Characterization of the novel *HLA-DQA1*01:89* allele by sequencing-based typing

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Marine Cargou, CHU de Bordeaux, Laboratoire d'Immunologie et Immunogénétique, Hôpital Pellegrin, Place Amélie Raba Léon, 33076 Bordeaux Cedex, France. Email: marine.cargou@chu-bordeaux.fr *HLA-DQA1*01:89* differs from *HLA-DQA1*01:01:01:01* by one nucleotide substitution in codon -5 in exon 1.

K E Y W O R D S

HLA, HLA-DQA1*01:89, novel allele, sequencing-based typing

We report here a novel HLA-DQA1*01 allele, now named DOA1*01:89 that carries one nucleotide substitution in exon 1 when compared with the DQA1*01:01:01:01 allele, identified in a patient awaiting kidney transplantation. The HLA typing was performed using Next Generation Sequencing (AllType NGS, One Lambda, Canoga Park, CA) on the Ion S5 system platform (ThermoFisher Scientific, Waltham, MA),¹ from exons 1 to 4. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This donor was found to have a new DQA1*01 allele and was consequently typed A*01:01, 02:01; C*02:02, 12:02; B*27:05, 52:01; DRB1*01:01, 15:02P; DRB5*01:02; DOA1*01:03, 01:89; DOB1*05:01P, 06:01; DPA1*01:03, 01:03; DPB1*04:01, 04:01. Using the IPD-IMGT/HLA Database,² nucleotide sequence alignment with HLA-DQA1 alleles shows that this new allele has one nucleotide change from DQA1*01:01:01:01 in codon -5 in

exon 1, where $C \rightarrow A$, resulting in a coding change $(AGC \rightarrow AGA, Serine \rightarrow Arginine, Figure 1)$. This nucleotide change was confirmed by performing the typing twice in two different laboratories. We were confident in the phasing as the sample displayed a mean read length of 337 base pairs over all the loci, the mismatched A base was attributed 280 times to the new HLA-DQA1*01. The nucleotide sequence of the exons 1 to 4 of the new allele has been submitted to the GenBank database (Accession No. ON135541) and to the IPD-IMGT/HLA Database (Submission No. HWS10061018). The name DOA1*01:89 has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in April 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,³ names will be assigned to new sequences as they are identified. Lists of such new names will be published in the following WHO Nomenclature Report.

AUTHOR CONTRIBUTIONS

WILEY_HLA

Marine Cargou and Jonathan Visentin contributed to the design of the study. Marine Cargou and Jonathan Visentin participated in the writing of the paper. Marine Cargou, Marco Andreani, Antonio Giuseppe Bianculli, Gwendaline Guidicelli, and Jonathan Visentin participated in the performance of the research. Marine Cargou, Marco Andreani, Antonio Giuseppe Bianculli, Gwendaline Guidicelli, and Jonathan Visentin participated in data analysis. Marco Andreani, Antonio Giuseppe Bianculli, and Gwendaline Guidicelli were involved in critical revision of the manuscript.

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CONFLICT OF INTEREST

The authors declare no potential conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions. The sequence is freely available in the IPD-IMGT/ HLA Database.

ORCID

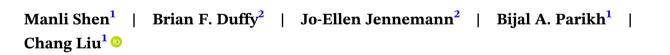
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A novel *HLA-DQA1*01* allele, *HLA-DQA1*01:99*, identified by next-generation sequencing



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Chang Liu, Department of Pathology and Immunology, Washington University in St. Louis, 660 South Euclid Avenue, Campus Box 8118, St. Louis, MO 63110, USA. Email: cliu32@wustl.edu *DQA1*01:99* differs from *DQA1*01:01* by a missense nucleotide substitution in exon 4.

K E Y W O R D S DQA1*01:99, HLA novel alleles, next-generation sequencing