HLA Alleles Are Race Specific

Here are just a few of the vast numbers of studies which prove that HLA alleles are inherited and race specific:


“A Unique African HLA Haplotype May Identify a Population at Increased Risk for Kidney Graft Rejection”

By Pauline C Creemers (immunology Department, UCT Medical School Cape Town, South Africa) and Delawir Khan (Nephrology Department, University of Cape Town Medical School)

“Unique HLA alleles and MHC haplotypes have been identified in the Cape Colored and in the black South African populations. . . . Because HLA haplotypes are inherited ‘en-bloc’ as ancestral haplotypes that vary considerably between races.”


“HLA Diversity: Detection and Impact on Unrelated Hematopoietic Stem Cell Donor Characterization and Selection”

By Carlyn Katovich Hurley, Georgetown University Medical Center, Washington DC, USA, as published in the International Journal of Hematology, 76 (2002) Supplement II.

“The alleles differ also in frequency in different populations. Thus, the search for a DRB1*0302 matched donor, for example, should be focused on populations of direct African origin since this allele is extremely rare in Caucasian or Oriental populations.”

“These frequencies must be taken into account as patients are evaluated for unrelated donor transplantation in order to estimate their probability of finding an allele matched donor to design a search strategy.”

3. [http://www.ebi.ac.uk/imgt/hla/help/ethnic_help.html](http://www.ebi.ac.uk/imgt/hla/help/ethnic_help.html)

The European Bioinformatics Institute has the following to say on race and HLA alleles:

“The ethnic origins qualifier is used to describe the ethnic group and geographical location of the cell donor. The ethnic origin qualifier allows the user to query the ethnic group or geographical location of the cell donor. This can be used in population genetics studies of the HLA alleles. The origin of the cell donor can be used to infer which alleles are found in particular ethnic groups, and the geographical spread of HLA alleles.”

The European Bioinformatics Institute has, on the site given above, a
searchable HLA database where it is possible to look up specific HLA alleles and see in which racial groups they are dominant.


Here, the Indian based Dalistan Journal, discusses how HLA haplotypes were used to distinguish between Indo-European origin and non-Indo-European population elements in India:

"Racial Origin of Caste System Vindicated"

"While all non-Dalit, non-Adivasi castes in North India are of Aryan descent, in South India only the Brahmins are Aryans. Here are two abstracts from two papers establishing that the South Indian Brahmins are of Caucasian origin, in contrast to the Dravidians who are of Negroid stock [Iyer] [Caste] [Ravi]

Abstract - "Seventy-four randomly sampled Iyers, a Brahmin population of Tamil Nadu and preachers and followers of the Advaita philosophy, living in Madurai, were studied for their HLA-A, HLA-B, HLA-C, HLA-DR, HLA-DQ, C4A, C4B, and BF polymorphisms and compared with other populations. HLA alleles A1, A11.1, A24, A33, B35, B44, B51, B52, B57, Cw4, Cw6, Cw7, DR4, DR7, DR8, DR10, DR11, DR15, and DQ1 and C4A*3, C4A*4, C4A*6, C4A*Q0, C4B*1, and BF*S were represented in 15% of the samples studied. HLA alleles A25, A69, Cw3, Cw8, B45, B14, B39, B18, B50, and B56 were not identified. Various populations of Tamil Nadu were compared, but the Iyers of Madurai formed a separate cluster with Sourashtrans of Madurai and major group 4 (various Brahmin populations of Tamil Nadu); hill tribes (Irulas, Malayalis, and Badagas) and caste groups in the plains (Kallars and Nadars) formed distinct clusters. Comparison of the Iyers with other Indian and world populations revealed that Iyers form a distinct branch of the Indo-European and Central Asian tree. The Bhargavas of Lucknow, another Brahmin caste group from Uttar Pradesh, did not cluster with the Iyers but clustered with Central Asian populations. The Punjabis of Delhi clustered with European and Middle Eastern populations."

(Sources: [Caste] = `HLA antigens in South India: II. Selected caste groups of Tamil Nadu', Rajasekar, R., Kakkanaiah, V. N. and Pitchappan, R. M., Department of Immunology, School of Biological Sciences, Madurai Kamaraj University, India; Tissue Antigens. 30(3):113-8, September 1987.

[Iyer] = `HLA affinities of Iyers, a Brahmin population of Tamil Nadu, South India.', Balakrishnan, K., Pitchappan, R. M., Suzuki, K., Kumar, U. S., Santhakumari, R. and Tokunaga, K., Unit of Immunogenetics, School of Biological Sciences, Madurai Kamaraj University, Madurai, India; Human Biology. 68 (4) pp. 523-37, August, 1996.


HCV Info and Support Monthly Magazine July 2001

"Race and HLA-II Alleles Combine to Influence Hepatitis C Persistence"
"WESTPORT, CT (Reuters Health) Jul 26 - Race combines with class II human leukocyte antigens (HLAs) to determine whether hepatitis C virus (HCV) infection persists, according to a report in the July 1st issue of the Journal of Infectious Diseases.

Vigorous CD4+ T-cell responses, mediated by class II HLAs, contribute to viral clearance in early HCV infection, the authors explain, and a previous association between viral clearance and the class II allele DQB1*0301 was shown in European individuals.

Dr. Chloe L. Thio from the Johns Hopkins Medical Institutions in Baltimore and colleagues sought to determine whether other class II HLA alleles contributed to viral clearance and whether these contributions differed according to the race of the individual.

Besides confirming the increased frequency of DQB1*0301 in subjects with viral clearance, the authors report a significantly increased frequency of DQB1*0501 and DRB1*0101, but only in whites.

In combination, the DQB1*0501-DRB1*0101 haplotype was associated with HCV clearance in whites, but not in blacks, the report indicates.

Similarly, DRB1*0301 and the haplotypes DQB1*0201-DRB1*0301 and DQA1*0501-DQB1*0201-DRB1*0301 were more strongly associated with viral persistence in whites than in blacks, the researchers note.

"The genes associated with HCV outcomes are different based on ethnic groups," Dr. Thio told Reuters Health. "The hope is to find genes that are associated with HCV outcomes to help us understand HCV pathogenesis which could help us to find treatments. Such HLA findings can also be used in vaccine development."

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