The name *DPB1*1461:01* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in February 2023. The nucleotide sequence of *DPB1*1461:01* was submitted to the IPD-IMGT/HLA Database in February 2023 and assigned an accession number (HWS10065069). This follows the agreed policy that subject to the conditions stated in the most recent Nomenclature Report,[5] 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

Keerthi Shetty conceived the report, performed the experiment, analyzed the data, and wrote the paper along with Akanksha Sharma. Bagirath Raghuraman and B. R. Prathip Kumar arranged for samples from patients and family. Manjula Das reviewed and finalized the paper.

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CONFLICT OF INTEREST STATEMENT

All the authors confirm that there are no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data supporting this study's findings are available in repositories: GenBank (OQ225487 and OQ225489) and IPD-IMGT/HLA Database (HWS10065069).

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Characterization of the novel *HLA-DPB1*1463:01N* allele by sequencing-based typing

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*HLA-DPB1*1463:01N* differs from *HLA-DPB1*02:01:02:04* by one nucleotide substitution in codon 128 in exon 3.

KEYWORDS

HLA, *HLA-DPB1*1463:01N*, novel allele, sequencing-based typing

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AA Codon                 95                  100                 105                 110                 115
DPB1*02:01:02:04   TC CAG CCT AGG GTG AAT GTT TCC CCC TCC AAG AAG GGG CCC TTG CAG CAC CAC AAC CTG CTT GTC TGC CAC GTG
DPB1*1463:01N      -- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon                120                 125                 130                 135                 140
DPB1*02:01:02:04   ACG GAT TTC TAC CCA GGC AGC ATT CAA GTC CGA TGG TTC CTG AAT GGA CAG GAG GAA ACA GCT GGG GTC GTG TCC
DPB1*1463:01N      --- --- --- --- --- --- --- --- --- --- T-- *** *** *** *** *** *** *** *** *** *** *** *** ***

AA Codon                145                 150                 155                 160                 165
DPB1*02:01:02:04   ACC AAC CTG ATC CGT AAT GGA GAC TGG ACC TTC CAG ATC CTG GTG ATG CTG GAA ATG ACC CCC CAG CAG GGA GAT
DPB1*1463:01N      *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***

AA Codon                170                 175                 180                 185
DPB1*02:01:02:04   GTC TAC ACC TGC CAA GTG GAG CAC ACC AGC CTG GAT AGT CCT GTC ACC GTG GAG TGG A
DPB1*1463:01N      *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *
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FIGURE 1 Alignment of the sequence of exon 3 of *HLA-DPB1*1463:01N* with the sequence of *HLA-DPB1*02:01:02:04*. Dashes indicate nucleotide identity with the HLA-*DPB1*02:01:02:04* allele. Numbers above the sequence indicate codon position.

We report here a novel HLA-DPB1 allele, now named *HLA-DPB1*1463:01N* that carries one nucleotide substitution in exon 3 when compared with the *HLA-DPB1*02:01:02:04* 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 3.0 (One Lambda). This donor was found to have a new DPB1 allele and was consequently typed *A*02:01, 02:06; B*51:01, 51:01; C*14:02, 15:02; DRB1*04:07, 11:01; DRB3*02:02; DRB4*01:03; DQA1*03:03, 05:05; DQB1*03:01, 03:01; DPA1*01:03, 01:03; DPB1*1463:01N, 03:01*. Using the IPD-IMGT/HLA database,[2] nucleotide sequence alignment with HLA-DPB1 alleles shows that this new allele has one nucleotide change from *HLA-DPB1*02:01:02:04* in codon 128 in exon 3 where C → T, resulting in a coding change (CGA → TGA, Arginine → STOP, Figure 1). This nucleotide change was confirmed using other NGS reagents provided by GenDX NGSgo-MX6-1 (Utrecht, Netherlands) run on the Illumina MiSeq system (San Diego, CA) and analyzed with the NGSEngine software (GenDX, version 2.26). We were very confident in the phasing as the sample displayed a mean read length of 306 base pairs over all the loci, the mismatched T base was attributed 771 times to the new *HLA-DPB1*1463:01N* allele and can be only attributed to this allele because it was possible to discriminate from the associated HLA-*DPB1*03:01:01:01* allele by virtue of four variant positions each distant by less than 100 base pairs. HLA typing by Luminex reverse sequence-specific oligonucleotide (SSO) was performed (One Lambda Labtype XR, Canoga Park, CA).[3] With this assay (lot 004, catalog RSSO2P_010_04), the most likely HLA-typing of the donor was *DPB1*02:EFWDV, 03:EBKTD* (most likely allele *DPB1*02:01, 03:01*, respectively) without any bead modification. Indeed the IPD-IMGT/HLA Database 3.51.0 release describe few other HLA-DPB1 alleles displaying a TGA sequence in codon 128, also identified as null alleles, the manufacturer did not include probes targeting this codon. As a null allele, the *HLA-DPB1*1463:01N* is clinically significant in both organ and allogeneic hematopoietic cell transplantation. The coding nucleotide sequence of the new allele has been submitted to the GenBank database (Accession No. OQ378319) and to the IPD-IMGT/HLA database (Submission No. HWS10065193). The name *HLA-DPB1*1463:01N* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in February 2023. 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.[4]

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, Vincent Elsermans, Isabelle Top, Mamy Ralazamahaleo, and Jonathan Visentin participated in the performance of the research. Marine Cargou, Vincent Elsermans, Isabelle Top, Mamy Ralazamahaleo, and Jonathan Visentin participated in data analysis. Vincent Elsermans, Isabelle Top, and Mamy Ralazamahaleo 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 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 *KIR3DL3*116* allele identified in a Chinese Han individual

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The novel *KIR3DL3*116* allele differs from the closest allele *KIR3DL3*00902* by a single missense mutation.

KEYWORDS
*KIR3DL3*116*, novel allele, sequencing-based typing (SBT)

The Killer-cell Immunoglobulin-like Receptors (KIRs) are mainly expressed on natural killer (NK) cells and a few subsets of T cells. KIR molecules interact with the HLA class I ligands, which play an important role in the immune surveillance and elimination of tumor and virus-infected cells through innate immune pathways.