# **Guidelines for ISBT Naming of Blood Group Alleles**

## **Purpose**

To provide instructions on how to name alleles that encode blood group antigens and phenotypes for use in transfusion medicine.

#### Overview

The rules described below have been developed for use in transfusion medicine.

The name used by transfusion medicine practitioners ("transfusion medicine name") is easily recognisable and can be used when only a small region of a gene has been sequenced or when a single nucleotide polymorphism (SNP) in an allele has been analysed. This name comprises the ISBT gene symbol and a serological representation of the allele (i.e., the phenotype or absence of antigen encoded). This terminology is acceptable for use in reports, correspondence, and publications relating to the transfusion medicine discipline.

# Rules for "transfusion medicine names" for alleles determined by DNA-based assays

- For alleles write the gene symbol (as above), followed by an asterisk (e.g.,  $FY^*$ ), followed by one of the following:
  - o For alleles representing polymorphic, very common, or single rare antigens: use ISBT assigned antigen name, e.g., FY\*01, YT\*02. Alternatively, where letters are commonly used, symbols such as JK\*A or FY\*B are permissible.
  - o For an absence of a very common antigen where there is no antithetical antigen: write a minus sign and the antithetical ISBT antigen name, e.g., *CROM\*01.−05*, *OK\*01.−01*.
  - o For multiple rare antigens: write the phenotype name, e.g., GYP\*GP.Mur.
  - For null (silenced alleles) phenotypes: write symbol and number of background allele followed by N, then a period and a sequential number, e.g., *JK\*02N.01* or *JK\*01N.04*. Numbers will be assigned by the ISBT Working Party.
  - o For previously described "mod" phenotypes: write symbol and number of background allele followed by M, then a period and a sequential number, e.g., *KEL\*02M.1*. Numbers will be assigned by the ISBT Working Party.
  - O Hybrid alleles are defined where there is clear evidence of exon exchange, e.g., *GYP\*GP.Hil* or *GYP\*(A-B)Hil*, *RHD\*06.02* or *RHD\*D-CE(4-6)-D*; *ABO\*O.(O.02-B.01).01* or *ABO\*O.[O.02(1-5)-B(6-7)].01*
- Use the ISBT gene symbol (e.g., FY, DI, GE). Exceptions to this are: GYPA, GYPB, RHD, RHCE.
- All allele names are italicized.
- In cases of partial analysis of the allele, names may be truncated at any period (full stop), according to the amount of information available or required, e.g., *RHD\*05.01* or *RHD\*DV.01* could be *RHD\*05* or *RHD\*DV*.

- Genotypes/haplotypes are written, e.g., JK\*01/02, GYP\*01,03/01,04, KEL\*02,04/02,04 or, if determined by hemagglutination,  $Jk^a/Jk^b$ , MS/Ms,  $kKp^b/kKp^b$ .
- Alleles that encode some ISBT numbered antigens, but which do not differ from the Reference Allele, will not be given an allele name, e.g., LW6 (LW<sup>ab</sup>).
- Alleles not relevant to transfusion medicine are not necessarily listed.
- Phenotypes and alleles may be listed in more than one place.
- Information will be obtained from DNA from any source or from RNA obtained from erythroid cells.
- The allele name can be used even when only the relevant SNP (or other change diagnostic for the allele, e.g. *RHCE* intron 2 polymorphism associated with *RHCE\*02*) has been analysed, even though in some cases this may not reflect the true allele (e.g., *JK\*02* or *JK\*B* can be used when 838A is detected, even though on rare occasions an undetected inactivating mutation elsewhere in the gene may mean that no JK2 antigen is produced).
- Provide only coding changes from the reference DNA and changes that cause a detectable change in antigen expression (e.g., affect splicing). Silent (synonymous) changes are not given in the tables, nor are alleles that differ only by silent polymorphisms.
- For carbohydrate blood groups, the allelic background numbering will not necessarily reflect the allelic relationships, e.g. *ABO* null alleles, which give rise to the group O phenotype and which are based on an A allelic background, will be named as O alleles
- Missense (non-synonymous) nucleotide changes are written in the format 1057C>T or 1057T.
- When describing the amino acid change encoded by a specific allele, the allele name should be given followed by the predicted amino acid change, e.g. *YT\*02* encoding His353Asn (or H353N) [and the Yt<sup>b</sup> antigen].
- Amino acids may be abbreviated to either the three letter or one letter code, e.g. His353 or H353. The three letter code is encouraged as it gives greater clarity.
- Numbering of nucleotides (nts) begins with #1 as the A of the initiating ATG.
- Numbering of amino acids (AA) begins with #1 as the initiation Met, regardless of
  whether it, or a signal/leader sequence, is cleaved from the mature protein. This
  means a change from the more commonly used numbering for some systems, e.g.,
  MNS, LW, and Cromer systems.
- For alleles inferred by hemagglutination write the ISBT traditional antigen name italicized, e.g.,  $Fy^a$ ,  $Yt^b$ .
- Original papers will not be given as they are hyperlinked from dbRBC.

### Some useful references:

Daniels, et al., Vox Sang 2004;87:304-16. ISBT/IBGRL website <a href="http://ibgrl.blood.co.uk/">http://ibgrl.blood.co.uk/</a> dbRBC <a href="http://www.ncbi.nlm.nih.gov/gv/mhc/xslcgi.cgi?cmd=bgmut/home">http://www.ncbi.nlm.nih.gov/gv/mhc/xslcgi.cgi?cmd=bgmut/home</a> Garratty, et al., Transfusion 2000;40:477.

**Information included on each blood group system page for "transfusion medicine names".** The purpose of this classification is for transfusion medicine and therefore not necessarily complete.

- A brief description
- CD number
- ISBT gene name
- Number of exons
- Location of the initiation codon, e.g., at the beginning of exon 1; within exon 2.
- Where the stop codon is located.
- Data base information:
  - o GenBank NM#. If an allele has not been placed under the NM# umbrella, use the unique GenBank #.
  - o Entrez Gene ID
- The reference allele name
  - o Accession number
  - o Preferred name
  - o Acceptable name. In many cases alternative terminologies are given and may be employed according to the users' needs.
- A table for each blood group system in which the reference allele is shaded.
  - o ISBT numerical and traditional phenotype name.
  - O Antigens that have no antithetical antigen, which are present or absent on the protein encoded by the reference allele, will be listed (e.g., Dr(a+) in CROM, and Ls(a-) in GE) at the top of the table. In the case of carbohydrate antigens where the gene encodes an enzyme, this information will not be included.
  - o Null alleles and mod alleles to be grouped together with subheadings
- Some genes that do not encode blood group antigens or blood group glycosyltransferases, but have a well recognised effect on blood group phenotypes, will be included, e.g., *KLF1*.

Reference allele YT*01 encodes YT1				
Phenotype	Allele Name	Nucleotide change	Exon	Amino acid change
YT:1 or Yt(a+)	<i>YT*01</i> or <i>YT*A</i>			
YT:2 or Yt(b+)	<i>YT*02</i> or <i>YT*B</i>	1057 C>A	2	His353Asn