A PROSPECT FOR GENETIC IMPROVEMENT OF CHRONIC DISEASE RESISTANCE IN SWINE

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INTRODUCTION

The chronic infection in swine induces economical losses, such as growth delay, decline in feed efficiency, concurrence of secondary infection, and an increase in the health cost by medical treatment and medication. The objects of the present study is to evaluate the possibility of genetic improvement for higher resistance against Atrophic Rhinitis (AR) and Mycoplasmal Pneumonia of swine (MPS).

MATERIALS AND METHODS

The various breeds, number of animals used and traits measured were given in Table 1 for each swine farm investigated. The five immunities, delayed type hypersensitivity (DTH), phagocytic activity (PA), specific IgG and IgM antibody response (IgG, IgM) and activity of the alternative pathway of complement (CMP), were measured for each individual.

Table 1. The breeds or crossbred, number of animals used and traits measured in each farm

Farm	Breed	No. of animals	Traits measured
A	L,W,D	100	DTH, IgG
B	Duroc	718	DTH, IgG, IgM, CMP, PA, AR, MPS, DG

LWD: three-way cross produced by (F_1(LW) from Landrace(L)×Large White(W))♀×Duroc(D)♂

When the animals reached 70 Kg of body weight, the first immunization was practiced with approximately 10^8 of sheep red blood cells (SRBC). The second immunization was given 1 week after the first immunization. Two days after the second immunization, the area (mm^2) of the swelling (DTH) were measured. The blood sample was collected when the body weight of animals reached 105kg. As an index of PA, the activity of neutrophiles and monocytes in the peripheral blood was measured using chemiluminescence detector. The remaining whole blood sample was centrifuged and the separated plasma was used to measure the total concentration of anti-SRBC IgG and IgM by ELISA. The separated plasma was used also for measuring CMP. The morbid changes caused by AR in two full-brothers of the candidates were graded into -1~3 according to the degree of atrophy in nasal concha, when they were sacrificed at 105 kg of body weight. The area (cm^2) of the morbid changes by MPS in the full-brothers were measured at the same time. Further Daily body weight gain (DG, g/day) was evaluated. The least-squares

variance analyses (Harvey, 1990) of all the data were practiced. The genetic and phenotypic parameters were estimated by the method of restricted maximum likelihood (REML). The three selection indices for relative desired gains (Yamada *et al*., 1975) were made to delete the morbid changes by AR and MPS from the population.

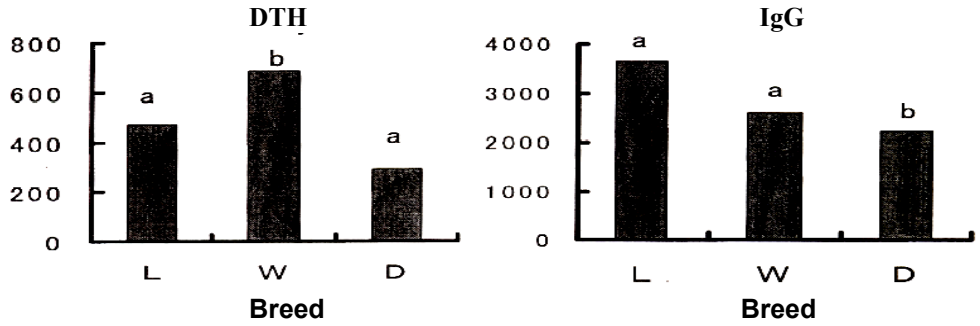

Figure 1. The breed differences in the immunities. L : Landrace, W : Large white, D : Duroc. The different letters mean the statistically significant difference ($p<0.001$) between the two breeds

Figure 1 shows the least-squares estimates of the two immune responses for the three breeds in Farm A. In DTH, Large White was significantly ($p<0.001$) higher than the other two breeds, and in IgG, Duroc was significantly ($p<0.001$) lower the other two breeds. These differences suggests that the between breeds genetic variation is exist.

Table 2 and 3 show the genetic and phenotypic parameters of the traits estimated. The underlined diagonal elements are the heritability estimates, the upper diagonal elements are the genetic correlations and the lower diagonal elements are the phenotypic correlations. As shown in Table 2, relatively higher heritability of DTH and IgG were estimated in Farm A. Further the genetic correlation between them was positive and high. These parameters mean that it is easy to improve the two traits simultaneously. The heritability estimates of the immunities in Farm B (Table 3) were low and the genetic correlations between them were almost positive. The low heritabilities were estimated since this population was in the fifth, sixth and seventh generation of closed hard breeding and had relatively small genetic variance. In Farm B, the nine genetic correlations between the morbid change and immunity were negative. This means the genetic improvement for higher immunities will bring us decrease of the morbid changes as correlated responses.

Table 2. The genetic and phenotypic parameters of immunities in Farm A

Farm A	DTH	IgG
DTH	0.47	0.60
IgG	0.06	0.78

Table 3. The genetic and phenotypic parameters in Farm B

Farm B	DG	DTH	IgG	IgM	CMP	PA	AR	MPS
DG	0.41	0.47	0.49	0.05	0.07	-0.43	-0.20	0.01
DTH	0.05	0.05	0.40	0.05	0.15	0.12	-0.88	0.07
IgG	0.16	-0.06	0.09	0.66	0.16	0.56	-0.60	-0.77
IgM	0.03	-0.05	0.90	0.11	0.11	0.64	-0.24	-0.45
AP	0.05	-0.04	-0.11	-0.12	0.03	0.25	-0.23	-0.21
PA	-0.03	0.00	-0.01	0.01	-0.14	0.04	-0.54	-0.73
AR	-0.02	0.04	0.09	0.23	-0.28	0.02	0.27	0.33
MPS	0.10	0.02	0.02	-0.02	-0.60	-0.14	-0.00	0.07

The prediction of responses to repeated selection based on the selection indices were practiced using the parameters of Farm B since the data of all the traits were available only in Farm B (Table 4). The breeding goal was defined as the condition in which we can find almost no morbid changes by AR and MPS in the population. It was predicted that we will be able to reach the selection goal in 2.4 generations of selection based on the selection index consists of the morbid change caused by AR and MPS in two full brothers of candidates. The second selection index for the same breeding goal was made assuming it is not possible to take the data of morbid changes by AR and MPS in the relatives. Then the selection has to be based only on the immunities of the animals. It was predicted that it requires 3.9 generations of selection to reach the breeding goal. The last prediction of selection response based on a selection index consists of morbid changes and immunities requires 2.3 generations. In the present study, it was hopefully predicted that 3 or 4 generations of selection based on the indices brings us a population in which we can find almost no morbid changes by AR and MPS. However if only the morbid changes were used as the selection criterion, the genetic gain per generation will decrease with the generation of selection because of the decrease of the morbid changes themselves. To resolve this problem, when it is possible to get both the data of the immunities and the morbid changes, it's better to use all the data for a selection index to reach the selection goal in the shorter generations of selection.

Table 4. The prediction of selection response in Farm B

Trait to be improved	Population mean	Target	Desired gain
AR (-1～3)	-0.42	-1.00	-0.58
MPS (cm^2)	11.40	0.00	-11.40

Traits used in the selection index	Number of generation to reach the goal	The correlated response in DG (g/day)
1. AR, MPS	2.4	+6.08
2. DTH, IgG, IgM, CMP, PA	3.9	+16.41
3. IgG, IgM, PA, AR, MPS	2.3	+10.29

There is another problem that the heritabilities of the immunities.
The 1st index was based on the two full-brothers' morbid changes of each candidate and the 2nd index was based on the five immunities of candidate itself. The 3rd index was based on both the morbid changes and immunities. The selection responses were predicted assuming that the intensities of selection were unity in the selection indices.

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