Journal of Animal Science and Technology 52(6) 451~457, 2010
DOI:10.5187/JAST.2010.52.6.451

SLA Homozygous Korean Native Pigs and Their Inbreeding Status Deduced from the Microsatellite Marker Analysis

Woo-Young Jung[1], Hyun-Tae Lim[2], Jae-Sam Lim[3], Sung-Bok Kim[3], Jin-Tae Jeon[2] and Jun-Heon Lee[1]*

[1]Department of Animal Science and Biotechnology, Chungnam National University, Daejeon 305-764, Korea,
[2]Division of Animal Science, College of Agriculture, Gyeongsang National University, Jinju 660-701, Korea,
[3]Livestock Technology Research Institute, Cheongyang-gun, Chungcheongnam-do 345-811, Korea

ABSTRACT

The porcine MHC (Major Histocompatibility Complex), encoding the SLA (Swine Leukocyte Antigen) genes, is one of the most significant regions associated with immune rejection in relation to transplantation. In this study, three SLA class I (*SLA-1, SLA-3, SLA-2*) loci and three SLA class II (*DRB1, DQB1, DQA*) loci were investigated in the previously unidentified Korean native pig (KNP) population that was closely inbred in the Livestock Technology Research Station in Cheongyang, Korea. Total thirteen KNPs from four generations were genotyped for the SLA alleles and haplotypes were investigated using PCR-SSP (Sequence-Specific Primer) method. The results showed that all of these KNPs had Lr-56.30/56.30 homozygous haplotype, indicating high level of inbreeding in the SLA genes. The inbreeding status of these animals was also investigated using microsatellite (MS) markers. From the 50 MS markers investigated, 17 MS markers were fixed in all generations and the fixed alleles are increased as 26 loci for the fourth generation. Two MS markers, S0069 and SW173, were heterozygous for all the animals tested. Observed and expected heterozygosities were calculated and the average inbreeding coefficients for each generation were also calculated. In the fourth generation, the average inbreeding coefficients was 0.732 and this may increase with further inbreeding process. Analysis of the SLA haplotypes and MS alleles can give important information for breeding the pigs for xenotransplantation studies.

(**Key words :** Haplotype, KNP, Microsatellite marker, PCR-SSP, SLA, Xenotransplantation)

INTRODUCTION

Pigs have been considered as the potential xenograft donors due to the similarity of their size and physiology to humans. Also, pigs have relatively little ethical issues compared with the primates. In order to use pigs for the xenotransplantation, controlling of the immune rejection is the major obstacle and large efforts have been carried out for overcoming this problem. The porcine MHC (Major Histocompatibility Complex), encoding the SLA (Swine Leukocyte Antigen) genes, is one of the most significant regions associated with immune rejection response. The porcine MHC antigens recognize self and non-self peptides on the surface of cells to T-lymphocytes and ultimately act as triggers to start the immune rejection cascade. Based on their biological functions, the MHC antigens were divided into three classes, SLA class I, II and III, respectively. Most nucleated cells can express SLA class I genes which are recognized by CD8+ T cells (Shishido et al., 1997). SLA class II genes are expressed on antigen presenting cells (APC) and are recognized by CD4+ T cells. On the other hand, SLA class III genes having wide range of functions and some of them are related to the complement cascade (Naziruddin et al., 1998). In 2002, SLA Nomenclature Committee of the International Society for Animal Genetics (ISAG) has been established for the systematic nomenclature of the class I and class II SLA alleles (Smith et al., 2005a; Smith et al., 2005b; Ho et al., 2009a; Ho et al., 2009b; Ho et al., 2010a). The recent updates of SLA alleles can also be found in Immunopolymorphism Database-Major Histocompatibility Complex (IPD-MHC) website (http://www.ebi.ac.uk/ipd/mhc/sla/).

The SLA genes are highly polymorphic and play very important roles in regulating the immune system against

* Corresponding author : Dr. J. H. Lee, Division of Animal Science and Biotechnology, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Korea. Tel: 82-42-821-5779, Fax: 82-42-825-9754, E-mail: junheon@cnu.ac.kr

infectious diseases. Therefore, the relationships between SLA haplotypes and immune response to various infectious diseases were observed (Lunney and Murrell, 1988; Mallard et al., 1989). Also, results indicated that reproductive performance and production traits were related with SLA polymorphism (Renard and Vaiman, 1989; Gautschi and Gaillard, 1990). In relation to xenotransplantation research, SLA allele- or haplotype-specific xenogenic T-cell response has been observed in human to porcine xenografts (Xu et al., 1999; Yamada et al., 1995).

Until now, many breeds of pigs were used for the characterization of SLA alleles and haplotypes. About 30 years ago, National Institutes of Health (NIH), USA, established MHC inbred miniature pig lines (Sachs et al., 1976) and have been widely used for xenotransplantation researches. Since then, two groups in the world have developed MHC inbred pig lines, called Westran and Yucatan miniature pigs which can be used for the xenotransplantation researches (Lee et al., 2005; Smith et al., 2005a). Later on, SLA alleles have been investigated in Clawn miniature pigs by the Japanese group using polymerase chain reaction-sequence specific primer (PCR-SSP) and polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) techniques (Ando et al., 2005). Therefore, it is clear that the development of SLA homozygous pig lines is very important in the future use of these animals, especially in the xenotransplantation researches. In Korea, SLA alleles and haplotypes were investigated in 115 pigs derived from three generations of the Korean native pigs, which have been maintained in the National Institute of Animal Science in Jeju island. As the results, the Korean native pigs have seven haplotypes and the identified homozygosity was 27.4% (Cho et al., 2010).

In this study, we investigated six SLA loci in the Korean native pig population, which was maintained as a small closed colony at the Livestock Technology Research Institute in Cheongyang, Korea and this herd was not investigated previously. The information in this article can give the general guidelines for using Korean native pigs in the xenotransplantation researches.

MATERIALS AND METHODS

1. Animals and extraction of DNA from blood

Four generations of KNPs containing three males and ten females were maintained at Livestock Technology Research Institute in Korea and blood samples of these pigs were collected for examining *SLA-1*, *SLA-2*, *SLA-3*, *DRB1*, *DQB1* and *DQA* alleles. The KNP used in this study are the different population from the previous KNP population of Cho et al. (2010). The Cho et al. (2010) population is the descendant of founder population of KNP in Korea and the pigs used in this study are from local farms in Korea with unknown history. The appearance of these two KNP populations was the same, assuming that these two pig populations have same origin. Genomic DNA was extracted from the blood using PrimePrep™ Genomic DNA Isolation kit (Genetbio, Korea) according to a modified manufacturer's protocol and stored at −20℃ until use. The concentration of extracted genomic DNA samples was measured by NanoDrop 2000C spectrophotometer (Thermo Scientific, USA).

2. SLA genotyping by PCR-SSP method

In this study, PCR-SSP (Sequence-specific primer) method was used for discriminating SLA alleles and haplotypes in KNPs. The information of 47 primer pairs for SLA class I alleles (*SLA-1*, *SLA-3*, *SLA-2*), 47 primer pairs for SLA class II alleles (*DRB1*, *DQB1*, *DQA*) and positive control primers for the porcine α-actin (*ACTA1* gene) was already obtained from description published by Ho et al. (2009a, 2010a). The PCR amplification was carried out under the condition of denaturation for 10 min at 94℃ followed by 35 cycles of 96℃ for 15 s, 65℃ for 20 s and 72℃ for 20 s, with final extension of 3 min at 72℃, then holding at 4℃ using a 96-well MJ Research PTC-200 thermal cycler (Bio-Rad, USA). PCR reactions lding aed 25 ng of KNP genomic DNA, 10X PCR gold buffer (Applied Biosystems, USA)olding at 4℃25 mM $M4Cl_2$ (Applied Biosystems, USA), 2.5 mM of each dNTPs (Genetbio, Korea), 10 pmol of forward and d aerse primer pairs, 1X Cresol Red loading buffer (1.0 mM Cresol Red in 1750 mM sucrose), 1.5 Unit of AmpliTaq Gold polymerase (Applied Biosystems, USA), 0.5 pmol porcine positive control primers designed from α-actin gene (*ACTA*1) and 0.5 ug of acetylated BSA (Promega, USA) in a total volume of 5 $\mu\ell$. In order to investigate the reagent contamination, negative control was set up for each typing. The PCR products were confirmed by direct gel loading using 2% standard 1X TAE agarose gel at 150V for 5 min using the Micro SSP™ Gel System (One Lambda, USA).

3. Microsatellite (MS) analysis

For the MS genotyping in 13 KNPs, the information of total fifty microsatellite markers [SSC1 (SW1515, S0331, SW1301); SSC2 (SW256, SW776, SW1879); SSC3 (SW2021, SW1443, SW1327); SSC4 (S0301, SW1364, MP77); SSC5 (SW1482, SW963, SW1383); SSC6 (SW2406, S0059, S0121); SSC7 (SW1873, SW1369, SW2108); SSC8 (SW2410, S0069, KS188), SSC9 (SW911, SW1434, SW2093); SSC10 (SW830, SW173, SW1829); SSC11 (SW1460, SW1648); SSC12 (SW 957, SW1962, SWR1021); SSC13 (SWR1941, S0283, KS604); SSC14 (SW857, SW2519, SW2515); SSC15 (SW1562, SW1263, KS135); SSC16 (S0111, SW81); SSC17 (SWR1004, SW1920); SSC18 (SB8, SW1682)] and primers were selected from the published MS marker list in the USDA map (http://www.marc.usda.gov/genome/genome.html). Two or three MS markers were randomly selected from each of the porcine chromosome 1 to 18. The PCR reactions were performed for genotyping 50 MS loci in 13 KNPs with one of the three (HEX, NED and FAM) fluorescence dye-labeled primers. The PCR amplification was carried out in a 7.5 $\mu\ell$ total volume containing 25 ng of genomic DNA, 10X reaction buffer (Genetbio, Korea), 2.5 mM of each dNTPs (Genetbio, Korea), 10 pmol of each primers, 1X Prime Taq polymerase (Genetbio, Korea). Following initial denaturation at 95℃ for 5 min, 30 cycles of 94℃ for 1 min, 55~66℃ for 1 min and 72℃ for 1 min with extension of 5 min at 72℃ were performed. The PCR products were analyzed using the ABI Prism® 3130xl genetic analyzer and GeneMapper software version 4 (Applied Biosystems, USA). In order to calculate the level of the inbreeding coefficients, microsatellite genotypes were analyzed using Cervus® 3.0 software.

RESULTS AND DISCUSSION

In order to analyze SLA alleles and haplotypes of the Korean native pig population, PCR amplifications were conducted from three SLA class I (*SLA-1*, *SLA-3* and *SLA-2*) loci and three SLA class II (*DRB1*, *DQB1* and *DQA*) loci using PCR-SSP typing method with allele-specific primers indicated in Table 1. As described previously, positive control primers (α-actin, *ACTA1* gene), were multiplexed into each reaction to distinguish true negative reaction from false negative reactions (Martens et al., 2003). Based on the inheritance and segregation of the alleles in the pedigree, Lr-56.0/56.0 for SLA class I and Lr-0.30/0.30 for SLA class II, r-0pectively, were observed in all Korean native pig individuals (Fig. 1). This indicated thatn the used in this stu30 had onl0 ree,h(Maz0gous haplotype Lr-56.30/56.30 with *SLA-1**11XX, *SLA-3**03XX and *SLA-2**15XX alleles for SLA class I genes and *DRB1**11XX (1LA1/1Lac21), *DQB1* *05XX and *DQA**02XX alleles for SLA class II genes (Fig. 2). Recently, nidurous SLA alleles and haplotypes have beenonsa1)cterized in many breeds of pigI, Especially, SLA class I haplotype Lr-56.0 has already beenoobserved in the c(Mdurc1LA1pig herds and SLA class II haplotype Lr-0.30 has been also found in Duroc pig lines (Soe et al., 2008). Both Lr-56.0 and Lr-0.30 have their high resolution counterpart, which were Hp-56.0 and Hp-0.30. However, the combination of SLA haplotype Lr-56.30, which was identified in the KNPs, was not found in other breeds including Large White, NIH, Yucatan, Meishan, Duroc, Hanford, Banna, Clawn, Hampshire, Sinclair and commercial breeds (Ho et al., 2009a).

In this study, we examined the SLA haplotypes in a small population of Korean native pigs, which were isolated from 1986 in research center in Chungnam province in Korea and they were expected to be the different population from the previous results of Cho et al. (2010). Previously, the KNPs in Jeju province had six class I haplotypes (Lr-5.0, 7.0, 31.0, 56.0, 59.0, and 65.0) and five class II haplotypes (Lr-0.1, 0.13, 0.23, 0.30, and 0.34). Especially, SLA haplotype Lr-56.30 was one of the most prevalent haplotype in KNPs from Jeju province (Cho et al., 2010). In this study, all the pigs investigated had Lr-56.30, indicating that two different KNP populations (Jeju and Cheongyang) were originated from

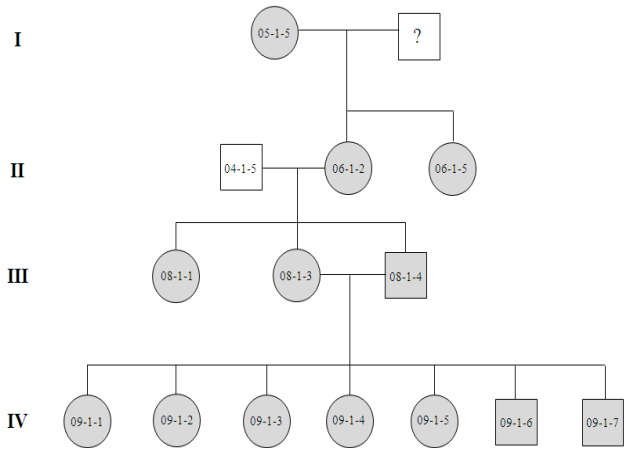

Fig. 1. Pedigree of the Korean native pig population used in this study. Grey color indicates the 13 KNPs used for SLA and MS analysis.

Table 1. Sequence-specific primer information for typing SLA class I and II alleles in Korean native pigs[1)]

SLA class	Specificity		Primer sequence (5'→ 3') (F: forward; R: Reverse)	Primer position	Product size (bp)
	Group[2)]	Allele			
I	SLA-1*08XX(all)	SLA-1*0801/08an03/08Lw02/08ms05/ 08pt13/08sk11/08sm08/08sy01	F: GtGGACTCCCGCTTCTTCATT R: CTCCCGATCCCAATACTCCG	+135 +233	138
	SLA-1*11XX(all)	SLA-1*1101~03/11mp11/11yn01	F: GTGTYCCGGCCCGACC R: TGTGCGYTGCCCATGACAC	+112 +260	182
	SLA-1*12XX(all)	SLA-1*1201/12hy01/12Lw01	F: GTTCGACAGCGACGCCCTC R: GGTTAATCTGTGCGGTTTCCTTGA	+186 +263	119
	SLA-1*15XX(all)	SLA-1*1501	F: CCCCACTCCCTcAGCTATTTCTC R: TGTAGTAGCCGCGCAGGGTC	+89 +300	253
	SLA-3*03XX(all)	SLA-3*0301~04/03an02/03an04/03an05/03pt31	F: TCYTCCTCCRCGGGTACCA R: GAGCCACTCCACACASGC	+404 +550	183
	SLA-3*05XX(all)	SLA-3*0501~03/05sw01	F: CGTGGAaGAtACGCAGTTCGTGT R: GTCTGTGCGTTGTCCTTGCTGA	+166 +260	138
	SLA-3*07XX(all)	SLA-3*070101~02/07Lw02/07rh34	F: CGACCGCaGGAAGCCCCGT R: CTCATCCCAATACTCCTGCCA	+126 +238	151
	SLA-2*05XX(all)	SLA-2*0501~03/05rh03/05rh34/05sy01	F: CGGGCGCCGTGGATAGAGA R: CCTCGCTCTGGTTGTAGTAGCCAAG	+232 +316	127
	SLA-2*06XX(all)	SLA-2*0601~02/06an03/06me01/06sv01	F: CGCCCCGAATCCGAGGAAA R: GGKTGTTCAGGYYCMCTCGGTA	+207 +292	125
	SLA-2*15XX(all)	SLA-2*1501	F: CGACCKCaGGAAGCCCCGT R: CGCGCAGGKTGTTCAGGC	+126 +293	203
	SLA-2*16XX(all)	SLA-2*1601	F: CCGCTTCCTCACCGTCGGGT R: GTAGTAGCCGCGCAGGGTG	+151 +309	196
	SLA-2*jh02	SLA-2*jh02	F: CGtGGACTCCCGCTTCCTCA R: TCGGTAAGTCTGTGCGGTTTCCTTGTAA	+142 +270	175
II	DRB1*01XX(all) DRB1*be01/ha01/ha04/Lu02	0101~02 be01/ha04/me02	F: CAGAAGCAGTACTATAACGGAGAGGAGC R: GTTGTGTCTGCAGTACGTGTCCACCG	+196 +308	162
	DRB1*01XX(all) DRB1*be01/ha04/me02	0101~02 be01/ha04/me02	F: CGCATTTCTTGTTTCTGGTGAAAGA R: CCGCATCTGCTCCAGGAGG	+125 +285	203
	DRB1*04XX	0401~04/04ga01/04ta01	F: CGCATTTCTTGTTTCTGSGGAAGG R: CGCCCGCTTCTGCTCCAT	+124 +289	206
	DRB1*10XX(all) DRB1*er01/La03	1001/10jh01/10ka06/10Lu03/10sp07 er01/La03	F: ACGCAGCGCATTTCTTCTTTATGGA R: GGTACTCGCCCACGTCGCTA	+119 +210	135
	DRB1*11XX(all)	1101~02/11ac21/11br02/11sp01/11zs10	F: CGAGTTCtGGGAAGTGACCGAAT R: GTGTCTGCAGTACGTGTCCACTG	+244 +308	109
	DRB1*04XX DRB1*11XX	0403~04 1101/11ac21	F: ACGGAGCGGGTGAGGTTTC R: CTTGtCGTCTGGCCGCCCAAAT	+166 +243	117
	DQB1*01XX(all)	0101/01be01/01ha01/01Lu01/01me03/ 01sh01	F: GATACATCTACAACCAGGAGGAGCTT R: GGTAGTTGTGTTTGCACACCG	+207 +326	165
	DQB1*03XX(all)	0301~03	F: TTCCAGTTTAAGGGCGAGTGCTACTTCTA R: GGCTGTTCCAGGAGTCGGCCT	+149 +266	166
	DQB1*04XX(all)	040101~02/0402/0402we01/04hg09/ 04sk51/04sp16	F: CAGCGGGTGTGGAGCGTGGA R: CCTCTATCTGGTAGTTGTGTTTGCACACA	+179 +327	197
	DQB1*05XX(all)	0501~03/05sp06	F: GCAGCGGGTGCGGCTCT R: TATCTGGTAGTTGTGTTTGCACACC	+175 +327	193
	DQB1*06XX(all)	0601~02/06sp01	F: ACtCAGCGGGTGCGGCA R: GCCTTCCTCTATCTGGTAGTTGTGTTTGC	+173 +332	204
	DQA*01XX(all)	0101~03/01ch01/01my01	F: ACTGTGTTTTCCAAGTCTCCAGTGATA R: GAAGCTGGTCTCAGAAAAACCTTTGA	+372 +461	141
	DQA*02XX(all)	0201~05/0201~05/02cs01/02xu01	F: GGCTTAAATGTCTACCAGTCTTACGGTC R: GTTGGAACGTTTAATCAGGRTGTTCAAA	+130 +285	210

[1)] Primer sequences have previously been published (Ho et al., 2009b; Ho et al., 2010).
[2)] "all" indicates all the published allele (s) that have been assigned to the group by the SLA Nomenclature Committee (Ho et al., 2009a; Smith et al., 2005b).

the same population sharing the same SLA haplotypes (Table 2). Based on the discussion about the origin of Cheongyang population, a few founder animals were transferred to Cheongyang from NIAS in Seonghwan after transferring KNP animals from Jeju to NIAS. Therefore the Cheongyang population should have the Jeju SLA alleles based on the known history of these pigs.

In order to calculate the inbreeding coefficients in the KNP population, fifty microsatellite (MS) markers were used. These MS markers were randomly selected from each of the porcine chromosome 1 to 18. Using the selected 50 MS markers, genotyping were performed and the results were

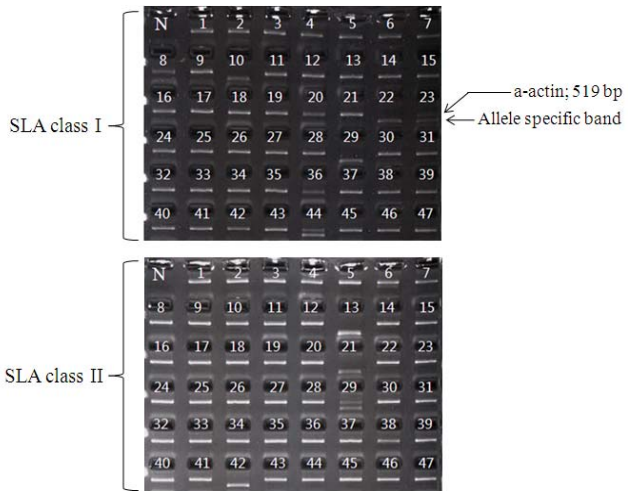

Fig. 2. The SLA genotyping analysis of the Korean native pig with haplotype Lr-56.0/56.0 (lane 10; *SLA-1**11XX, lane 22; *SLA-3**03XX, lane 44; *SLA-2**15XX) for SLA class I and haplotype Lr-0.30/0.30 (lane 13 and 21; *DRB1**11XX (1101/11ac21), lane 29; *DQB1**05XX, lane 42; *DQA**02XX) for SLA class II by low-resolution PCR-SSP method. The PCR products of range from 89 to 311 bp were amplified with the sequence-specific primers designed to discriminate SLA class I and II alleles. The size of designed positive control primers (porcine α-actin, *ACTA1* gene; 516 bp) are always larger than product sizes of allele-specific primers and the porcine α-actin primers was multiplexed into each reaction to distinguish real negative DNA bands from false negative reactions. A negative control is set up without DNA in order to check the reagent contamination.

analyzed. As the results, 17 loci (SW253, SW776, SW1879, SW1327, S0301, SW1383, S0121, SW2410, SW2093, SW 1962, SWR1941, SW857, SW2519, SW2515, SW1920, SB58, and SW1682) of the 50 MS markers were fixed in all generations of the KNP population. Also, 26 loci of the 50 markers were fixed at the 1st generation and 29, 31, 37 loci, in average, were fixed in the 2nd, 3rd, and 4th generations, respectively. However, two MS markers, S0069 and SW173, were heterozygous for all animals tested. The estimated average inbreeding coefficients in each generation were 0.511, 0.572, 0.613, and 0.732, respectively, and this may increase with further inbreeding process (Table 3). When we compare the inbreeding status of Westran pigs, the estimated inbreeding coefficient in generation 10 was 0.98159. This indicates that most of the alleles are homozygous in Westran pig breed and they are more inbred than Korean native pigs. The SLA analyses of the Westran pigs show that they have only one homozygous haplotypes consisted of haplotype Hp-8.0 for class I and Hp-0.9 for class II (Lee et al., 2005), which was different from the KNPs. Even though the identified inbreeding coefficient level of the KNPs in Cheongyang population was not as high as Westran pigs, KNPs in Cheongyang population were more inbred than the commercial pigs.

In conclusion, we have characterized the KNP SLA haplotype Lr-56.30 with PCR-SSP method in the Korean native pig population in Cheongyang, Korea. We have also investigated inbreeding coefficients of the KNPs using 50 MS markers. The SLA haplotypes and MS analysis of Korean native pigs in this study can provide important information for the breeding of pigs for the biomedical re searches and xenotransplantation studies. However, during the writing stage of this manuscript, all the Korean native pigs used in this study were killed because of foot-and- mouth disease outbreak in Cheongyang area in May 2010. Therefore, it is highly suggested to keep the valuable genetic resources in at least two different locations. If one of the

Table 2. SLA haplotypes and their frequencies identified in Korean native pigs from Jeju and Cheongyang populations

Population	SLA haplotype	Haplotype frequency (%)	Reference
Jeju	Lr-7.23	39.0	Cho et al. (2010)
	Lr-31.13	6.1	
	Lr-56.30	37.8	
	Lr-59.1	13.4	
	Lr-65.34	3.7	
Cheongyang	Lr-56.30	100	This study

Table 3. Estimation of inbreeding coefficients of 13 KNPs using MS markers in four generations

Generation	ID of KNP	No. of Total marker.	No. of heterozygote marker	No. of homozygote marker	Observed heterozygosity	Expected heterozygosity	Inbreeding Coefficient (IC)	Average of IC
I	05-1-5	50	24	26	0.48	0.982	0.511	0.511
II	06-1-2	50	19	31	0.38	0.980	0.612	0.572
	06-1-5	50	23	27	0.46	0.982	0.532	
III	08-1-1	50	21	29	0.42	0.981	0.572	0.613
	08-1-3	50	17	33	0.34	0.981	0.653	
	08-1-4	50	19	31	0.38	0.982	0.613	
IV	09-1-1	50	13	37	0.26	0.981	0.735	0.732
	09-1-2	50	17	33	0.34	0.981	0.653	
	09-1-3	50	10	40	0.20	0.978	0.796	
	09-1-4	50	14	36	0.28	0.983	0.715	
	09-1-5	50	15	35	0.30	0.980	0.694	
	09-1-6	50	13	37	0.26	0.979	0.734	
	09-1-7	50	10	40	0.20	0.977	0.795	

locations is affected by severe disease, we can still use the animals from another location.

ACKNOWLEDGEMENTS

This work was supported by a grant (No. 20070401034031) from BioGreen21 program, Rural Development Administration, The Republic of Korea and by a grant (No. 20100023352) from National Research Foundation of Korea, The Republic of Korea.

REFERENCES

Ando, A., Ota, M., Sada, M., Katsuyama, Y., Goto, R., Shigenari, A., Kawata, H., Anzai, T., Iwanaga, T., Miyoshi, Y., Fujimura, N. and Inoko, H. 2005. Rapid assignment of the swine major histocompatibility complex (SLA) class I and II genotypes in Clawn miniature swine using PCR-SSP and PCR-RFLP methods. Xenotransplantation 12:121-126.

Cho, H. O., Ho, C. S., Lee, Y. J., Cho, I. C., Lee, S. S., Ko, M. S., Park, C., Smith, D. M., Jeon, J. T. and Lee, J. H. 2010. Establishment of a resource population of SLA haplotype-defined Korean native pigs. Molecules and Cells 29:493-499.

Gautschi, C. and Gaillard, C. 1990. Influence of major histocompatibility complex on reproduction and production traits in swine. Animal Genetics 21:161-170.

Ho, C. S., Lunney, J. K., Ando, A., Rogel-Gaillard, C., Lee, J. H., Schook, L. and Smith, D. M. 2009a. Nomenclature for factors of the SLA system, update 2008. Tissue Antigens 73:307-315.

Ho, C. S., Lunney, J. K., Franzo-Romain, M. H., Martens, G. W., Lee, Y, J., Lee, J. H., Wysoki, M., Rowland, R. R. R. and Smith, D. M. 2009b. Molecular characterization of swine leukocyte antigen class I genes in outbred pig populations. Animal Genetics 40:468-478.

Ho, C. S., Lunney, J. K., Lee, J. H., Franzo-Romain, M. H., Martens, G. W., Rowland, R. R. R. and Smith, D. M. 2010a. Molecular characterization of swine leukocyte antigen (SLA) class II genes in outbred pig populations. Animal Genetics 41:428-432.

Lunney, J. K. and Murrell, K. D. 1988. Immunogenetic analysis of Trichinella spiralis infections in swine. Veterinary Parasitology 29:179-193.

Lee, J. H., Simond, D., Hawthorne, W. J., Walters, S. N., Patel, A. T., Smith, D. M., O'Connell, P. J. and Moran, C. 2005. Characterization of the swine major histocompatibility complex alleles at eight loci in Westran pigs. Xenotransplantation 12: 303-307.

Mallard, B. A., Wilkie, B. N. and Kennedy, B. W. 1989. Genetic and other effects on antibody and cell mediated immune response in swine leukocyte antigen (SLA)-defined miniature pigs. Animal Genetics 20:167-178.

Martens, G. W., Lunney, J. K., Baker, J. E. and Smith, D. M. 2003. Rapid assignment of swine leukocyte antigen haplotypes in pedigreed herds using a polymerase chain reaction-based assay. Immunogenetics 55:395-401.

Naziruddin, B., Durriya, S., Phelan, D., Duffy, B. F., Olack, B., Smith, D., Howard, T. and Mohanakumar, T. 1998. HLA antibodies present in the sera of sensitized patients awaiting renal transplant are also reactive to swine leukocyte antigens. Transplantation 66:1074-1080.

Remard, C. and Vaiman, M. 1989. Possible relationships between SLA and porcine reproduction. Reprodution, Nutrition, Development 29:569-76.

Sachs, D. H., Leight, G., Cone, J., Schwarz, S., Stuart, L. and Rosenberg, S. 1976. Transplantation in miniature swine. I. Fixation of the major histocompatibility complex. Transplantation 22:559-567.

Shishido, S., Naziruddin, B., Howard, T. and Mohanakumar, T. 1997. Recognition of porcine major histocompatibility complex class I antigens by human CD8+ cytolytic T cell clones. Transplantation 64:340-346.

Smith, D. M., Lunney, J. K., Ho, C. S., Martens, G. W., Ando, A., Lee, J. H., Schook, L., Renard, C. and Chardon, P. 2005a. Nomenclature for factors of the swine leukocyte antigen class II system, 2005. Tissue Antigens 66:623-639.

Smith, D. M., Lunney, J. K., Martens, G. W., Ando, A., Lee, J. H., Ho, C. S., Schook, L., Renard, C. and Chardon, P. 2005b. Nomenclature for factors of the SLA class-I system, 2004. Tissue Antigens 65:136-149.

Seo, O. K., Ohba, Y., Imaeda, N., Nishii, N., Takasu, M., Yoshioka, G., Kawata, H., Shigenari, A., Uenishi, H., Inoko, H., Ando, A. and Kitagawa, H. 2008. Assignment of the SLA alleles and reproductive potential of selective breeding Duroc pig lines. Xenotransplantation 15:390-397.

Xu, X. C., Naziruddin, B., Sasaki, H., Smith, D. M. and Mohanakumar, T. 1999. Allele-specific and peptide-dependent recognition of swine leukocyte antigen class I by human cytotoxic T-cell clones. Transplantation 68:473-479.

Yamada, K., Sachs, D. H. and Dersimonian, H. 1995. Human antiporcine xenogeneic T cell response. Evidence for allelic specificity of mixed leukocyte reaction and for both direct and indirect pathways of recognition. Journal of Immunology 155: 5249-5256.

(Received Aug. 5, 2010; Revised Nov. 22, 2010; Accepted Nov. 26, 2010)