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Importance of the Major Histocompatibility Complex (Swine Leukocyte Antigen) in Swine Health and Biomedical Research

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Supplemental Figures Tables
Importance of the MHC (SLA) in swine health and biomedical research

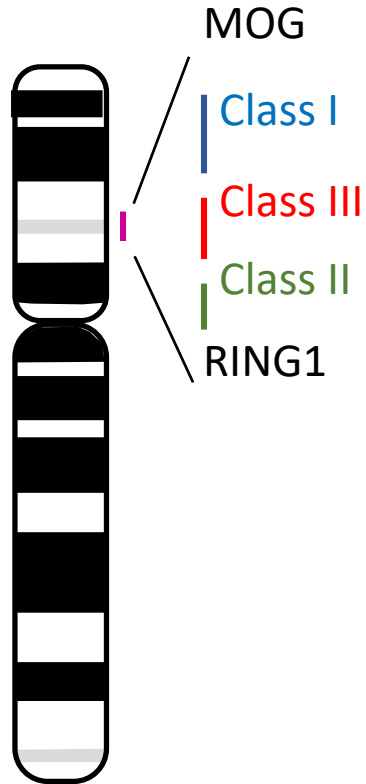
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Supplemental Figure 1. Chromosomal mapping of the human (HLA complex) and swine MHC (SLA complex)

a

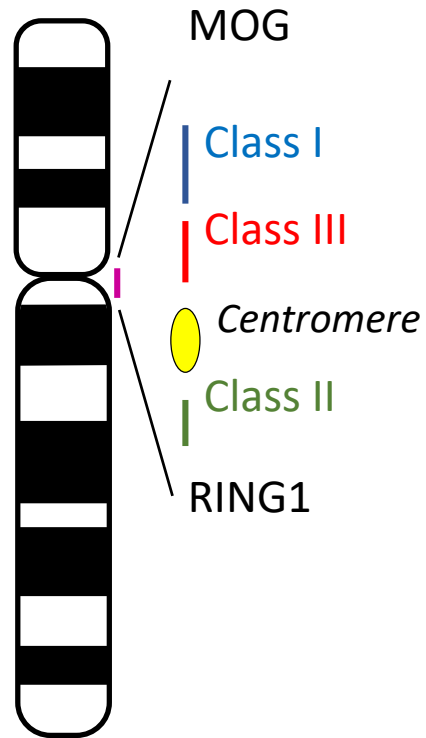
HSA 6p21



HLA complex

Human Leucocyte Antigen

SSC 7p11-7q11



SLA complex

Swine Leucocyte Antigen

b



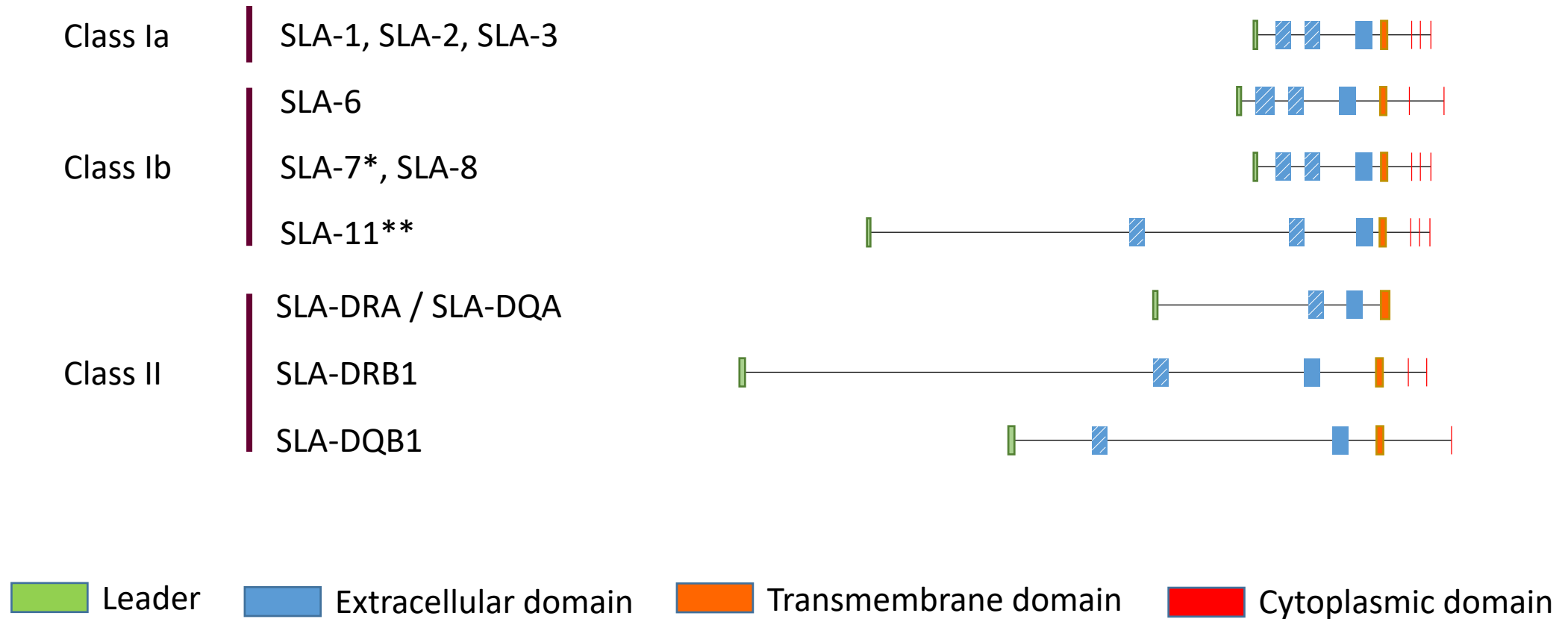
Supplemental Figure 1. Chromosomal mapping of the human (HLA complex) and swine MHC (SLA complex). A. Schematic representation of the chromosome mapping and orientation of the HLA complex on HSA 6p21 and of the pig SLA complex on both sides of the centromere on swine chromosome 7 (SSC7). B. Fluorescent in situ hybridization (FISH) map demonstrating SLA location on SSC7 p11 using a YAC clone containing SLA class Ia genes (adapted from Velten F, Rogel-Gaillard C, Renard C, Pontarotti P, Tazi-Ahnini R, et al. 1998. A first map of the porcine major histocompatibility complex class I region. *Tissue Antigens* 51:183–94).

Supplemental Figure 2. Detailed Physical Map of SLA genes

	Position	Name	Position	Name	Position	Name	Position	Name	Position	Name
7	22 595 564	22 606 449+ MOG	23 190 757	23 207 872- DHX16	23 705 030	23 706 737- LTB	23 994 844	23 996 220- ZBTB12	24 801 579	24 804 929- BTLN1*
7	22 607 422	22 612 063- ZFP57	23 214 057	23 220 314- PPP1R18	23 709 238	23 709 354- LST1	24 020 625	24 034 027+ C2	24 825 043	24 830 651+ SLA-DRA
7	22 621 686	22 624 180- ZNRD1-AS1	23 222 942	23 225 483+ NRM	23 713 919	23 714 208- NCR3	24 034 666	24 039 904+ CFB	24 845 879	24 856 577- SLA-DRB4**
7	22 624 616	22 625 409- ZNRD1	23 230 102	23 243 496- MDC1	23 720 533	23 720 866- AIF1	24 042 670	24 042 810- NELF-E	24 867 532	24 873 086- SLA-DRB3**
7	22 635 242	22 635 930+ PPP1R11	23 250 014	23 251 285+ TUBB	23 742 342	23 755 930+ PRRC2A	24 047 993	24 057 566+ SKIV2L	24 882 460	24 894 274- SLA-DRB2**
7	22 638 362	22 642 627- RNF39	23 262 617	23 264 275- FLOT1	23 758 043	23 767 712- BAG6	24 057 765	24 059 521- DXO	24 900 987	24 914 022- SLA-DRB1
7	22 668 950	22 681 032- TRIM31	23 266 307	23 266 798- IER3	23 770 895	23 772 781+ APOM	24 059 919	24 066 731+ STK19	24 953 480	24 959 313+ SLA-DQA
7	22 703 720	22 717 543+ TRIM40	23 380 960	23 390 612+ DDR1	23 774 207	23 775 097- C6orf47	24 067 878	24 082 949+ C4A	24 967 891	24 968 603- SLA-DQB2**
7	22 718 105	22 729 173- TRIM10	23 399 297	23 416 175+ VAR2L	23 777 298	23 779 237- GPANK1	24 086 354	24 088 300+ CYP21A2	24 969 034	24 977 238- SLA-DQB1
7	22 731 742	22 742 647+ TRIM15	23 421 081	23 421 232- SFTA2	23 783 119	23 785 736+ CSNK2B	24 094 065	24 150 584- TNXB	24 987 819	24 988 724- SLA-DOB2*
7	22 756 339	22 767 712- TRIM26	23 436 524	23 439 340+ DPCR1	23 786 970	23 787 784+ LY6G5B	24 161 530	24 171 225- ATF6B	24 992 845	25 001 720+ SLA-DRB5**
7	22 794 608	22 805 457+ TRIM26	23 443 720	23 448 956+ MUC21	23 791 581	23 793 911- LY6G5C	24 172 263	24 173 384- FKBPL	25 026 027	25 027 468- SLA-DYB*
7	22 824 137	22 827 965+ SLA-1b*	23 455 726	23 456 455+ MUC22	23 801 333	23 814 852- ABHD16A	24 183 943	24 185 590- PRRT1	25 030 435	25 038 196- SLA-DOB1
7	22 851 888	22 854 942+ SLA-5b*	23 515 759	23 516 607- C6orf15	23 818 669	23 821 522+ LY6G6F	24 189 529	24 200 027+ PPT2	25 045 921	25 056 294- TAP2
7	22 868 078	22 871 144+ SLA-9*	23 521 036	23 522 217- CDSN	23 823 769	23 824 299- LY6G6E	24 202 829	24 204 070+ EGFL8	25 059 023	25 061 532- PSMB8
7	22 888 634	22 892 409+ SLA-1a*	23 540 746	23 541 138- PSORS1C2	23 827 020	23 828 633+ LY6G6D	24 205 940	24 208 478- AGPAT1	25 063 184	25 071 824- TAP1
7	22 916 978	22 920 064+ SLA-5a*	23 544 712	23 557 507- CCHCR1	23 830 246	23 830 999- LY6G6C	24 215 691	24 217 978+ RNF5	25 075 279	25 077 229+ PSMB9
7	22 938 234	22 942 761+ SLA-3*	23 559 276	23 561 586+ TFC19	23 835 252	23 836 425+ LY6G6B	24 219 358	24 220 781- AGER	25 119 273	25 125 100- SLA-DMB
7	22 956 090	22 959 511+ SLA-2*	23 564 910	23 570 599- POU5F1	23 839 185	23 841 388- DDAH2	24 223 194	24 229 737- PBX2	25 133 494	25 137 959- SLA-DMA
7	22 974 434	22 977 527+ SLA-4*	23 603 786	23 605 903+ MIC-2*	23 843 091	23 846 907- CLIC1	24 231 886	24 255 024- NOTCH4	25 156 541	25 161 971+ BRD2
7	23 000 771	23 015 527- SLA-11*	23 619 392	23 622 373- MIC-1*	23 853 926	23 870 066+ MSH5	24 276 552	24 286 956+ BTNL5	25 178 866	25 182 665- SLA-DOA
7	23 047 216	23 047 674- TRIM39	23 622 374	23 625 867+ SLA-8*	23 875 620	23 885 421- VWA7	24 326 155	24 334 951+ BTNL6	25 205 505	25 232 024- COL11A2
7	23 064 441	23 066 267+ RPP21	23 634 733	23 638 561- SLA-7*	23 886 990	23 899 598- VARS	24 408 487	24 409 986- C6orf10	25 237 133	25 242 773- RXRB
7	23 102 879	23 111 046- GNL1	23 645 615	23 649 244- SLA-6*	23 900 742	23 901 188- LSM2	24 499 275	24 499 823+ BTNL7*	25 243 429	25 246 833+ SLC39A7
7	23 113 401	23 118 903+ PRR3	23 654 902	23 655 787+ MCCD1	23 910 408	23 912 330- HSPA1L	24 517 891	24 518 442- BTNL8*	25 247 865	25 248 904+ RING2
7	23 135 288	23 143 432+ ABCF1	23 659 170	23 667 616- DDX39B	23 915 074	23 916 993+ HSPA1A	24 682 974	24 683 519- BTLN9*	25 252 577	25 255 204+ RING1
7	23 149 935	23 158 749- PPP1R10	23 671 911	23 672 685- ATP6V1G2	23 925 931	23 927 850+ HSPA1B	24 726 892	24 727 458- BTLN10*		
7	23 166 076	23 172 714+ MRPS18B	23 674 527	23 684 873+ NFKBIL1	23 954 267	23 957 943- NEU1	24 764 765	24 765 175- BTLN4*		
7	23 173 466	23 185 260+ ATAT1	23 696 206	23 698 142+ LTA	23 960 137	23 961 617- SLC44A4	24 787 140	24 787 679+ BTLN3*		
7	23 187 160	23 190 108+ C6orf136	23 699 627	23 701 605+ TNF	23 978 013	23 992 676- EHMT2	24 793 588	24 795 223- BTLN2		

Supplemental Figure 2. Detailed Physical Map of SLA genes from Sscrofa11.1. The SLA class I and II genes are in blue and green font, respectively. The * symbol notes swine specific loci for which no orthology is found with HLA loci. The ** symbol notes genes found in HLA, but without a clear orthology relationship with their SLA counterparts.

Supplemental Figure 3. Gene structure of the SLA class Ia, class Ib and class II genes.



Supplemental Figure 3. Gene structure of the SLA class Ia, class Ib and class II genes. The exons are represented by boxes and the introns by lines proportional to their size and connecting the exons. The exons corresponding to the peptide leader are represented in green; the exons corresponding to the extracellular domains ($\alpha 1$, 2 and 3 for class I genes and $\alpha 1$ and 2 for class II genes) are represented in blue; the exons corresponding to the transmembrane domain are represented in yellow; the exons corresponding to cytoplasmic tail are represented in red. The most polymorphic exons (exons 2 and 3 for class I genes and exon 2 for class II genes) are represented by striped boxes. * On this figure, the *SLA-7* gene comprises eight exons as annotated from Sscrofa1.1 assembly and as reported by Hu et al. (3) ; a gene structure with seven exons has also been described by Crew et al. (11) but has not been presented on this scheme. **The classification of SLA-11 as a class Ib protein coding gene is still provisional and needs to be confirmed.

Supplemental Table 1: Available typing methods for assessing SLA diversity

Method	Starting material	Requirements	Animal throughput	Accuracy/ resolution	Missing alleles	Cost	Turn-around time	Interpretation/ bioinformatics	References
PCR-sequence-specific primers (PCR-SSP)	gDNA	Sets of SLA allele group-defined primers	intermediate	low	low	intermediate	low	low	Ho et al. 2009
DNA-based high-resolution genotyping	gDNA	Sets of SLA locus-defined nested primers	intermediate	high	low	high	intermediate	intermediate	Le et al. 2015
Hybridization DNA capture-based sequencing	gDNA	SLA locus-based capture array	high	high	low	high	intermediate	high	Lee et al. 2018
PCR-SSOP Luminex	gDNA	SLA allele group-defined oligoprobes	intermediate	low	intermediate	intermediate	intermediate	intermediate	Ando et al. 2011
Sequence-based typing (SBT)	RNA	Sets of SLA locus-defined primers	low	high	intermediate	high	high	intermediate	Ho et al. 2006
2 nd Generation Pyrosequencing	RNA library	All known SLA class I loci defined a set of universal primers	high	high	low	high	intermediate	high	Kita et al. 2012
Sequence-based typing (SBT) by RNASeq	RNA library	Sets of SLA locus-defined primers	high	high	low	high	intermediate	high	Sørensen et al. 2017

Abbreviations: gDNA, genomic DNA; SLA, swine leucocyte antigen; SSOP, sequence-specific oligonucleotide probes.

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