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

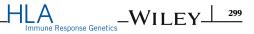
K E Y W O R D S

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

We report here a novel HLA-DQA1*02:01 allele, now named DOA1*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-DOA1 alleles shows that this new allele has one nucleotide change from DQA1*02:01:01:02 in codon 105 in exon 3, where $C \rightarrow A$, (CCC \rightarrow 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

AA Codon DOA1*02:01:01:02	90 NG GTT CCT GNG GTC	95 ACA GTG TTT TCC AAG	100 TCT CCC GTG ACA CTG GGT CA	105	110 TC TCT CTT CTC
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 CA	C TCA GTC ACA GAA GO	GT 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 CT	C ACC TTC CTC CCT TC	CT 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 AA	AA CAC TGG G	
DQA1*02:01:14					

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.

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

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K E Y W O R D S 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