

amino acid arginine and may therefore affect antigen-presenting properties of the HLA molecule.

The nucleotide sequence of the novel allele was submitted to GenBank and IPD-IMGT/HLA Databases and the accession numbers OP559474 and HWS10064273 were assigned. The name *C*15:255* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in December 2022. 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

Mirzokhid Rakhmanov, Martin Bernheiden, and Murielle Verboom carried out NGS data acquisition, analyzed and interpreted the NGS data. Murielle Verboom performed Sanger sequencing. Florian Emmerich and Mirzokhid Rakhmanov analyzed data and submitted the allele sequence to GenBank. Mirzokhid Rakhmanov and Florian Emmerich wrote the manuscript. All authors have read and approved the final manuscript.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

ACKNOWLEDGMENT

Open Access funding enabled and organized by Projekt DEAL.

DATA AVAILABILITY STATEMENT

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

ORCID

Florian Emmerich  <https://orcid.org/0000-0002-1099-9634>

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How to cite this article: Rakhmanov M, Bernheiden M, Verboom M, Emmerich F. Next-generation sequencing reveals a novel HLA-C allele, *HLA-C*15:255*. *HLA.* 2023;102(1):100-102. doi:[10.1111/tan.15038](https://doi.org/10.1111/tan.15038)

Characterization of the novel *HLA-DRB1*01:140* allele by sequencing-based typing

Marine Cargou¹  | Vincent Elsermans²  | Isabelle Top² |
Gwendaline Guidicelli¹ | Jonathan Visentin^{1,3} 

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

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

³Univ. 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-DRB1*01:140* differs from *HLA-DRB1*01:02:01:01* by one nucleotide substitution in codon 147 in exon 3.

KEYWORDS

HLA, *HLA-DRB1*01:140*, novel allele, sequencing-based typing

We report here a novel HLA-DRB1 allele, now named *HLA-DRB1*01:140*, that carries one nucleotide substitution in exon 3 when compared to the *HLA-DRB1*01:02:01:01*

allele, identified in a patient awaiting kidney transplantation. The HLA typing was performed using Next Generation Sequencing (AllType NGS, One Lambda, Canoga Park, CA)

AA Codon		100		105		110		115																		
DRB1*01:02:01:01	TT	GAG	CCT	AAG	GTG	ACT	GTG	TAT	CCT	TCA	AAG	ACC	CAG	CCC	CTG	CAG	CAC	CAC	AAC	CTC	CTG	GTC	TGC	TCT	GTG	
DRB1*01:140	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AA Codon		120		125		130		135		140																
DRB1*01:02:01:01	AGT	GGT	TTC	TAT	CCA	GGC	AGC	ATT	GAA	GTC	AGG	TGG	TTC	CGG	AAC	GGC	CAG	GAA	GAG	AAG	GCT	GGG	GTG	GTG	TCC	
DRB1*01:140	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AA Codon		145		150		155		160		165																
DRB1*01:02:01:01	ACA	GGC	CTG	ATC	CAG	AAT	GGA	GAT	TGG	ACC	TTC	CAG	ACC	CTG	GTG	ATG	CTG	GAA	ACA	GTT	CCT	CGG	AGT	GGA	GAG	
DRB1*01:140	---	---	G--	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AA Codon		170		175		180		185																		
DRB1*01:02:01:01	GTT	TAC	ACC	TGC	CAA	GTG	GAG	CAC	CCA	AGT	GTG	ACG	AGC	CCT	CTC	ACA	GTG	GAA	TGG	A						
DRB1*01:140	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						

FIGURE 1 Alignment of the sequence of exon 3 of *HLA-DRB1*01:140* allele with the sequence of *HLA-DRB1*01:02:01:01*. Dashes indicate nucleotide identity with the *HLA-DRB1*01:02:01:01* allele. Numbers above the sequence indicate codon position.

on the Ion S5 system platform (ThermoFisher Scientific, Waltham, MA),¹ from exons 2 to 6. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This patient was found to have a new *DRB1*01* allele and was consequently typed *A*01:01, 29:02; B*18:01, 37:01; C*05:01, 06:02; DRB1*01:140, 07:01; DRB4*01:01; DQA1*01:01, 02:01; DQB1*02:02, 05:01P; DPA1*01:03, 02:12; DPB1*15:01, 85:01*. Using the IPD-IMGT/HLA Database,² nucleotide sequence alignment with HLA-DRB1 alleles shows that this new allele has one nucleotide change from *DRB1*01:02:01:01* in codon 147 in exon 3, where C → G resulting in a new protein (CTG → GTG, Leucine → Valine, 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 303 base pairs over all the loci, the mismatched G base was attributed 988 times to the new *HLA-DRB1*01* allele and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-DRB1*07:01:01:01* allele by virtue of 2 variant positions each distant by less than 100 base pairs. HLA typing by Luminex reverse sequence-specific oligonucleotide (SSO) was performed (One Lambda Labtype, Canoga Park, CA).³ With this assay (lot 006, catalog RSSOX2B1_006_03), the most likely HLA-typing of the donor was *DRB1*01:DWJJD, 07:DVYJB* (most likely allele *DRB1*01:02, 07:01*, respectively) without any bead modification. Indeed the IPD-IMGT/HLA Database 3.50.0 release describe few other HLA-DRB1 alleles displaying a GTG sequence in codon 147, explaining why the manufacturer did not include probes targeting this codon. The analysis of the localization of this amino-acid and its antibody accessibility with the pHLA3D database⁴ indicated that this amino-acid is located out of the peptide binding groove while it is surface accessible. Then, despite

the fact that Leucine and Valine are amino-acids having similar physico-chemical properties, a transplanted organ from a donor expressing the *HLA-DRB1*01:140* allele could lead to a humoral allo-sensitization which cannot be detected by current solid-phase assays. In case of a suspicious antibody-mediated rejection, only the use of donor's cells to perform a retrospective crossmatch could allow the diagnosis. The nucleotide sequence of the new allele has been submitted to the GenBank database (Accession No. OP807952) and to the IPD-IMGT/HLA Database (Submission No. HWS10064315). The name *DRB1*01:140* 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,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, Gwendaline Guidicelli, and Jonathan Visentin participated in the performance of the research. Marine Cargou, Vincent Elsermans, Isabelle Top, Gwendaline Guidicelli, and Jonathan Visentin participated in data analysis. Vincent Elsermans, Isabelle Top, and Gwendaline Guidicelli 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>




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How to cite this article: Cargou M, Elsermans V, Top I, Guidicelli G, Visentin J. Characterization of the novel *HLA-DRB1*01:140* allele by sequencing-based typing. *HLA*. 2023;102(1):102-104. doi:10.1111/tan.14992

Characterization of the novel HLA-DRB1 allele, *HLA-DRB1*04:328* in a Chinese individual

Jingjing Zhang^{1,2}  | Nanying Chen^{1,2} | Chen Chen^{1,2}  | Wei Zhang^{1,2} | Faming Zhu^{1,2} 

¹HLA Typing Laboratory, Blood Center of Zhejiang Provinc, Hangzhou, China

²HLA Typing Laboratory, Key Laboratory of Blood Safety Research of Zhejiang Provinc, Hangzhou, China

Correspondence

Faming Zhu, Blood Center of Zhejiang Province, Key Laboratory of Blood Safety Research of Zhejiang Province, JianYe Road 789, Hangzhou, Zhejiang Province 310052, China.
Email: zfm00@hotmail.com

Funding information

Science Research Foundation of Zhejiang Healthy Bureau, Grant/Award Number: 2021KY651

*HLA-DRB1*04:328* shows a single nucleotide substitution at position 143 A>T when compared with *HLA-DRB1*04:05:01:01*.

KEYWORDS

*HLA-DRB1*04:328*, new allele, next-generation sequencing

There are 35,820 HLA alleles identified in populations around the world according to the latest release of the IPD-IMGT/HLA Database (Version 3.51.0 January 2023), including 4374 alleles for the HLA-DRB1 locus.¹ Here, we describe the novel HLA-DRB1 allele, officially named

as *HLA-DRB1*04:328*, that has been found in a Chinese cord blood donor.

The sample of the proband was originally genotyped for the HLA-A, -B, -C, -DRB1, -DQB1 loci using the AllType™ NGS 11-loci amplification kit (One Lambda,