A novel allele, *HLA-C*15:227*, identified when typing COVID-19 patients

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Funding information
Ministry of Science and Higher Education of the Russian Federation, Grant/Award Number: 075-15-2019-1789

*HLA-C*15:227* differs from *HLA-C*15:02:01:01* by a single nonsynonymous change (368A → G Tyrosine 99 to Cysteine).

KEYWORDS
*HLA-C*15:227*, NGS HLA typing, novel HLA allele

The IPD-IMGT/HLA Database currently has information on more than 20,000 human leukocyte antigen (HLA) class I alleles and more than 6200 of these are alleles of HLA-C gene.[1] In this report, we describe the sequence of a novel HLA-C allele. It was identified in a COVID-19 patient, using a next-generation sequencing (NGS) method for HLA typing.

The genomic DNA was extracted from peripheral blood cells using a commercial kit "Proba MCh-Max," according to the manufacturer's instructions (DNA-technology, Moscow, Russia) on automatic DNA extraction station "DT-stream" (DNA-technology, Moscow, Russia). It was typed for HLA-alleles at the A, B, C, DRB1, and DQB1 loci using reagents "HLA-expert" (DNA-technology, Moscow, Russia), sequenced on MiSeq (Illumina, The United States), and analyzed with "HLA-expert" software (DNA-technology, Moscow, Russia).

The sequence of *HLA-C*15:227* differs from *HLA-C*15:02:01:01* by nonsynonymous mutation (A → G) at position 368, resulting in change from TAT (Tyrosine) to TGT (Cysteine) at codon 99 in exon 3. The complete HLA typing of patient with the novel *HLA-C*15:227* allele was: *HLA-A*29:02:01G*, *32:01:01G*; *HLA-C*06:02:01G*, *15:227*; *HLA-B*50:01:01G*, *51:01:01G*; *HLA-DRB1*04:04:01G*, *07:01:01G*; *HLA-DQB1*02:01:01G*, *03:02:01G*.

The novel allele was submitted to GenBank (accession number MT896389) and the IPD-IMGT/HLA Database[1] and was officially assigned by the World Health

Organization (WHO) Nomenclature Committee for Factors of the HLA System in September 2020. List of such new names were published in the following WHO Nomenclature Report.[2]

The *HLA-C*15:227* allele was confirmed in the Research Laboratory of Applied Immunogenetics by NGS typing with the VariFind HLA solution IL kit (Parseq Lab Co, Saint Petersburg, Russia), the whole HLA-C (except the 3′-UTR region) gene was amplified by long PCR at 1st step. Once the library for NGS was obtained, it was then sequenced using a MiSeq (Illumina, The United States) and analyzed by VariFind HLA Software v2.2 (Parseq Lab Co, Saint Petersburg, Russia).

ACKNOWLEDGMENT

This research was funded by grant number 075-15-2019-1789 from the Ministry of Science and Higher Education of the Russian Federation allocated to the Center for Precision Genome Editing and Genetic Technologies for Biomedicine.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

Valery Cheranev: Registering novel allele. Maria Loginova: Confirmatory HLA-typing, writing a manuscript. Tatjana Jankevic: Primary HLA-typing. Svetlana Kutyavina: Confirmatory HLA-typing. Denis Rebrikov: Recruiting bone marrow donors, collection blood samples.

DATA AVAILABILITY STATEMENT

Data is available from the IPD-IMGT/HLA Database. GenBank accession number-MT896389.

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How to cite this article: Cheranev V, Loginova M, Jankevic T, Kutyavina S, Rebrikov D. A novel allele, *HLA-C*15:227*, identified when typing COVID-19 patients. *HLA*. 2021;97:377–378. https://doi.org/10.1111/tan.14199