

Temporal Evolution of HLA Distribution: A 25-Year Single-Center Immunogenetic Analysis

Emel Yantır¹ , Ertuğrul Çolak² 

¹Eskişehir Osmangazi University Faculty of Medicine, Department of Immunology, Eskişehir, Türkiye; ²Eskişehir Osmangazi University Faculty of Medicine, Department of Immunology, Department of Biostatistics, Eskişehir, Türkiye

Abstract

Objective: The HLA system exhibits significant population variability due to demographic history. As a migration crossroad, Türkiye has a complex genetic structure. This study analyzes 25 years of data from a single center in West-Central Anatolia to document the evolution of regional HLA distribution between low-migration (2001-2011) and high-migration (2011-2025) periods and to evaluate its implications for transplantation immunology.

Materials and Methods: In this retrospective study, HLA-A, -B, -C, -DRB1, -DQB1, and -DPB1 data from 6550 healthy donors were analyzed. The cohort was divided into two periods: 2001-2011 (n=2089) and 2011-2025 (n=4461). Genotyping was performed via PCR-SSO. Population genetics analyses, including Hardy-Weinberg Equilibrium (HWE) and Linkage Disequilibrium (LD), were conducted using PyPop software. Statistical significance of allele frequency differences was assessed using Fisher's Exact test.

Results: Statistically significant frequency changes were detected in 18 alleles ($p < 0.05$). In the post-2011 period, Middle Eastern/Asian-origin alleles (e.g., B*52, DRB1*03) increased, while European-associated alleles (e.g., B*44, DQB1*05) decreased. The high-migration cohort showed significant deviation from HWE due to excess homozygosity, indicating a "Wahlund effect" and population stratification. Furthermore, LD between HLA-C and HLA-B weakened significantly, whereas the strong LD between DRB1 and DQB1 was preserved. Specific haplotypes like A*30~B*51~C*16~DRB1*13 disappeared, replaced by new ones such as A*01~B*08~C*07~DRB1*03.

Conclusion: Dynamic changes in the gene pool directly affect donor matching probabilities and transplantation strategies. These findings highlight the necessity of periodically updating transplantation registries and donor search algorithms to reflect the current genetic profiles of populations.

Keywords: HLA Antigens, emigration and immigration, biological evolution, linkage disequilibrium, genetics population

OP-01

Correspondence

Emel Yantır

E-mail

dremelyntr@gmail.com

Published

July 13, 2026

DOI

10.36519/tji.2026.op1



This work is licensed under the Creative Commons Attribution-NonCommercial-NonDerivatives 4.0 International License (CC BY-NC-ND 4.0).