

NEW ALLELE ALERTS

Discovery of a novel HLA class I allele, *HLA-B*38:75*, in an Indian umbilical cord blood sample

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Email: drvinayak@regrow.inThe novel HLA allele *HLA-B*38:75* differs from *B*38:02:01* by nonsynonymous change in codon 50.**KEYWORDS**

cord blood units, human leukocyte antigen, next generation sequencing

The HLA genes, located within the human major histocompatibility complex on the short-arm chromosome 6 (6p21.3), are known for their extreme polymorphism and encode the diverse HLA class I and II antigen-presenting molecules. According to the IPD-IMGT/HLA Database, the HLA-B gene is most polymorphic encoding over 6500 alleles (Release 3.27.0 July 2019).¹ The number of HLA alleles recognized is continuously increasing with the development of genotyping technologies.

We discovered the novel HLA-B allele during routine HLA typing of samples derived from umbilical cord blood by next generation sequencing (NGS) method. In comparison to traditional HLA DNA typing methods, the NGS technique has several advantages: first, it allows generation of haplotype sequencing from a single DNA molecule; second, it resolves the problem of phase ambiguity and last, millions of sequencing reads are produced by massive level of parallelism. As such, NGS is expected to

Segment : Exon2

AA Codon					5					10					15					20
B*38:02:01	GC	TCC	CAC	TCC	ATG	AGG	TAT	TTC	TAC	ACC	TCC	GTG	TCC	CGG	CCC	GGC	CGC	GGG	GAG	CCC
B*38:75	--	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AA Codon					25					30					35					40
B*38:02:01	CGC	TTC	ATC	TCA	GTG	GGC	TAC	GTG	GAC	GAC	ACG	CAG	TTC	GTG	AGG	TTC	GAC	AGC	GAC	GCC
B*38:75	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AA Codon					45					50					55					60
B*38:02:01	GCG	AGT	CCG	AGA	GAG	GAG	CCG	CGG	GCG	CCG	TGG	ATA	GAG	CAG	GAG	GGG	CCG	GAA	TAT	TGG
B*38:75	---	---	---	---	---	---	---	---	---	-T-	---	---	---	---	---	---	---	---	---	---
AA Codon					65					70					75					80
B*38:02:01	GAC	CGG	AAC	ACA	CAG	ATC	TGC	AAG	ACC	AAC	ACA	CAG	ACT	TAC	CGA	GAG	AAC	CTG	CGC	ACC
B*38:75	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
AA Codon					85					90										
B*38:02:01	GCG	CTC	CGC	TAC	TAC	AAC	CAG	AGC	GAG	GCC	G									
B*38:75	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIGURE 1 Alignment of the exon 2 sequences of *HLA-B*38:02:01* with the new variant *B*38:75*. Dashes indicate nucleotide sequence identity to *B*38:02:01*. Numbers above correspond with the codon position

provide highly accurate, reproducible, more effective, and high-throughput genotyping of HLA gene.²

Briefly, DNA was extracted from whole blood using FABG reagent (Favorprep, Genomic DNA Mini Kit, Taiwan). The concentration of the extracted nucleic acid was measured using a Qubit dsDNA BR Assay Kit (Thermo Fisher Scientific). DNA concentration of 10 ng/μL was used for HLA sequencing and typing testing by using Illumina MiSeq/HiSeq, and analysis of data was done using in-house software (Histo S).

Point mutation, recombination, and gene conversion—such events have all been shown in the generation of novel HLA alleles. HLA polymorphism is mainly located in the exons that encode the α1 and α2 (HLA class I, exons 2-3) and the α1 and β1 (HLA class II, exon 2) domains which bind processed peptides.³ In our HLA registry, we discovered the novel allele, now named *HLA-B*38:75*, which differs from the *HLA-B*38:02:01* allele by a nonsynonymous substitution (CCG to CTG, proline to leucine) in codon 50 in exon 2 (Figure 1).

The nucleotide sequence described in this study has been submitted to the GenBank and was allotted the accession number MG756820. The name *B*38:75* has been officially assigned by the World Health Organization (WHO) Nomenclature Committee in September 2018. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,⁴ 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.

CONFLICT OF INTEREST

The authors have declared no conflicting interests.

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