

Identification of a New HLA-B*27 Allele, B*27:05:31, in a Russian Individual

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Introduction

The human leukocyte antigen (HLA) genes are the most polymorphic in the human genome. According to the World Health Organization (WHO) Nomenclature Committee for Factors of the HLA System in July 2015, a total of 10 297 HLA class I alleles and 3 543 HLA class II alleles have been described [1]. Currently, there are over 4700 HLA-B alleles described [2].

It is well documented that the frequencies of HLA alleles differ with different ethnic groups. For example, the frequency of B*27 alleles in Caucasian populations varies between 0.0% and 8.8%, while in Oriental populations this may exceed 10% [3]. Russia is a multinational state with a poly-ethnic population. At present, information about the ethnic polymorphism of HLA in Russia is negligible. In this study, we describe the identification of a new allele, B*27:05:31, in a Russian individual.

Genomic DNA was isolated from frozen collected anticoagulated ethylene diaminetetraacetic acid (EDTA) whole blood of Russian unrelated hematopoietic stem cell volunteer by using the QIAamp DNA Blood Mini Kit on the automatic workstation QIAcube (Qiagen, Hilden, Germany). It was typed for the HLA-A, HLA-B, HLA-C and HLA-DRB1 loci. HLA alleles were sequenced through exons 2-4 in both directions using reagent kit AlleleSEQR HLA from Celera (Abbott, IL, USA) and analyzed with SBTengine software (GenDx, Utrecht, Netherlands). The sample showed the following genotypes: HLA*A02, 11, HLA-B*27NEW, 56, HLA-C*01, 02, HLA-DRB1*01, 09.

The complete sequence for this sample for the HLA-A, HLA-B, HLA-C, HLA-DRB1 and HLA-DQB1 loci was obtained by Next Generation Sequence (GenDx, Utrecht, Netherlands) on the platform IonTorrent. HLA typing results analyzed with NGSengine (GenDx, Utrecht, Netherlands). The sample showed the following genotypes: HLA*A02:01:01:01/02:01:01:01L, 11:01:01:01, HLA-B*27NEW,

56:01:01:01, HLA-C*01:02:01, 02:02:02:01, HLA-DRB1*01:01:01, 09:01:02/09:21, DQB1*03:03:02, 05:01:01:02.

AA Codon	188	190	198	200	208	
B*27:05:02	AC CCC CCA AAG ACA CAC	GTG ACC CAC CAC CCC ATC TCT GAC CAT GAG GGC ACC CTG AGG TGC TGG GGC CTG GGC				
B*27:05:31	AC CCC CCA AAG ACA CAC	GTG ACC CAC CAC CCC ATC TCT GAC CAT GAG GGC ACC CTG AGG TGC TGG GGC CTG GGC				
AA Codon	210	218	220	228	230	
B*27:05:02	TTC TAC CCG GCG GAG ATC ACA	CTG ACC TGG CAG CCG GAT GGC GAG GAC CAA ACT CAG GAC ACT GAG CTT GTG GAG				
B*27:05:31	TTC TAC CCG GCG GAG ATC ACA	CTG ACC TGG CAG CCG GAT GGC GAG GAC CAA ACT CAG GAC ACT GAG CTT GTG GAG				
AA Codon	238	240	248	250	258	
B*27:05:02	ACC AAA CCA GCA GGA GAT AGA	ACC TTC CAG AAG TGG GCA GCT GTG GTG GTC CTT TGT GGA GAA GAG CAG AGA TAC				
B*27:05:31	ACC AAA CCT GCA GGA GAT AGA	ACC TTC CAG AAG TGG GCA GCT GTG GTG GTC CTT TGT GGA GAA GAG CAG AGA TAC				
AA Codon	260	268	270			
B*27:05:02	ACA TGC CAT GTA CAG CAT GAG	GGG CTG CCG AAG CCC CTC ACC CTG AGA TGG G				
B*27:05:31	ACA TGC CAT GTA CAG CAT GAG	GGG CTG CCG AAG CCC CTC ACC CTG AGA TGG G				

Figure 1: Comparison of exon 4 sequences for alleles B*27:05:02 and B*27:05:31. B*27:05:31 differs from B*27:05:02 by an A to T in codon 235 as indicated by a box. This figure is derived from the IMGT/HLA database [2].

The new allele B*27:05:31 differs from B*27:05:02 by an A>T in exon 4, but the change codon 235 from CCA to CCT does not change the amino acid (Pro) (Figure 1). The name HLA-B*27:05:31 allele was officially assigned by the WHO Nomenclature Committee in February 2015. The nucleotide sequence is available in the European molecular biology laboratory (EBML) sequence database under the accession number LN810554.

References

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