A new *GYPB*04*(164T>G, Phe55Cys) allele with a phenotypic partial character of small s

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Background

The S and s antigens of the MNSs blood group system are caused by a single SNP at coding nucleotide (nt) 143C>T (Thr48Met) of *GYPB*. Antigens S^D+ and Mit+ result from SNPs at nts 161G>A (Arg54His) and 173C>G (Pro58Arg) respectively and underline the immunohematological relevance of this area proximal to the trans-membrane region of the protein on the outer RBC surface. In general, new blood group antigens may be discovered by diagnostic antibodies, discrepancies in pheno-/genotyping, or due to responders' antibodies.

Methods

Human and monoclonal anti-s typing reagents were applied (Medion Grifols Diagnostics, Duedingen, CH; BioRad, Cressier, CH; Merck-Millipore, Darmstadt, DE) using gel-card, in tube and lateral flow-card assays. Genotyping (MNSs, Inno-Train, Kronberg, DE) and sequencing were performed (Meyer S. et al Br J Haematol. 2016). Trans-membrane helix location was predicted using HMMTOP, PHOBIUS, SOSUI, TMPRED, disulphide-bonds using DiANNA, and N-glycosylation using NetOGlyc.

Results

Initial phenotyping discrepancies were observed using human anti-s (gel-card) and monoclonal anti-s (in tube) in two unrelated blood donors (table 1). Samples were heterozygous for *GYPB*03/04* (S/s) and both *GYPB*04* (s) exons 4 showed the same new mutant allele *GYPB*04*(164T>G, Phe55Cys). moAB clones P3Y326Bn5 used in tube and P3BER in lateral flow assays, delivered reliable positive reactions for this new s, whereas moAB P3YAN3 failed to detect it. Software did not predict a change in the trans-membrane helix, nor disulphide-bonds. Still, changes in N-glycosylation of the mutated protein were assessed.

Conclusion

We describe a partial s. Anti-s was not detected in either donor. Potentially, family analysis could deliver this pre-requisite for considering *GYPB*04*(164T>G, Phe55Cys) as a true new MNSs antigen. Still, partial character of the new s and the location of the mutation in a highly antigenetically relevant part of the peptide are of significance.

anti-s antibodies (AB) tested

method applied	manu-facturer	tested in	testing	type of antibody	clone number	control Ss	donor 1 (male)	donor 2 (female)
gel-card	Diagnostic Grifols	Zurich	initial	human	n.a.	+	+	+
tube-technique	Bio-Rad	Zurich	initial	moAB IgG	P3YAN3	+	-	-
gel-card	Bio-Rad	Zurich	advanced	human	n.a.	+	+	+
tube-technique	Merck-Millipore	Düdingen	advanced	moAB IgG	P3Y326Bn5	+	+	+
lateral-flow-card	Medion Grifols Diagnostics	Düdingen	advanced	moAB IgM	P3BER	+	+	+

Negative DAT with Anti-Human Globulin Mono-Type, Lot 654912015A, exp. 2016-03-31 (Medion Grifols Diagnostics) in all cases

Table 1: Phenotyping discrepancies were observed in two unrelated donors using human anti-s (gel-card) and monoclonal anti-s (in tube). Initial genotyping (MNSs, Innotrain, Kronberg, DE) showed heterozygosity for *GYPB*03/04* (S/s) and subsequent sequencing revealed the same new mutant allele *GYPB*04*(164T>G, Phe55Cys). moAB clones P3Y326Bn5 used in tube and P3BER in lateral flow assays, delivered reliable positive reactions for this new s, whereas moAB P3YAN3 failed to detect it.