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LETTER TO EDITOR

Mexican Human Leukocyte Antigen Alleles Might Predict Clinical Outcome in SARS-CoV-2 Infected Patients

Country border lines are illusory and do not restrain the spread of pathogens. For instance, the US has now become the epicenter of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic, but just South of its border, in Mexico, confirmed cases have only surpassed a thousand patients, and fatalities are less than a hundred. Such drastic differences replicate worldwide, with no merit due to health-care policies, but probably to ancestry and genetics.

Human leukocyte antigen (HLA) genes dictate the immune response to pathogens. Interestingly, HLA genes are the most polymorphic in the human genome and are non-randomly inherited as conserved blocks. The distribution of HLA alleles is determined by ancestry and natural selection through infectious diseases.

The immunogenetics of the Mexican population has been shaped by the infectious pandemics of the 16th century that killed more than half of the Native population[1] and a highly heterogeneous combination of Amerindian, Caucasian, and African HLA haplotypes[2]. Thus, the immunogenetics of the Mexican population has stirred great interest. Moreno-Estrada et al.[3] demonstrated that Mexican Mestizos can be genetically stratified into substructures concordant with indigenous ancestry, and these groups can be as genetically differentiated as Asians are from Europeans, along with considerable differences in biomedical traits.

The progression from a viral infection to clinical disease, with varying degrees of severity, is determined by a complex interaction between the virus and the host immune system. Specific HLA alleles favor antigen presentation of immunodominant viral epitopes and clearance of the infection, while others impair peptide presentation, mount a weak immune response, and are unable to eradicate the infection[4]. Studies on HIV/AIDS have consistently corroborated such correlation: among untreated patients with almost insignificant viral loads, or "elite" responders, the HLA-B*57 allele is *significantly increased* compared to non-controllers[5], which represents an interesting paradigm. Hence, it is of utmost relevance to analyze the HLA haplotypes of patients capable of mounting an effective immune response against the SARS-CoV-2 and compare them with those who develop severe manifestations.

Our research group has just begun collaborating in a project aimed to analyze the HLA haplotypes of mild, severe, and fatal cases of SARS-CoV-2 infection in Mexico. This study will potentially provide the groundwork to translate the immunogenetics discipline into infectology, epidemiology, and public health, whereby impacting on health-care policies tailored for the Mexican population that in the face of future pandemics might prioritize genetically susceptible individuals.

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REFERENCES

1. Acuna-Soto R, Stahle DW, Therrell MD, Griffin RD, Cleaveland MK. When half of the population died: the epidemic of hemorrhagic fevers of 1576 in Mexico. FEMS Microbiol Lett. 2004;240:1-5.
2. Zúñiga J, Yu N, Barquera R, Alosco S, Ohashi M, Lebedeva T, et al. HLA class I and class II conserved extended haplotypes and their fragments or blocks in Mexicans: implications for the study of genetic diversity in admixed populations. PLoS One. 2013; 8:e74442.
3. Moreno-Estrada A, Gignoux CR, Fernández-López JC, Zakharia F, Sikora M, Contreras AV, et al. Human genetics. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science. 2014;344:1280-5.
4. Unanue ER, Turk V, Neefjes J. Variations in MHC class II antigen processing and presentation in health and disease. Annu Rev Immunol. 2016;34:265-97.
5. Martin MP, Carrington M. Immunogenetics of HIV disease. Immunol Rev. 2013;254:245-64.

Rafael Garcia-Silva, Susana Hernandez-Dono, Lourdes Mena, and Julio Granados

Immunogenetics Division, Department of Transplantation, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico City, Mexico

*Corresponding author:
Julio Granados
E-mail: julgrate@yahoo.com