Inbreeding Levels and Pedigree Structure of Landrace, Yorkshire and Duroc Populations of Major Swine Breeding Farms in Republic of Korea

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ABSTRACT : The registration data of 15 populations from nine major swine breeding farms were investigated to check levels of inbreeding and the current status of pedigree structures of breeding stocks. The average rate of inbreeding per generation was 0.208%, 0.209%, 0.098%, 0.307% and 0.071% for farms D, S, K, H, and Y in Duroc, 0.071%, 0.188%, 0.685%, 0.336%, and 0.449% for farms S, H, C, J, and W in Landrace, and 0.243%, 0.123%, 0.103%, 0.165%, and 0.286% for farms D, S, G, H, and J in Yorkshire, respectively. The average inbreeding rate was highest for Landrace, intermediate for Yorkshire, and lowest for Duroc farms. In Landrace and Yorkshire populations there were few immigrant animals per generation. In Duroc, however, there were quite large numbers of immigrant animals per generation compared to other breeds. The effective population sizes calculated from the average rate of inbreeding were distributed between 73.0 and 708.7. Specific values were 204.8, 239.7, 508.8, 163.0 and 708.2 for farms D, S, K, H, and Y in Duroc, 708.7, 266.5, 73.0, 148.9, and 111.3 for farms S, H, C, J, and W in Landrace, and 205.5, 406.0, 486.9, 302.6 and 175.0 for farms D, S, G, H, and J in Yorkshire, respectively. The values were acceptable for natural selection for fitness and inbreeding depression. The results showed that there was no cause for concern over the current inbreeding level of major swine breeding farm populations and the inbreeding level was within an acceptable range. (**Key Words :** Inbreeding, Inbreeding Coefficient, Swine, Pedigree Structure, Effective Population Size)

INTRODUCTION

In swine breeding industry, crossing between inbred lines or between different pure breeds has been used to produce hybrid vigour for the next generation. It is natural for swine breeders to maintain several purebred lines or breeds for this purpose hence, inbreeding is inevitable problem for them. The consequence of inbreeding is the reduction of the mean phenotypic value associated with decrease in reproductive capacity, physiological efficiency and fitness (Falconer and Mackay, 1996; Mandal et al., 2004; Singh. and Gurnani, 2004). For this reason swine breeders are always concerned in keeping the inbreeding level of their breeding stocks to minimum as they pursue improvement in performance.

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Swine breeding companies were founded in early 80's using selection index as the major method to select seed stocks for next generation. It was until late 90's that inbreeding level was elucidated as a problem coupled with the change in selection method from selection index based on phenotypic values to breeding values by Best Linear Unbiased Prediction (BLUP). It is known that selection based on breeding values estimated by BLUP, increased the level of inbreeding compared to selection index or phenotypic selection (Smith, 1988; Quinton et al., 1992). However, mating program and level of inbreeding were regarded as business secret in swine breeding farms therefore no studies were conducted and reported about the actual inbreeding levels of the breeding stocks in Korea. The objectives of this study were to investigate levels of inbreeding and the current status of pedigree structures of breeding stocks in major swine breeding farms in Korea.

MATERIALS AND METHODS

Pedigree data

The data were taken from purebred registry records of Korea Animal Improvement Association (KAIA), a breed

Table 1. Number of records and generations by breed and farm

Birth year	Breed/farm[1]														
	Duroc					Landrace					Yorkshire				
	D	S	K	H	Y	S	H	C	J	W	D	S	G	H	J
1985	27		11	5	53		13			3				1	
1986	239		168	28	171		90	23		38				34	
1987	502		211	52	63		87	8		196				33	
1988	345		169	88	58		223	92		158				178	
1989	631		211	22	111		61	117		99				101	
1990	413		342	69	175		185	66		201				172	
1991	471		474	27	321		294	117		300				257	
1992	1,053		623	45	311		313	58		965				334	
1993	1,596		644	82	366		192	84		1,838				277	
1994	1,427		768	91	520		353	120		1,085				428	
1995	1,773		513	202	687		468	203		789				609	
1996	414		264	109	705		433	70	36	617				622	35
1997	1,993	81	175	134	875	234	416	57	190	120		561		684	227
1998	1,771	698	95	188	843	573	546	229	1,419	343		865	648	780	1,626
1999	1,714	982	256	187	665	729	625	338	1,886	425	396	903	1,396	786	2,321
2000	2,652	1,782	764	930	165	1,639	1,745	487	2,953	479	1,675	1,929	2,734	3,152	4,304
2001	3,448	3,276	1,228	1,616	405	2,025	2,126	466	5,030	1,179	4,032	2,505	4,385	4,310	6,242
2002	2,250	2,691	1,957	3,068	449	2,166	3,046	2,600	4,929	1,544	4,102	2,725	3,226	6,096	6,119
2003	844	2,390	1,475	2,250		2,555	3,076	1,007	5,560	331	3,652	2,984	3,309	6,035	6,671
2004		1,733	629	1,562		2,855	2,292	3,670	5,509	405	4,396	3,012	3,699	3,446	7,776
Total	23,563	13,633	10,977	10,755	6,943	12,776	16,584	9,812	27,512	11,115	18,253	15,484	19,397	28,335	35,321
Number of generation[2]	14	8	15	15	14	7	12	9	9	13	5	7	7	13	8

[1] The same alphabet means same farm.

[2] Number of generation was calculated while sorting animals in the pedigree by descent.

association for beef cattle, dairy cattle, swine, and rabbit in Korea.

Five major farms based on the number of heads registered were selected for each breed; Landrace, Yorkshire and Duroc. The selected farms were all great-grand-parent stock farms and the mating was conducted according to pre-planed individual mating plan in all farms. Prior to 1990s both natural service and artificial insemination were used thereafter AI was predominant.

The oldest animal in the data was restricted to 1985 and further animals were deleted, because the swine registration program of KAIA was settled down in 1986 (NLRI, 2005) and few animals were registered before 1986. As shown in Table 1, there were five farms for each breed and a total of nine unique breeding farms were included for this study.

Inbreeding coefficient and pedigree structure

All animals in pedigree files were sorted in chronological order by using simple iterative algorithm (L. R. Schaeffer, personal communication) similar to that of "stack" in Animal Breeders' Tool Kit (ABTK) developed by Golden et al. (1992):

(1) Denoted all animals as generation number 1 and set iteration to 0:

$G(i) = 1, i = 1, 2, \dots n$, and

iteration $= 0$

where n = number of animals in pedigree, G = vector of where n = number of animals in pedigree, G = vector of generation number of animals, $G(i)$ = element of vector G for i^{th} animal, and iteration was used for counting the number of rounds

(2) Set count to 0 and increase iteration by 1:

count $= 0$

iteration $=$ iteration$+1$

(3) For each animal, read sire, s, and dam, d, of animal i. Find it in the pedigree and add $G(i)+1$ to $G(s)$ and $G(d)$ only if $G(s)(G(d))$ is smaller than $G(i)+1$:

if $(G(s)<G(i) + 1)$ $G(s) = G(i)+1$, count $=$ count$+1$

if $(G(d)<G(i) + 1)$ $G(d) = G(i)+1$, count $=$ count$+1$

(4) Performed steps (2), (3) until no further changes in the value of G. except existence of loop in the pedigree. If there is a loop in the pedigree, program should be stopped after certain number of iterations. The criteria for iteration

Table 2. Mean level of inbreeding (%) for each generation and farm in Duroc

Gen	Farm D				Farm S				Farm K				Farm H				Farm Y			
	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]
0	214	0.00			92	0.00	0.00	0.00	339	0.00			80	0.00			158	0.00		
1	4	0.00			1	0.00	0.00	0.00	4	0.00			1	0.00			1	0.00		
2	8	0.00	0.00	0.00	12	0.00	0.00	0.00	6	0.00	0.00	0.00	7	0.00	0.00	0.00	2	0.00	0.00	0.00
3	14	0.89	3.34	12.50	24	0.52	2.55	12.50	10	0.00	0.00	0.00	11	0.00	0.00	0.00	13	0.00	0.00	0.00
4	28	0.11	0.59	3.13	40	0.39	2.02	12.50	14	0.00	0.00	0.00	11	1.85	4.46	14.06	15	0.00	0.00	0.00
5	41	0.53	2.20	12.50	54	0.95	3.30	18.75	16	0.00	0.00	0.00	13	0.93	2.34	7.42	25	0.63	2.55	12.50
6	44	0.14	0.66	3.13	103	0.85	3.14	25.00	20	0.78	2.46	9.38	15	0.96	3.63	14.06	30	0.78	2.68	12.50
7	58	0.58	2.01	13.28	219	1.01	3.33	25.00	21	0.54	1.08	3.52	25	0.73	2.11	7.42	37	0.46	1.79	10.16
8	71	1.08	2.24	12.50	13,180	1.45	3.29	28.13	26	1.27	2.84	12.50	40	0.47	2.19	12.50	34	1.05	1.68	6.25
9	95	1.77	3.53	14.58					26	2.13	5.43	25.00	37	1.41	3.67	12.96	41	0.96	2.47	14.45
10	113	1.52	2.28	10.94					29	1.80	2.64	9.52	46	2.76	4.95	25.00	58	0.42	0.99	4.35
11	173	1.89	2.77	14.97					43	2.79	4.76	25.00	61	1.90	2.49	12.50	89	0.42	0.98	4.64
12	292	1.80	2.73	14.58					102	2.04	4.35	25.00	90	2.77	3.57	17.19	150	0.63	1.51	7.81
13	813	2.13	3.20	25.00					236	2.10	3.92	18.78	180	2.67	3.44	16.02	436	0.69	1.60	12.50
14	21,809	2.68	3.40	31.77					647	1.78	4.49	34.43	461	3.11	3.73	26.27	6,012	0.92	2.28	25.81
15									9,777	1.39	3.40	34.43	9,757	4.25	4.60	32.08				
Total[1]	23,777				13,725				11,316				10,835				7,101			

[1] Animals in base population (generation 0) were added to total number of animals.

[2] Minimum inbreeding coefficient was 0 for all generations and farms.

Table 3. Mean level of inbreeding (%) for each generation and farm in Landrace

Gen	Farm S				Farm H				Farm C				Farm J				Farm W			
	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]
0	298	0.00			181	0.00			56	0.00			87	0.00			80	0.00		
1	2	0.00			5	0.00			4	0.00			4	0.00			6	0.00		
2	15	0.00	0.00	0.00	8	0.00	0.00	0.00	31	0.40	2.25	12.50	14	0.00	0.00	0.00	14	0.00	0.00	0.00
3	38	0.00	0.00	0.00	17	0.00	0.00	0.00	51	1.47	5.39	25.00	30	0.00	0.00	0.00	19	0.66	2.87	12.50
4	84	0.00	0.00	0.00	22	1.28	5.34	25.00	94	0.30	2.60	25.00	45	0.14	0.65	3.13	27	0.38	1.80	9.38
5	160	0.29	2.15	25.00	37	0.01	0.06	0.39	159	0.54	2.01	12.50	62	0.69	1.52	6.25	29	0.98	1.87	6.45
6	471	0.13	0.82	12.50	50	0.13	0.88	6.25	270	2.86	5.54	25.00	94	0.91	1.60	7.03	32	2.36	2.80	10.16
7	12,006	0.42	2.97	25.78	64	0.16	0.67	3.13	488	3.53	4.88	31.25	199	1.45	2.07	12.50	34	3.64	2.96	11.52
8					88	0.54	1.37	6.25	1,067	4.69	4.69	32.03	583	1.71	2.02	9.38	37	3.95	2.91	11.52
9					152	0.90	2.23	15.63	7,648	5.39	5.03	37.11	26,481	2.66	2.38	26.56	51	7.26	6.20	28.13
10					321	0.89	2.43	25.00									96	5.69	5.23	21.84
11					978	1.14	2.74	25.39									194	5.35	5.79	28.08
12					14,842	2.07	3.16	26.81									586	4.95	5.31	29.20
13																	9,990	5.35	5.42	29.20
Total[1]	13,074				16,765				9,868				27,599				11,195			

[1] Animals in base population (generation 0) were added to total number of animals.

[2] Minimum inbreeding coefficient was 0 for all generations and farms.

number should be larger than actual generation number of a certain population and 20 was used in this study because there was no population that exceed 20 generation:

if (count>0 and iteration <20) goto (2)

The inbreeding coefficients were calculated using the algorithm of Meuwissen and Luo (1992). All individuals in the base population were assumed unrelated with an inbreeding coefficient of zero. Sire or dam which had less than two progenies and was not listed as an individual in the pedigree was deleted.

The rate of inbreeding was calculated as:

$$\Delta F = \frac{1}{n-1}\Sigma_{t=2}^{n}\Delta F_t,$$

Where n is the number of generation for each breed and farm, $\Delta F_t = (F_t - F_{t-1})/(1-F_{t-1})$ and F_t = the average inbreeding coefficient of individuals born in generation t (Falconer and Mackay, 1996).

For each animal, pedigree dissection was performed by tracing backwards its ancestors and classified it into 4 groups; 00G (no known parent), 01G (traced back 1 generation), 02G (traced back 2 generations) and 03G (traced back 3 generations) and >03G (traced back more than 3 generations).

RESULTS AND DISCUSSION

Inbreeding

The descriptive statistics for inbreeding coefficients across generations is presented in Tables 2, 3 and 4 for Duroc, Landrace, and Yorkshire, respectively. Figures 1 to 3 shows some typical patterns of the changes of inbreeding levels with proportions of individuals (%) with inbreeding coefficients greater than zero.

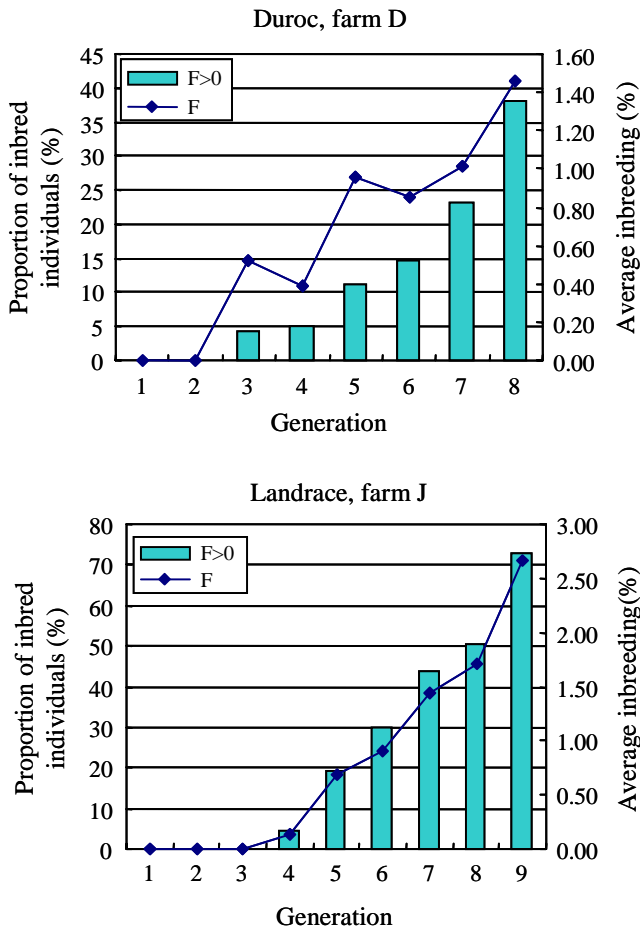As shown in Table 1, generation numbers varied from 5

Figure 1. Pattern I, average inbreeding coefficients (%) and proportion of animals (%) with inbreeding coefficients greater than zero.

Figure 2. Pattern II, average inbreeding coefficients (%) and proportion of animals (%) with inbreeding coefficients greater than zero.

to 15 because each farm had different starting point in its breeding program. The base population consisted of animals with both parents missing in the stacked pedigree. Therefore, an unrelated newly infused animal from different population, including its sire and dam was treated as base population which was used in the calculation of inbreeding coefficient.

In Duroc, the levels of average inbreeding for all farms ranged from 0.11 to 4.25%, which generally followed an increasing trend as generation increased (Figure 1). All the three farms followed this trend except for two farms, K and Y. Farm K, showed steady increased until generation 11 with average inbreeding coefficient, 2.79% then declined continuously until the 15th generation. It implied some management intervention to control inbreeding level in the farm (Figure 2). However, farm Y (Figure 3) showed no pattern as opposed to the three farms. There seemed to be some problems in efficiency of managing proper mating system between generations 5 and 9, although the level was only 1%. Overall, Duroc population in Korea revealed low average inbreeding levels far lower than the 10% as cited in
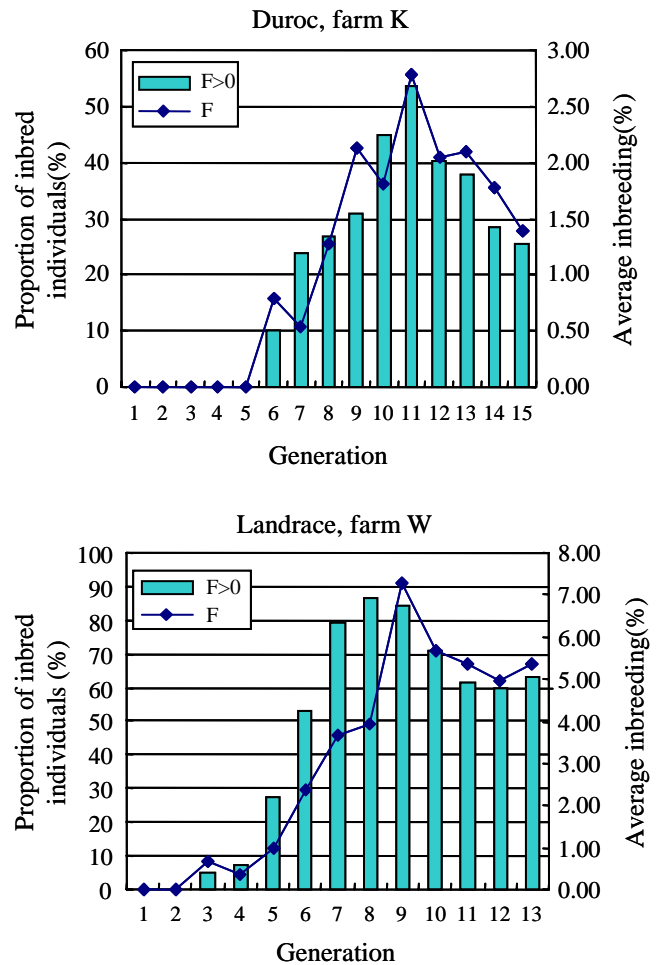
NSIF, 1987. At 10% level it would lead to reduction in number of born alive (NBA) by 0.3, 2.3 lb in 154-day weight (154 dWT) depression in growth rate.

The average inbreeding level for Landrace, ranged from 0.01 to 7.26%. All farms except farm W showed steady increase up to the last generation (Figure 1). In farm W, the average inbreeding level increased until generation 9 with level 7.26% then continuously declined up to the 13th generation. It indicated some management actions to handle inbreeding level of its population. Although farm H with the number of generations more than others showed only 2.07% at generation 12. It implied two phenomena; either the farm implemented sound mating program or open their population to allow immigration of animals from other farms. Furthermore, selection intensity was not that high.

In Yorkshire, the average inbreeding level ranged from 0.06 to 1.98%. Of the five farms studied, four farms had fewer generations compared to Duroc and Landrace. The average inbreeding levels of last generation were 0.62, 0.74, and 0.97 in farms G, S, and D, respectively. Inbreeding levels of other two farms, H and J were 1.97% and 1.98%

Table 4. Mean level of inbreeding (%) for each generation and farm in Yorkshire

Gen	Farm D				Farm S				Farm G				Farm H				Farm J			
	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]	N	Mean	SD	Max[2]
0	199	0.00			250	0.00			268	0.00			198	0.00			102	0.00		
1	45	0.00			2	0.00			2	0.00			1	0.00			4	0.00		
2	115	0.00	0.00	0.00	25	0.00	0.00	0.00	13	0.00	0.00	0.00	3	0.00	0.00	0.00	33	0.00	0.00	0.00
3	252	0.22	1.46	12.50	63	0.00	0.00	0.00	65	0.00	0.00	0.00	5	0.00	0.00	0.00	48	0.00	0.00	0.00
4	825	0.65	1.68	12.50	104	0.06	0.61	6.25	132	0.47	2.40	12.50	11	0.00	0.00	0.00	77	0.16	12.50	0.00
5	17,016	0.97	2.29	26.56	221	0.18	1.74	25.00	261	0.15	0.98	12.50	19	0.16	0.00	0.72	123	0.66	12.50	0.00
6					651	0.33	1.90	25.78	877	0.28	1.48	12.50	36	0.87	0.00	4.27	222	0.87	0.00	1.47
7					14,418	0.74	3.53	29.69	18,047	0.62	2.96	25.00	76	0.08	0.00	0.72	676	1.18	0.00	1.96
8													94	0.44	0.00	2.03	34,138	1.98	0.00	2.29
9													134	0.31	0.00	1.14				
10													249	0.74	0.00	2.02				
11													531	1.08	0.00	2.45				
12													1,601	1.14	0.00	2.44				
13													25,575	1.97	0.00	3.17				
Total[2]	18,452				15,734				19,665				28,533				35,423			

[1] Animals in base population (generation 0) were added to total number of animals.

[2] Minimum inbreeding coefficient was 0 for all generations and farms.
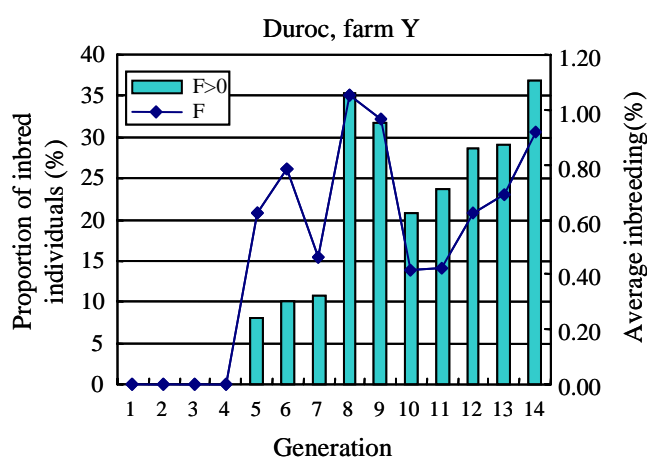

Figure 3. Pattern III, average inbreeding coefficients (%) and proportion of animals (%) with inbreeding coefficients greater than zero.

during last generation, respectively. Farm J reached 1.98% in 8 generations while farm H reached similar level in 13 generations. This could be explained by the higher selection intensity of farm J compared to farm H, or the population size of farm J was smaller than that of farm H. It implied that the farm implemented a sound mating program or open their population to allow immigration of animals from other farms. In all farms across breeds, the maximum average inbreeding levels were lower than 10%, therefore very low inbreeding depressions were expected. However, there were some individuals whose inbreeding levels exceeded 30% that leads to depression of 0.9 head in NBA, 22.2lb in 154dWT (NSIF, 1987).

The rate of inbreeding (ΔF) is more important than the actual inbreeding level (F) because it measures how many more generations a population can be kept before reaching the critical inbreeding level. The rate of inbreeding (ΔF) calculated from actual inbreeding levels relative to the previous generation using the formula of Falconer and Mackay (1996) and effective population size, N_e were shown in Table 5.

In Duroc, the average rate of inbreeding per generation for farms D, S, and H was 0.208%, 0.209%, and 0.307% respectively and was much higher compared to farms K and Y, which was 0.098% and 0.071%, respectively. Take the generation number of farm K, 15 and Y, 14 into account, the differences strongly suggest that population should be under open breeding scheme. Likewise, only farm S showed 0.071% of average rate of inbreeding per generation compared to other four farms which ranged from 0.188% to 0.685% in Landrace. However, in Yorkshire the rate ranged from 0.103% to 0.286% with little differences compared to Landrace and Duroc.

The effective population sizes calculated from the rate of inbreeding ΔF were 204.8, 239.7, 508.8, 163.0 and 708.2 for farms D, S, K, H, and Y, respectively in Duroc, 708.7, 266.5, 73.0, 148.9, and 111.3 for farms S, H, C, J, and W, respectively in Landrace, and 205.5, 406.0, 486.9, 302.6 and 175.0 for farms D, S, G, H, and J, respectively in Yorkshire. The range of effective population sizes was distributed between 73.0 and 708.7. The estimated effective population sizes were above the minimum value 40 according to the study on dairy cattle (Goddard and Smith, 1990). They reported the minimum reference value was 40 animals for maximizing net genetic response for total economic merit in dairy cattle. The values were also acceptable for natural selection for fitness and inbreeding depression balance, the effective population sizes between 30 and 250 where fitness is maintained by natural selection (Meuwissen and Wolliams, 1994).

Pedigree structure

The proportions of individuals (%) with inbreeding coefficients greater than zero to is presented in Table 6. As the proportions of individuals (%) with inbreeding

Table 5. The rates of increase in inbreeding coefficients, ΔF_t, ΔF and effective population size (Ne)

Generation	Breed/farm														
	Duroc					Landrace					Yorkshire				
	D	S	K	H	Y	S	H	C	J	W	D	S	G	H	J
2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.403	0.000	0.000	0.000	0.000	0.000	0.000	0.000
3	0.893	0.521	0.000	0.000	0.000	0.000	0.000	1.072	0.000	0.658	0.223	0.000	0.000	0.000	0.000
4	-0.788	-0.131	0.000	1.847	0.000	0.000	1.278	-1.189	0.139	-0.284	0.431	0.060	0.473	0.000	0.162
5	0.422	0.566	0.000	-0.932	0.625	0.293	-1.284	0.244	0.549	0.603	0.319	0.117	-0.325	0.164	0.496
6	-0.394	-0.104	0.781	0.032	0.157	-0.162	0.114	2.327	0.225	1.393		0.155	0.133	0.705	0.211
7	0.438	0.165	-0.244	-0.231	-0.319	0.292	0.033	0.689	0.545	1.318		0.407	0.335	-0.793	0.313
8	0.501	0.444	0.737	-0.268	0.589		0.382	1.209	0.261	0.321				0.354	0.817
9	0.704		0.866	0.948	-0.088		0.361	0.727	0.969	3.449				-0.131	
10	-0.258		-0.332	1.369	-0.551		-0.005			-1.699				0.433	
11	0.380		1.001	-0.887	0.003		0.246			-0.357				0.342	
12	-0.097		-0.764	0.889	0.205		0.938			-0.427				0.061	
13	0.337		0.058	-0.107	0.068					0.418				0.847	
14	0.561		-0.322	0.451	0.228										
15			-0.405	1.183	0.000										
ΔF (%)[1]	0.208	0.209	0.098	0.307	0.071	0.071	0.188	0.685	0.336	0.449	0.243	0.123	0.103	0.165	0.286
Ne[2]	240.8	239.7	508.8	163.0	708.2	708.7	266.5	73.0	148.9	111.3	205.5	406.0	486.9	302.6	175.0

[1] $\Delta F = \dfrac{1}{n-1}\Sigma_{t=2}^{n}\Delta F_t$, where n is the number of generation for each breed and farm, $\Delta F_t = (F_t - F_{t-1})/(1 - F_{t-1})$ and F_t is the average inbreeding coefficient of

individuals born in generation t (Falconer and Mackay, 1996).

[2] Effective population size, $N_e = \dfrac{1}{2\Delta F}$ (Falconer and Mackay, 1996).

Table 6. Proportion of individuals (%) with inbreeding coefficients greater than zero

Generation	Breed/farm														
	Duroc					Landrace					Yorkshire				
	D	S	K	H	Y	S	H	C	J	W	D	S	G	H	J
1	0.0	0	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.0	0	0.00	0	0	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	7.1	4.2	0.00	0	0	0.00	0.00	7.84	0.00	5.26	3.17	0.00	0.00	0.00	0.00
4	3.6	5.0	0.00	18.2	0	0.00	9.09	2.13	4.44	7.41	18.91	0.96	3.79	0.00	1.30
5	7.3	11.1	0.00	15.4	8.0	0.29	2.70	10.69	19.35	27.59	27.23	3.17	3.45	5.26	23.58
6	4.5	14.6	10.0	13.3	10.0	0.13	2.00	39.63	29.79	53.13		10.75	5.02	5.56	36.94
7	17.2	23.3	23.8	16.0	10.8	0.42	7.81	64.14	43.72	79.41		12.42	7.06	1.32	41.72
8	31.0	38.2	26.9	5.0	35.3		21.59	81.26	50.60	86.49				6.38	64.60
9	37.9		30.8	18.9	31.7		41.45	89.84	72.92	84.31				14.18	
10	53.1		44.8	50.0	20.7		40.19			70.83				27.71	
11	52.0		53.5	62.3	23.6		45.50			61.34				46.89	
12	52.7		40.2	67.8	28.7		70.55			59.73				53.40	
13	56.5		37.7	64.4	29.1					62.94				75.24	
14	67.4		28.4	69.2	36.9										
15			25.4	84.0											

coefficients greater than zero increased, the average level of inbreeding increased as well. Although the rate of increase of inbreeding level was not linear and the patterns were different from farm to farm, the patterns could be categorized into three groups. Out of the total 15 farms, 12 of which farms D, S and H in Duroc, farms S, H, C, and J in Landrace and all farms in Yorkshire were classified as pattern I (Figure 1). Farm K in Duroc, farm W in Landrace were grouped into pattern II (Figure 2), while farm Y in Duroc was assigned to pattern III (Figure 3). As shown in Table 6 and Figure 1 pattern I, the increased of the proportions of individuals (%) with inbreeding coefficients greater than zero was accompanied with increased of average inbreeding levels. Moreover, farms showed proportion of >03G steadily increased as the generation

increased. Likewise, in 00G and 01G proportion revealed steady decreased as the generation increased (Table 7).

Farm K shown as a model of pattern II (Figure 2, Table 7), revealed that increased of proportion in 00G and 01G between generations 10 and 15 related to decreased of inbreeding level. It implied that new animals were infused into the existing population to control inbreeding level.

Moreover, pattern III (Figure 3) showed the mixture of patterns I, II and I again. It seems that farms classified as patterns II and III encountered difficulties in controlling inbreeding level and might have changed their breeding strategies.

The average inbreeding rate is highest for Landrace, intermediate for Yorkshire, and lowest for Duroc farms. In Landrace and Yorkshire populations there were few

Table 7. Proportion of animals grouped by the number of generation traced back to its ancestor for each generation

Generation	Pattern I (Landrace, farm J)					Pattern II (Duroc, farm K)					Pattern III (Duroc, farm Y)				
	00G*	01G	02G	03G	>03G	00G	01G	02G	03G	>03G	00G	01G	02G	03G	>03G
0	100.0					100.0					100.0				
1		100.0				75.0	25.0				100.0				
2		85.7	14.3				83.3	16.7				100.0			
3		73.3	23.3	3.3			60.0	30.0	10.0			84.6	15.4		
4		35.6	51.1	11.1	2.2	7.1	42.9	28.6	14.3	7.1		33.3	53.3	13.3	
5	1.6	21.0	37.1	32.3	8.1	6.3	25.0	31.3	25.0	12.5	4.0	12.0	40.0	36.0	8.0
6		19.1	24.5	33.0	23.4	5.0	15.0	25.0	20.0	35.0	6.7	3.3	30.0	20.0	40.0
7		17.1	17.6	19.6	45.7	9.5	4.8	19.0	14.3	52.4	2.7	8.1	10.8	21.6	56.8
8	0.3	14.4	20.6	14.4	50.3	3.8	7.7	3.8	11.5	73.1	5.9	5.9		11.8	76.5
9		0.1	10.7	16.4	72.8		7.7	3.8	7.7	80.8	2.4	17.1		2.4	78.0
10							10.3	6.9	6.9	75.9	5.2	15.5	3.4	1.7	74.1
11						2.3	14.0	7.0	7.0	69.8	2.2	6.7	10.1	7.9	73.0
12						6.9	11.8	9.8	7.8	63.7	1.3	6.7	13.3	10.0	68.7
13						2.5	18.6	6.4	5.9	66.5		11.9	8.0	8.3	71.8
14						0.3	13.0	15.5	6.6	64.6	0.2	3.0	4.3	4.3	88.2
15						0.1	9.6	8.8	8.7	72.8					

All farms showed same pattern, i.e. pattern I except farm K (Duroc), farm Y (Duroc) and farm W (Landrace), those were classified as pattern II, pattern II and pattern III, respectively.

* 00G: animal with no parents, 01G: animal with parent(s), 02G: animal with parent and grand parent(s), 03G: animal with parent(s) and grand-grand parent(s), >03G: animal with grand-grand parent(s) or higher.

immigrant animals per generation. In Duroc, however, there were quite large number of immigrant animals per generation compared to other breeds.

From the results, it is clear that new animals were introduced into current population to regulate its inbreeding level in farms grouped as pattern II or III and implied that those farms might not focus on the selection methodology. According to the simulation study of Quinton et al. (1992) if low to moderate inbreeding levels are targeted, as in a closed line of limited size, then selection on phenotype can yield higher genetic responses than selection on BLUP. Therefore, it would be helpful for swine breeding farms suffering from high level of inbreeding or farms insisting closed breeding scheme to implement phenotypic selection rather than complicated BLUP selection.

The results showed no cause for concern over the current inbreeding level of major swine breeding farm populations and the inbreeding level was under control in all major breeding farms fell within proper range. However, farm H for Duroc, farm C and W for Landrace, and farm D and J for Yorkshire should pay attention to the inbreeding level and effective population size if the increasing rate of inbreeding was not prearranged.

It might not be true to generalize these results to the whole swine population in the breeding farm, but it would be helpful to check current status of inbreeding levels of populations and to build new breeding program or scheme.

LIMITATION OF THE STUDY

This study used the purebred registry records of Korea Animal Improvement Association (KAIA) therefore restricted to the pedigree of registered animals only from which the findings were based.

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