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# Killer-cell Immunoglobulin-like Receptor (KIR) Nomenclature Report, 2002

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## INTRODUCTION

During discussion at the WHO Nomenclature Committee for Factors of the HLA System meeting in Victoria, Canada, in May 2002, it was decided to form a subcommittee to coordinate the naming of alleles of the genes encoding the killer-cell immunoglobulin-like receptors (KIRs) [1]. These genes are encoded on chromosome 19 (19q13.4) and have varying degrees of polymorphism. The receptors encoded by the *KIR* genes are expressed by natural killer (NK) cells and a subset of T cells and some of them have been shown to have specificity for determinants of human leukocyte antigen (HLA) class I molecules. The extracellular ligand-binding part of KIR consists of two or three immunoglobulin (Ig)-like domains. The discussions which took place in Victoria futher to earlier discussions on KIR nomenclature at the NK Polymorphism meeting (27–29 July 2001) in Cambridge, UK. In addition, a request has been made by the International Union of Immunological Societies (IUIS) to provide a standardized nomenclature for the expressed protein products of the KIR genes.

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## KIR GENE NOMENCLATURE

The first KIRs to be defined were inhibitory receptors, and when initially coined, the acronym stood for killer-cell inhibitory receptor. With appreciation that this family of molecules included both activating and inhibitory receptors, the KIR acronym was retained and is now accepted as an abbreviation for Killer-cell Immunoglobulin-like Receptor [2]. Unlike HLA genes, which for practical and historical reasons are named by the WHO Nomenclature Committee for Factors of the HLA System, the naming of KIR genes is the responsibility of the HUGO Genome Nomenclature Committee (HGNC). Agreement was reached with the HGNC for naming the *KIR* genes, and a total of 17 genes have been recognized and named (Table 1), the ones most recently assigned being *KIR2DL5A*, *KIR2DL5B*, *KIR2DP1*, *KIR3DL3*, and *KIR3DP1*. The subcommittee will continue to work closely with the HGNC in the future to ensure all newly described genes are assigned appropriate names.

The names given to the *KIR* genes are based on the structures of the molecules they encode. The first digit following the KIR acronym corresponds to the number of Ig-like domains in the molecule and the "D" denotes "domain." The D is followed by either an "L," indicating a "Long" cytoplasmic tail, an "S" indicating a "Short" cytoplasmic tail, or a "P" for "pseudogenes." The final digit indicates the number of the gene encoding a protein with this structure. Thus *KIR2DL1*, *KIR2DL2*, and *KIR2DL3* all encode receptors having two extracellular Ig-like domains and a long cytoplasmic tail [3]. Where two or more genes have very similar structures and have very similar sequences, they may be given the same

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**TABLE 1** KIR gene names

| Gene Symbol | Protein symbol | Description | Aliases | Reference or submitting author |
|---|---|---|---|---|
| *KIR2DL1* | KIR2DL1 | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 | cl-42, nkat1, 47.11, p58.1, CD158a | (10, 11) |
| *KIR2DL2* | KIR2DL2 | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 | cl-43, nkat6, CD158b1 | (10, 11) |
| *KIR2DL3* | KIR2DL3 | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 | cl-6, nkat2, nkat2a, nkat2b, p58, CD158b2 | (10, 11) |
| *KIR2DL4* | KIR2DL4 | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 | 103AS, 15.212, CD158d | (12) |
| *KIR2DL5A* | KIR2DL5A | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A | KIR2DL5.1, CD158f | (13) |
| *KIR2DL5B* | KIR2DL5B | Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5B | KIR2DL5.2, KIR2DL5.3, KIR2DL5.4 | (13) |
| *KIR2DS1* | KIR2DS1 | Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 | EB6ActI, EB6ActII, CD158h | (14) |
| *KIR2DS2* | KIR2DS2 | Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 | cl-49, nkat5, 183ActI, CD158j | (10, 11) |
| *KIR2DS3* | KIR2DS3 | Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3 | nkat7 | (15) |
| *KIR2DS4* | KIR2DS4 | Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 | cl-39, KKA3, nkat8, CD158i | (11, 15) |
| *KIR2DS5* | KIR2DS5 | Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5 | nkat9, CD158g | (15) |
| *KIR2DP1* | KIR2DP1 | Killer cell immunoglobulin-like receptor, two domains, pseudogene 1 | KIRZ, KIRY, KIR15, KIR2DL6 | (13) |
| *KIR3DL1* | KIR3DL1 | Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 | cl-2, NKB1, cl-11, nkat3, NKB1B, AMB11, KIR, CD158e1 | (10) |
| *KIR3DL2* | KIR3DL2 | Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 | cl-5, nkat4, nkat4a, nkat4b, CD158k | (10) |
| *KIR3DL3* | KIR3DL3 | Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3 | KIRC1, KIR3DL7, KIR44, CD158z | (16) |
| *KIR3DS1* | KIR3DS1 | Killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1 | nkat10, CD158e2 | (15) |
| *KIR3DP1* | KIR3DP1 | Killer cell immunoglobulin-like receptor, three domains, pseudogene 1 | KIRX, KIR48, KIR2DS6, KIR3DS2P, CD158c | (13) |

number but distinguished by a final letter; for example, the *KIR2DL5A* and *KIR2DL5B* genes [4]. The similarity of these two genes suggests they are related by a recent gene duplication event.

Certain *KIR* genes have arisen through recombination between two other *KIR* genes and are effectively functional hybrids of the parent genes. The question for gene nomenclature is whether the recombinant gene should have a new unique name or be given a name that in some way represents its evolutionary ontogeny. If we consider

a hypothetical recombination between *3DL1* and *3DL2*, we could name the new product according to these parent genes, either by concatenating their names (*i.e., 3DL13DL2*) or by arbitrarily choosing to name the gene after the parent that has contributed the 5′ end of its sequence (*i.e., 3DL1* if the recombination was 5′ *3DL1* × *3DL2* 3′ or *3DL2* if the recombination was 5′ *3DL2* × *3DL1* 3′). This system of naming derived from the parent gene makes many assumptions about the nature of the recombination and the function of the new gene and presumes that there have been no further modifications to the gene that would merit providing a new name. The alternative of assigning a new name to the recombinant gene using the same criteria that have been applied in naming all other new *KIR* genes (based on domain structure, cytoplasmic tail length and sequence similarity) avoids the ambiguities of these assumptions. In this case, the new gene could be assigned *3DL"n,"* in which "n" represents the next number in the series.

Perhaps the simplest solution to naming alleles of a recombinant gene is to assign the allele with the gene name of the gene contributing the Ig-like domains, providing sufficient homology is maintained. In such situations in which the 3′ region of the recombinant allele is inconsistent with the L/S designation of the gene, a suffix would be added to the allele name to indicate the aberrant nature of the allele. Using this nomenclature, it would be possible to rename the alleles of the *3DS1* gene, which behave as alleles of the *3DL1* gene, in the *3DL1* series with an "S" suffix to indicate their short tail.

## KIR PROTEIN NOMENCLATURE

Consistent with standard genetic nomenclature, the names of genes and alleles are given in italic typeface. The names for the KIR proteins are the same as those used for the *KIR* genes; however, they will be presented as normal typeface (Table 1).

Like other cell surface molecules of the immune system, the KIR molecules have also been given a CD designation and are recognized as members of the CD158 series (see the list of aliases and previous designations given in Table 1) [5–7].

## KIR ALLELE NOMENCLATURE

Following the success of the nomenclature used for HLA alleles, it was decided to name *KIR* allele sequences in an analogous fashion. After the gene name, an asterisk will be used as a separator before a numerical allele designation. The first three digits of the numerical designation will be used to indicate alleles that differ in the sequences of their encoded proteins. The next two digits will be used to distinguish alleles that only differ by synonymous (noncoding) differences within the coding sequence. The final two digits will be used to distinguish alleles that only differ by substitutions in an intron, promoter, or other noncoding region of the sequence. A complete listing of all *KIR* allele sequences assigned official names can be found in Table 2.

Evidence exists indicating that the *3DS1* and *3DL1* genes behave as alleles of the same gene. It is likely that at some time in the future the alleles of these genes will be combined under one gene name. To avoid confusion, it has been decided to name the alleles of both genes in a single numeric series, thus *3DL1*001* to *3DL1*009* are followed by *3DS1*010* to *3DS1*014*. Likewise the alleles of the *2DL5A* and *2DL5B* genes have also been named in a single series because of the similarity of these sequences.

## NAMING KIR HAPLOTYPES

The *KIR* gene family forms part of the leukocyte receptor complex (LRC), which includes several related gene families that encode cell-surface receptors of the immune system and have extracellular regions made up of Ig-like domains. Within the LRC the *KIR* genes appear the most variable. In addition to allelic polymorphism, there is haplotypic variability due to the different number and kind of *KIR* genes. This situation is analogous to that of the HLA-DRB genes, but contrasts with that of the HLA class I gene organization, which is relatively fixed. Because haplotypic diversity is a major contributor to the population diversity of KIR and of NK cell repertoires, there was agreement amongst the committee that it would be useful to devise a robust and versatile nomenclature system that could be used to describe the gene content of different KIR haplotypes. With this in mind it was suggested that each KIR haplotype be designated "KH," followed by a hyphen and then a unique three-digit number, assigned sequentially indicating the different haplotypes. This system would allow 999 KIR haplotypes to be named.

Two kinds of KIR haplotype have been described based upon gene content and are designated A and B. No single specific criterion distinguishes all A and B haplotypes, a current working definition being as follows. Group B haplotypes are characterized by one or more of the following genes: *KIR2DL5*, *KIR2DS1*, *KIR2DS2*, *KIR2DS3*, *KIR2DS5*, and *KIR3DS1*. Conversely, group A haplotypes are characterized by the absence of all these genes. As a consequence of these differences, the B haplotypes have more genes encoding activating KIR than A haplotypes. Different investigators have used different criteria to distinguish A and B haplotypes, and certain haplotypes are assigned differently when using these different criteria ([8, 9] and other refs). The committee felt that the distinction between A and B haplotypes is a useful one, having potential biological and medical sig-

**TABLE 2** KIR allele names

| Allele name | Previous name | Cell ID | Accession number | Reference or submitting author |
|---|---|---|---|---|
| *2DL1*001* | NKAT1 | ? | L41267 | (10) |
| *2DL1*002* | cl-42 | ? | U24076 | (11) |
| *2DL1*00301* | cl-47.11 | NK-lib | U24078 | (11) |
| *2DL1*00302* | 2DL1M, 2DL1v2 | MU | AF285431 | (17) |
| *2DL1*004* | 2DL1v | NV | AF022045 | (18) |
| *2DL1*005* | 2DL1W102, 2DL1v3 | WC | AF285432 | (17) |
| *2DL2*001* | cl-43 | ? | U24075 | (11) |
| *2DL2*002* | NKAT6 | ? | L76669 | (15) |
| *2DL2*003* | 2DL2v2, 2DL2M | MU | AF285434 | (17) |
| *2DL2*004* | 2DL2v1 | WC | AF285433 | (17) |
| *2DL3*001* | NKAT2, cl-6 | ?, NK3.3 | L41268, U24074 | (10, 11) |
| *2DL3*002* | NKAT2a | ? | L76662 | (15) |
| *2DL3*003* | NKAT2b | ? | L76663 | (15) |
| *2DL3*004* | KIR-023GB | ? | U73395 | (19) |
| *2DL3*005* | 2DL3v | PP | AF022048 | (18) |
| *2DL3*006* | 2DL3W308 | WC | AF285435 | (17) |
| *2DL4*00101* | NK3.3#27 | NK3.3 | X99480 | (20) |
| *2DL4*00102* | 2DL4v1 | PP, NV | AF034771 | (18) |
| *2DL4*00201* | 15.212 | ? | X97229 | (20) |
| *2DL4*00202* | 2DL4v2 | PP, NV | AF034772 | (18) |
| *2DL4*003* | KIR103AS | YT, NK92 | U71199 | (12) |
| *2DL4*004* | KIR103LP | ? | AF002979 | (21) |
| *2DL4*005* | 2DL4v3 | NV | AF034773 | (18) |
| *2DL4*006* | 2DL4v4 | RR | AF285436 | (17) |
| *2DL4*007* | — | LP | AF276292 | A. Selvakumar, New York, USA |
| *2DL5A*001* | 2DL5.1 | NV, XX-1060P11 | AF204903, AF217485, AL133414 | (13, 22, 23) |
| *2DL5B*002* | 2DL5.2 | NV | AF217486 | (22) |
| *2DL5B*003* | 2DL5.3 | WCS | AF217487 | (22) |
| *2DL5B*004* | 2DL5.4 | CC | AF260138, AF260139, AF260140, AF260141 | (22) |
| *2DS1*001* | Eb6ActI | PA | X89892 | (14) |
| *2DS1*002* | 2DS1v | NV | AF022046 | (18) |
| *2DS1*003* | Eb6ActII | GT | X98858 | (24) |
| *2DS1*004* | 2DS1v1 | WC | AF285437 | (17) |
| *2DS2*001* | NKAT5, cl-49 | ?, ? | L41347, U24079 | (10, 11) |
| *2DS2*002* | 183ActI | 23D | X89893 | (14) |
| *2DS2*003* | TG14#35 | TG14 | AJ002103 | R. Biassoni, Genova, Italy |
| *2DS2*004* | 2DS2v1 | WC | AF285438 | (17) |
| *2DS2*005* | 2DS2v2 | FC | AF285439 | (17) |
| *2DS3*00101* | NKAT7 | ? | L76670 | (15) |
| *2DS3*00102* | 59C_K3 | Pag1 | X97231 | R. Biassoni, Genova, Italy |
| *2DS3*00103* | 2DS3v | NV | AF022047 | (18) |
| *2DS4*00101* | cl-39, cl-17, KKA3_34-52 | ?, ?, 4053, Mal 43-52 | U24077, AF002255, AJ417555, X94609 | (11, 25, 26), HW. Chan, Pittsburgh, USA |
| *2DS4*00102* | NKAT8 | ? | L76671 | (15) |
| *2DS4*002* | 2DS4v1 | RR | AF285440 | (17) |

(Continued)

**TABLE 2** KIR allele names (*Continued*)

| Allele name | Previous name | Cell ID | Accession number | Reference or submitting author |
|---|---|---|---|---|
| *2DS4*003* | Deletion V, KIR1D | 3321 | AJ417554 | (26, 27) |
| *2DS5*001* | NKAT9 | ? | L76672 | (15) |
| *2DS5*002* | — | NV | AF208054 | (28) |
| *2DS5*003* | — | WC | AF272389 | (28) |
| *2DP1*001* | KIR15 | NV | AF204906, AF204907, AF204908 | (13) |
| *2DP1*002* | — | CTB-61M7 | AC011501 | (29) |
| *3DL1*00101* | NKAT3, cl-11, AMB11.115 | ?, ?, AMB11 | L41269, U30274, X94262 | (10, 30, 31) |
| *3DL1*00102* | Nnkat-3 | ? | AF262968 | (32) |
| *3DL1*002* | NKB1, cl-2 | NKB1, ? | U31416, U30273 | (30, 33) |
| *3DL1*003* | 3DL1v | NV | AF022049 | (18) |
| *3DL1*00401* | W204 | WC | AF262970 | (32) |
| *3DL1*00402* | M322 | MU | AF262969 | (32) |
| *3DL1*006* | NJN55 | ? | AF262972 | (32) |
| *3DL1*007* | r3k10 | RR | AF262973 | (32) |
| *3DL1*008* | r3k2 | RR | AF262974 | (32) |
| *3DL1*009* | — | 3321, 4053 | AJ417556, AJ417557 | (34) |
| *3DL2*001* | NKAT4 | ? | L41270 | (10) |
| *3DL2*002* | cl-5, AMC5 | ?, ? | U30272, X94374 | (30, 31) |
| *3DL2*003* | 1.1, NKAT4A | ?, ? | X94373, L76665 | (15, 31) |
| *3DL2*004* | 17.1C | ? | X93595 | (31) |
| *3DL2*005* | NKAT4b | ? | L76666 | (15) |
| *3DL2*006* | 3DL2Wv2 | WC | AF262966 | (32) |
| *3DL2*007* | b3DL2b | BS | AF262965 | (32) |
| *3DL2*008* | r3k17 | RR | AF262967 | (32) |
| *3DL2*009* | rrk100 | RR | AF263617 | (17) |
| *3DL2*010* | — | ? | AY059418 | (35) |
| *3DL2*011* | — | ? | AY059419 | (35) |
| *3DL2*012* | — | ? | AY059420 | (35) |
| *3DL3*001* | KIRCI | ? | AF072407, AF072408, AF072409, AF072410 | (16) |
| *3DL3*00201* | KIR44a | NV, UV5HL9-5B | AF204909, AF204910, AF204911, AC006293 | (13, 29) |
| *3DL3*00202* | KIR44b | NV | AF204912, AF204913, AF204914 | (13) |
| *3DL3*003* | KIRC1 | XX-1060P11 | AL133414 | (23) |
| *3DL3*004* | 3DL7 | ? | AF352324 | (36) |
| *3DS1*010* | NKAT10, 3DS1*001 | ? | L76661 | (15) |
| *3DS1*011* | C97.12#5, 3DS1*002 | ? | X97233 | R. Biassoni, Genova, Italy |
| *3DS1*012* | KIR-123FM, 3DS1*003 | ? | U73396 | (19) |
| *3DS1*013* | 3DS1v, 3DS1*004 | NV | AF022044 | (18) |
| *3DS1*014* | 3DS1*005 | 4373 | AJ417558 | (34) |
| *3DP1*001* | KIR48a | NV | AF204915, AF204916, AF204917 | (13) |
| *3DP1*002* | KIRX | XX-1060P11 | AL133414 | (23) |
| *3DP1*00301* | KIR48b | NV | AF204918, AF204919, AF204920 | (13) |
| *3DP1*00302* | 2DS6 | CTB-61M7 | AC011501 | (29) |

nificance, and that efforts should be made to develop a consistent and logical set of criteria for distinguishing them. It was proposed that as part of the haplotype nomenclature the letters A or B would follow the three-digit number. So a haplotype may, for example, be named KH-001A or KH-022B.

To supplement the haplotype name and provide further information, it was suggested that following the

haplotype designation a 17-digit binary code would indicate the presence or absence of the genes on the haplotype. Each digit in the code would represent a distinct gene: a "1" indicating presence of the gene, a 0′ its absence. Thus a full haplotype name could be given as KH-001A-11100010011011011. This system can readily accommodate the discovery of additional *KIR* genes by simple introduction of another digit. Wherever possible the order of the genes in the full haplotype designation will reflect their order in the genome. However, when digits are added to represent newly discovered genes, they will be placed at the end of the code in the order of their discovery.

To refine haplotype definition, a further series of digits could be used to indicate which allele for each *KIR* gene is present on a haplotype. It is suggested that such an addition would only be made to the nomenclature once it had become a common practice to type *KIR* genes at the allele level.

## NAMING KIR GENOTYPES

As well as assigning unique designations to KIR haplotypes, it was also thought useful to provide a nomenclature system to describe KIR genotypes. It was suggested that each genotype would be indicated by the prefix "KG" followed by a hyphen, in turn followed by a unique four-digit number. This would then be followed with an optional hyphen and 17-digit binary code. As in the naming of haplotypes, the binary code would indicate the presence (a 1) or absence (a 0) of KIR genes in the genotype. So a KIR genotype may be written KG-0202-1111010110110110l. The order of genes would be as used for the haplotype code.

Further refinements of this system to indicate the presence of null alleles or to demonstrate homozygosity of alleles have been suggested. However, in the short term it has been recommended that the community gains familiarity with the system as proposed before implementing any additional complexity.

## KIR SEQUENCE DATABASE

In collaboration with the European Bioinformatics Institute, the KIR-DB—a database of the nucleotide and protein sequence alignments for all of the officially recognized *KIR* alleles—has been established. Together with the sequences, information is given on the nomenclature assigned to the different *KIR* alleles. In the near future further tools for the submission and analysis of *KIR* sequences will be made available from the web site. The KIR-DB may be accessed via the World Wide Web at http://www.ebi.ac.uk/ipd/kir/.

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