Porcine major histocompatibility complex

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The major histocompatibility complex in swine (swine leucocyte antigen: SLA) is located on chromosome 7 with the class I and class III regions separated by the centromere from the class II region. The overall molecular organisation of the class I and III regions is well known, but further research is needed to establish that of the class II region. Approximately sixty genes have been characterised to date, including ten tightly packed SLA class I sequences. The exact number of functional polymorphic class I genes, as defined by serology, probably varies from one to four, depending on the haplotype. At least two other distantly class I-related gene families exist. The numerous and significant associations reported between SLA haplotypes and physiological traits are described. These traits include immune responsiveness to a variety of microbes and metazoan parasites, and male and female production and reproduction performance. The results obtained suggest that selection for specific SLA haplotypes may assist in the improvement of porcine production.

Keywords

Introduction

The swine major histocompatibility complex (MHC), named SLA (swine leucocyte antigen) was identified in 1970 (76, 81), several decades after identification of the mouse H-2 complex (22) and the human HLA (human leucocyte antigen) system (12). Early experiments emphasised the role of MHC as a strong histocompatibility system, while serological tests revealed both a high level of polymorphism and genetic complexity. At present, the molecular organisation of the SLA complex is partly unravelled and represents the best-defined genetic region in swine. The MHC specialised class I and class II proteins are essential in the development and control of specific immune responses. Other genes of the MHC region are involved in the non-specific branch of the immune defence system, such as the C2-Bf and C4 complement components. Similarly, the tumour necrosis factor (TNF) gene family plays a prominent role in these mechanisms as well as in the development of the lymphoid tissues (46). Finally, the SLA region has been shown to affect a number of biological characteristics including productive and reproductive performance, thus the SLA region is of great importance for selection in the swine industry.

Chromosomal map of the swine leucocyte antigen complex

The SLA complex was mapped near the centromere of chromosome 7 (19, 52): the SLA class I and class III regions were assigned to the 7p1.1 band on the short arm while the SLA class II region was assigned to the 7q1.1 band on the long arm (73). The current view of SLA region is shown diagrammatically in Figure 1. This diagram is based on serological, genetical and molecular biological results obtained in National Institutes of Health (NIH) Miniature swine and swine from commercial breeds, by pulse field gel electrophoresis (PFGE), cosmids and yeast artificial
Fig. 1
Chromosomal map of the swine leucocyte antigen complex and the human leucocyte antigen region
The swine leucocyte antigen class I region

Current understanding of the overall physical organisation of the SLA complex is a result of the extensive use of molecular biology techniques. It is nevertheless important to emphasise the historical as well as the practical importance of the SLA class I serology, the understanding of which has led to knowledge of the SLA region. Furthermore, SLA class I serology still remains a powerful, quick and inexpensive tool for analysing large numbers of individuals.

Serological comparison tests

The anti-SLA reagents used in serological comparison tests are produced essentially by full thickness dermo-epidermal allografts or injections of peripheral blood leucocytes, lymph node or spleen cells. Following continuous exchanges of reagents and information between a limited number of laboratories, the first official international comparison test was held in 1986. The joint report issued in 1988 presented the results of the comparison of 157 selected alloantisera tested on lymphocytes from 264 unrelated Landrace or Large White pigs (53). Among the 31 SLA specificities characterised, eighteen (designated W1 to W18) were defined internationally. Most of these specificities were tentatively assigned to one of the three class I series which are presumed to exist and were based on results from serological, genetical and biochemical studies.

In addition to the conventional allo-anti-SLA reagents, a number of monoclonal antibodies have been produced. In general, these were shown to recognise monomorphic determinants common to most class I molecules or semi-public specificities shared by several SLA class I molecules (29). In fact, monoclonals capable of identifying SLA private specificities have not been produced so far.

The swine leucocyte antigen haplotype chart and polymorphism

A haplotype consists of a combination of alleles of genes located on the same chromosome. Analysis of more than 500 SLA serologically informative families revealed the repeated occurrence of at least 68 haplotypes in numerous swine commercial breeds worldwide. An updated version of the previous SLA haplotype chart is given in Table I. The NIH Miniature a haplotype was found to share class I specificities with the standard haplotype H10, while the d haplotype resembled the haplotype H04. The NIH c haplotype did not correlate with any of the haplotypes of the chart. Unlike other haplotypes, the SLA H04 haplotype was found in a majority of breeds and is considered to be one of the ancestral haplotypes in swine. Furthermore, there is clear haplotype-to-haplotype variation in the number of SLA class I genes expressed. Although most SLA haplotypes code for at least two or three distinct class I molecules, some haplotypes appear to control one or even four – and exceptionally five – SLA class I molecules.

The overall level of swine MHC polymorphism is not known, as SLA tests have been carried out thus far on about twenty breeds out of the 300 or more breeds which exist throughout the world.

The genomic swine leucocyte antigen class I region

Like the MHC class I genes in other species, the SLA class I molecules consist of a heavy glycoprotein chain of about 45 kiloDaltons (kDa) which is non-covalently associated with the swine β2-microglobulin, a polypeptide of 11.7 kDa. The heavy chain is a transmembrane molecule, encoded within the SLA complex, which expresses all the polymorphisms observed. The β2-microglobulin is monomorphic and is coded for by a gene which has been mapped to the chromosome 1q1.7 region (59).

The SLA class I classical molecules are expressed ubiquitously although there is wide variation in the level of expression among tissues and cells.

Number of swine leucocyte antigen class I genes

The first SLA functional class I gene to be characterised, designated PD1, was recovered in 1982 from a NIH Miniature pig homozygous for SLA haplotype d genomic library (72). Further screening of dd genomic libraries in phage and cosmids led to the characterisation of six more non-allelic SLA class I sequences named PD14, PD7, PD6, PD15, PD8 and PD4 (16). Thus, a total of seven class I sequences were found to be present on haplotype d. More recently, a laboratory in Germany has identified seven to nine class I genes in a different miniature swine breed by screening a cosmids library with an HLA cDNA (complementary DNA) probe (68).

Restriction fragment length polymorphism (RFLP) analyses by Southern blotting of the SLA class I genes in both the NIH Miniature lines (72) and in commercial breeds in the United States of America (USA) and Europe revealed a limited number of bands compatible with the cloning findings (8, 69). Thus, the swine carries a significantly lower number of class I sequences than rodents and humans, in which 20 to 40 class-I bands are observed, among which only a minority of bands correspond to classical class I genes.
Table I
Swine leucocyte antigen haplotype chart

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(a) Belgian haplotype

Structure of the swine leucocyte antigen class I gene

Swine leucocyte antigen classical class I genes

The genomic structure of the MHC PD1, PD7 and PD14 genes corresponds to the canonical model found for all classical class I genes, and consists of a leader sequence, three exons encoding corresponding extracellular domains, a transmembrane exon and three intracytoplasmic exons. The PD1 and PD14 sequences were highly homologous in both coding and non-coding regions, with an average homology of 88% and 80%, respectively (66). The deduced amino acid residue differences were essentially concentrated in exon 2 and more specifically clustered in positions 63 to 77. By contrast, the exon 3 sequences differed by 14 substitutions scattered throughout the whole exon. Although the PD7 gene is closely related to PD1 and PD14, with 81% and 85% homology in the coding regions, respectively, its expression level was very low when compared to PD1 and PD14.

Swine leucocyte antigen class I divergent gene

The PD6 gene represents a divergent monomorphic member of the SLA class I family and has an overall homology of only 55% with PD1 or PD14 (13). The size and the eight-exon organisation of PD6 are similar to the other class I genes with open reading frames for exons 1 to 6; however, PD6 has a codon stop in exon 7. A human or mouse counterpart of swine PD6 sequence has not been found. In vivo expression of PD6 products could not be revealed, while PD6 transcripts were present mainly in secondary lymphoid tissues and preferentially in peripheral T cells as compared to B cells. The PD6 gene was also transcribed in mouse cells and upregulated by interferon treatment. Among the remaining sequences, PD15 represented a pseudogene while PD4 and PD8 were not characterised further.

Molecular organisation of the swine leucocyte antigen class I region

Pulse field gel electrophoresis has shown that the three classical genes PD1, PD14 and PD7 are located on a 320 kilobase (kb) genomic fragment, while the PD6 and PD15 sequences could not be located more than 500 kb apart, as quoted in Schook et al. (67). More recently, the use of evolutionary conserved anchor genes together with SLA class I genes permitted the construction of a contig of overlapping YAC clones spanning about 1.2 Mb of the SLA class I region (9) of a Large White male (Fig. 1). Within this contig there was perfect conservation of the order of the anchor genes between swine and humans. Actually, the conservation of the synteny could be extended possibly far beyond the MHC region as it includes the butyrophilin sequence, which is
located presumably several tens of megabases away from the MHC. As shown in Figure 1, from the centromeric region onwards there are the class III pig counterpart of the HLA-B-associated transcript 1 (BAT1) genes, at least two divergent members of the class I gene family including SLA-6, the cell growth-regulated gene SCI, the octamer transcription factor 3 gene POUSF1, the skin-associated protein gene S, the guanosine-5'-triphosphate (GTP)-binding protein gene HR1, the ring-finger-protein gene RF50, the myelin oligodendrocyte glyco-protein gene MOG, and finally an olfactory receptor gene cluster. Of the seven class I sequences included here, five (SLA-1, SLA-3, SLA5, SLA-9 and SLA-10) were found within a segment of less than 180 kb. Partial sequencing of these genes suggested that the SLA-2 and SLA-3 genes were probably allelics of the NIH classical PD14 and PD7 genes, respectively. The SLA-1 and SLA-10 sequences closely resembled the NIH PD1 gene, while SLA-5 and SLA-9 where slightly less homologous. The SLA-4 gene was found to contain a stop codon in exon 4. Among the two most centromeric class I-related genes were SLA-6 (which is identical to the NIH PD6 gene) and the SLA-7 gene, which appeared not to be related to any of the described sequences. Remarkably, in contrast to the anchor genes framework, the class I gene organisation and spatial location differed greatly between humans and swine. Thus, while all functional SLA class I genes are clustered in less than 180 kb, the HLA classical class I genes are spread over a 2 Mb segment.

The swine leucocyte antigen class II region

Swine leucocyte antigen class II serology
Characterisation of SLA class II serology has met with limited success because of the existence of a wide range of class II cross-reactions which precluded its use in routine tests. A number of monoclonal antibodies produced mainly against MHC class II specificities in the mouse and other species were found to react with swine cells. An updated list of these reagents was provided recently (36). Some of these monoclonals recognise either SLA-DR or SLA-DQ antigens, but most appeared to react with monomorphic determinants. Only two monoclonals have been reported to recognise private polymorphic determinants of swine class II antigens.

Swine leucocyte antigen class II proteins
Biochemical and serological studies demonstrated the expression of SLA-DQ and DR molecules but not the swine counterpart of the human DP third series (7, 49). As in other species, these molecules are heterodimers which consist of a heavy chain (alpha) with a molecular weight of approximately 34 kDa and a light chain (beta) of about 29 kDa. Both chains, which associate non-covalently, have a transmembrane and a cytoplasmic tail and are encoded by genes in the MHC complex.

SLA class II antigens are found mainly on lymphoreticular B and macrophage cells and on a significant fraction (60% to 70%) of circulating T cells. Parenchymatous cells, such as kidney cells, also express class II molecules physiologically.

Swine leucocyte antigen class II molecular analysis

Southern blot analyses of swine class II genes revealed the existence of one to two DQA and DRA genes but more DQB and DRB sequences per haplotype (8, 65). These analyses also revealed extensive cross-hybridisation between the SLA-DQB and DRB genes. Cloning experiments subsequently demonstrated a unique DRA monomorphic gene in the NIH lines. On the other hand, the DQA gene (and especially the DQB and DRB genes) were shown to be highly polymorphic.

The predicted structure of the miniature swine DQA and of the DQB genes confirmed the overall organisation established for their counterpart genes in rodents and man. Thus, the swine DQA sequence consists of a leader peptide, two extracellular domains (exons 2 and 3) the transmembrane domain (exon 4) and the cytoplasmic tail. Domain sizes are conserved, and so the locations of cysteine residues are found at positions 111 and 167 and the two glycosylations sites at positions 82-84 and 122-124. Similar structures were deduced from the sequences of the other swine class II genes. The comparison of the NIH swine DQB c and d alleles revealed 18 nucleotide substitutions in the first domain, and only one was silent. The remaining part of the two sequences differed by only three nucleotides, with one leading to the replacement of an amino acid in the second domain. The alignment of the allelic sequences DRB c and d revealed a total of 42 nucleotide substitutions of which twelve were located in the first extracellular domain (residues 1-94), three in the region encoding the second extracellular domain (residues 95-188) and one in the exon encoding the transmembrane portion (residues 198-220). Remarkably, ten of the substitutions in the first domain consisted of amino acid replacements and two were silent, as were all substitutions in the second domain. Of the ten predicted replacement substitutions, six (60%) were situated in positions corresponding to the putative antigen recognition site (24, 25).

SLA class II expression and DRB and DQA exon 2 sequences have also been analysed recently in commercial breeds of swine in Norway and the USA by the reverse transcriptase-polymerase chain reaction (RT-PCR) and the PCR-RFLP techniques (70, 75). Addition of the results obtained in these breeds to those of the NIH miniatures gives a total of seven DQB and thirteen DRB alleles, thus confirming the polymorphism of the class II region revealed earlier by cellular tests. Preliminary results indicate that the SLA class II region may cover at least 450 kb (67).

The swine leucocyte antigen class III region

As shown in Figure 1, the genomic organisation of the SLA class III region spans about 700 kb of DNA and contains 33 characterised genes (50). Comparison with the corresponding human region confirmed the good overall conservation of this segment of the MHC between mammal species. The biggest difference concerned the 21-hydroxylase-complement C4 component (CYP21-C4) locus, with only one CYP21 and one
C4 gene present in swine, whereas in humans, mice and probably in ruminants species, the CYP21-C4 group underwent independent tandem duplications. Interestingly, the majority of well-documented SLA recombinants occurred within the class III region which suggests that recombination hot spots may exist in this chromosomal segment. There is limited information on the polymorphism of SLA class III genes except some RFLP data concerning the complement C4 component and CYP21. For the latter, six allelic patterns were obtained in 31 Large White pigs bearing a large panel of SLA haplotypes (20). Similarly, a dinucleotide repeat (TG) 23 close to the TNF-α locus has been isolated, which allowed the characterisation of six alleles (34).

**Involvement of the major histocompatibility complex in physiology and pathological syndromes**

In higher vertebrate species including the chicken, laboratory rodents, farm animals and humans, the MHC region was shown to affect a variety of biological parameters more or less profoundly (30, 71). In humans, the MHC complex has been associated significantly with disease susceptibility in various syndromes, often in conjunction with other unlinked genes (10, 14). Similarly, specific HLA haplotypes were found to increase resistance towards life-threatening infectious pathogens including bacteria, protozoa and nematodes (1, 26, 47). In swine, investigations of the role of the SLA complex have concerned the immune responsiveness, disease resistance and associations with reproduction and production traits.

The swine leucocyte antigen complex and cutaneous malignant melanoma

Segregation analyses of the occurrence of melanocytic lesions in the American miniature pig Sinclair line suggested a two-loci model involving an undefined major initiator gene and a second locus located within the SLA region (4, 27, 74). One particular haplotype appeared to be necessary for the tumour initiator locus to be fully penetrant. In a herd of pigs with Sinclair origins in the Czech Republic, the reappearance of the malignant melanoma also seemed to correlate with an ancestral SLA haplotype (28). On the other hand, segregation studies of melanocytic lesions in crosses with the Munich miniature swine Troll in Germany showed no SLA-complex influence (48).

Swine leucocyte antigen and immune responsiveness

The role of the SLA complex in allograft tissues and organs has been fully assessed and therefore represents a very well characterised model for self versus non-self recognition experiments. The first evidence that the SLA complex was responsible for at least part of the genetic control of the immune response against conventional antigens was obtained from a herd of related Large White pigs in which only the haplotypes SLA H10 and H12 were segregating. Pigs homozygous for haplotype H10 and H12 had lower primary immune responses to both low and high doses of hen egg white lysozyme (HEWL) than heterozygous H10/H12 pigs. Challenged homozygous H12 and heterozygous H10/H12 had significantly better secondary responses than the homozygous H10 group (77). Similar studies performed in the NIH Miniature lines by a group in the USA confirmed that the SLA complex affected the immune response against HEWL and the synthetic peptide (T,G)-A--L (37). Thus, the SLA aa, dd and gg animals (the g haplotype is a recombinant haplotype comprising the class I genes from haplotype c and the class II region from haplotype d), were high responders for HEWL while the cc pigs were low responders. Conversely, dd- and gg-bearing pigs did not respond to (T,G)-A--L, while aa and cc pigs produced specific antibodies.

Scientists in Canada have also performed extensive investigations of the influence of the SLA complex on a number of immune parameters against a wide range of antigens in the NIH Miniature lines, using both in vivo and in vitro tests. Overall, the conclusion of these research efforts was that the SLA complex exhibited some role (although usually a moderate one) in the immune response. Thus, in 8-week-old piglets the SLA haplotypes contributed slightly (P < 0.1) to the variation in serum immunoglobulin (IgG) concentration while the sire, dam and litter effects were predominant (44). Pigs with the dd, dg and gg genotypes were associated with higher serum IgG levels. Similarly, the pigs bearing these haplotypes also produced more antibody to sheep red blood cells and (T,G)-A--L, while dg and gg pigs developed higher primary antibody response to HEWL (42). The antibody avidity tests to HEWL after primary and booster immunisations revealed no significant influence of the SLA genotype, while pigs of the dd genotype had greater avidity maturation between primary and secondary responses than other genotypes (2).

Cellular activity was measured using the delayed hypersensitivity test to bacillus Bilié-Calmette-Guérin (BCG). The challenge injection of purified tuberculin derivative 21 days after showed most marked reactions in the dd, dg and gg pigs. In contrast, hypersensitivity to dinitrochlorobenzene was lower in the dg and gg pigs compared to the other genotypes (42).

In vitro tests of phagocytic and bactericidal action of peripheral blood monocytes of 4- and 8-week-old pigs against Salmonella Typhimurium and Staphylococcus aureus showed that the effects of the SLA haplotypes on both bacteria were generally significant (33). Furthermore, serum agglutinating antibody titre and O-polysaccharide (O-ps) specific peripheral blood lymphocyte blastogenesis were measured following two parenteral vaccinations with an aromatic-dependent mutant of 5. Typhimurium and an oral challenge with virulent bacteria (35). While in most cases only luter significantly influenced both parameters, the SLA complex influenced significantly the degree of O-ps specific lymphocyte proliferation six days after the second vaccination (P < 0.004). In addition, the dd and gg homozygous and dg...
heterozygous pigs generally behaved as a group distinct from the other genotypes. In Yorkshire pig lines divergent for the antibody and cell-mediated immune response, the same authors found no apparent effect of selection for high and low responsiveness in swine on monocyte O-2 production and SLA-DR and SLA-DQ expression (23).

In a similar quantitative immunological testing approach carried out in several commercial swine breeds in Germany, significant breed differences were found for most of the traits tested, some which were related to the MHC region (5). Similarly, the immune response in commercial pig breeds in the USA to inactivated Bordetella bronchiseptica vaccine was affected mainly by the breed and dam, while the SLA haplotype also had some limited effect (60). More recently, a possible disease susceptibility and resistance pattern in porcine reproductive and respiratory syndrome virus associated with the SLA complex has been reported (32).

Regarding the biology of the SLA complex in virally infected swine, the expression in spleen of SLA class I and II antigens was followed in Yorkshire pigs which were inoculated with either a highly virulent or a less virulent African swine fever virus (ASFV) isolate (21). Spleen staining with specific anti-SLA class I and anti class II monoclonals revealed a general decrease of SLA molecule expression at three days post inoculation. However, pigs inoculated with the moderately virulent isolate showed an upregulated expression of both SLA classes on day four (when compared to the controls) which paralleled the recovery of the spleen macrophage population and the major increase of spleen T cells. As the pigs which recover from ASFV infection have circulating virus-specific cytotoxic T lymphocytes which readily lyse viral infected target cells upon in vitro restimulation, the role of the SLA as a restriction element has been investigated in infected NIH Miniature swine lines (43). The results were less clear than expected. Thus, although cc effectors in general preferentially lysed cells bearing cc SLA class I antigens, the restriction effect was less clear-cut with the dd and aa effector cells, which appeared to have broader lysis capacities.

The role of the swine MHC loci in natural resistance against the nematode Trichinella spiralis has also been studied in SLA homozygous NIH Miniature lines (38). Preliminary studies revealed that after a low inoculum dose, swine homozygous for the SLA haplotype c exhibited a lower burden of muscular larvae than the dd and aa swine (40). Although not statistically significant, this possible resistance was correlated with the development of an earlier antibody response and perhaps with a higher cellular response too. When challenged by a secondary infection, all three lines were protected, but the aa pigs showed a significant reduction in the number of encysted muscular larvae compared to the other two lines. Further research revealed that just one 'c' haplotype was enough to ensure a higher resistance level in about half (50%) of the pigs following a challenge inoculation in comparison to 8% in pigs without this haplotype (39). Altogether, these results were interpreted as evidence for the role of one gene of the SLA region and another elsewhere in the genome.

**Complement activity**

Despite the presence of numerous potential important genes within the SLA class III region, no pathologies have been related to this region so far. Evidence for the control of global serum haemolytic activity levels by the SLA complex was obtained by measuring complement haemolytic 50 activity in Large White related pigs previously tested for their immune response capability against HEWL (78). The SLA H12 homozygous pigs and the SLA H10/H12 heterozygous pigs displayed significantly lower haemolytic activity than the SLA H10 homozygous animals. The role of SLA control was not confirmed in the NIH Miniature lines (43).

**The swine leucocyte antigen complex and production performances**

With regard to investigations carried out to assess the influence of the SLA region on swine production performance, some scientists concluded an absence of (or at best a small) effect (83). The majority of reports, however, revealed significant associations with one or several traits. As shown in Table II, a wide variety of productive and reproductive traits was affected by SLA specific haplotypes as reviewed recently (67, 82). In particular, phenotypically identical haplotypes may have opposite effects in different breeds: for example, haplotype H04 and carcass fat content. Conversely, the haplotype H12 influenced growth rate favourably in both Large White and Meishan pigs. A haplotype may exhibit pleiotropic effects such as the 'Landrace' haplotype SLA H23, which was found to be strongly associated with carcass leanness and muscle malic enzyme activity and moderately associated with ham development.

A number of reproduction traits were also affected by the SLA complex, including the ovulation rate, embryo development and litter size. The latter trait is generally affected negatively in litters where SLA homozygous piglets are expected, though occasionally the opposite was observed. Thus, in a Swiss study of Landrace families, larger litters were found with SLA haplotypes H16 and H24. In a separate study, SLA H16 homozygous sows had significantly more mummies than non-H16 homozygous dams. Investigation of male reproductive traits revealed that several SLA haplotypes were associated with the genital tract development and with the tissue androgenese level.

**Conclusion**

A number of significant advances have been achieved recently concerning the molecular organisation of the swine MHC-chromosomal region. The development of new tools for class I and above all class II allele studies is currently
Table II
Associations between production, carcass and reproduction traits and the swine leucocyte antigen complex

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RFLP: restriction fragment length polymorphism
NIH: National Institutes of Health
SLA: swine leucocyte antigen

underway and should contribute to an improvement in the precision of the tests. In addition to the class I and class II processed-peptide presenting molecules whose function is crucial in the immune response, more than fifty genes have been identified in the SLA region. These include the divergent class-I-related sequences whose functions are totally unknown, as are those of many of the remaining genes of this region. Future work should be devoted to the characterisation of some of these functions, which represents a necessary step for a fuller comprehension of SLA region involvement in swine production performance. Nevertheless, it appears possible to use the available information even now in selection programmes. Thus, a policy of not mating parents with common SLA haplotypes might be advisable to avoid piglet deficits. Similarly, selection for some specific SLA haplotypes related to carcass traits and disease resistance may make sense in certain breeds and lines. Continued analysis of the SLA region at both the molecular level and in the context of
production, reproduction and disease-related traits is needed to unravel further this important complex of genes and their functions.

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Le complexe majeur d’histocompatibilité des porcins
M. Vaiman, P. Chardon & M.F. Rothschild

Résumé
Le complexe majeur d’histocompatibilité des porcins (antigène leucocytaire du porc ; en anglais : swine leucocyte antigen : SLA) est porté par le chromosome 7, les régions des classes I et III étant séparées par le centromère de la région de la classe II. Alors que l’organisation moléculaire générale des régions des classes I et III est parfaitement connue, les travaux de recherche doivent être poursuivis pour mieux comprendre celle de la région de la classe II. Environ soixante gènes ont été caractérisés à ce jour, y compris dix séquences SLA de classe I étroitement groupées. Le nombre exact des gènes polymorphes fonctionnels de la classe I, tel que défini par la sérologie, varie probablement de un à quatre, selon l’haplotype. Il existe, au moins, deux autres familles de gènes ayant une relation lointaine avec la classe I. Les auteurs décrivent les associations nombreuses et importantes observées entre les haplotypes SLA et les caractères physiologiques. Ces caractères comprennent la qualité de la réponse immune à divers microbes et parasites métazoaires, ainsi que les performances en matière de production et de reproduction des mâles et des femelles. Les résultats obtenus montrent que la sélection en fonction d’haplotypes SLA spécifiques peut contribuer à améliorer la production porcine.

Mots-clés

El complejo mayor de histocompatibilidad del cerdo
M. Vaiman, P. Chardon & M.F. Rothschild

Resumen
El complejo mayor de histocompatibilidad del cerdo, o antígeno leucocitario porcino (swine leucocyte antigen, SLA), se encuentra en el cromosoma 7. Las regiones de la clase I y la clase III están separadas de la región de la clase II por el centrómero. Aunque se conoce bien la organización molecular general de las regiones de la clase I y la clase III, es necesario estudiar con más profundidad la de la región de la clase II. Hasta la fecha se han caracterizado aproximadamente sesenta genes, entre ellos un compacto agregado de diez secuencias que codifican moléculas SLA de la clase I. El número exacto de genes polimórficos funcionales de la clase I, tal y como pueden caracterizarse por serología, varía
probablemente, según el haplotipo, entre uno y cuatro. Existen por lo menos otras dos familias de genes lejanamente relacionadas con la clase I. Se exponen aquí los numerosos y significativo casos descritos de correlación entre haplotipos del SLA y rasgos fisiológicos. Entre tales rasgos figuran la capacidad de respuesta inmunitaria a diversos microorganismos y parásitos metazoos, así como la eficiencia de producción de machos y hembras y el rendimiento reproductor. Los resultados obtenidos sugieren que la selección de ciertos haplotipos concretos del SLA podría resultar útil para mejorar la producción porcina.

**Palabras clave**
Cartografía – Cerdo – Complejo mayor de histocompatibilidad – Genética – Rasgos de producción – Respuesta inmunitaria.

**References**


