

CHARACTERIZATION OF 69 NOVEL HLA ALLELES IDENTIFIED IN CROATIA

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The introduction of Sequence Based Typing (SBT) and Next-Generation Sequencing (NGS) methods into routine histocompatibility laboratories for both allogeneic hematopoietic stem cell transplantation (allo-HSCT) and solid organ transplantation has made it possible to sequence the entire spectrum of HLA genes and simplifying the identification of numerous novel HLA alleles.

Over the last 10 years, we have identified 69 novel alleles. Among novel alleles, 52 (75.4%) belong to HLA class I genes (13 HLA-A, 24 HLA-B, and 15 HLA-C) while 17 (24.4%) novel alleles belong to HLA class II genes (1 HLA-DRB1, 2 HLA-DRB3, 1 HLA-DQA1, 4 HLA-DQB1, and 9 HLA-DPB1). Among identified alleles, 24 (34.8%) novel sequences were found to encode a new protein, 8 (11.6%) novel sequences contained a synonymous substitution within coding region, and 37 (53.6%) novel sequences contained polymorphisms in intronic regions. Two of these novel alleles were seen to be null alleles (DRB3*01:132N and DRB3*01:133N). In terms of frequency, the novel alleles HLA-A*01:200 and HLA-DPB1*1146:01 are considered common in our population, as each was identified in more than five individuals, while the novel HLA-C*04:477 allele was detected twice and is classified as a well-defined allele.

In conclusion, the ongoing identification and reporting of novel HLA alleles enriches our understanding of HLA diversity and ensures keeping IPD-IMGT/HLA database up-to-date.

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