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Development of Techniques and Breeding Strategies for Pig Strain Improvement in Japan

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Abstract
Distributed over many farms, more than 40 pig strains have been developed since the early 1980s. Although until recently, only the selection index method had been used for pig strain development, it is being replaced by the BLUP method, supplemented with molecular genetic information. Here, these techniques and challenges for the future are described.

Discipline: Animal industry
Additional key words: BLUP, marker-assisted selection

Introduction

The pig breeds raised in Japan comprise Landrace, Large White, Hampshire, Duroc and Berkshire. The pigs bred for meat are mainly crossbreeds of these pure breeds, accounting for about 90% of the total. In order to increase the efficiency of pig production, strains within a single breed are developed by systematic breeding.

In 1970, a standard model pig strain development plan was formulated[5]. By 1994, 46 strains had been developed and these are used and reared in pig farms in Japan. Currently studies are carried out to develop an additional 11 strains (Table 1). The selection index method which had been exclusively used for pig strain development until recently, is being replaced by the Best Linear Unbiased Prediction method (BLUP), supplemented with molecular genetic information. In this paper emphasis was placed on describing the principles underlying current pig strain development programs, and some of the challenges for the future were outlined.

Background of pig strain development

Crossbreeding of pigs in Japan began with the introduction of Landrace in the early 1960s. The first crossbreeds were Middle White with Landrace, and Berkshire with Landrace. It was anticipated that crossbreeding would produce heterosis effects not only in the feed consumption of growing pigs, but also in the number of sows and boars in each litter. Many crossbreeding experiments were undertaken to evaluate crossing patterns economically suitable. However, clear results were not obtained from these experiments because there were excessive genetic variations within the breeds. It was therefore deemed necessary to develop superior strains which were more uniform genetically. To achieve this objective, a project was initiated in 1970 to develop new strains by closed-herd breeding over several generations and carried out in some of the national livestock

Table 1. Pig strains developed in Japan (1994)

Breed name	Developed strains	Strains under development	Proposed strains	Total
Landrace	23	6		29
Large White	15		1	16
Hampshire	3	1		4
Duroc	3	2		5
Berkshire	2	1		3
Synthetic		1	2	3
Total	46	11	3	60

breeding stations and prefectural livestock experimental stations.

Procedures for pig strain development

The basic procedures used for strain development have been and largely continue to be as follows (Fig. 1):

(1) Sows and boars are selected from pigs at home and/or abroad as source materials for improvement.

(2) They are intermated and 10+ boars and 50+ sows are selected from the young pigs thus born.

(3) These boars and sows are then used for the formation of a foundation group.

(4) This foundation group acts as a closed herd and the renewal of generations is undertaken exclusively from within the group.

(5) According to the predetermined target of improvement, the next generation of 10+ boars and 50+ sows is produced by the selection index method.

(6) Selection index is compiled from a number of desirable characteristics, i.e. average daily gain ranging from 30 to 90 kg, backfat thickness measured ultrasonically, loin-eye-area between the 5th and 6th thoracic vertebrae and ham as a percentage of carcass weight, etc. The information on daily gain and backfat thickness is derived from individual live pigs and that on loin-eye area and ham percentage from the carcasses of 2 or 3 full-sib pigs. These procedures are gradually being replaced by the

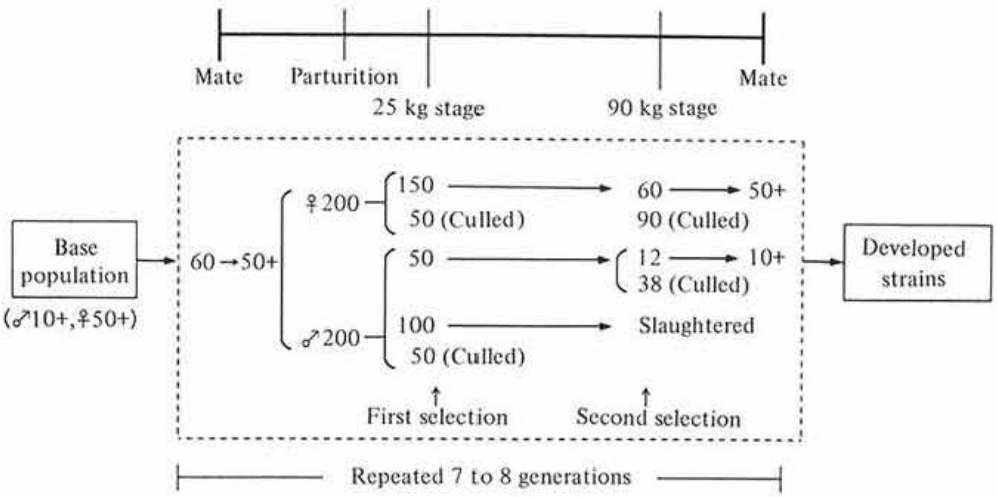

Fig. 1. Standard pig breeding plan in a closed herd

BLUP method.

(7) This process is repeated until the mean coefficient of relationship of the group exceeds 20%.

(8) Only the first farrow of each generation is used to produce the subsequent generations and the time lag between generations for breeding is 1 year. Also 20% of the boars and 10% of the sows of each generation are carefully selected. Normally, the development of a strain is completed within 7 to 8 generations.

Utilization of developed pig strains

Fig. 2 shows a typical process of pork production using pig strains. Developed pig strains are maintained and multiplied in order to distribute them more widely among farmers. The standard distribution package for strains consists of 5+ male pigs and/or 10+ female pigs. The sexes are either distributed singly or jointly depending on the farmer requirement. At first each farmer crosses these strains with strains of another breed; for example Landrace (L female) is crossed with Large White (W male) producing LW females that are subsequently used for breeding more females. Then these LW females are crossed with male pigs [mainly Duroc (D)] and these 3 crossed pigs (LWD) are used for fattening.

Official regulations and criteria

There are official regulations covering the registration and development of pig strains in Japan[4]. A Pig Strain Development Committee was set up by the Japanese Pig Registration Association, composed of representatives of each of the national and prefectural livestock experimental stations. These stations undertake the actual development of pig strains. This committee is responsible for resolving matters

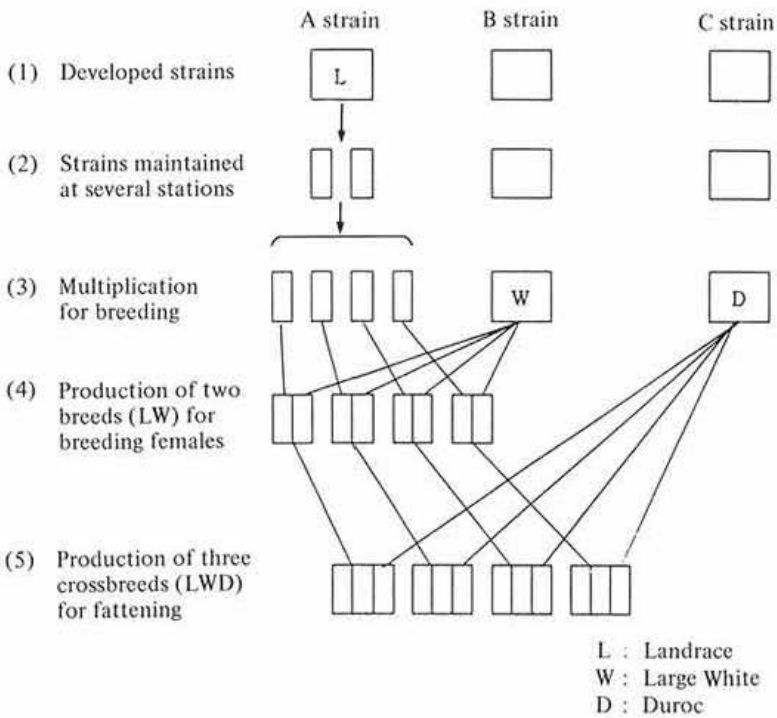

Fig. 2. A typical process of pork production using pig strains

concerning pig strain development; i.e. the authorization of pig strain development, the designation of pig strains for maintenance and the formation of institutes for these purposes. Individual pig strains have to fulfill the following requirements related to their development, in order to be eligible for designation as a unique strain:

(1) Designation criteria

(a) Each strain of pig must consist of herds composed of a minimum of 5 and 30 male and female pigs, respectively.

(b) Average relationship coefficient within each strain must exceed 20% and the relationship coefficient between each individual within the strain must exceed 10%. These data indicate that all the members of each unique strain must be related to the level of either the half-sib or first cousin.

(c) The meat production performance levels must exceed that set up for the performance and/or progeny tests in the manual of Pig Performance and Progeny Test Procedure.

(2) Maintenance criteria

(a) The first three of these criteria are the same as the designation criteria listed above.

(b) The designated strain must not be crossed with pigs from another strain.

How to maintain the genetic structure

The genetic structure of the designated pig strains should remain, as far as possible, unaltered from that existing at the time of the designation. In order to fulfill this condition, the following practices are recommended:

(1) As far as possible, equal numbers of both male and female pigs of the strain should be reared in any herd.

(2) When one male or female has to be culled, it is recommended that the same sex progeny of that pig be kept and used for breeding.

(3) It is preferable that the duration of the breeding period of the animals of each sex be the same.

(4) The average relationship and inbreeding coefficients of each pig strain must be maintained slightly above their initial population level to avoid inbreeding depression. For this reason, intense inbreeding, such as the mating of half-sibs or full-sibs, should be avoided.

(5) To increase the effective population size, it is preferable to keep the largest possible male population for breeding.

(6) It is highly desirable that pigs of the same strain, reared at different stations, be exchanged between stations to reduce the incidence of inbreeding depression within herds with a limited number of animals.

(7) A criterion value, the Coefficient of Genetic Contributory Variation (CGCV), has been developed and used in order to analyze the change of the genetic structure of pig strains. The CGCV measures the degree of contribution of each pig designated as a unique strain at the source stage, to the succeeding stage and it indicates how the male and female

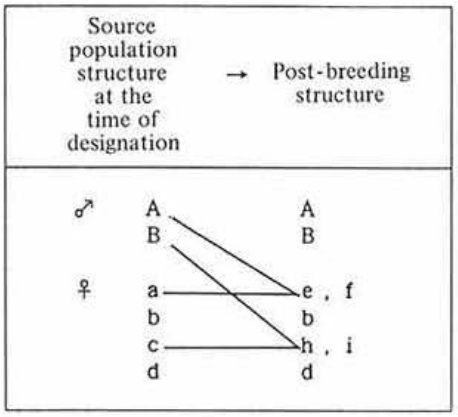

Fig. 3. Hypothetical inter-breeding plan
The source population is assumed to be composed of two males (A, B) and four females (a, b, c, d). In the succeeding stage, two females (a, c) are culled and their female offsprings (e, f, h, i) are introduced into the population. A CGCV value is obtained, calculated as indicated in Fig. 4.

ratios change compared to the source one.

The CGCV is calculated as follows:

$$CGCV = \sum \frac{(\text{realized value for male} - \text{source value for male})^2}{\text{source value for male}} + \sum \frac{(\text{realized value or female} - \text{source value for female})^2}{\text{source value for female}}$$

The term source value refers to the male and female ratios corresponding to the source population of the pig strain at the time of designation. Realized value refers to the ratios of the male and female existing after breeding which produced a second generation. Figs. 3 and 4 show an example of numerical matrix for the calculation of CGCV. Breeders are requested to restrict this value to 0.2 or less and to try to abide by that restriction. It is necessary that this value be calculated annually for each herd and reported to the Pig Strain Development

Item		Source population structure at the time of designation					
		♂		♀			
		A	B	a	b	c	d
Source population structure at the time of designation	♂ A	1					
	B		1				
	R. C. ♂ **	0.5	0.5	0	0	0	0
	♀ a			1			
	b				1		
	c					1	
	d						1
	R. C. ♀ ***	0	0	0.25	0.25	0.25	0.25
	R. C. ****	0.25	0.25	0.125	0.125	0.125	0.125

↓

Item		Source population structure at the time of designation					
		♂		♀			
		A	B	a	b	c	d
Post-breeding structure	♂ A	1					
	B		1				
	R. C. ♂ **	0.5	0.5	0	0	0	0
	♀ e	0.5	0	0.5	0	0	0
	f	0.5	0	0.5	0	0	0
	b				1		
	h	0	0.5	0	0	0.5	0
	i	0	0.5	0	0	0.5	0
	d						1
	R. C. ♀ ***	0.167	0.167	0.167	0.167	0.167	0.167
	R. C. ****	0.333	0.333	0.083	0.083	0.083	0.083

* Coefficient of Genetic Contributory Variation (CGCV) measures the degree of contribution of each pig, upon designation as a unique strain at the source stage to the succeeding generation.

** Relative contribution rate of each source male pig.

*** Relative contribution rate of each source female pig.

**** Relative contribution rate of each source pig.

$$CGCV^{*} = \frac{(0.333-0.25)^2}{0.25} \times 2 + \frac{(0.083-0.125)^2}{0.125} \times 4 = 0.111$$

Fig. 4. Example of numerical matrix of the calculation of CGCV

Committee along with the performance test data of each herd.

Research strategies to develop further improved strains

1) Developmental programs for strains with multiple herds

The average herd size for developed pig strains is 10–15 male and 50–60 female pigs. Several research stations have developed independently a number of pig strains. Unfortunately, until now, the herd size at each station has restricted the degree of genetic improvement that could be achieved because of the limited genetic variation. A more fruitful approach genetically could be achieved by obtaining a number of herds which could be interbred to promote genetic improvement. It is necessary to ensure that these programs are implemented for multiple pig herds which practice interbreeding. Obviously an association to monitor and control this interbreeding system should be established (Fig. 5).

2) Development of synthetic strains from hybrid breeds

Until now, all the developed pig strains have originated from pure breed stocks, e.g. those of Landrace, Large White, Hampshire and Duroc. For pork production on the farm, these pure strains were crossed with one another to

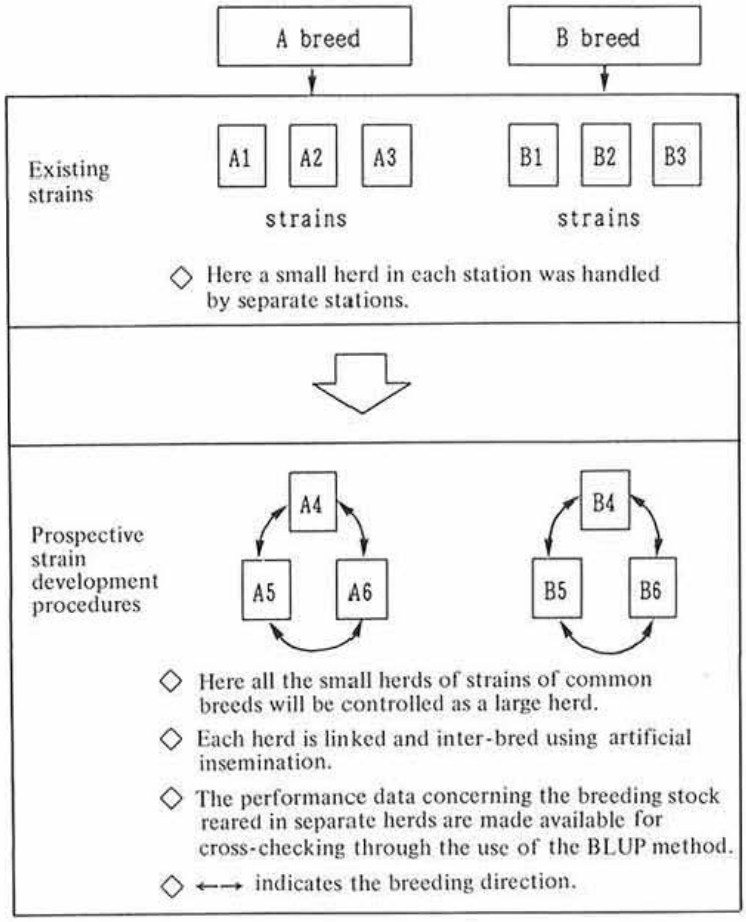

Fig. 5. Strain development using multiple herds

promote heterosis. However, further heterosis can be as readily obtained by crossing synthetic breeds derived from multiple crossbred animals, as by crossing purebred stock. Commercial companies, especially non-Japanese ones, have developed synthetic breeds for commercial pig production, the constitution of which remains a secret. Synthetic breeds, having genes from many different breeds within one breed, can be expected to display a wider genetic variation than that of purebred animals. To make the most of this approach, it is very important to develop appropriate procedures for producing such synthetic strains from existing strains.

3) Application of BLUP method for multiple traits based on animal model

Many traits cannot be easily improved by conventional selection methods due to their low heritability. Of these traits, typical ones include reproduction performance traits, e.g. litter size, etc. and disease resistance traits, e.g. *Hemophilus* infection, etc. Recently, BLUP has become widely recognized as a standard method for estimating breeding values for beef and dairy cattle selection programs.

BLUP advantages are as follows[2]: (1) More accurate prediction of breeding values through the use of information on all the pig relationships. (2) More accurate comparison of animals at different times or under different management systems by correcting environmental factors. (3) More direct comparison among animals by using different levels of relevant information and/or by allowing comparisons across different generations.

The use of BLUP to collect the performance data related to the breeding stocks reared in separate herds enables intergenerational cross-checking of such data. This creates a larger core population for selection and development programs than previously available. If BLUP were used for pig strain development, it is obvious that BLUP would have a major impact on strain development, mainly by facilitating more accurate prediction of the genetic merit of breeding stock animals. Low, but valuable, inheritable traits are especially responsive to improvement through the use of BLUP, in contrast to other existing development methods. For the convenience of pig breeders, a calculation program for breeding value suitable for personal computer was developed[8,9] by applying the BLUP method for multiple traits, based on an animal model.

4) Application of molecular genetics to genome analysis

Traditional breeding methods for the development of pig strains depend on the phenotypic assessment of performance, i.e. average daily gain, backfat thickness, rib-eye area, etc. Such complex phenotypes are the product of both genetic and environmental factors, the relative importance of which is difficult to assess. In future, biotechnology could facilitate and improve the accuracy of such assessments through the determination of the specific DNA part responsible for the desired phenotypic traits[3]. This strategy could have a significant impact on livestock improvement. Until now, the use of molecular genetics has been mostly confined to the laboratory research stage and only a few techniques have been developed for practical application to general pig breeding. Further basic studies, some of which are outlined in the following part are required to make molecular genetic methods more readily available and practical for everyday use in the field.

One basic study necessary for utilizing genome analysis more widely involves the detection of the critical marker genes indicating the loci of the genes linked with the desired production traits. To optimize the efficiency and efficacy of genome analysis, international cooperation is essential, especially for pig genome mapping. It is also necessary to develop key statistical procedures, e.g. specific statistical procedures for (1) effective design

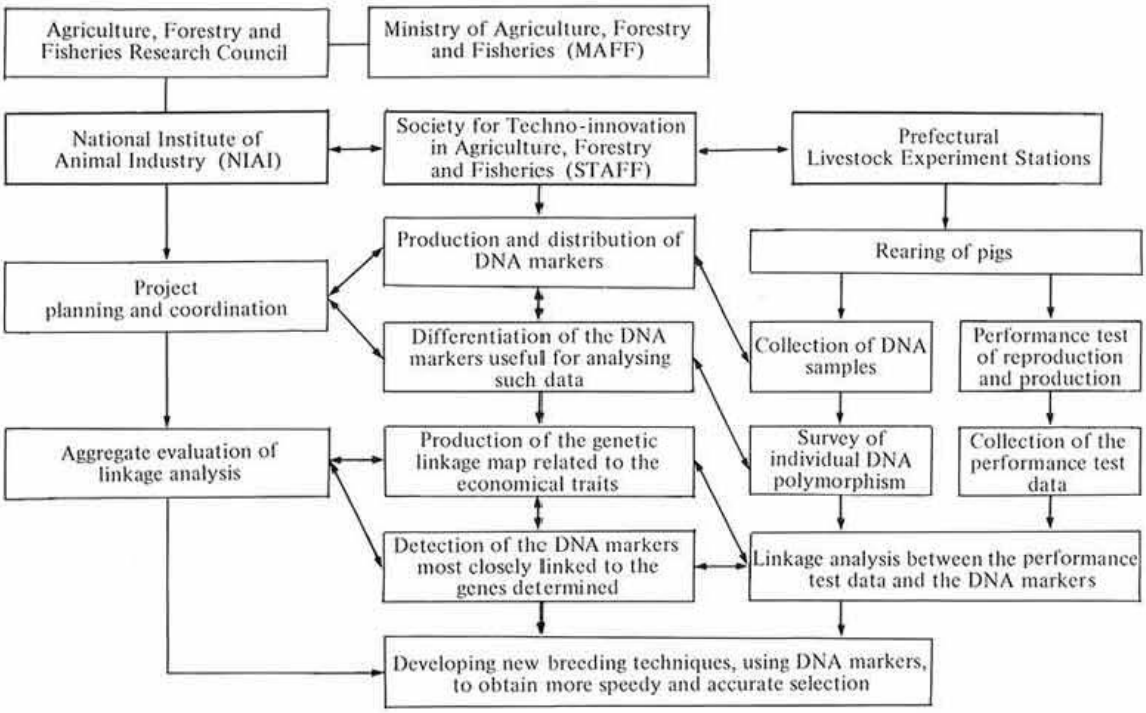

Fig. 6. Outline of the project for the development of livestock breeding techniques using DNA markers linked to economic traits (Flow chart)

of experiments to detect marker genes[10], (2) linkage analyses applicable to non-inbred populations[7], (3) to establish marker-assisted selection procedures using marker genes which can stand for the true genes responsible for the desired phenotypic characteristics, etc. In 1994, a new project aimed at the utilization of molecular information for pig selection criteria was initiated in collaboration with prefectural pig breeding stations (Fig. 6).

Conclusion

In recent years several pig traits have been improved by systematical pig strain development. For example, the daily weight gain of male Landrace increased by 700 to 850 g per day (Obata and Satoh, unpublished data). These results were obtained by using traditional breeding methods based on selection indexes. However, the use of the BLUP method for evaluating multiple traits based on an animal model should enable a more precise estimation of male and female breeding values and is already contributing to the promotion of the genetic improvement of pigs. Both for the development and maintenance of pig strains, this procedure is likely to have a definite and substantial impact on pig improvement.

Although it is sometimes considered that molecular technology will not have as great an impact on current pig strain improvement, this assumption may not be valid. What is certain is that further improvements could be obtained and that further research relating to molecular genetics, e.g. for application to breeding to improve meat quality, disease resistance, etc., should be carried out. It is our contention that substantial improvements can be obtained using molecular genetics. One fundamental step in that direction was achieved in January of this year when the Genetic Society of America

reported the identification of 383 porcine DNA marker genes[6]. Furthermore, genetic mapping of quantitative trait loci for growth and fatness in pigs was reported[1]. This fact indicates that new developments in pig breeding research have been made. For pig strain improvement, it is important to combine simultaneously the use of new techniques of statistical and genome analysis.

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