CONFLICT OF INTEREST

The authors have declared no conflicting interests.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in the IPD-IMGT/HLAdatabase.

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REFERENCES

1. Robinson J, Barker DJ, Georgiou X, Cooper MA, Flicek P, Marsh SGE. IPD-IMGT/HLA database. *Nucleic Acids Res*. 2020; 48:D948-D955.
2. Marsh SGE, Albert ED, Bodmer WF, et al. Nomenclature for factors of the HLA system. *Tissue Antigens*. 2010;75:291-455.

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Characterization of the novel HLA-B*08:302 allele by sequencing-based typing

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*HLA-B*08:302* differs from *HLA-B*08:01:01:01* by one nucleotide substitution in codon 116 in exon 3.

KEYWORDS
HLA, *HLA-B*08:302*, novel allele, sequencing-based typing

We report here a novel *HLA-B*08* allele, now named *B*08:302* that carries one nucleotide substitution in exon 3 when compared to the *B*08:01:01:01* 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 1 to 7. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This donor was found to have a new *B*08* allele and was consequently typed *A*01:01, 11:01*; *B*08:302*, *35:08*; *C*03:03, 07:01*; *DRB1*03:01*, *13:03*; *DRB3*01:01*, *01:01*; *DQA1*05:01*, *05:05*; *DQB1*02:01*, *03:01P*; *DPA1*01:03*, *02:01*; *DPB1*02:01*, *11:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-B alleles shows that this new allele has one nucleotide change from *B*08:01:01:01* in codon 116 in exon 3 where T → C, resulting in a coding change (TAC → CAC, Tyrosine → Histidine, Figure 1). This nucleotide change was confirmed using other NGS reagents provided by Immucor (Mia Fora NGS Flex, Norcross, GA) run on the Illumina MiSeq system (San Diego, CA) and analyzed with the Mia Fora Flex software (Immucor, version 5.1). We were very confident in the phasing as the sample displayed a mean read length of 324 base pairs over all the loci, the mismatched C base was attributed 179 times to the new *HLA-B*08* allele and can be only attributed to this allele

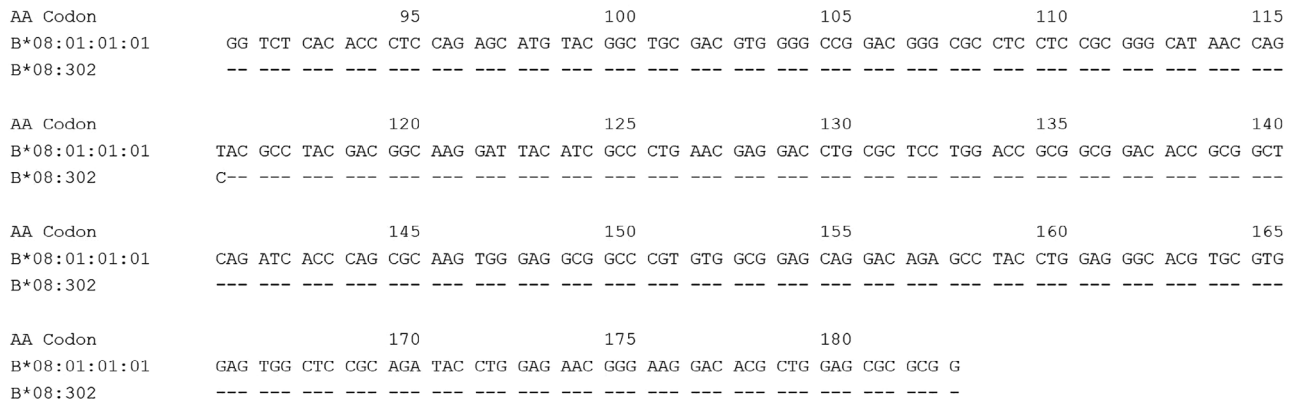

FIGURE 1 Alignment of the sequence of exon 3 of *HLA-B*08:302* with the sequence of *HLA-B*08:01:01:01*. Dashes indicate nucleotide identity with the *HLA-B*08:01:01:01* allele. Numbers above the sequence indicate codon position.

because it was possible to discriminate from the associated *HLA-B*35:08:01:01* allele by virtue of 11 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 006, catalog RSSOX1B_007_02), the pattern of positive beads did not result in an acceptable HLA typing. We had to modify the bead #600 and bead #706 from negative to positive to obtain a *HLA-B*08:01* result. Indeed beads #600 and #706 displayed oligonucleotides targeting the sequence surrounding codon 116. The analysis of the localization of this amino-acid and its antibody accessibility with the pHLA3D database[4] indicated that this amino-acid is located into the peptide binding groove. As such this could have an importance in both allogeneic hematopoietic stem cell transplantation and solid organ transplantation. The coding nucleotide sequence of the new allele has been submitted to the GenBank database (Accession No. ON933816) and to the IPD-IMGT/HLA Database (Submission No. HWS10062188). The name *B*08:302* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in August 2022. 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

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, Elodie Wojciechowski and Jonathan Visentin participated in the performance of the research. Marine Cargou, Vincent Elsermans, Isabelle Top, Elodie Wojciechowski and Jonathan Visentin participated in data analysis. Vincent Elsermans, Isabelle Top and Elodie Wojciechowski 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.

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REFERENCES

1. Cargou M, Ralazamahaleo M, Blouin L, et al. Evaluation of the AllType kit for HLA typing using the ion torrent S5 XL platform. *HLA*. 2020;95(1):30-39. doi:10.1111/tan.13708
2. Robinson J, Barker DJ, Georgiou X, Cooper MA, Flicek P, Marsh SGE. IPD-IMGT/HLA Database. *Nucleic Acids Res*. 2020; 48(D1):D948-D955. doi:10.1093/nar/gkz950
3. Bouthemy C, Ralazamahaleo M, Jollet I, Filloux M, Visentin J, Guidicelli G. Improvement in HLA-typing by new sequence-specific oligonucleotides kits for HLA-A, -B and -DRB1 loci. *HLA*. 2018;92(5):279-287. doi:10.1111/tan.13382

4. Teles E, Oliveira DM, Marroquim MSC, de Serpa Brandão RMS, et al. pHLA3D: updating the database of predicted three-dimensional structures of HLA with HLA-DR, HLA-DQ and HLA-DP molecules. *Hum Immunol*. 2021;82(1):8-10. doi:10.1016/j.humimm.2020.10.007
5. Marsh SGE, Albert ED, Bodmer WF, et al. Nomenclature for factors of the HLA system, 2010. *Tissue Antigens*. 2010;75(4):291-455. doi:10.1111/j.1399-0039.2010.01466.x

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Characterization of the novel *HLA-B*15:01:01:65Q* allele by sequencing-based typing

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*HLA-B*15:01:01:65Q* differs from *HLA-B*15:01:01:01* by one nucleotide substitution in the splice site in the beginning of intron 3.

KEYWORDS
HLA, *HLA-B*15:01:01:65Q*, novel allele, sequencing-based typing

We report here a novel *HLA-B*15* allele, now named *HLA-B*15:01:01:65Q* identified in a volunteer bone marrow donor, who gave is consent for HLA typing. The HLA typing was performed using Next Generation Sequencing (NGSgo kit, GenDX, Utrecht, The Netherlands), performed on the Illumina MiSeq platform (Illumina, San Diego, California). This donor was found to have a new B*15 allele and was consequently typed *HLA-A*02:01P, 02:01P*; *-B*15:01:01:65Q, 44:02:01:01*; *-C*03:03P, 05:01P*; *-DRB1*07:01P, 11:01P*; *-DQB1*03:01:01G, 03:03P*.

Using NGSEngine software (v. 2.24.0.25185, according to version 3.44 of the IPD-IMGT/HLA Database[1]), we demonstrated that *HLA-B*15:01:01:65Q* differed from *HLA-B*15:01:01:01* by a single nucleotide change at position 993, at the beginning of intron 3, where G → T (Figure 1). This nucleotide replacement in the splicing region might impact the protein's cell surface expression. This nucleotide change was confirmed by NGS typing on the Ion S5 system platform (ThermoFisher Scientific, Waltham, Massachusetts), using TypeStream Visual software (v. 2.0.1).[2] We were very confident in the phasing as the sample displayed a mean read length of 135 base pairs over all the loci, the mismatched T base was attributed 554 times to the new *HLA-B*15* allele and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-44:02:01:01* allele by virtue of 5 variant positions each distant by less than 100 base pairs.

The nucleotide sequence of the new allele has been submitted to the GenBank database (Accession number ON649889) and to the IPD-IMGT/HLA Database (Submission number HWS10061736). The name