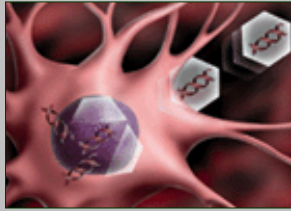


Imunogenetika a imunogenomika



Imunogenetika

Definice

- **Klasická**
- **Aktuální**

Imunogenetika

Definice

➤ **Klasická**

Definice

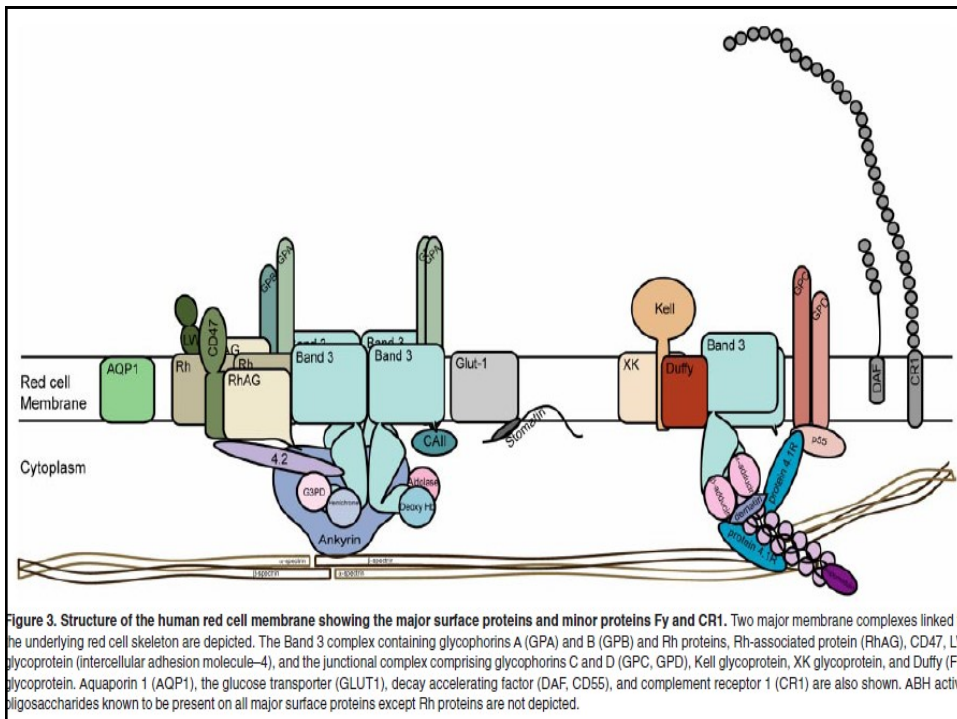
Klasická

**Studium genetických rozdílů
pomocí imunologických
metod**

Definice

Klasická

Genetika krevních skupin



Definice

Krevní skupiny

- **Gen:** *krevněskupinový system*
- **Alela:** krevní (feno)skupina
- **Epitop:** krevní faktor

KS systémy lidí a zvířat

Dělení

- **Primární a sekundární**
- **Jednoduché a komplexní**
- **Jiná dělení**

KS systémy lidí

- ✓ 36 krevněskupinových systémů
- ✓ 41 genů
- ✓ >300 antigenních determinant
- ✓ Přirozené funkce vs. antigenita:
transfúze, těhotenství

Table 1 Human blood group systems

No.	Name	System symbol and ISBT ^a gene name ^b	No. of antigens	HUGO ^c gene symbol(s)	Chromosome
001	ABO	ABO	4	<i>ABO</i>	9
002	MNS	MNS	46	<i>GYP A, GYP B, GYP E</i>	4
003	P	P1	1	<i>P1</i>	22
004	Rh	RH	50	<i>RHD, RHCE</i>	1
005	Lutheran	LU	19	<i>BCAM</i>	19
006	Kell	KEL	31	<i>KEL</i>	7
007	Lewis	LE	6	<i>FUT3</i>	19
008	Duffy	FY	6	<i>DARC</i>	1
009	Kidd	JK	3	<i>SLC14A1</i>	18
010	Diego	DI	21	<i>SLC4A1</i>	17
011	Yt	YT	2	<i>ACHE</i>	7
012	Xg	XG	2	<i>XG, CD99</i>	X/Y
013	Scianna	SC	7	<i>ERMAP</i>	1
014	Dombrock	DO	6	<i>ART4</i>	12
015	Colton	CO	3	<i>AQP1</i>	7
016	Landsteiner–Wiener	LW	3	<i>ICAM4</i>	19
017	Chido/Rodgers	CH/RG	9	<i>C4A, C4B</i>	6
018	H	H	1	<i>FUT1</i>	19
019	Kx	XK	1	<i>XK</i>	X
020	Gerbich	GE	8	<i>GYP C</i>	2
021	Cromer	CROM	15	<i>CD55</i>	1
022	Knops	KN	9	<i>CR1</i>	1
023	Indian	IN	4	<i>CD44</i>	11
024	Ok	OK	1	<i>BSG</i>	19
025	Raph	RAPH	1	<i>CD151</i>	11
026	John Milton Hagen	JMH	5	<i>SEMA7A</i>	15
027	I	I	1	<i>GCNT2</i>	6
028	Globoside	GLOB	1	<i>B3GALT3</i>	3
029	Gill	GIL	1	<i>AQP3</i>	9
030	RHAG	RHAG	3	<i>RHAG</i>	6

^a International Society of Blood Transfusion
^b System symbol shown; gene symbol in italics
^c Human Genome Organisation

KS systémy lidí a zvířat

Molekulární podstata

- Proteiny a jejich geny
- Polysacharidy, enzymy a jejich geny

Table 1
A summary of blood group systems, gene locations, gene products, and antigen moieties.

System name (Number)	Chromosome location	Gene product	Antigenic moiety*	References
ABO (00 1)	9q34	α 1,3-N-acetylgalactosaminyl-transferase, α 1,3-galactosyl-transferase	(1,3)N-Acetylgalactose,* (1,3)Galactose	Yamamoto et al. [43]
MNS (00 2)	4q28-31	Glycophorin A Glycophorin B	Type I glycoprotein Type I glycoprotein	Siebert and Fukuda [44] Siebert and Fukuda [45]
P (0 0 3)	22q13	α 4Gal	(1-4)Galactose	Thuesson et al. [46]*
Rh (0 0 4)	1p36.2-34	Rh D Rh CE	Multipass protein Multipass protein	Avent et al. [47] Cherif-Zahar et al. [18]
Lutheran (0 0 5)	19q13.2	Basal Cell Adhesion Molecule (BCAM)	Type I glycoprotein	Parsons et al. [48]
Kell (0 0 6)	7q33	Kell glycoprotein	Type II glycoprotein	Lee et al. [49]
Lewis (0 0 7)	19p13.3	α 3,4-fucosyltransferase-3 (FUT3)	(3-4)Fucose	Kukowska-Latallo et al. [50]
Duffy (0 0 8)	1q21-22	Duffy Antigen Receptor for Chemokines (DARC)	Multipass glycoprotein	Chaudhuri et al. [51]
Kidd (0 0 9)	18q11-12	Solute Carrier Family 14 member 1 (SLC14A1)	Multipass glycoprotein	Olives et al. [52]
Diego (0 1 0)	17q21-21	Solute Carrier Family 4 Anion Exchanger (SLC4A1)	Multipass glycoprotein	Tanner et al. [53]
Yt (0 1 1)	7q22	Acetylcholinesterase	Glycosylphosphatidylinositol (GPI)-linked protein	Lapidot-Lifson et al. [54]
Xg (0 1 2)	Xpter-22	Xg glycoprotein	Type I glycoprotein	Ellis et al. [55]
Scianna (0 1 3)	1p34	Erythroblast Membrane-Associated Protein (ERMAPP)	Type I protein	Xu et al. [56]
Dombrock (0 1 4)	12p13-12	ADP-ribosyltransferase-4 (ART4)	GPI-linked protein	Gubin et al. [57]
Colton (0 1 5)	7p14	Aquaporin-1 (AQP1)	Multipass protein	Preston and Agre [58]
Landsteiner-Wiener (0 1 6)	19p13.3	Intercellular Adhesion Molecule-4 (ICAM4)	Type I glycoprotein	Bailly et al. [59]
Chido-Rogers (0 1 7)	6p21.3	Complement Component 4A	Soluble protein	Yu [60]
Hh (0 1 8)	19q13.3	α 1-2-Fucosyltransferase	(1,2)Fucose	Larsen et al. [61]
Kx (0 1 9)	Xp21	Kx glycoprotein	Xk glycoprotein	Ho et al. [62]
Gerbich (0 2 0)	2q14-21	Glycophorin C	Type I glycoprotein	Colin et al. [63]
Cromer (0 2 1)	1q32	Decay-Accelerating Factor (DAF)	GPI-linked	Medof et al. [64]
Knops (0 2 2)	1q32	Complement Receptor 1 (CR1)	Type I protein	Wong et al. [65]
Indian (0 2 3)	11pter-13	In(Lu)-related glycoprotein	Type I glycoprotein	Screation et al. [66]
Ok (0 2 4)	19p13.3	Basigin	Type I glycoprotein	Biswas et al. [67]
Raph (0 2 5)	11p15.5	Monoclonal Eleanor Roosevelt-2 (MER2)	Multipass glycoprotein	Bill et al. [68]
JMH (0 2 6)	15q22-23	Semaphorin-7A (SEMA7A)	GPI-linked	Lange et al. [69]
I (0 2 7)	6p24-23	β 1,6-N-acetylglucosaminyltransferase	(1,6)N-Acetylglucose	Bierhuizen et al. [70]
Globoside (0 2 8)	3q25	β 1,3-N-acetylgalactosaminyltransferase	(1,3)N-Acetylgalactose	Amado et al. [71]
GL (0 2 9)	9p13	Aquaporin-3 (AQP3)	Multipass protein	Ishibashi et al. [72]
RHAG	6p21-11	Rh associated glycoprotein	Multipass glycoprotein	Ridgwell et al. [73]

* Antigenic moiety refers to those molecules that express blood group antigens.

* all carbohydrate transferases are type II proteins.

* published abstract.

KS systémy lidí a zvířat

Funkce

- **Strukturní**
- **Receptorová**
- **Transportní**
- **???**

738 Hum Genet (2009) 126:729–742

Table 6 Some red cell surface proteins: their structures and putative functions

Proteins	Blood group system	Structure	Function on erythroid cells
Urea transporter (UT)-B	Kidd	T3 (10 span)	Urea transport
Aquaporin 1	Colton	T3 (6 span), Aquaporin SF	Water channel
Aquaporin 3	Gill	T3 (6 span), Aquaporin SF	Water and glycerol channel
Band 3, anion exchanger 1 (CD233)	Diego	T3 (14 span), long cytosolic N-terminal domain. Core of band 3/Rh complex	Exchanges $\text{HCO}_3^-/\text{Cl}^-$. Links membrane to membrane cytoskeleton
Rh-associated glycoprotein (CD241)	RHAG	T3 (12 span), part of band 3/Rh complex	Probably involved in CO_2/O_2 or possibly $\text{NH}_4^+/\text{NH}_3$ transport
RhD and RhCE (CD240)	Rh	T3 (12 span), unglycosylated, part of band 3/Rh complex	Possibly involved in CO_2/O_2 or $\text{NH}_4^+/\text{NH}_3$ transport, or in maintenance of cell shape
Xk protein	Kx	T3 (10 span), unglycosylated. Linked to Kell glycoprotein	Homology with neurotransmitter transporters
Duffy antigen receptor for chemokines (DARC, CD234)	Duffy	T3 (7 span), G protein-coupled SF	Binds chemokines, possibly for removal from peripheral blood
Lutheran glycoprotein (CD329)	Lutheran	T1, IgSF (IgV-V-C2-C2-C2)	Probably adhesion/receptor, possibly involved in erythropoiesis. Binds laminin 511 and 521
Intercellular adhesion molecule-4 (ICAM-4, CD242)	LW	T1, IgSF (IgI-I). Part of band 3/Rh complex.	Probably adhesion/receptor involved in stability of erythroblastic islands. Binds Integrins.
Erythroblast membrane-associated protein (ERMAP)	Scianna	T1, IgSF (IgV)	Probably adhesion/receptor
Basigin (CD147)	Ok	T1, IgSF (IgC2-V)	Probably adhesion/receptor
Decay accelerating factor for complement (CD55)	Cromer	T5, GPI-linked. 4 CCP SF domains	Inhibits activity of C3 convertases. Protects cell from lysis by autologous complement
CD59		T5, GPI-linked. Single Ly-6 domain	Inhibits assembly of membrane attack complex. Protects cell from lysis by autologous complement
Complement component (3b/4b) receptor 1 (CD35)	Knops	T1, ~30 CCP SF domains	Binds and processes immune complexes
CD44	Indian	T1, Link module SF of proteoglycans	Probably adhesion/receptor. Binds hyaluronan
Xg glycoprotein	Xg	T1, highly glycosylated, SGP	Possibly adhesion/receptor
CD99	Xg	T1, highly glycosylated, SGP	Possibly adhesion/receptor
Semaphorin 7A (CD108)	JMH	T5, GPI-linked. Semaphorin SF	Possibly adhesion/receptor
CD151	Raph	T3 (4 span), Tetraspanin SF	Might associate with integrins to generate laminin-binding complexes
Acetylcholinesterase	Yt	T5, GPI-linked	Enzyme
Kell glycoprotein (CD238)	Kell	T2, large EC globular domain, linked to Xk protein	Endopeptidase. Possibly processes endothelin-3 from big endothelin-3
ADP-ribosyltransferase 4 (CD297)	Dombrock	T5, GPI-linked	Possibly transfer of ADP-ribose, if active
Glycophorins C (CD236C) and D (CD236D)	Gerbich	T1, highly glycosylated, SGP	Links membrane to membrane cytoskeleton. Could contribute to glycocalyx
Glycophorin A (CD235A)	MNS	T1, highly glycosylated, SGP. Part of band 3/Rh complex	Could contribute to glycocalyx. Interacts with band 3 to enhance anion transport and band 3 trafficking
Glycophorin B (CD235B)	MNS	T1, highly glycosylated, SGP.	Could contribute to glycocalyx

T1 type 1, single membrane span, external N-terminus, T2 type 2, single membrane span, internal N-terminus, T3 type 3, multiple membrane span, T5 type 5, glycosylphosphatidylinositol (GPI)-linked, SGP sialoglycoprotein, IgSF immunoglobulin superfamily, EC extracellular, SF superfamily, CCP complement control protein

KS systémy lidí a zvířat

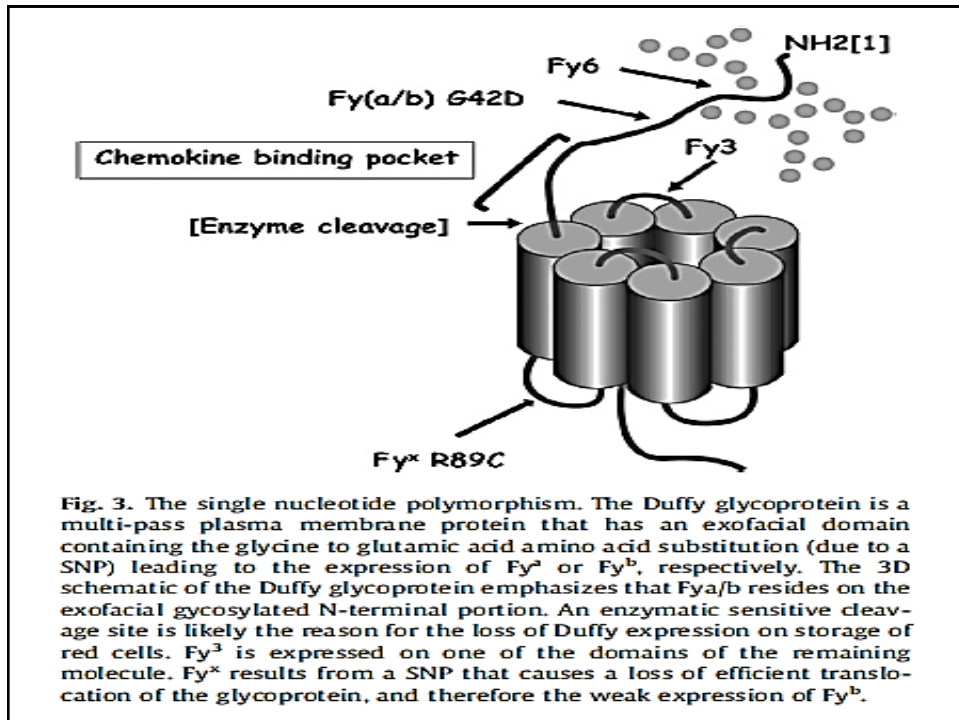
Polymorfismus

- Různé typy
- Kvalitativní i kvantitativní efekty
- Asociace s nemocemi

56 *G.A. Denomme/Transfusion and Apheresis Science 44 (2011) 53-63*

Table 2
Common Blood Group Antigens and the Associated Nucleotide Differences.

ISBT system name (Symbol) number	Target antigen (Target allele)	ISBT gene name (RefSeqGene)	Amino acid; Nucleotide change
ABO (ABO) 0 0 1	A (ABO-A1) A2 (ABO-A2) B (ABO-B1)	ABO (NG_006669.1)	A (consensus) +21 amino acids (fs); 1061ΔC Arg176Gly; 526C>G Gly235Ser; 703G>A Leu266Met; 796C>A Gly268Ala; 803G>C 116Stop (fs); 261AG Ser20Leu, Gly24Glu; nt59C>T, 71G>A+72T>G
MNS (MNS) 0 0 2	O (ABO-O1) M (GYPA-M) N (GYPA-N) S (GPB-S) s-(GPB-s) S silenced	GYPA (NG_007470.2) GYPB (NG_007483.1)	Thr48Met; 143T>C exon 5/6 deletion + fs; 230C>Taa 58-90 deletion; intron 5+5g>t exon 4 and 7; multiple SNPsno gp; gene deletion (common) no change; intron 2 190 bp insertionSer103Pro; 307T>C Pro226Ala; 676C>G Leu245Val; 733C>G Gly336Cys; 1006G>T His77Arg; 230A>G
Rh (RH) 0 0 4	D (RHD) D negative (-) C (RHCE-C) C (RHCE-c) E (RHCE-E) e (RHCE-e) V & VS V (VS-)	RHD (NG_007494) RHCE (NG_009208)	no change; intron 2 190 bp insertionSer103Pro; 307T>C Pro226Ala; 676C>G Leu245Val; 733C>G Gly336Cys; 1006G>T His77Arg; 230A>G
Lutheran (LU) 0 0 5	Lu ^a (LU-A) Lu ^b (LU-B)	LU (NG_007480.1)	Met193Thr; 578T>C Trp281Arg; 841T>C
Kell (KEL) 0 0 6	K (KEL-01) k (KEL-02) Kp ^a (KEL-03) Kp ^b (KEL-04) Js ^a (KEL-06) Js ^b (KEL-07)	KEL (NG_007492.1)	Pro597Leu; 1790C>T
Duffy (FY) 0 0 8	Fy ^a (FY-A) Fy ^b (FY-B) Fynull (FY)	FY (NG_011626.1)	Gly42Asp; 125G>A
Kidd (JK) 0 0 9	Jk ^a (JK-A) Jk ^b (JK-B)	JK (NG_011775.1)	No protein; -67>c (no transcript) Asp280Asn; 838G>A
Diego (DI) 0 1 0	Di ^a (DI-A) Di ^b (DI-B)	DI (NG_007498.1)	Leu854Pro; 2561T>C His353Asn; 1057C>A
Yt (YT) 0 1 1	Yt ^a (YT-A) Yt ^b (YT-B)	YT (NG_007474.1)	Gly57Arg; 169G>A
Scianna (SC) 0 1 3	Sc1 (SC-01) Sc2 (SC-02)	SC (NG_008749.1)	Asp265Asn; 793A>G Gly108Val; 323G>T Thr117Ile; 350C>T Ala45Val; 134C>T Gln70Arg; 308A>G
Dombrock (DO) 0 1 4	Do ^a (DO-A) Do ^b (DO-B) Hy (HY) Jo ^a (JO)	DO (NG_007477.1)	Ala193Pro; 679G>C Val1561Met; 4681G>A Lys1590Glu; 4768A>G
Colton (CO) 0 1 5	Co ^a (CO-A) Co ^b (CO-B)	CO (NG_007475.1)	Arg1601Gly; 4801A>G
Landsteiner-Wiener (LW) 0 1 6	LW ^a (LW-A) LW ^b (LW-B)	LW (NG_007728.1)	
Cromer (CR) 0 2 1	Cr ^a (CR-A)	CROM (NG_007465.1)	
Knops (KN) 0 2 2	Kn ^a (KN-A) Kn ^b (KN-B) Mc ^a (KN-03) Mc ^b (KN-05) SP (KN-04) ViI (KN-07)	KN (NG_007481.1)	



KS systémy lidí

Význam: transfúze, nemoci

- ✓ **ABO, Fut1, Fut2, Fut3**
- ✓ **Rh**
- ✓ **Kell**
- ✓ **Duffy**
- ✓ **.....**

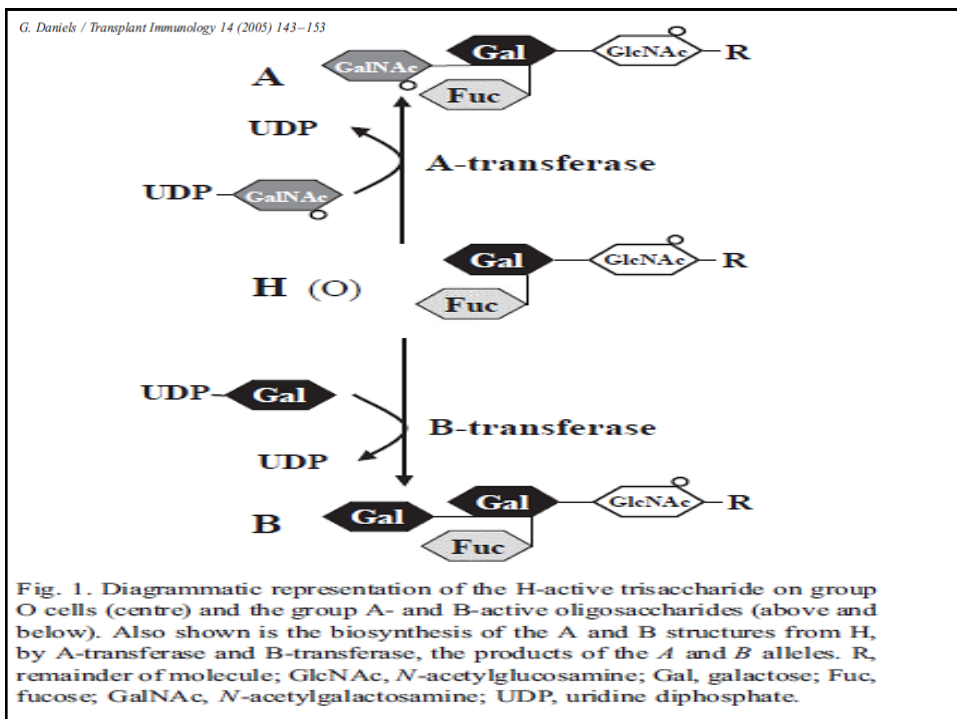
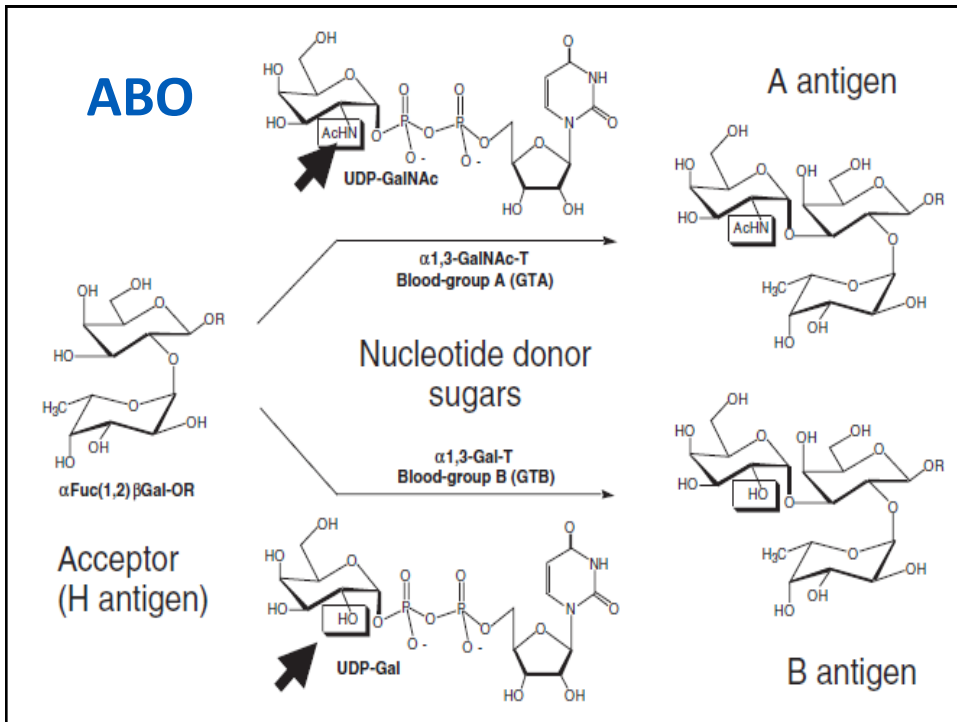


Fig. 1. Diagrammatic representation of the H-active trisaccharide on group O cells (centre) and the group A- and B-active oligosaccharides (above and below). Also shown is the biosynthesis of the A and B structures from H, by A-transferase and B-transferase, the products of the A and B alleles. R, remainder of molecule; GlcNAc, N-acetylglucosamine; Gal, galactose; Fuc, fucose; GalNAc, N-acetylgalactosamine; UDP, uridine diphosphate.

Genetika ABO

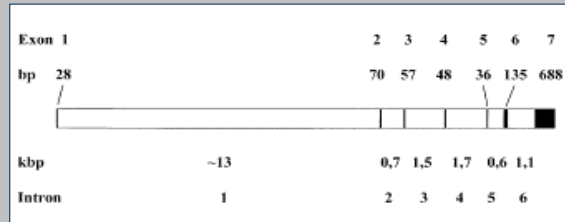


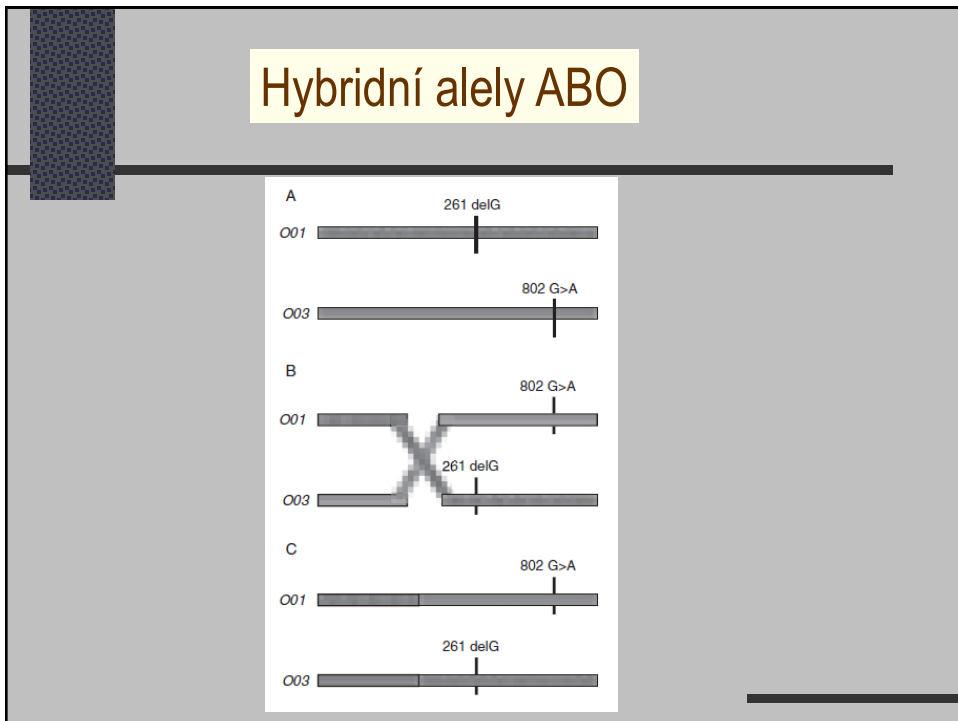
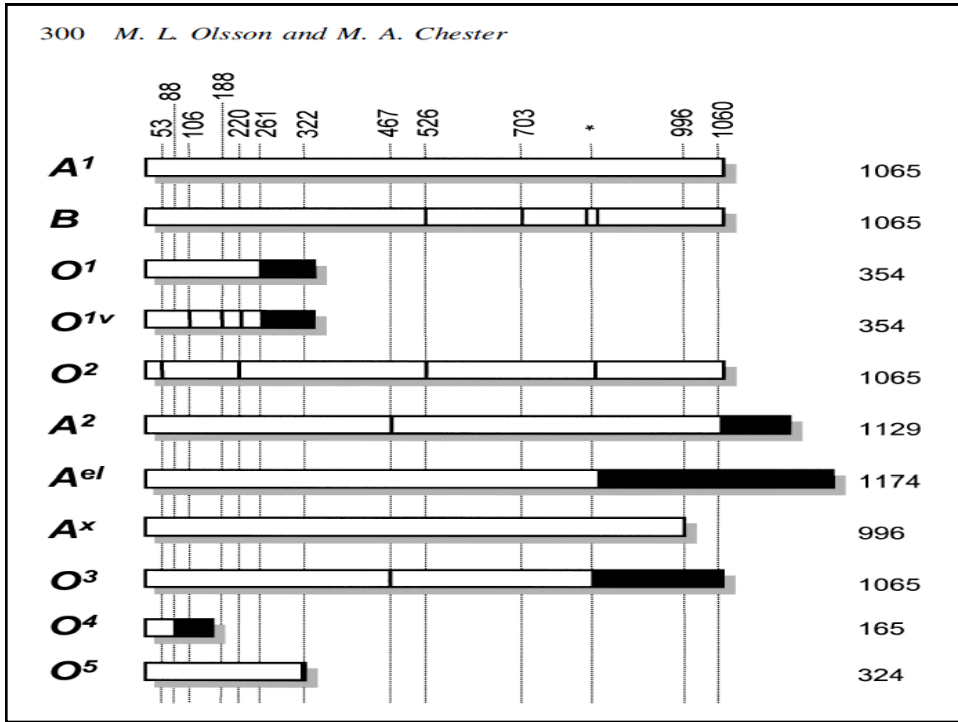
Table 1. Comparison of the Nucleotide Residues that Produce Amino Acid Substitutions Discriminating GTA from GTB

Glycosyl-transferase	Nucleotide (amino acid) residue			
	526 (176)	703 (235)	796 (266)	803 (268)
GTA	C (Arg)	G (Gly)	C (Leu)	G (Gly)
GTB	G (Gly)	A (Ser)	A (Met)	C (Ala)

NOTE. Although 4 other nucleotides are polymorphic between the consensus *A101* and *B* alleles, they do not alter the amino acid sequence of the enzyme.

Polymorfismus ABO

Exon	1	2	3	4	5	6	7
nt. position		53	106	188 189	220	261 297 323	467 526 646 657 681 703 771 796 802 803 829 930 1061 1062 1096 1126
Consensus		G	G	G C	C	G A T	C C T C G G C C G G G C G G T
<i>A¹-1</i>							
<i>A¹-2</i>							T
<i>A²</i>							T
<i>B</i>						G	G T A A C A A
<i>O¹</i>						-	
<i>O^{iv}</i>			T	A T	T	- G	A A T A A
<i>O²</i>		T			T	G	G A A
Amino acid		18	36	63 63	74	87 99	156 176 216 219 227 235 257 266 268 268 277 310 354
Consensus		Arg	Val	Arg Arg	Pro	Val Thr	Pro Arg Phe His Pro Gly Pro Leu Gly Gly Val Leu Pro
Change		Leu	Phe	His	Ser		Leu Gly Ile Ser Arg Ala Met



Fut1, Fut2 (Fut3)

- ✓ V těsné vazbě na chromosomu 19q13.3
- ✓ 70 procent nukleotidové sekvenční identity
- ✓ Jeden exon CDS
- ✓ Přenos terminální fukózy na preexistující β - galaktózu
- ✓ FucT1 exprimována v buňkách mesodermálního původu
- ✓ FucT2 exprimována v buňkách endodermálního původu
- ✓ FucT3 exprimována v epiteliálních buňkách

ABO a Fut2,3: Lewis

ABH, Infection and Immunity 427

Table 1 Biosynthesis of ABH and Lewis glycans on Type 1 and Type 2 precursors

Type 1 Glycans		Type 2 Glycans	
Non-Secretor (se/se)	Secretor (Se/-)		
Gal β 1-3 GlcNAc 1-9 R 1-9 R	Gal β 1-3 GlcNAc 2)	Gal β 1-94 GlcNAc 1-9 R 2	Gal β 1-94 GlcNAc 1-9 R 2
FUT 3 (Lewis transferase) 4 ↑ Fuc α 1 Le ^a	FUT 3 (Lewis transferase) ↑ Fuc α 1 Le ^a	FUT 3 (Lewis transferase) ↑ Fuc α 1 Le ^a	FUT 3 (Lewis transferase) ↑ Fuc α 1 Le ^a
FUT 3	↓ FUT 2 (Se transferase)	↓ FUT 1 (H transferase)	
No synthesis of H, hence no synthesis of A, B or Le ^a	Gal β 1-93 GlcNAc 1-9 R 1-9 R 2 3 Fuc α 1 H antigen	Gal β 1-93 GlcNAc 2 4 Fuc α 1 Fuc α 1 H, Le ^a	Gal β 1-94 GlcNAc 1-9 R 2 3 Fuc α 1 Fuc α 1 H antigen H, Le ^a
↓ A or B transferase ↓	↓ A or B transferase ↓	↓ A or B transferase ↓	↓ A or B transferase ↓
	GalNAc/Gal α 1 ↓ ↓ Gal β 1-93 GlcNAc 1-9 R 1-9 R 2 3 Fuc α 1 A/B antigen	GalNAc/Gal α 1 ↓ ↓ Gal β 1-93 GlcNAc 2 4 Fuc α 1 Fuc α 1 A/B, Le ^a	GalNAc/Gal α 1 ↓ ↓ Gal β 1-94 GlcNAc 1-9 R 2 3 Fuc α 1 Fuc α 1 A/B antigen A/B, Le ^a

Abbreviations: Fuc, L-fucose; Gal, D-galactose; GalNAc, N-acetyl-D-galactosamine; GlcNAc, N-acetyl-D-glucosamine.

Fut a nemoci

- ✓ Oh fenotypy normální, *FUT1* mutace náhodně distribuované v populacích
- ✓ *FUT2* asociovány s chorobami, nulové alely evolučně výhodnější?

Table 2 Effects of the FUT2 "non-secretor" status on different pathophysiological conditions

Condition	Effect	Reference(s)
<i>Helicobacter pylori</i> infection	Lower susceptibility	[73-75]
Symptomatic Norovirus infection	Resistance/protection	[28, 78, 79]
Rotavirus A infection	Resistance	[85]
Urinary tract infections	Increased (in B and AB blood group women)	[86]
Acute uncomplicated pyelonephritis	Increased (in women)	[88]
Oral or vaginal <i>Candida</i> infections	Increased	[89-91]
<i>H. influenzae</i> infection	Increased susceptibility	[92]
<i>N. meningitidis</i> and <i>S. pneumoniae</i> infections	Increased susceptibility	[93]
Axillary lymph node metastasis	Increased risk (in breast cancer patients)	[109]

Clinic Rev Allerg Immunol (2015) 48:182-191

Genetika Rh

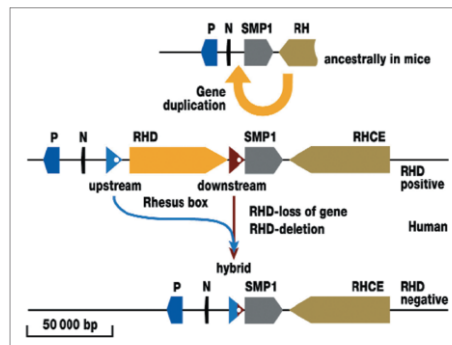


Figure 1 - Duplication of the RH gene and deletion of the RHD gene. The ancestral condition is shown as the RH gene locus in the mouse. The single RH gene is adjacent to the three genes *SMP1*, P29-associated protein (P) and NPD014 (N). Duplication created a second, reversed RH gene in humans, which is located between N and *SMP1*. At the insertion points before and after the RHD gene is a DNA segment about 9,000 nucleotides or base pairs (bp) long. The two DNA segments flank the RHD gene and are termed the upstream or downstream Rhesus box. In the RHD positive haplotype, the RHD gene could be lost again through recombination (figure 3). The scale gives the approximate length of 50,000 nucleotides in the genomic DNA.

Blood Transfus 2007; 5: 50-57

Genetika Rh

474

L. Raud et al. / *Transfusion Clinique et Biologique* 24 (2017) 472–475

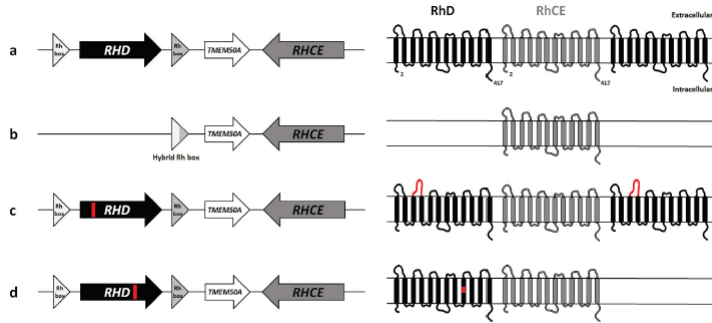


Fig. 1. Schematic representations of the *RH* locus genomic organization (left) and Rh protein membrane expression (right) in the presence of the *D*+ (a), *D*- (b), partial *D* (c) and weak *D* (d) alleles. The 5'- and 3'-Rh boxes are in light and dark gray, respectively; single-nucleotide variations (a) and protein motifs affected by the amino acid substitution (b) are in red.

54 antigenů

Genetika Rh

Table 3 Frequencies of some Rh antigens in three populations

Antigen	English (%)	Nigerian (%)	Chinese (%)
D	83	95	100
C	68	17	94
c	81	99	43
E	29	23	36
e	98	99	96

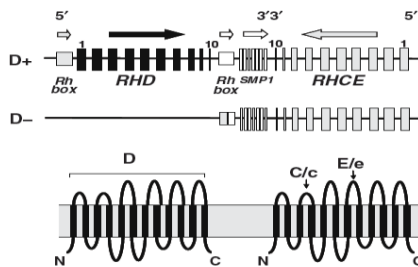
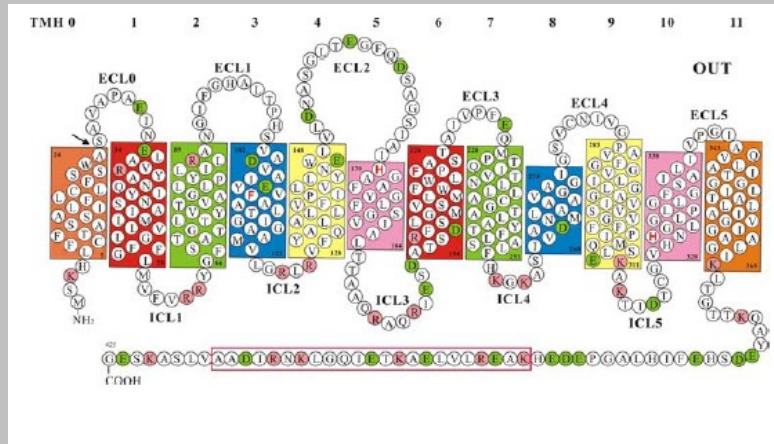


Fig. 3 Top the Rh genes, showing the ten exons of *RHD* and *RHCE* in opposite orientation on the chromosome, *SMP1* between them, and the *Rh* boxes flanking *RHD*. Below that is the *D*-negative haplotype, in which *RHD* is deleted, giving rise to a hybrid *Rh* box. Bottom diagrammatic representation of the *D* and *CcEe* polypeptides, which span the membrane 12 times and have internal *N*- and *C*-termini and six extracellular loops. The amino acid substitutions that define the *C/c* and *E/e* polymorphisms reside in the second and fourth loops of the *CcEe* polypeptide, respectively

Rh protein



Rh protein

Hum Genet (2009) 126:729–742

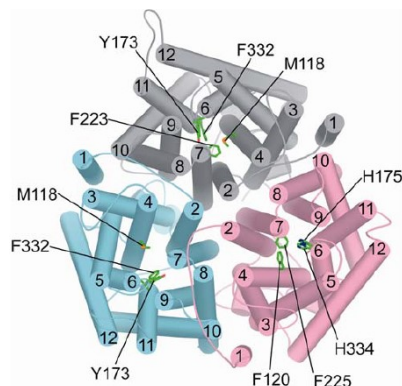


Fig. 4 Homology model of an Rh protein. RhAG heterotrimer viewed from the extracellular side. RhAG, RhD, and RhCE subunits are colored pink, grey and cyan, respectively; transmembrane helices are numbered. From Burton and Anstee (2008), with permission

KS systémy lidí a zvířat

Praktický význam

- **Krevní transfúze**
- **Inkompatibilita matka/plod**
- **Markery** *mapovací, asociační, populační*
- **Asociace s nemocemi**
- **Paternita**

KS systémy zvířat

Zvláštnosti a význam

- **Komplexní systémy**
- **Krevní transfúze**
- **Inkompatibilita matka/plod**
- **Markery** *mapovací, asociační, populační*
- **Asociace s nemocemi**
- **Paternita**

Skot	Locus	Chrom.	Linkage group	Syteny group	Antigens
	A	15	5	19	A D H Z'
	B	29	12	27	B G ₁ I ₂ K O ₁ O ₂ O ₃ O ₄ P ₁ P ₂ Q ₁ Q ₂ T ₁ T ₂ Y ₁ Y ₂ A' B' D' E' ₁ E' ₂ E' ₃ F' G' I' J' ₁ J' ₂ K' O' P' Q' Y' B'' G'' I''
	C	18		9	C ₁ C ₂ E R ₁ R ₂ W X ₁ C' L'
	F/V	21	7		F ₁ V ₁
	J	11	2	16	J
	L	3		6	L
	M	23	1	20	M M'
	S	21	7	4	S ₁ U ₁ U ₂ H' U' ₁ U' ₂ H'' S'' U''
	Z	8 (10 ^{ref10})	12	18 (5 ^{ref10})	Z
R'/S'	16		1	R' ₁ S'	
T'	19		21	T'	

Psi a kočky

Table 1. Geographic Distribution of Blood Types in Domestic or Nonpurebred Cats

Country	Reference	Type A (%)	Type B (%)
USA (by region)	16		
Northeast	16	99.7	0.3
North central/rocky mountain	16	99.4	0.4
Southeast	16	98.5	1.5
Southwest	16	97.5	2.5
West coast	16	94.8	4.7
Australia	8	73.3	26.3
England	17	97.0	3.0
France	17	85.0	15.0
Switzerland	17	99.6	0.4
Finland	17	100	0.0
Italy	17	88.8	11.2
Netherlands	17	96.1	3.9
Scotland	17	97.1	2.9
Austria	17	97.0	3.0
Germany	18	92.6	6.7
Denmark	19	98.1	1.9

Table 2. Blood Type B Frequencies in United States Purebred Cats*

Purebred Cats	Frequency of Type B Cats
Siamese, Oriental Shorthair, Burmese, Tonkinese, and Russian Blue	0%
Maine Coon, Norwegian Forest Cat	<5%
Abyssinian, Himalayan, Birman, Persian, Somali, and Sphinx	5%-25%
Devon Rex, British Shorthair	25%-50%