POPULATION FEATURES OF HLA-DRB POLYMORPHISM IN THE UZBEK POPULATION OF SAMARKAND REGION

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Abstract. The Samarkand region represents one of the most historically and ethnically diverse areas of Central Asia. This study investigates the polymorphism and population distribution of HLA-DRB alleles among the Uzbek population of the region. Using molecular genetic typing methods, we analyzed allele frequencies, heterozygosity levels, Hardy–Weinberg equilibrium, and regional variability. The results demonstrate a high level of genetic diversity, reflecting historical admixture between Europoid and Mongoloid populations. The most frequent alleles were HLA-DRB1*01:01 (0.112), HLA-DRB1*03:01 (0.104), and HLA-DRB1*04:01 (0.097). High heterozygosity (93.2%) indicates strong adaptive immune potential. These findings are important for transplantation medicine, population genetics, and personalized healthcare.

Keywords: HLA-DRB, polymorphism, population genetics, Uzbekistan, Samarkand, immunogenetics, allele frequency, heterozygosity

The Samarkand region of Uzbekistan is one of the most ancient and culturally significant areas of Central Asia, distinguished by its rich historical heritage and complex ethnic composition. Located at the crossroads of major trade and migration routes, including the Great Silk Road, this region has been a center of interaction between diverse populations for centuries [3]. Historical processes such as the Arab expansion, Turkic migrations, and Mongol conquests have contributed to the formation of a genetically heterogeneous population. As a result, the modern Uzbek population of the Samarkand region reflects a combination of Europoid and Mongoloid genetic components, making it an important subject for population genetic and immunogenetic studies [1]. The development of modern molecular genetics has provided new opportunities to investigate the genetic structure of populations at a deeper level. Among the most informative systems for such studies is the Human Leukocyte Antigen system, which plays a fundamental role in the regulation of immune responses. In particular, the HLA-DRB locus, belonging to the major histocompatibility complex class II, is highly polymorphic and encodes the β-chain of HLA-DR molecules [2]. These molecules are expressed on antigen-presenting cells, including B lymphocytes, dendritic cells, and macrophages, and are responsible for presenting exogenous peptides to CD4+ T cells. Due to its high variability, the HLA-DRB locus is widely used in studies of population genetics, transplantation compatibility, susceptibility to infectious and autoimmune diseases, and personalized medicine [4, 5]. The aim of this study was to investigate the polymorphism and population distribution of HLA-DRB alleles in the Uzbek population of the Samarkand region, as well as to assess genetic diversity, heterozygosity, and population structure. The study was conducted on a representative sample of individuals from different districts of the Samarkand region, including urban and rural populations (Samarkand city, Samarkand district, Taylak, Jomboy, and Pastdargom). All participants were unrelated individuals of Uzbek ethnicity. Genomic DNA was extracted from peripheral blood samples using standard protocols. HLA-DRB genotyping was performed using polymerase chain reaction PCR-based methods with sequence-specific primers and/or high-resolution sequencing techniques. The analysis included the identification of alleles at the HLA-DRB1 locus as well as its paralogous genes DRB3, DRB4, and DRB5. Pseudogenes DRB2, DRB6-DRB9 were not included in the analysis due to their lack of expression.

Allele frequencies were calculated based on direct counting, considering two alleles per individual. Population genetic parameters, including allele frequency (p), expected homozygosity (p^2), and heterozygosity (2p(1-p)), were calculated according to the Hardy-Weinberg equilibrium model. Additional statistical indicators such as mean allele frequency, standard deviation, coefficient of variation, and overall heterozygosity were also determined. Comparative analysis with historical serological data and international databases IMGT-HLA was performed to assess population similarities and differences.

Genotyping results revealed a total of 17 functional alleles across the HLA-DRB locus, including DRB1 and its paralogs. Among these, the most frequent alleles were HLA-DRB1*01:01 (frequency 0.112), HLA-DRB103:01* (0.104), and HLA-DRB1*04:01 (0.097), indicating their dominant role in the population. Alleles such as HLA-DRB101:02 (0.082) and DRB301:01 (0.082) were observed at moderate frequencies, while several alleles including DRB108:01, DRB111:01, DRB114:01, and DRB115:01 were classified as low-frequency variants (0.022-0.030). Among the paralogous genes, DRB301:01 (0.082), DRB401:01 (0.067), and DRB501* (0.060) were the most common, although overall these loci were less frequent compared to DRB1, reflecting their conditional expression linked to specific haplotypes. Population genetic analysis demonstrated a high level of heterozygosity (93.2%) and low homozygosity (6.77%), indicating substantial genetic diversity within the population. The coefficient of variation (51.8%) further confirmed significant allele frequency dispersion, characteristic of highly polymorphic loci. Hardy–Weinberg equilibrium analysis showed that the population maintains genetic stability, with a predominance of heterozygous genotypes across all alleles. This high heterozygosity suggests strong adaptive potential of the immune system and the ability to respond to a wide range of pathogens. Analysis of sex-based distribution revealed that allele frequencies were nearly equal between males and females, indicating no significant gender-related differences and supporting the presence of genetic equilibrium within the population. Regional analysis showed that allele diversity was highest in Samarkand city and Jomboy district, likely due to higher population density and historical migration activity, while relatively lower diversity was observed in Pastdargom district.

A comparative analysis between historical serological data from the 1990s and modern molecular genetic findings demonstrated general consistency in overall trends, while also highlighting the advantages of high-resolution genotyping. Earlier serological studies identified antigens such as DR7, DR1, DR9, and DR2 as the most frequent. Molecular analysis clarified that these correspond to specific alleles, including DRB1*01:01 and DRB1*01:02 for DR1, DRB1*07:01 for DR7, and DRB1*15:01 for DR2. Importantly, modern techniques also enabled the identification of DRB3, DRB4, and DRB5 alleles, which were not detectable using serological methods, thus providing a more detailed and accurate characterization of the population’s immunogenetic profile. Comparison with global population data revealed that the Samarkand population shares similarities with European and Central Asian populations, particularly in the frequencies of DRB1*01:01, DRB1*03:01, and DRB1*04:01 alleles. At the same time, significant differences were observed compared to East Asian populations, where these alleles occur at much lower frequencies. This pattern supports the hypothesis of mixed Europoid–Mongoloid genetic ancestry and reflects the historical processes of migration and admixture in the region.

In conclusion, the Uzbek population of the Samarkand region is characterized by a highly polymorphic HLA-DRB gene pool, with a predominance of DRB1 alleles, substantial heterozygosity, and balanced allele distribution across sexes and regions. These findings highlight the genetic diversity and adaptive potential of the population and have important implications for transplantation compatibility, immunogenetic research, and personalized medicine. The results also contribute to a deeper understanding of population genetics in Central Asia and provide a valuable basis for future studies on disease associations and immune response variability.

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