Nomenclature for factors of the SLA system, Update 2018



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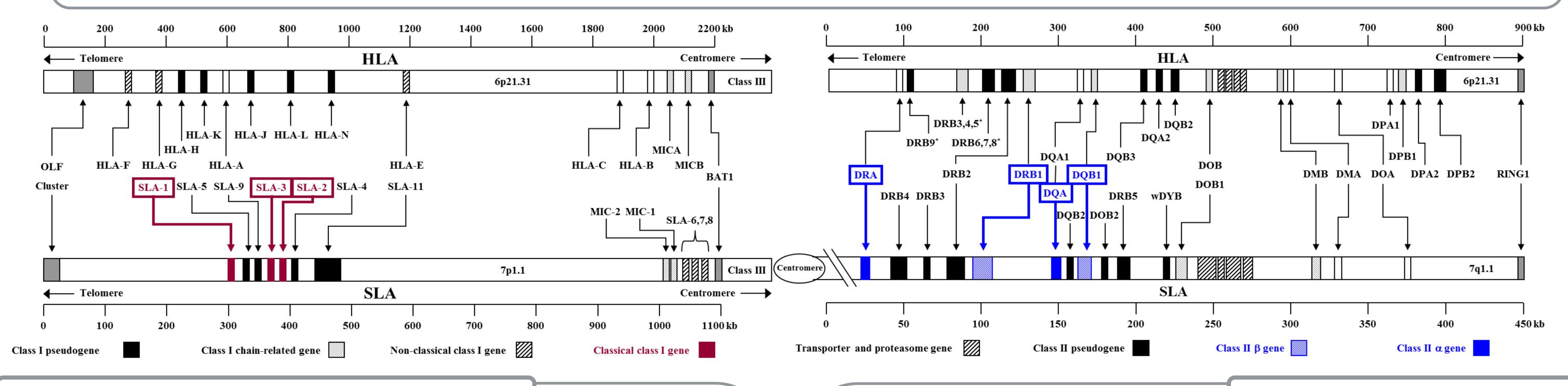
Background & Objectives

A systematic nomenclature for the genes, alleles and haplotypes of the swine major histocompatibility complex (MHC) is critical for research in swine genetic diversity, immunology, health, vaccinology, and organ or cell transplantation. The Swine Leukocyte Antigen (SLA) system is among the most well characterized MHC systems in non-human animal species. To date, 259 class I and 227 class II alleles are officially designated. Additionally, 67 class I (1-2-3) and 54 class II (DRB1-DQB1) haplotypes are designated at the allele level.

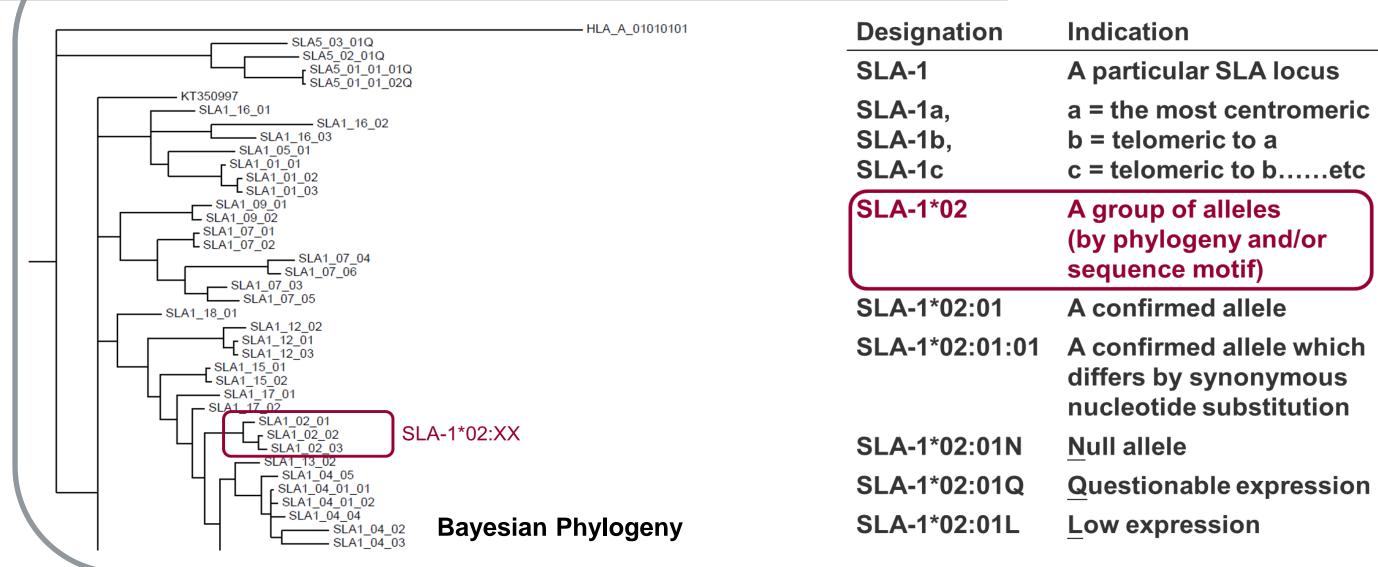
Recent evidence has suggested certain loci in the SLA system previously recognized as pseudogenes (e.g. SLA-9, SLA-11, DQB2 and DOB2) may be expressed at the transcript level for some haplotypes. Continuous efforts on characterizing SLA alleles and haplotypes and studying their diversity in various pig populations will further deepen our understanding of the architecture and polymorphism of the SLA system and their role in disease, vaccine and allo- or xeno-graft responses.

Human MHC (HLA) vs. Swine MHC (SLA) class I + II

Genomic organization of the MHC class I and class II region of the human leukocyte antigen (HLA) and swine leukocyte antigen (SLA) complexes. Modified after Lunney et al. (2009) Dev. Comp. Immunol. 33:362-74. Note: Not all the genes are shown here and the scale is approximate. Typical SLA class I and SLA class II genes that most researchers are interested in typing for their immune, disease and transplantation studies are indicated in red and blue, respectively.



SLA Nomenclature System (similar to WHO HLA)



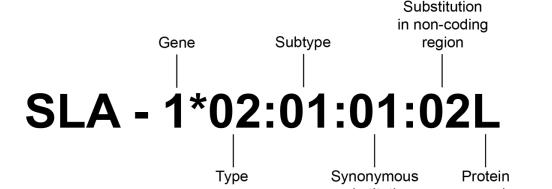
Definition of SLA Haplotypes SLA-1 SLA-3 SLA-2 DRB1 DQB1 0.1

Low-resolution (Lr) haplotypes are identified by a PCR-based typing assay and define the MHC background of an animal on allelegroup level → e.g., **SLA-1*01:XX**; **DRB1*01:XX**. **High-resolution (Hr) haplotypes** are defined on allele level by

sequence-based typing methods → e.g., **SLA-1*01:01**; **DRB1*01:01**.

Major Changes since 2016

O The adoption of the "colonized" nomenclature of the HLA system



- Methods for grouping and naming of SLA alleles are redefined Bayesian Phylogeny, # of AA substitutions and Sequentially
- O All tentative, unconfirmed SLA alleles are assigned official numerical allele names, e.g.: SLA-1*08pt13 → SLA-1*08:07

Endeavors of the ISAG/VIC IUIS SLA Nomenclature Committee

- O To validate newly identified SLA sequences according to the guidelines established for maintaining high quality standards of the accepted sequences.
- O To assign appropriate nomenclatures for new alleles as they are validated.
- O To serve as a curator of the IPD-MHC SLA Database and the repository of **SLA** sequences and haplotypes.
- O Work with journal editors to make official nomenclature as a requirement for non-human MHC sequences.

Assigned Alleles and Proteins

	Description	Locus	# Alleles	# Proteins		
SLA class I	Classical	SLA-1	89	87		
	(la α-chain)	SLA-2	93	90	Growth of SLA Database (2002-2018)	
		SLA-3	39	37		
	Non-classical	SLA-6	10	10	# Alleles # Proteins 500	
	(lb α-chain)	SLA-7	3	3		
		SLA-8	5	5		
	Other	SLA-12	6	6	450	
	Pseudogenes		14	0	400	
	Total number		259	238	400	
SLA class II	α-chain	DRA	14	6	350	
	β-chain	DRB1	99	92	250	
	α-chain	DQA	26	24		
	β-chain	DQB1	53	48		
	α-chain	DMA	7	5		
	β-chain	DMB	1	1		
	α-chain	DOA	2	2	200	
	β-chain	DOB1	3	3	2002 2008 2010 2012 2013 2014 2016 2017	
	Pseudogenes		22	0		
	Total number		227	181		

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