) groups, which result in a significant differentiation between Mexican Indigenous and Mestizos (51.2% vs. 23.8%; $p < 0.01$) (Fig. 3).

Predicted genetic risk for worldwide populations was estimated with the proportion of risk-alleles for the analyzed SNVs (Fig. 4). The European (EUR) population exhibited the highest proportion of individuals classified in the risk category (87.5%), followed by East Asian (EAS) and Mexican Mestizo populations (76.2%). In contrast, Mexican Indigenous populations showed the lowest proportion of individuals in the risk category (48.8%).

These findings indicate a clear interpopulation variability in the cumulative distribution of inflammatory-related risk alleles, with Indigenous Mexican populations exhibiting the lowest predicted genetic risk under the three-locus model.

Discussion

Inflammatory diseases arise from complex interactions between genetic and environmental factors, with functional variants in *IL6* (rs1800795), *IL1B* (rs1143627), and *TNF* (rs1800629) contributing to interindividual variability in inflammatory responses. In this study, we characterized the allele and genotype distributions of these variants in Mexican Mestizo and Indigenous populations, revealing significant differences in the distribution of inflammatory risk alleles compared with global populations.

Mexican Mestizos exhibited higher frequencies of risk alleles than Indigenous groups, whereas European populations showed the highest frequencies worldwide. These findings highlight the genetic heterogeneity underlying inflammatory susceptibility and emphasize the importance of population-specific genetic backgrounds when assessing disease risk. Although our study does not establish direct genotype–phenotype associations, the observed distribution patterns may be relevant in the context of the high prevalence of obesity in Mexico (Barquera et al. 2024), a condition strongly associated with chronic low-grade inflammation.

Our findings are consistent with previous reports showing that the GG genotype of *IL6* (rs1800795) and *TNF* (rs1800629) predominates in Mexican Mestizo populations (Posadas-Sánchez et al. 2024; Torres-Poveda et al. 2025; Valdez-Velazquez et al. 2024), a pattern also observed in individuals with Maya ancestry (Nakazawa-Ueji et al. 2024; Valencia Villalvazo et al. 2012). Likewise, the heterozygous genotype of *IL1B* (rs1143627) has been reported as the most frequent in Mestizos (Gallegos-Arreola et al. 2024; Mendoza-Carrera et al. 2019). However, limited data on Indigenous populations may bias frequency estimates given their substantial ancestral contribution in Mexico.

In contrast to the Mestizo population, Indigenous groups exhibited markedly lower frequencies of the C allele at rs1800795 and the A allele at rs1800629, both commonly associated with enhanced pro-inflammatory responses. Notably, the Tarahumara population was monomorphic for the G allele at rs1800795, whereas the Purepecha, Nahua, and Maya

populations were monomorphic for the G allele at rs1800629. The presence of monomorphic profiles at these loci indicates reduced genetic variability in key inflammatory pathways among Indigenous populations.

Such patterns likely reflect the combined effects of population history, including founder events, genetic drift, and long-term demographic isolation, which have characterized many Native American groups (Rangel-Villalobos et al. 2016). In addition, selective pressures may operate differently across populations, favoring adaptation to local environmental conditions. This phenomenon has been documented in Indigenous populations from central Mexico, where pathogen-rich environments appear to have shaped variation in immune-related pathways (Reynolds et al. 2019). Comparable patterns have been reported in African populations, which exhibit monomorphism at several loci when contrasted primarily with European populations, underscoring the influence of distinct evolutionary trajectories and demographic histories on genetic diversity (Babenko et al. 2019; Juárez-Luis et al. 2023).

All analyzed Mexican populations conformed to Hardy–Weinberg equilibrium (HWE) for the evaluated variants. This observation suggests the absence of major genotyping errors, strong ongoing directional selection, or recent admixture events substantially affecting these loci. Conformity with HWE expectations is generally interpreted as evidence of population genetic stability and methodological robustness in population-based studies, thereby supporting the reliability of the reported allele and genotype frequency estimates (Graffelman & Weir 2016). Conversely, deviations from equilibrium may indicate selective pressures acting on specific genotypes or population stratification, in which individuals from genetically distinct subgroups with different allele frequencies are analyzed together (Luis Royo 2021).

Taken together, these findings support the interpretation that the current distribution of inflammatory gene variants in Mexican populations is shaped primarily by long-term demographic and evolutionary processes rather than by recent perturbations. This underscores the importance of incorporating historical and population-specific contexts when interpreting genetic susceptibility to inflammatory diseases.

Genetic distance analyses further reflected the complex demographic history of Mexican populations. Most Mestizo groups clustered closely together, whereas Indigenous populations formed a distinct cluster and showed greater genetic proximity to the African reference population. This population structure reinforces one of the central findings of this study: Mestizo groups exhibited a significantly higher proportion of cumulative genetic risk compared with Indigenous populations ($p < 0.01$). Considering that the functional implications of these alleles have been previously documented, the observed distribution patterns suggest that genetic background may contribute to interpopulation differences in susceptibility to low-grade inflammatory processes in Mexico.

In contrast, previous studies have reported higher genetic risk among populations with greater Native American ancestry for variants associated with cardiovascular disease and low HDL-cholesterol levels when compared with diverse global populations (Acuña-Alonzo et al. 2010; Zamudio-Felix et al. 2025). These apparently divergent findings underscore the context-dependent nature of genetic susceptibility. Genetic variants are not intrinsically pathogenic or protective; rather, their biological effects depend on population-specific genetic architecture, linkage disequilibrium structure, environmental exposures, and evolutionary history. Consequently, a variant associated with increased inflammatory risk in Mestizo populations may not confer the same effect in Indigenous groups, and vice versa. Failure to account for such population-specific contexts may lead to inaccurate interpretations of genetic risk and limit the generalizability of association studies, particularly in admixed populations (Cavazos & Witte 2020; Gurdasani et al. 2019).

Interestingly, the European population appeared as the most genetically distinct group in the dendrogram, exhibited the highest number of risk alleles, and showed the greatest proportion within the cumulative risk category (87.5%). In contrast, the African population and Indigenous groups—particularly the Tarahumara—displayed the lowest frequency within the risk category. Similar patterns were reported by Babenko et al. (2019), who observed a higher genetic risk profile for obesity-associated variants in European populations compared with other global groups (Babenko et al. 2019). One possible explanation for this distribution is ascertainment bias, as many single-nucleotide variants (SNVs) have been identified through genome-wide association studies (GWAS) conducted predominantly in European ancestry populations, potentially

inflating the apparent frequency of “risk” alleles in Europeans relative to other ancestries (Kim et al. 2018). Nonetheless, careful interpretation requires variant-specific analyses within each population context.

In summary, this study provides a comprehensive population-based characterization of functional inflammatory gene variants in Mexican Mestizo and Indigenous populations, revealing significant intergroup differences in allele frequencies and inferred cumulative genetic risk. The integration of allele distribution analyses, HWE testing, and genetic distance approaches highlights the strong influence of ancestry, demographic history, and evolutionary processes on the genetic architecture of inflammatory susceptibility. Although the genetic diversity of the three variants analyzed has been scarcely explored in Mexican Mestizo and Indigenous populations, limiting direct biomedical extrapolation, our findings provide valuable baseline data for future research.

Several limitations should be acknowledged, including the absence of direct genotype–phenotype association analyses and the relatively small sample size, which may constrain the clinical interpretation of inferred risk. Despite these limitations, our results emphasize the importance of variant-specific and population-aware approaches in genetic research, particularly in admixed settings. Such strategies are essential for improving our understanding of inflammatory disease mechanisms in Mexican populations and may ultimately inform more precise and population-tailored preventive or therapeutic interventions.

Conclusion

This study provides robust evidence of substantial genetic heterogeneity between Mexican Mestizo and Indigenous populations in key functional variants of *IL6* (rs1800795), *IL1B* (rs1143627), and *TNF* (rs1800629), genes critically involved in inflammatory regulation. The significantly higher cumulative load of inflammatory risk alleles observed in Mexican Mestizo and European populations highlights the marked population specificity of genetic susceptibility profiles.

These findings reinforce the necessity of incorporating ancestry-informed frameworks into genetic and biomedical research, particularly in admixed populations such as those in Mexico. Ignoring population structure may obscure genuine biological differences, distort risk estimation, and reduce the translational relevance of association studies. By establishing baseline population-level data for these functional inflammatory variants, this study contributes meaningful evidence toward more precise, equitable, and population-aware strategies for understanding and managing inflammation-related diseases.

Declarations

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Author contributions JIRR: writing—original draft preparation, methodology, GAN: review and editing, HRV: Instrument and DNA population sample provision, data analysis, review and editing, conceptualization, KGB: funding acquisition, project administration, statistical analysis, review and editing, conceptualization.

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Data availability All data related to this study are presented in the manuscript.

Conflict of interest The authors declare no conflict of interest.

Ethical approval The study was conducted in accordance with the ethical guidelines of the Helsinki Declaration. Approval for the project was obtained from the Ethics and Research Committee of the Centro Universitario de la Ciénega at the

Universidad de Guadalajara (CUCI-UdeG, Mexico) (N° 33949). The confidentiality and anonymity of all participants were strictly maintained throughout the study.

Informed consent Informed consent was obtained from all individual participants included in the study.

Supplementary Information Additional supporting information can be found online in the Supplementary Information section.

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Figures

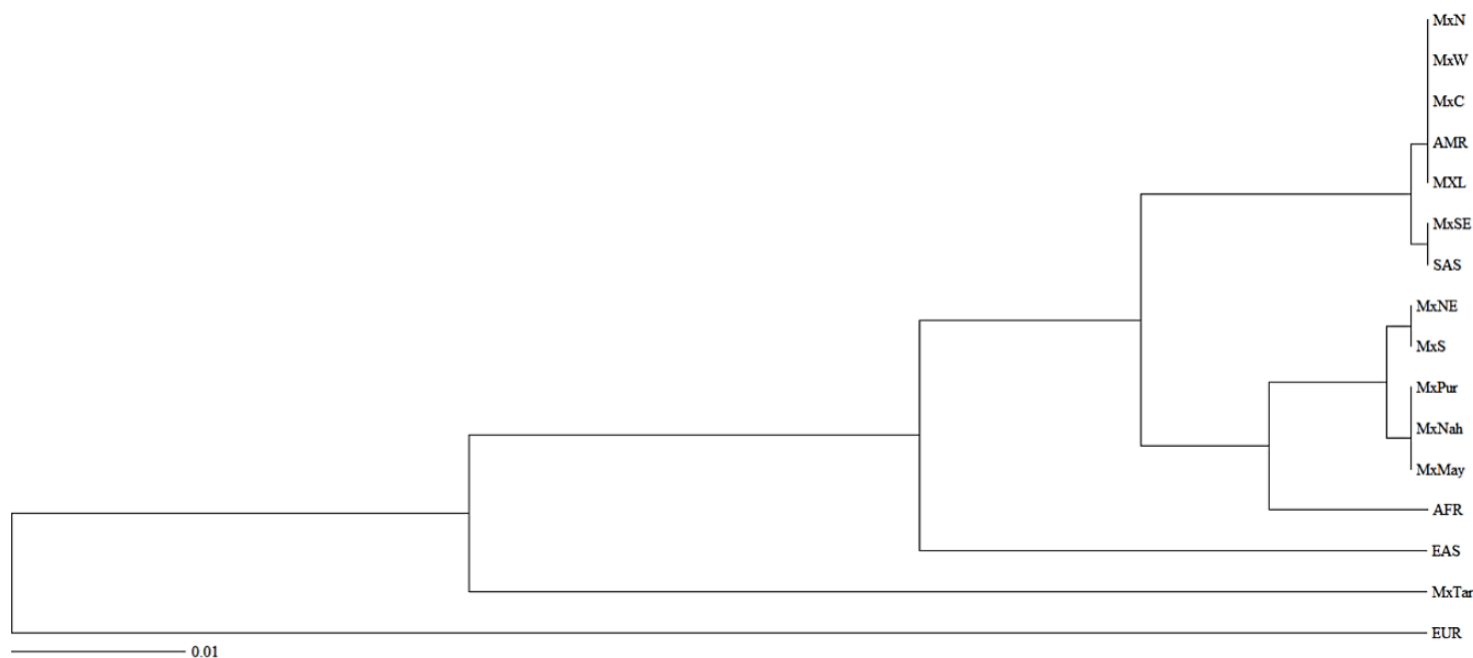


Figure 1

NJ tree representing F_{st} distances between Mexican and worldwide populations based on the IL6 (rs1800795), IL1B (rs1143627) and TNF (rs1800629) variants. Please check abbreviations in Study populations and Statistical analysis sections

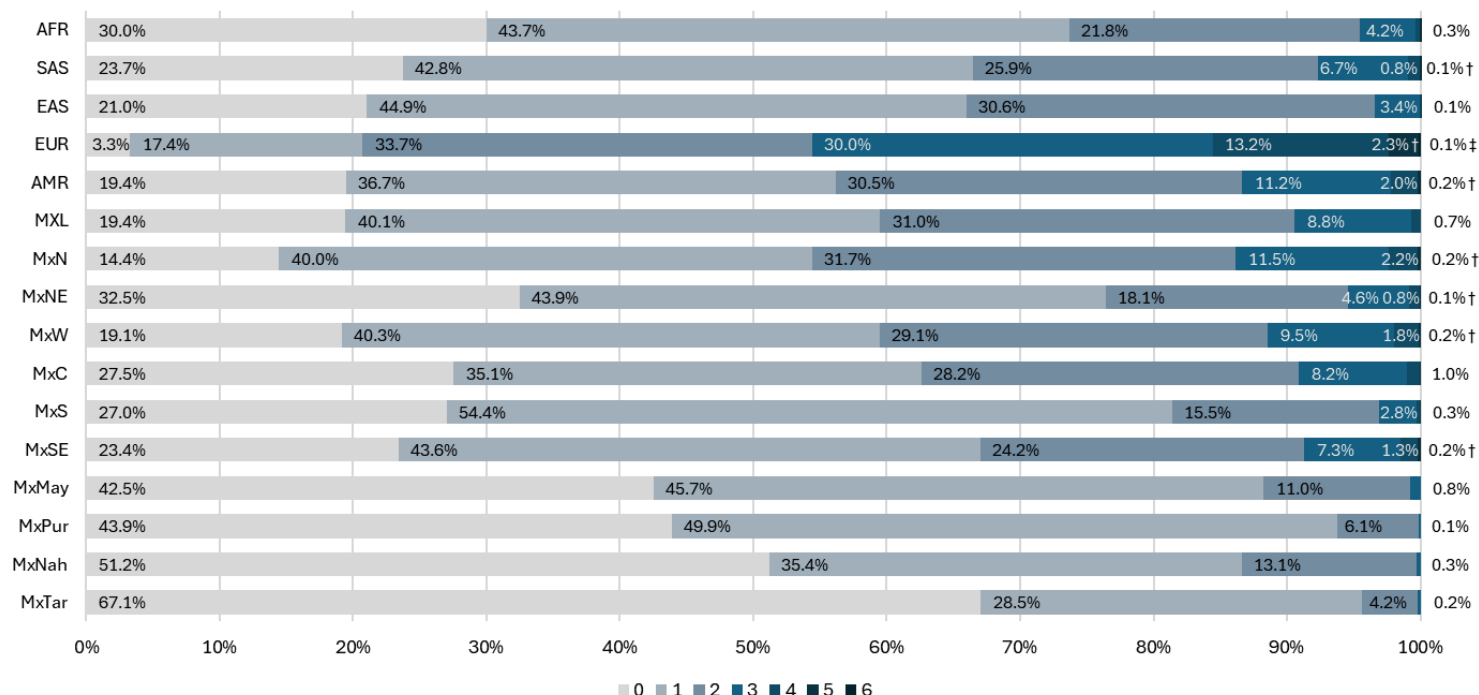


Figure 2

Number of risk alleles in Mexican and worldwide populations based on IL6 (rs1800795), IL1B (rs1143627) and TNF (rs1800629) variants. † Percentage with five risk alleles; ‡ Percentage with six risk alleles. Please check abbreviations in Study populations and Statistical analysis sections

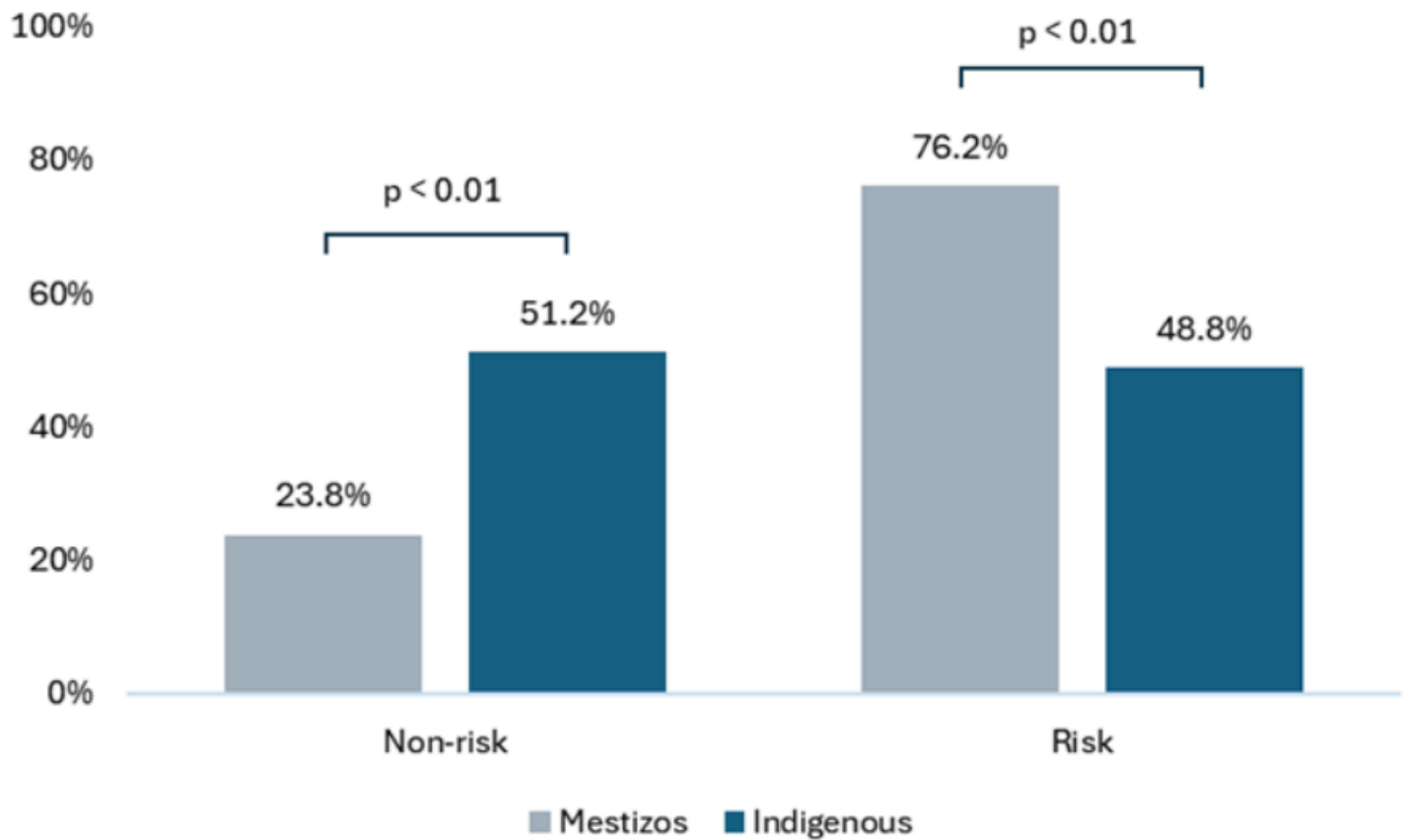


Figure 3

Non-risk and risk percentage in Mestizos and Indigenous Mexican populations based in IL6 (rs1800795), IL1B (rs1143627) and TNF (rs1800629) variants. Categories were defined based on the combination of alleles for the analyzed SNVs: Non-risk (0 risk alleles) and Risk (≥ 1 risk alleles; C allele of rs1800795, T allele of rs1143627 and A allele of rs1800629)

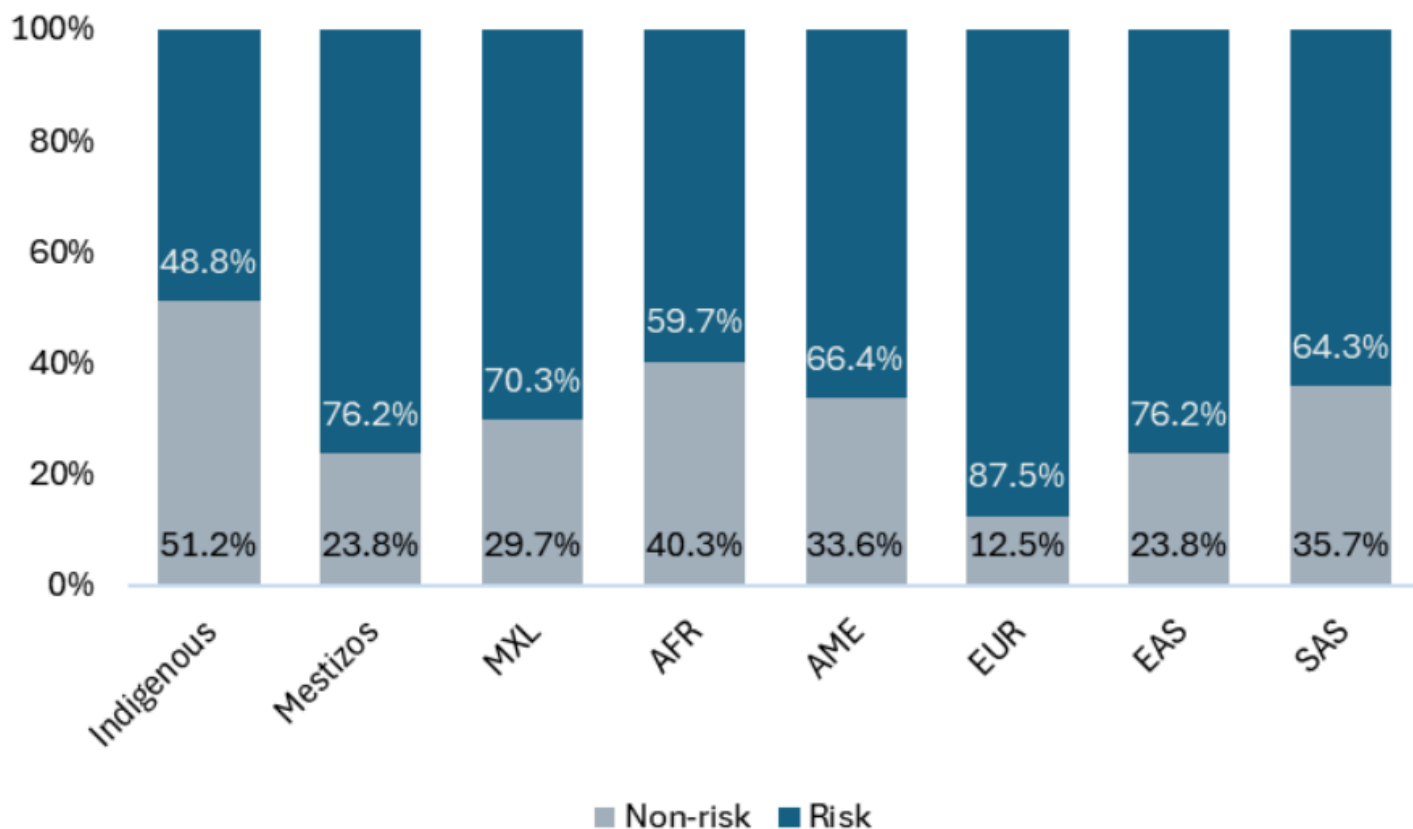


Figure 4

Non-risk and Risk percentage in Mexican and worldwide populations based on IL6 (rs1800795), IL1B (rs1143627) and TNF (rs1800629) variants. Please check abbreviations in Study populations and Statistical analysis sections

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