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Genetic Improvement for Meat Production and Quality using Physiological Traits and DNA Markers and Possibility of Disease Resistance in Pigs

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Summary

This paper reports results from a seven-generation genetic selection experiment to develop an excellent line of Duroc breed in meat production and meat quality traits. It also describes genetic correlations between meat quality and various production traits and physiological traits such as serum insulin like growth factor 1 (IGF-1) and leptin concentration. This study introduces the possibility of genetic improvement using DNA marker for Duroc pigs. Recently, pork that is produced without antibiotic feed additives is demanded internationally, thereby necessitating some other means to improve pigs' disease resistance. A pig-breeding program for the goal of higher disease resistance has begun. This report presents the possibility of genetic improvement of pig's disease resistance based on statistical breeding theory, on DNA marker information, and on its actual implementation.

Our laboratory investigates the genetic improvement of reproduction, meat production, feed efficiency, and disease resistance. These genetic improvements are studied with various statistical, molecular, physiological and immunogenetic approaches. These studies mainly use beef and dairy cattle, sheep and swine. Laboratory animals are also used for basic studies as pilot subjects for domestic animals. This review first introduces results of a direct selection experiment for meat quality and the correlated response of physiological traits and QTL analysis for meat quality using a DNA marker. Next, genetic improvement for disease resistance in pigs will be introduced.

In Japan, pork with a high added value of safety and deliciousness is demanded to compete with increased pork imports. With that background, selection experiment for meat production traits and intramuscular fat (IMF) for Duroc breed was conducted at the Miyagi Prefecture Livestock Experiment Station. Various detailed measurements of meat quality were examined in

selection experiment. Furthermore, the effectiveness of serum insulin like growth factor 1 (IGF-1) and leptin as physiological genetic indicator of meat performance traits was investigated after the fourth generation. In addition, the DNA of 1646 individual pigs with their performance test records was collected and preserved during this experiment. At present, the analysis of relation of IMF with DNA makers is proceeding.

Since last December, addition of antifungal agents to domestic animal feed has been scheduled for prohibition in Japan. Increased resistance to antibiotics of bacillus is engendered by the use of sub-therapeutic antibiotics that are added to the pigs' feed. Such practices present the danger of antibiotic-resistant bacillus infection of humans. Moreover, the danger exists of antibiotics and antifungal agents remaining in the meat, which may cause allergic and other reactions in humans. Japanese people demand delicious and safe pork. The market also demands meat produced without the use of potentially harmful agents. To address such concerns, breeding for disease resistance is necessary. In cooperation with Tohoku University, the Miyagi Prefecture Livestock Experiment Station has begun a selection experiment of the fifth generation for the atrophic rhinitis (AR) and mycoplasma pneumonia in swine (MPS). Potential relationships among candidate genes for health and immune response will also be investigated.

1. Selection Experiment for High Meat Quality

To develop an excellent line of Duroc breed in terms of performance traits and meat quality traits, selection was conducted over seven generations for growth rate (DG), real-time ultrasound loin eye muscle area (EM), backfat thickness (BF), and intramuscular fat content (IMF). Those performance traits were measured on 1646 pigs; meat quality traits were measured on 547 pigs. Meat quality traits were IMF and tenderness (TEND), which were measured 24 h after slaughter in *M. longissimus* taken two sections above the last rib. Selection was based on a selection index method that was constructed using four traits (DG, EM, BF, and IMF), at the first and second generations of selection. After the third generation, expected breeding values (EBVs) for four traits were obtained from analyses of performance and meat quality data. Selection of boars and gilts was based on an aggregated value that was constructed by crossing each EBV and relative weight. Heritability estimates for DG, EM, BF, IMF, and TEND were 0.48, 0.45, 0.72, 0.46, and 0.45, respectively. Selection and correlated responses were estimated from predicted breeding values using genetic parameters derived from multivariate restricted maximum likelihood (REML) analysis. Although the desired gains were not achieved completely for DG, EM, and BF, the total genetic gain of IMF at the seventh generation (1.20%) exceeded the initially intended desired gain (0.7%); the phenotypic mean of the IMF level reached about 5.0% (Suzuki *et al.*,

2002). This Duroc population had more IMF content in *M. longissimus* than Berkshire breed. Regarding fatty acid of inner and outer subcutaneous fat, Berkshire contained significantly higher concentration of saturated fatty acids, but had lower concentration of unsaturated fatty acid than Duroc. Consequently, the melting point of inner and outer subcutaneous fat and perirenal fat of Berkshire was markedly higher than that of Duroc. Furthermore, no breed difference was found in concentration of saturated fatty acids of intramuscular fat, but Duroc had more oleic acid (C18 : 1) than Berkshire (Suzuki *et al.*, 2003)

2. Genetic Correlation between Physiological Traits and Meat Production, and Meat Quality Traits in Duroc Pigs

We examined whether serum IGF-1 concentration is appropriate for use as a physiological predictor for genetic improvement of meat production and meat quality traits in Duroc pigs. Serum IGF-1 concentration of boars and gilts at the fourth generation of selection and that of boars, gilts, and barrows from the fifth to seventh generations of selection were measured at 8 week (IGF1-8W) for 832 animals and again at the time they reached 105 kg of body weight (IGF1-105KG) for 834 animals. A multivariate REML procedure was used to estimate genetic parameters with a model incorporating generation of selection, sex, common environmental effects of litters, and individual additive genetic effects. Heritability estimates for IGF1-8W and IGF1-105KG were 0.23 ± 0.02 and 0.26 ± 0.03 , respectively. The estimates of common environmental effect for IGF1-8W and IGF1-105KG were 0.20 ± 0.02 and 0.03 ± 0.01 , respectively. Positive genetic correlations were estimated between IGF1-8W and DG (0.26 ± 0.08), EM (0.22 ± 0.10), and IMF (0.32 ± 0.10). Moreover, positive genetic correlation between IGF1-105KG and EM was 0.42 ± 0.08 . These results indicate that serum IGF-1 concentration at an early stage of growth was effective for prediction of IMF, but it was not a reliable physiological predictor of genetic merit of meat production traits (Suzuki *et al.*, 2004).

Next, we estimated genetic parameters between serum leptin concentration and meat production traits. We measured leptin concentration of full brothers of candidates from the fifth to the seventh generation. Heritability estimates of direct and common environmental effects were high for leptin concentration (0.65 ± 0.02 and 0.18 ± 0.04). Genetic and phenotypic correlations between leptin concentration and backfat thickness were high (0.69 ± 0.08 and 0.51 , respectively), but those with intramuscular fat were low (0.22 ± 0.06 and 0.24 , respectively). This result demonstrates that the serum leptin concentration reflects the amount of the fat accumulation of the whole body in pigs. Moreover, leptin concentration was not effective as an index of the growth rate (genetic correlation : -0.14 ± 0.05 , phenotypic correlation : 0.08).

3. Association of IMF with Candidate Genes in Duroc Pigs

We investigated the association of intramuscular fat with candidate genes in Duroc pigs. The relation between IMF and Heart Fatty Acid Binding Protein (H-FABP) gene, which was the candidate gene, was examined. Breeding values of IMF by MspI polymorphism, HaeIII polymorphism, and HinfI polymorphism, which were restricted fragment length polymorphism (RFLP) of H-FABP gene, were presumed to be independent variables. Subsequently, multiple regression analysis was performed using all breeding values as dependent variables. Consequently, the partial regression coefficients of MspI polymorphism and HaeIII polymorphism were found to be statistically significant. The coefficient of determination of multiple regression was 0.39 when MspI polymorphism and HaeIII polymorphism were set as independent variables. Therefore, these two DNA polymorphisms explained about 40% of the total variance of IMF breeding values. Sato *et al.* (2003) reported the results of a genome scan showing evidence for significant quantitative trait loci affecting intramuscular fat content on SSC 7 in F₂ resource population by crossing a Meishan sow and a Duroc boar. We plan to investigate QTL analysis within this Duroc breed using DNA microsatellite markers.

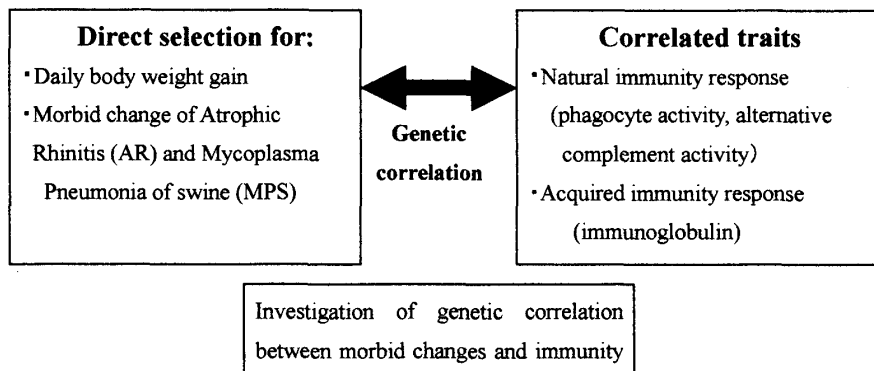
4. Genetic Improvement of Chronic Disease Resistance in Pigs

1) Genetic Parameters Estimates in Duroc Pigs

The potential for genetic improvement of resistance against chronic infectious diseases was investigated in Duroc pigs described in the previous section. Three immunities were measured for each individual. Furthermore, the morbid changes caused by AR and MPS were measured in two full-brothers of the candidate. Genetic and phenotypic parameters of delayed type hypersensitivity, phagocyte activity (PA), antibody productivity (AP), morbid changes engendered by AR and MPS, DG, BF, and EM were estimated using REML. Two selection indices were made based on those parameters to delete morbid changes attributable to AR and MPS from the population. One index was based on morbid changes in the two full-brothers of the candidate; another index was based on the three immunities of the candidate itself. Intensities of selection were assumed as unity in the indices. Seven or eight generations of selection based on the indices were inferred to be sufficient to yield a population showing almost no morbid changes by AR and MPS (Nishida *et al.*, 2001).

2) Selection Experiment for Chronic Disease Resistance in Landrace Pigs

Based on the information garnered from results with Duroc pigs, a selection experiment for higher growth rate and disease resistances with Landrace pigs



Morbid changes are assumed as direct selection traits at the beginning of the selection. The genetic correlation of morbid traits and immune response are estimated at this stage. The frequency of the morbid changes is expected to decrease as selection advances. Selection traits may be changed to immune traits with a high genetic correlation with morbid status at the stage. Strong genetic correlations between morbid change and immune response traits were previously estimated in Duroc pigs.

FIG. 1. Genetic selection scheme for disease resistance in pigs.

began in 2004 at the Miyagi Prefecture Livestock Experiment Station. In that experiment, the Experiment Station examines the performance traits and morbid changes by AR and MPS. In addition, our laboratory examines the immunological traits. The genetic selection scheme of disease resistance in pigs is shown in Fig. 1. Traits to be improved are the degree of morbid changes by AR and MPS. In addition to the morbid changes, some immune response phenotypes (PA, AP and activity of alternative complement pathway) will be used as selection criteria. Further, quantitative trait loci (QTL) analysis on morbid changes, and immunological traits within Landrace breed will be practiced in this project.

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