No. OQ174841) and to the IPD-IMGT/HLA Database[5] (Submission No. HWS10065109). The name *HLA-C*07:1058* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System[6] in January 2023. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report, 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

Adèle Dhuyser and Alice Aarnink performed the research. Michaël Pérès, Adèle Dhuyser, Thomas Morel and Alice Aarnink analysed the data. Maël Silva Rodriguez and Adèle Dhuyser wrote the manuscript. Michaël Pérès, Thomas Morel and Alice Aarnink were involved in the critical review of the article.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data supporting the findings of this paper are available upon request from the corresponding author.

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Characterization of the novel *HLA-C*12:384* allele by sequencing-based typing

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*HLA-C*12:384* differs from *HLA-C*12:03:01:02* by one nucleotide substitution in codon 42 in exon 2.

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KEYWORDS

HLA, *HLA-C*12:384*, novel allele, sequencing-based typing

We report here a novel *HLA-C*12* allele, now named *HLA-C*12:384* that carries one nucleotide substitution in exon 2 when compared to the *HLA-C*12:03:01:02* 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 8. The reads were analyzed using the TypeStream Visual Software version 3.0 (One Lambda). This donor was found to have a new *C*12* allele and was consequently typed *A*29:02, 31:01*; *C*08:02, 12:384*; *B*35:08, 44:03*; *DRB1*07:01, 13:01*; *DRB3*01:01*; *DRB4*01:01P*; *DQA1*01:03, 02:01*; *DQB1*02:02, 06:03*; *DPA1*01:03, 02:01*; *DPB1*04:01, 10:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-C alleles shows that this new allele has one nucleotide change from C*12:03:01:02 in codon 42 in exon 2, where G → A, resulting in a coding change (AGT → AAT, Serine → Asparagine, 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 confident in the phasing as the sample displayed a mean read length of 339 base pairs over all the loci, the mismatched A base was attributed 198 times to the new *HLA-C*12* allele and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-C*08:02:01:05* allele by virtue of two 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 02A, catalog RSSOX1C_02A_03), the most likely HLA-typing of the donor was *C*08:DWJJA*, 12:03:36 without any bead modification. We had to modify the bead #004 from positive to negative to obtain a *HLA-C*12:03:01* result. Indeed the bead #004 displayed oligonucleotides targeting the sequence surrounding codon 42 and was indicated by the manufacturer as reactive for the *HLA-C*12:123* which has an AAT in codon 42. Indeed, the IPD-IMGT/HLA Database 3.52.0 release describes only a few other HLA-C alleles displaying an AAT sequence at codon 42. 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. OQ606806) and to the IPD-IMGT/HLA Database (Submission No. HWS10065701). The name *C*12:384* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in March 2023. This follows the agreed policy that,

```
AA Codon                    5                   10                  15                  20                  25
C*12:03:01:02   GC TCC CAC TCC ATG AGG TAT TTC TAC ACC GCC GTG TCC CGG CCC GGC CGC GGA GAG CCC CGC TTC ATC GCA GTG
C*12:123
C*12:384

AA Codon                    30                  35                  40                  45                  50
C*12:03:01:02   GGC TAC GTG GAC GAC ACG CAG TTC GTG CGG TTC GAC AGC GAC GCC GCG AGT CCA AGA GGG GAG CCG CGG GCG CCG
C*12:123                                                                    -A-
C*12:384                                                                    -A-

AA Codon                    55                  60                  65                  70                  75
C*12:03:01:02   TGG GTG GAG CAG GAG GGG CCG GAG TAT TGG GAC CGG GAG ACA CAG AAG TAC AAG CGC CAG GCA CAG GCT GAC CGA
C*12:123
C*12:384

AA Codon                    80                  85                  90
C*12:03:01:02   GTG AGC CTG CGG AAC CTG CGC GGC TAC TAC AAC CAG AGC GAG GCC G
C*12:123                                                            --- -
C*12:384                                                            --- -
```

FIGURE 1 Alignment of sequences of exon 2 of *HLA-C*12:384* and *C*12:123* with the sequence of *C*12:03:01:02*. Dashes indicate nucleotide identity with the HLA-*C*12:03:01:02* allele. Numbers above the sequence indicate codon position.

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 STATEMENT

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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The new *HLA-DQB1*05:304* allele identified in an Italian patient

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*DQB1*05:304* allele was identical to *DQB1*05:02:01* except for a single nucleotide substitution.

KEYWORDS

*HLA-DQB1*05* new, new allele, next generation sequencing