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NEW ALLELE ALERT

Identification of the Novel *HLA-DPB1*1758:01* Allele by Pacbio Sequencing

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Received: 15 April 2025 | **Revised:** 17 April 2025 | **Accepted:** 22 April 2025

Keywords: *HLA-DPB1*1758:01* | new allele | Pacbio sequencing

ABSTRACT

The novel *HLA-DPB1*1758:01* allele differs from *HLA-DPB1*1273:01* by one nucleotide substitution in Exon 4.

In this report, we describe the identification of the novel allele *HLA-DPB1*1758:01*, which was identified by PacBio's Single Molecule Real-Time (SMRT) sequencing (PacBio, Menlo Park, CA, USA) of a sample from a Chinese haematopoietic stem cell donor.

Genomic DNA was isolated from a peripheral blood sample using commercial kits (Tiangen Biochemical Technology Co. Ltd., Beijing, China). Full-length gene segments of *HLA-A*, *HLA-B*, *HLA-C*, *HLA-DQB1*, *HLA-DPB1*, *HLA-DQA1* and *HLA-DPA1* were amplified with locus-specific primers. Additionally, the *DRB1/3/4/5* genes were targeted using two primer pairs to amplify exon 1 and exons 2–6 individually. Next, SMRT sequencing of the amplicons was carried out using the PacBio Sequel II Platform, while readings were analysed by PB AMPLICON ANALYSIS (PBAA) software (Version 1.0.3).

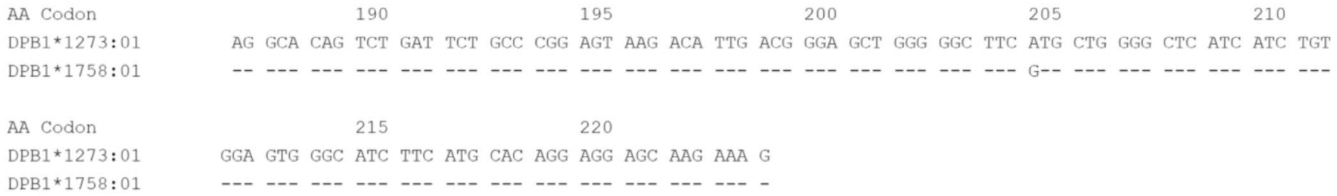
The complete HLA typing of the 67-year-old donor was as follows: *A*11:01, 33:03*; *B*40:01, 58:01*; *C*03:02, 07:02*; *DRB1*09:01, 11:01*; *DRB3*02:02, DRB4*01:03*; *DQA1*03:02, 05:05*; *DQB1*03:01, 03:01*; *DPA1*02:02, 04:01*; *DPB1*05:01, 1758:01*.

Using *HLA-DPB1*1273:01* sequence alignment from the IPD-IMGT/HLA 3.60.0 database [1], it was clear that the investigated allele differed from the allele *DPB1*1273:01* at nucleotide 700 located in exon 4. The observed nucleotide substitution produced a non-synonymous variation from A to G at nucleotide 700, in codon 205 (ATG vs. GTG) resulting in a change from Methionine to Valine (Figure 1), indicating the existence of a new allele.

The sequence of the *DPB1*1758:01* allele was submitted to Genbank and IPD-IMGT/HLA Database (the accession numbers are PQ858443 and HWS10093477, respectively).

The name *DPB1*1758:01* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in January 2025. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report

https://doi.org/10.1111/tan.70220



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AA Codon                       190                 195                 200                 205                 210
DPB1*1273:01        AG GCA CAG TCT GAT TCT GCC CGG AGT AAG ACA TTG ACG GGA GCT GGG GGC TTC ATG CTG GGG CTC ATC ATC TGT
DPB1*1758:01        -- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- G-- --- --- --- --- --- ---

AA Codon                       215                 220
DPB1*1273:01       GGA GTG GGC ATC TTC ATG CAC AGG AGG AGC AAG AAA G
DPB1*1758:01       --- --- --- --- --- --- --- --- --- --- --- --- -
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FIGURE 1 | Comparison of the exon 4 sequences of the *HLA-DPB1*1273:01* and *HLA-DPB1*1758:01* alleles. The exon 4 sequences are shown in codons, numbered above. One nucleotide substitution in codon 205 present in *HLA-DPB1*1758:01* distinguishes it from the *HLA-DPB1*1273:01* allele. Identity between the two sequences is shown with dashes (–).

[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

Kun Ru and Yani Lin designed the study. Tongcui An provided genetic laboratory data. Dongmei Guo and Bin Chen analysed the data and wrote the manuscript. All authors read and approved the final version of the manuscript.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are openly available in Genbank at https://www.ncbi.nlm.nih.gov/nuccore/PQ858443 and IPD-IMGT/HLA Database (the accession numbers are PQ858443 and HWS10093477, respectively).

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