*DQB1*02:01:01:01, 06:03:01:19*; *DPA1*01:03:01, 02:01:02:02*; *DPB1*01:01:01, 02:01P*.

The names *HLA-DPA1*01:03:01:68*, *-DPA1*01:03:01:71*, *-DQA1*02:01:01:06*, and *-DQB1*06:03:01:19* have been officially assigned by the WHO Nomenclature Committee from November 2022 to January 2023. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[2] 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

Luis A. Marin Rubio and Jesus Ontañon design study and data analysis. Luis A. Marin Rubio submission of the new alleles to IPD-IMGT/HLA Database. Luis A. Marin Rubio wrote the manuscript. All authors read and approved the final version of the manuscript.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Characterization of the novel *HLA-DPA1*01:150* allele by sequencing-based typing

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*HLA-DPA1*01:150* differs from *HLA-DPA1*01:03:01:05* by one nucleotide substitution in codon 190 in exon 4.

KEYWORDS
HLA, *HLA-DPA1*01:150*, novel allele, sequencing-based typing

We report here a novel *HLA-DPA1*01* allele, now named *DPA1*01:150* that carries one nucleotide substitution in exon 4 when compared to the *DPA1*01:03:01:05* 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 3.0 (One Lambda). This patient was found to have a new *DPA1*01* allele and was consequently typed *A*01:01, 02:01*; *B*18:01, 38:01*; *C*07:01, 12:03*; *DRB1*04:04, 11:04*;

```
AA Codon              180                 185                 190                 195                 200
DPA1*01:03:01:05   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*01:150                --- ---                          -T-

AA Codon              205                 210                 215                 220                 225
DPA1*01:03:01:05   GTC GGC ATC ATC GTG GGC ACC GTC CTC ATC ATA AAG TCT CTG CGT TCT GGC CAT GAC CCC CGG GCC CAG GGG ACC
DPA1*01:150                                          --- ---                                                --- ---

AA Codon              230
DPA1*01:03:01:05   CTG TGA
DPA1*01:150
```

FIGURE 1 Alignment of the sequence of exon 4 of *HLA-DPA1*01:150* with the sequence of *HLA-DPA1*01:03:01:05*. Dashes indicate nucleotide identity with the *HLA-DPA1*01:03:01:05* allele. Numbers above the sequence indicate codon position.

*DRB3*02:02*; *DRB4*01:03*; *DQA1*03:03*, *05:05*; *DQB1*03:01P*, *04:02*; *DPA1*01:150*, *02:01*; *DPB1*04:02*, *14:01*. Using the IPD-IMGT/HLA database,[2] nucleotide sequence alignment with HLA-DPA1 alleles shows that this new allele has one nucleotide change from *DPA1*01:03:01:05* in codon 190 in exon 4, where C → T, resulting in a coding change (ACG → ATG, Threonine → Methionine, 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 321 base pairs over all the loci, the mismatched T base was attributed 57 times to the new *HLA-DPA1*01:150* allele and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-DPA1*02:01:01:02* allele by virtue of four variant positions each distant by less than 100 base pairs. The analysis of the localization of this amino acid and its antibody accessibility with the pHLA3D database[3] indicated that this amino-acid not surface accessible and not located close to the peptide binding groove. Then, its clinical significance seems minimal. The coding nucleotide sequence of the exons 1–4 of the new allele has been submitted to the GenBank database (accession no. OQ754735) and to the IPD-IMGT/HLA Database (submission no. HWS10065909). The name *DPA1*01:150* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in April 2023. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[4] names would 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, Marion Duclaut and Jonathan Visentin participated in the performance of the research. Marine Cargou, Marco Andreani, Paola Giustiniani, Marion Duclaut, and Jonathan Visentin participated in data analysis. Marco Andreani, Paola Giustiniani, and Marion Duclaut were involved in critical revision of the manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from thecorresponding 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-DPA1*02:03:05* allele by next generation sequencing

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*HLA-DPA1*02:03:05* differs from *HLA-DPA*02:03:04* by three nucleotide substitution located in exon 3.

KEYWORDS
HLA new allele, *HLA-DPA1*02:03:05*, next generation sequencing

The HLA system is one of the most polymorphic gene clusters in the human genome. To date, according to the IPD-IMGT/HLA Database (Release 3.51, January 2023), a total of a total of 531 HLA-DPA1 alleles have been identified, giving rise to 248 different proteins. Twenty-two of the HLA-DPA1 alleles are null alleles.[1,2]

Next generation sequencing (NGS) has facilitated the sequencing of previously un-sequenced regions of HLA genes leading to the discovery of many novel alleles during routine laboratory testing. The availability of NGS testing and new genomic data, is transforming our understanding of the polymorphisms underlying the tremendous variation found in the HLA region.

This report describes the identification of the full genomic sequence of the *HLA-DPA1*02:03:05* allele identified in a 52-year-old male Caucasian, during a Lung patient workup for HLA class I (HLA-A, -B, and -C) and class II (HLA-DRB1 and -DQB1) typing by NGS. Briefly, genomic DNA was extracted on a Qiagen EZ1 DNA extraction instrument with Qiagen EZ1 Blood 350 µL Kit, from a sample of peripheral blood. Samples were amplified for 11 HLA loci (HLA-A, -B, -C, -DRB1, -DRB3/4/5, -DQA1, -DQB1, -DPA1 and -DPB1) by long range PCR using NGSgo kits (GenDx, Utrecht, The Netherlands). Amplification, library preparation, and sequencing were performed according to the vendor and laboratory specifications. The sequencing was performed on an MiSeq 100 system (Illumina, San Diego, CA) and was analyzed with NGSengine software (GenDx) software v. 2.27.2.27406 and the IPD-IMGT/HLA Database version 3.49.0 Genomic sequencing enables sequencing of the whole gene from the 5′-untranslated region (UTR) to the 3′-UTR. The reads were analyzed using the NGSengine Software. *HLA-DPA1*02:03:05*, when the generated sequence aligned with the most closely related sequence *HLA-DPA*02:03:04*, we observed the presence of three synonymous single nucleotide differences in Exon 3 at position 4287 (G > C) (codon 90 ACG- > ACC), resulting in no change in the amino Threonine, at position 4371 (T > C) (codon 118 AAT- > AAC) resulting in no change in the amino Asparagine, and at position 4398 (G > A) (codon 127 CCG- > CCA), resulting in no change in the amino Proline (Figure 1). This full-length sequence covers the 5′-untranslated region (UTR), all introns and exons and the 3′ UTR.