The names *DPA1*01:03:01:57* and *DPA1*02:01:01:29* have been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in March 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[4] 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

David J. Margolis and Dimitri S. Monos were involved in the design of the case–control study on atopic dermatitis. Georgios Damianos, Ioanna Pagkrati and Jamie L. Duke were involved in the genotyping and consensus sequence generation for the novel alleles. Georgios Damianos, Jamie L. Duke, and Dimitri S. Monos wrote the manuscript. All authors approved of the manuscript.

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CONFLICT OF INTEREST

Jamie L. Duke and Dimitri S. Monos receive royalties from Omixon. Dimitri S. Monos is also the Chair of the Scientific Advisory Board of Omixon and owns options in Omixon. David J. Margolis is or recently has been a consultant for Pfizer, Leo, and Sanofi with respect to studies of atopic dermatitis and served on an advisory board for the National Eczema Association.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in IPD-IMGT/HLA at https://www.ebi.ac.uk/ipd/imgt/hla/, reference number HLA34360 and HLA34329.

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Characterization of the novel *HLA-DPA1*02:01:21* allele by sequencing-based typing

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*HLA-DPA1*02:01:21* differs from *HLA-DPA1*02:01:01:03* by one nucleotide substitution in codon 190 in exon 4.

KEYWORDS
HLA, *HLA-DPA1*02:01:21*, novel allele, sequencing-based typing

We report here a novel *HLA-DPA1*02:01* allele, now named *DPA1*02:01:21* that carries one nucleotide substitution in exon 4 when compared with the *DPA1*02:01:01:03* allele, identified in 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 patient was found to have a new *DPA1*02:01* allele and was consequently typed *A*01:02, 24:02*; *B*18:01, 53:01*; C**02:10,16:01*; *DRB1*03:02, 07:01*; *DRB3*01:01; DRB4*01:03*; *DQA1*02:01, 04:01*; *DQB1*02:02, 04:02*; *DPA1*02:01:21, 02:02:02*; *DPB1*01:01, 17:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-DPA1 alleles shows that this new allele differs from *DPA1*02:01:01:03* in codon 190 in exon 4, where G → A (ACG → ACA, 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 295 base pairs over all the loci, the mismatched A base was attributed 169 times to the new *HLA-DPA1*02:01:21* allele. HLA typing by Luminex reverse sequence-specific oligonucleotide (SSO) was performed (One Lambda Labtype HD, Canoga Park, CA).[3] With this assay (lot 010, catalog RSSO2P_010_02), the HLA-typing of the *HLA-DPA1*02* allele was *HLA-DPA1*02:01:01*, 02:02:02 without any bead modification. Indeed the IPD-IMGT/HLA Database 3.50.0 release describes few other HLA-DPA1 allele displaying an ACA sequence in codon 190, explaining why the manufacturer did not include probes targeting this codon. The coding nucleotide sequence of the exons 1–4 of the new allele has been submitted to the GenBank database (Accession No. ON809566) and to the IPD-IMGT/HLA Database (Submission No. HWS10061882). The name *DPA1*02:01:21* 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,[4] 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

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, Paola Giustiniani, Gwendaline Guidicelli and Jonathan Visentin participated in the performance of the research. Marine Cargou, Marco Andreani, Paola Giustiniani, Gwendaline Guidicelli and Jonathan Visentin participated in data analysis. Marco Andreani, Paola Giustiniani 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.

```
AA Codon              180                 185                 190                 195                 200
DPA1*02:01:01:03    AG GCC CAA GAG CCA ATC CAG ATG CCT GAG ACA ACG GAG ACT GTG CTC TGT GCC CTG GGC CTG GTG CTG GGC CTA
DPA1*02:01:21       -- --- --- --- --- --- --- --- --- --- --- --A --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon              205                 210                 215                 220                 225
DPA1*02:01:01:03  GTG GGC ATC ATC GTG GGC ACC GTC CTC ATC ATA AAG TCT CTG CGT TCT GGC CAT GAC CCC CGG GCC CAG GGG CCC
DPA1*02:01:21     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon              230
DPA1*02:01:01:03  CTG TGA
DPA1*02:01:21     --- ---
```

FIGURE 1 Alignment of the sequence of exon 4 of *HLA- DPA1*02:01:21* with the sequence of *HLA-DPA1*02:01:01:03*. Dashes indicate nucleotide identity with the *HLA-DPA1*02:01:01:03* allele. Numbers above the sequence indicate codon position

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Characterization of the novel *HLA-DPB1*11:01:06* allele by sequencing-based typing

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*HLA-DPB1*11:01:06* differs from *HLA-DPB1*11:01:01:01* by one nucleotide substitution in codon 21 in exon 2.

KEYWORDS

HLA, *HLA-DPB1*11:01:06*, novel allele, sequencing-based typing

We report here a novel *HLA-DPB1*11:01* allele, now named *DPB1*11:01:06* that carries one nucleotide substitution in exon 2 when compared to the *DPB1*11:01:01:01* allele, identified in a volunteer bone marrow donor. 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 2 to 5. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This donor was found to have a new *DPB1*11:01* allele and was consequently typed *A*02:01*, *30:02*; *B*18:01*, *44:03*; *C*05:01*, *16:01*; *DRB1*03:01*, *07:01*; *DRB3*02:02*; *DRB4*01:01*; *DQA1*02:01*, *05:01*; *DQB1*02:01*, *02:02*; *DPA1*01:03*, *02:01*; *DPB1*11:01:06*, *104:01:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-DPB1 alleles shows that this new allele has one nucleotide change from *DPB1*11:01:01:01* in codon 21 in exon 2, where A → G, (ACA → ACG, Figure 1), not resulting in a coding change. This nucleotide change was confirmed using other NGS reagents provided by GenDX NGSgo-MX6-1 (Utrecht, Nederlands) run on the Illumina MiSeq system (San Diego, CA) and analyzed with the NGSEngine software (GenDX, version 2.26). We were confident in the phasing as the sample displayed a mean read length of 304 base pairs over all the loci, the mismatched G base was attributed 139 times to the new *HLA-DPB1*11:01:06* allele and can be only attributed to this allele because it was possible to discriminate