

single nucleotide substitution (G → A) in exon 2 at gDNA position 3941 (codon 33.a). Complete HLA assignment was as follows: *A*02:01:01:01*, *02:01:01:01*; *B*27:05:02*, *44:02P*; *C*02:02:02*, *05:01:01:02*; *DRB1*08:01P*, *12:01P*; *DRB3*02:02:01*; *DQA1*04:01:01:01*, *05:51*; *DQB1*03:01P*, *04:02:01:01*; *DPA1* 01:03:01*, *01:03:01*; *DPB1*03:01P*, *04:01P*.

The names *A*68:288*, *C*07:1012*, *C*12:364*, and *DQA1*05:51* have been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in March 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,² names would 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

Evgeny A. Leonov performed the NGS and wrote the article. Alena R. Abdrakhimova and Stanislav P. Khizhinskiy performed the NGS. Ekaterina G. Khamaganova supervised the work and was involved in writing the article. Elena N. Parovichnikova supervised the work and was involved in critical revision of the manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data is freely available from the IPD-IMGT/HLA database.

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The novel HLA class I allele, *HLA-B*14:110*, identified by next-generation sequencing

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The novel HLA-allele *B*14:110*, differs from *B*14:02:01:01*, by one nucleotide substitution, c.T247A in exon 2.

KEYWORDS

*HLA-B*14:110*, next-generation sequencing, novel HLA-allele

The numbers of identified HLA-alleles are rapidly increasing since the introduction of sequencing methods such as next-generation sequencing (NGS) for clinical

HLA typing. According to IPD-IMGT/HLA Database version 3.47 (2022-01),¹ a total of 8756 HLA-B alleles have been identified. At Aarhus University Hospital we

FIGURE 1 Sequence alignment of *HLA-B*14:02:01:01* and *HLA-B*14:110*, coding sequences (CDS). Identity to the *B*14:02:01:01* allele is shown with dashes (—), the exon boundaries are indicated by pipes (|).

AA Codon B*14:02:01:01 B*14:110	ATG CTG GTC ATG GCG CCC CGA ACC GTC CTC CTG CTG CTC TCG GCG GCC CTG GCC CTG ACC GAG ACC TGG GCC G GC	-20 -15 -10 -5 1
AA Codon B*14:02:01:01 B*14:110	TCC CAC TCC ATG AGG TAT TTC TAC ACC GCC GTG TCC CGG CCC GGC CGC GGG GAG CCC CGC TTC ATC TCA GTG GGC	5 10 15 20 25
AA Codon B*14:02:01:01 B*14:110	TAC GTG GAC GAC ACG CAG TTC GTG AGG TTC GAC AGC GAC GCC GCG AGT CCG AGA GAG GAG CCG CGG GCG CCG TGG	30 35 40 45 50
AA Codon B*14:02:01:01 B*14:110	ATA GAG CAG GAG GGG CCG GAA TAT TGG GAC CGG AAC ACA CAG ATC TGC AAG ACC AAC ACA CAG ACT GAC CGA GAG	55 60 65 70 75
AA Codon B*14:02:01:01 B*14:110	AGC CTG CGG AAC CTG CGC GGC TAC TAC AAC CAG AGC GAG GCC G GG TCT CAC ACC CTC CAG TGG ATG TAT GGC TGC	80 85 90 95 100
AA Codon B*14:02:01:01 B*14:110	GAC GTG GGG CCG GAC GGG CGC CTC CTC CGC GGG TAT AAC CAG TTC GCC TAC GAC GGC AAG GAT TAC ATC GCC CTG	105 110 115 120 125
AA Codon B*14:02:01:01 B*14:110	AAC GAG GAC CTG AGC TCC TGG ACC GCG GCG GAC ACC GCG GCT CAG ATC ACC CAG CGC AAG TGG GAG GCG GCC CGT	130 135 140 145 150
AA Codon B*14:02:01:01 B*14:110	GAG GCG GAG CAG CTG AGA GCC TAC CTG GAG GGC ACG TGC GTG GAG TGG CTC CGC AGA CAC CTG GAG AAC GGG AAG	155 160 165 170 175
AA Codon B*14:02:01:01 B*14:110	GAG ACG CTG CAG CGC GCG G AC CCC CCA AAG ACA CAT GTG ACC CAC CAC CCC ATC TCT GAC CAT GAG GCC ACC CTG	180 185 190 195 200
AA Codon B*14:02:01:01 B*14:110	AGG TGC TGG GCC CTG GGC TTC TAC CCT GCG GAG ATC ACA CTG ACC TGG CAG CGG GAT GGC GAG GAC CAA ACT CAG	205 210 215 220 225
AA Codon B*14:02:01:01 B*14:110	GAC ACC GAG CTT GTG GAG ACC AGA CCA GCA GGA GAC AGA ACC TTC CAG AAG TGG GCA GCT GTG GTG GTG CCT TCT	230 235 240 245 250
AA Codon B*14:02:01:01 B*14:110	GGA GAA GAG CAG AGA TAC ACA TGC CAT GTA CAG CAT GAG GGG CTG CCG AAG CCC CTC ACC CTG AGA TGG G AG CCA	255 260 265 270 275
AA Codon B*14:02:01:01 B*14:110	TCT TCC CAG TCC ACC GTC CCC ATC GTG GGC ATT GTT GCT GGC CTG GCT GTC CTA GCA GTT GTG GTC ATC GGA GCT	280 285 290 295 300
AA Codon B*14:02:01:01 B*14:110	GTG GTC GCT GCT GTG ATG TGT AGG AGG AAG AGT TCA G GT GGA AAA GGA GGG AGC TAC TCT CAG GCT GCG T CC AGC	305 310 315 320 325
AA Codon B*14:02:01:01 B*14:110	GAC AGT GCC CAG GGC TCT GAT GTG TCT CTC ACA GCT TGA	330 335

annually perform approximately 1000 high resolution HLA typing using NGS.

We report here a novel *HLA-B*14*-allele, now officially named *B*14:110*. The allele was identified in a patient HLA typed prior to listing for renal transplantation.

The novel allele was determined by NGS applying the Holotype HLA protocol (Omixon, Hungary) and the Illumina MiSeq platform (Illumina, USA). Data was aligned using HLA Twin software 4.4.1 (Omixon). The novel allele was verified with the AllType NGS protocol (One Lambda, USA).

The novel *B*14:110* allele has one nucleotide change when compared to the *B*14:02:01:01* allele at coding position c.247 T > A in exon 2. This non-synonymous codon change, TAT > AAT, results in an amino acid substitution from Tyrosine to Asparagine, both of which are neutral polar amino acids (Figure 1A). This novel position is located in the $\alpha 1$ helix of the peptide binding groove, which defines affinity to presented peptides. As the amino acid is located in the $\alpha 1$ helix and not pointing towards the peptide binding site, it is not expected to be directly involved in peptide binding (Figure 1B).²

The patient carrying the novel allele had the following extended genotype: *HLA-A*23:01:01:01*, *24:02:01G*; *B*14:110*, *35:02:01G*; *C*02:02:02G*, *04:01:01:06*; *DRB1*01:02:01:01*, *11:04:01*; *DQB1*03:01:01:02*, *05:01:01:01*; *DQA1*01:01:02*, *05:05:01:09*; *DPA1*01:03:01G*, *01:03:01G*; *DPB1*02:01:02:03*, *04:01:01:27*.

The novel sequence was submitted to GenBank under accession number OM687206. The name *B*14:110* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in March 2022. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report,³ 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

Marie Quach Lam, Maja Nørgaard: performed the analyses; **Maja Nørgaard, Marie Quach Lam, Mira Marie Laustsen:** handled and analyzed data; **Nicklas Heine Staunstrup, Mira Marie Laustsen, Pernille Koefoed-Nielsen:** wrote the paper; **Nicklas Heine Staunstrup, Pernille Koefoed-Nielsen:** supervision.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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The *HLA-B*15:02:01:05* allele identified by two next-generation sequencing methods in a Japanese individual

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*HLA-B*15:02:01:05* differs from *HLA-B*15:02:01:01* by four nucleotides in 3'UTR at positions 3435, 3457, 3472, and 3511.

KEYWORDS

*B*15:02:01:05*, *B*15:02:01:01*, Japanese

The *HLA-B*15:02* allele is the 36th most common HLA-B allele in the Japanese population¹ with an allele frequency of 0.041%. Here, we are reporting a novel *HLA-B*15:02:01:01* variant allele, now officially named as *HLA-B*15:02:01:05* by World Health Organization (WHO) Nomenclature Committee for Factors of the HLA System in December 2020. *HLA-B*15:02:01:05* was discovered in the project to evaluate the potential association of HLA alleles with the severity of Japanese COVID-19.²

Here, we report the first genomic full-length sequence of *B*15:02:01:05* with a total amplicon length of 4093 bp

genotyped by using AllType™ NGS Assays (One Lambda, West Hills, CA) on the Ion GeneStudio S5 (Thermo Fisher Scientific, Waltham, MA). Concordant HLA genotype assignments were carried out using both NGSengine® (2.22.0.22581) by the GenDX company (GenDX, Utrecht, the Netherlands) and HLATypeStream Visual (TSV v2.0; One Lambda).

Confirmation of novel HLA alleles were carried out by Pacbio Sequel sequencing using in-house primers developed in conjunction with H.U.Group Research Institute (Tokyo, Japan). Pacbio subreads and consensus