Characterization of the novel *HLA-A*24:585* allele by sequencing-based typing

Marine Cargou[1] | **Vincent Elsermans**[2] | **Isabelle Top**[2] | **Elodie Wojciechowski**[1,3] | **Jonathan Visentin**[1,3]

[1]CHU de Bordeaux, Laboratoire d'Immunologie et Immunogénétique, Hôpital Pellegrin, Bordeaux, France

[2]CHU de Lille, Institut d'Immunologie-HLA, Lille, France

[3]Univ. Bordeaux, CNRS, ImmunoConcEpT, UMR 5164, Bordeaux, France

Correspondence
Marine Cargou, CHU de Bordeaux, Laboratoire d'Immunologie et Immunogénétique, Hôpital Pellegrin, Place Amélie Raba Léon, 33076 Bordeaux Cedex, France
Email: marine.cargou@chu-bordeaux.fr,

*HLA-A*24:585* differs from *HLA-A*24:02:01:01* by one nucleotide substitution in codon -15 in exon 1.

KEYWORDS
HLA, *HLA-A*24:585*, novel allele, sequencing-based typing

We report here a novel *HLA-A*24* allele, now named *HLA-A*24:585*, that carries one nucleotide substitution in exon 1 when compared with the *HLA-A*24:02:01:01* 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 8. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This recipient was found to have a new *A*24* allele and was consequently typed *A*11:01, 24:585*; *B*35:01, 51:01*; *C*04:01, 16:02*; *DRB1*01:03, 11:01*; *DRB3*02:02*; *DQA1*01:01, 05:05*; *DQB1*03:01P, 05:01P*; *DPA1*01:03, 02:01*; *DPB1*02:01, 09:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-A alleles shows that this new allele has one nucleotide change from *A*24:02:01:01* in codon -15 in exon 1, where G → C resulting in a new protein (GTC → CTC, Valine → Leucine, 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 302 base pairs over all the loci, the mismatched C base was attributed 157 times to the new *HLA-A*24* allele, and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-A*11:01:01:01* allele by virtue of 6 variant positions each distant by less than 100 base pairs. The coding nucleotide sequence of the new allele has been submitted to the GenBank database (Accession No. OP807951) and to the IPD-IMGT/HLA Database (Submission No. HWS10064313). The name *A*24:585* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in November 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,[3] 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

```
AA Codon                  -20               -15               -10               -5
A*24:02:01:01    ATG GCC GTC ATG GCG CCC CGA ACC CTC GTC CTG CTA CTC TCG GGG GCC CTG GCC CTG ACC CAG ACC TGG GCA G
A*24:585         --- --- --- --- --- --- --- --- --- C-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -
```

FIGURE 1 Alignment of the sequence of exon 1 of *HLA-A*24:585* with the sequence of *HLA-A*24:02:01:01*. Dashes indicate nucleotide identity with the *HLA-A*24:02:01:01* allele. Numbers above the sequence indicate codon position.

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.

ACKNOWLEDGMENTS

The authors thank the technicians of the Bordeaux and Lille Immunology laboratories for their technical expertise.

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.

ORCID

Marine Cargou https://orcid.org/0000-0002-1141-1417
Vincent Elsermans https://orcid.org/0000-0002-0881-0695
Jonathan Visentin https://orcid.org/0000-0003-3795-8979

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. Barker DJ, Maccari G, Georgiou X, et al. The IPD-IMGT/HLA database. *Nucleic Acids Res*. 2023;51(D1):D1053-D1060. doi:10.1093/nar/gkac1011
3. 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

How to cite this article: Cargou M, Elsermans V, Top I, Wojciechowski E, Visentin J. Characterization of the novel *HLA-A*24:585* allele by sequencing-based typing. *HLA*. 2023;102(1):70-71. doi:10.1111/tan.14993

Identification of the novel *HLA-A*24:589* allele in a Korean deceased donor

Sohyun Kim | Eun Kyung Kwon | Eun Hee So | Hye-Jin Kim | Borae G. Park

KODA LAB, Korea Organ Donation Agency, Seoul, South Korea

Correspondence
Borae G. Park, KODA LAB, Korea Organ Donation Agency, 36, Chungjeong-ro Seodaemun-gu, Seoul, 03741, Korea.
Email: borae.park@gmail.com

The *HLA-A*24:589* allele differs from *A*24:02:01:01* by one nucleotide substitution in codon 145 (CGC > GGC).

KEYWORDS

*A*24:589*, HLA-A24, new allele

*HLA-A*24* is a frequent allele with an average frequency of 23.97% (9.5%–61.0%) in the Oriental population.[1] *HLA-A*24:02* showed the highest frequency in the Korean population with 19.33% of HLA-A alleles.[2] Here, we report a novel *HLA-A*24*, officially named as *A*24:589*, discovered during routine HLA typing of deceased organ donation and confirmed by next generation sequencing.

In our routine laboratory setting, low-resolution HLA typing was performed using LinkSeq HLA ABCDRDQDP+384 kit (One Lambda, Thermo Fisher Scientific Inc., USA) on the ViiA7 Real-Time PCR system (Applied Biosystems, Thermo Fisher Scientific Inc.) and analyzed with SureTyper software per the manufacturer's instruction. Next generation sequencing was performed using AllType NGS assay system (One Lambda) on Illumina (San Diego, California) MiSeq sequencing technology. Informed consent for genetic testing of HLA was obtained. Sequences were submitted to GenBank and the IPD-IMGT/HLA Database, and allele names were officially assigned by the