Characterization of the novel *HLA-DQA1*02:01:14* allele by sequencing-based typing

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*HLA-DQA1*02:01:14* differs from *HLA-DQA1*02:01:01:02* by one nucleotide substitution in codon 105 in exon 3.

KEYWORDS
HLA, *HLA-DQA1*02:01:14*, novel allele, sequencing-based typing

We report here a novel *HLA-DQA1*02:01* allele, now named *DQA1*02:01:14* that carries one nucleotide substitution in exon 3 when compared with the *DQA1*02:01:01:02* 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*02:01 allele and was consequently typed *A*23:01, 26:01*; *B*27:05, 44:03*; *C*01:02,*04:01*; *DRB1*07:01, 16:01*; *DRB4*01:01*; *DRB5*02:02*; *DQA1*01:02, 02:01:14*; *DQB1*02:02, 05:02P*; *DPB1*02:01, 03:01*. 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*02:01:01:02* in codon 105 in exon 3, where C → A, (CCC → CCA, Figure 1), not resulting in a coding change. 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 335 base pairs over all the loci, the mismatched A base was attributed 299 times to the new *HLA-DQA1*02:01*. The nucleotide sequence of the exons 1 to 4 of the new allele has been submitted to the GenBank database (Accession No. OP393480) and to the IPD-IMGT/HLA Database (Submission No. HWS10062890). The name *DQA1*02:01:14* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in September 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[3] names will be

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AA Codon                 90                  95                 100                 105                 110
DQA1*02:01:01:02    AG GTT CCT GAG GTC ACA GTG TTT TCC AAG TCT CCC GTG ACA CTG GGT CAG CCC AAC ACC CTC ATC TGT CTT GTG
DQA1*02:01:14       -- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --A --- --- --- --- --- --- ---

AA Codon                115                 120                 125                 130                 135
DQA1*02:01:01:02   GAC AAC ATC TTT CCT CCT GTG GTC AAC ATC ACC TGG CTG AGC AAT GGG CAC TCA GTC ACA GAA GGT GTT TCT GAG
DQA1*02:01:14      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon                140                 145                 150                 155                 160
DQA1*02:01:01:02   ACC AGC TTC CTC TCC AAG AGT GAT CAT TCC TTC TTC AAG ATC AGT TAC CTC ACC TTC CTC CCT TCT GCT GAT GAG
DQA1*02:01:14      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon                165                 170                 175                 180
DQA1*02:01:01:02   ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAT GAG CCT CTT CTG AAA CAC TGG G
DQA1*02:01:14      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -
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FIGURE 1 Alignment of the sequence of exon 3 of *HLA-DQA1*02:01:14* with the sequence of *HLA-DQA1*02:01:01:02*. Dashes indicate nucleotide identity with the HLA-*DQA1*02:01:01:02* allele. Numbers above the sequence indicate codon position

assigned to new sequences as they are identified. Lists of such new names will be published in the following WHO Nomenclature Report.

AUTHOR CONTRIBUTIONS

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, Maria Troiano, Gwendaline Guidicelli and Jonathan Visentin participated in the performance of the research. Marine Cargou, Marco Andreani, Maria Troiano, Gwendaline Guidicelli and Jonathan Visentin participated in data analysis. Marco Andreani, Maria Troiano and Gwendaline Guidicelli were involved in critical revision of the manuscript.

ACKNOWLEDGMENTS

The authors thank the technicians of the Bordeaux and Roma Immunology laboratories for their technical expertise.

CONFLICT OF INTEREST

The authors confirm that there are no conflicts 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.

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How to cite this article: Cargou M, Andreani M, Troiano M, Guidicelli G, Visentin J. Characterization of the novel *HLA-DQA1*02:01:14* allele by sequencing-based typing. *HLA*. 2023; 101(3):298-299. doi:10.1111/tan.14896

Characterization of the novel *HLA-DQA1*05:05:14* allele by sequencing-based typing

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*HLA-DQA1*05:05:14* differs from *HLA-DQA1*05:05:01:04* by one nucleotide substitution in codon −8 in exon 1.

KEYWORDS

HLA, *HLA-DQA1*05:05:14*, novel allele, sequencing-based typing

We report here a novel *HLA-DQA1*05:05* allele, now named *DQA1*05:05:14* that carries one nucleotide substitution in exon 1 when compared to the *DQA1*05:05:01:04* allele, identified in a volunteer bone