

# Characterization of the novel *HLA-B\*40:539* allele by sequencing-based typing

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*HLA-B\*40:539* differs from *HLA-B\*40:01:01* by one nucleotide substitution in codon 46 in exon 2.

## KEYWORDS

HLA, *HLA-B\*40:539*, novel allele, sequencing-based typing

We report here a novel *HLA-B\*40* allele, *B\*40:539* that carries one nucleotide substitution in exon 2 when compared to the *B\*40:01:01* allele, identified in a volunteer unrelated hematopoietic stem cell donor. The HLA typing was performed using Next Generation Sequencing reagents provided by Protrans (Protrans N5, Hockenheim, Germany) run on the Miseq system platform (Illumina, San Diego, CA). The reads were analyzed using the SeqPilot software (version 5.2.0) (JSI Medical Systems, Ettenheim, Germany).

The subject was found to have a new *B\*40* allele and was consequently typed *A\*02:01*, *68:02*; *C\*03:04*, *08:02*; *B\*14:02*, *40:539*; *DRB1\*01:02*, *13:01*; *DQB1\*05:01*, *06:03*; *DPB1\*13:01*, *13:01*. Using the IPD-IMGT/HLA Database,<sup>1</sup> nucleotide sequence alignment with *HLA-B* alleles shows that this new allele has one nucleotide change from *B\*40:01:01* in codon 46 of exon 2, where G → C resulting in a new protein (GAG → GAC, Glutamic acid → Aspartic acid, Figure 1). This polymorphism had previously been described in only

AA Codon		5		10		15		20		25																
<i>B*40:01:01</i>	GC	TCC	CAC	TCC	ATG	AGG	TAT	TTC	CAC	ACC	GCC	ATG	TCC	CGG	CCC	GCC	CGC	GGG	GAG	CCC	CGC	TTC	ATC	ACC	GTG	
<i>B*40:539</i>	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AA Codon		30		35		40		45		50																
<i>B*40:01:01</i>	GGC	TAC	GTG	GAC	GAC	ACG	CTG	TTC	GTG	AGG	TTC	GAC	AGC	GAC	GCC	ACG	AGT	CCG	AGG	AAG	GAG	CCG	CGG	GCG	CCA	
<i>B*40:539</i>	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AA Codon		55		60		65		70		75																
<i>B*40:01:01</i>	TGG	ATA	GAG	CAG	GAG	GGG	CCG	GAG	TAT	TGG	GAC	CGG	GAG	ACA	CAG	ATC	TCC	AAG	ACC	AAC	ACA	CAG	ACT	TAC	CGA	
<i>B*40:539</i>	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
AA Codon		80		85		90																				
<i>B*40:01:01</i>	GAG	AGC	CTG	CGG	AAC	CTG	CGC	GCC	TAC	TAC	AAC	CAG	AGC	GAG	GCC	G										
<i>B*40:539</i>	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

**FIGURE 1** Alignment of the sequence of exon 2 of *B\*40:539* with the sequence of *B\*40:01:01*. Dashes indicate nucleotide identity with the *HLA-B\*40:01:01* allele. Numbers above the sequence indicate codon position.

one other *HLA-B* allele. This nucleotide change was confirmed using DNA sequencing reagents provided by Protrans (Protrans S4 mono allelic SBT kits, Hockenheim, Germany) run on the ABI 3730xl (Applied Biosystems, Foster City, CA). Data were analyzed with SeqPilot software (version 5.2.0). Sequencing was performed in both directions (forward and reverse) for exons 2, 3, and 4. The nucleotide sequence of the new allele has been submitted to the GenBank database (accession number OK236546) and to the IPD-IMGT/HLA Database (Submission No. HWS10065787). The name *B\*40:539* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in April 2023. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,<sup>2</sup> 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.

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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 from the corresponding author upon reasonable request. The sequence is freely available in the IPD-IMGT/HLA Database.

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#### REFERENCES

1. Barker DJ, Maccari G, Georgiou X, et al. The IPD-IMGT/HLA database. *Nucleic Acids Res.* 2023;51(D1):D1053-D1060.
2. Marsh SGE, Albert ED, Bodmer WF, et al. Nomenclature for factors of the HLA system, 2010. *Tissue Antigens.* 2010;75(4):291-455.

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