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Abstract

This study aims to estimate the connectedness rating (CR) of Korean swine breeding herds. Using 104,380 performance and 83,200 reproduction records from three swine breeds (Yorkshire, Landrace and Duroc), the CR was estimated for two traits: average daily gain (ADG) and number born alive (NBA) in eight breeding herds in the Republic of Korea (hereafter, Korea). The average CR for ADG in the Yorkshire breed ranges from 1.32% to 28.5% depending on the farm. The average CR for NBA in the Yorkshire herd ranges from 0% to 12.79%. A total of 60% of Yorkshire and Duroc herds satisfied the preconditions suggested for genetic evaluation among the herds. The precondition for the genetic evaluation of CR for ADG, as a productive trait, was higher than 3% and that of NBA, as a reproductive trait, was higher than 1.5%. The ADG in the Yorkshire herds showed the highest average CR. However, the average CR of ADG in the Landrace herds was lower than the criterion of the precondition. The prediction error variance of the difference (PEVD) was employed to assess the validation of the CR, as PEVDs exhibit fluctuations that are coupled with the CR across the herds. A certain degree of connectedness is essential to estimate breeding value comparisons between pig herds. This study suggests that it is possible to evaluate the genetic performance together for ADG and NBA in the Yorkshire herds since the preconditions were satisfied for these four herds. It is also possible to perform a joint genetic analysis of the ADG records of all Duroc herds since the preconditions were also satisfied. This study provides new insight into understanding the genetic connectedness of Korean pig breeding herds. CR could be utilized to accelerate the genetic progress of Korean pig breeding herds.

Keywords: Connectedness rating, Yorkshire, Landrace, Duroc, Average daily gain, Number born alive

Introduction

The accuracy of estimated breeding value (EBV) for economic traits is crucial in animal breeding programs. The accuracy of the estimation relies on connectedness to perform genetic analysis between pig breeding herds. Connectedness rating (CR) refers to the genetic similarity or genetic relationships among different herds or populations of animals [1]. In the context of animal breeding programs, it is crucial to assess the CR between herds or populations because it significantly impacts the accuracy of EBV for economic traits, which relies on having enough genetic information from the different herds or populations to perform a thorough genetic analysis. When herds are genetically connected, it means that there are shared ancestors or common genetic backgrounds between them. This genetic connectedness enables higher accuracy breeding value estimations because more genetic information is available to make predictions about an animal's performance and breeding potential. On the other hand, if herds are genetically isolated or not well connected, the accuracy of EBV may be lower due to the limited genetic information available for analysis. In such cases, it becomes challenging to predict the performance of animals accurately, leading to less effective selection and breeding strategies. Therefore, understanding and evaluating these genetic links among herds or populations is essential in animal breeding programs to ensure accurate and successful genetic improvement of economically important traits in livestock affecting the prediction error variance of difference (PEVD) of EBV [2].

Many methods have been proposed to estimate CR [1, 3-5]. Among them, Mathur et al. [6] suggested the CR, which has gained popularity as a reliable measure for evaluating connectedness. Subsequent studies have validated its consistency in producing accurate results in various connectedness analyses [2, 7, 8]. In Korea, genetic progress on swine has been achieved mainly by importing breeding pigs from other countries. However, as consolidation among pig breeding companies and farms has progressed, the number of pig genetic resources imported each year has decreased. In addition, multiple breeding farms plan to work together on pig genetic analysis to maximize genetic progress and mitigate the need to import breeding pigs into Korea. However, if there is no genetic link between herds, the analysis of EBV between different farms would not be reliable or accurate. It has been reported that the accuracy of the genetic evaluation increases when the CR between the herds is high [2, 7-9].

In Korea, efforts are being made to utilize pig genetic resources at the national level. The Pig Improvement Network (PIN) is a project under the Ministry for Food, Agriculture, Forestry and Fisheries (MIFAFF) in Korea. It aims to improve and develop a unique Korean pig breed well-suited to the conditions in Korea by selecting, sharing, and evaluating excellent breeding stocks from various farms to secure genetic connections. The project is managed by the National Institute of Animal Science under the Rural Development Administration (RDA), which oversees project management and national-level genetic capacity evaluations. The Korean Animal Improvement Association (KAIA) is responsible for project implementation and performance testing. Currently, 19 pig farms are participating in this network, and three pig artificial insemination centers are in operation.

The PIN is focused on enhancing the competitiveness of the domestic pig industry and developing genetically superior pig breeds that are resilient and productive in the local environment. The collaboration between government agencies, research institutes, and pig farms allows for the comprehensive genetic evaluation and selective breeding required to achieve the project's goals. The core of this project lies in how efficiently and effectively genetic resources are shared among different farms. Therefore, this study aims to estimate the connectedness among swine herds in Korea using three different breeds (Yorkshire, Landrace and Duroc) for average daily gain (ADG) and number born alive (NBA).

Materials and Methods

Data preparation

Performance and reproduction data were collected from fifteen Korean pig breeding herds (8 Yorkshire herds, 5 Landrace herds and 4 Duroc herds) born between 1997 and 2016. Two traits were considered to calculate the connectedness between pairs of herds: ADG and NBA. The numbers of records per breed and farm are presented in Tables 1 and 2.

Statistical model for breeding value

Both ADG and NBA datasets were analyzed for each breed to estimate the breeding value using the following statistical model (1).

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Hd} + \mathbf{e} \qquad (1)$$

where **y** is the phenotype observation for ADG and NBA, **b** is a vector of fixed effects (herd effects), **a** is the vector of random effects (additive animal genetic effects), **d** is the vector of common litter effects, and **e** is a vector for environmental residuals ($\boldsymbol{e \sim N(0, I\sigma_e^2)}$). **X**, **Z** and **H** were used as incidence matrices corresponding to vectors **b**, **a** and **d** related to the random additive genetic effects ($\boldsymbol{a \sim N(0, A\sigma_a^2), d \sim N\left(0, I\sigma_d^2\right)}$). $\boldsymbol{\sigma_a^2}$, $\boldsymbol{\sigma_d^2}$ and $\boldsymbol{\sigma_e^2}$ represent the additive genetic variance, litter variance, and environmental residual variance, respectively.

Mixed model equation construction

The above statistical model was used to construct the mixed model equation (MME) resulting in equation (2).

$$\begin{bmatrix} X'X & X'Z & X'H \\ Z'X & H'H + I\alpha_2 & H'Z \\ H'X & Z'H & H'H + A^{-1}\alpha_1 \end{bmatrix} \begin{bmatrix} \hat{h} \\ \hat{d} \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ H'y \end{bmatrix} \qquad (2)$$

where, **A** is the numerator genetic relationship matrix for animals, $\boldsymbol{\alpha_1}$ refers to $\boldsymbol{\sigma_e^2/\sigma_a^2}$ and $\boldsymbol{\alpha_2}$ refers to $\boldsymbol{\sigma_e^2/\sigma_d^2}$. The ASReml package [10] was used for solving equation (2).

Estimation of connectedness rating

CR was defined by the following equation (3):

$$\boldsymbol{CR_{ij}} = \frac{\boldsymbol{cov(\hat{h}_i,\hat{h}_j)}}{\sqrt{\boldsymbol{var(\hat{h}_i)var(\hat{h}_j)}}} \tag{3}$$

The covariance for the herd and variance of estimation of each herd effect i and j were obtained by solving equation (2).

Evaluation of connectedness rating and its effect on comparison of estimated breeding value

According to Mathur *et al.* [11], the accuracy of an individual EBV is estimated using the prediction error variance corresponding to the animals. The PEVD can be used to validate the accuracy of EBVs of two individuals. PEVD is formularized as:

$$\mathbf{PEVD} = \mathbf{Var}(\hat{\boldsymbol{a}}_i - \hat{\boldsymbol{a}}_j) = \boldsymbol{Var}(\hat{\boldsymbol{a}}_i) + \boldsymbol{Var}(\hat{\boldsymbol{a}}_j) - \mathbf{2}\boldsymbol{cov}(\hat{\boldsymbol{a}}_{ij}) \tag{4}$$

PEVD can then be substituted as the variance of estimates of difference between herd effects (VHD) [11]:

$$\boldsymbol{VHD_{ij}} = \boldsymbol{Average}\left[\boldsymbol{PEV}\left(\hat{\boldsymbol{a}}_{ik} - \hat{\boldsymbol{a}}_{jk'}\right)\right]$$

$$\approx \boldsymbol{Var}\left(\hat{\boldsymbol{h}}_i - \hat{\boldsymbol{h}}_j\right) \cong \boldsymbol{Var}\left(\hat{\boldsymbol{h}}_i\right) + \boldsymbol{Var}\left(\hat{\boldsymbol{h}}_j\right) - \mathbf{2}\boldsymbol{cov}\left(\hat{\boldsymbol{h}}_{ij}\right) \tag{5}$$

Results

Connectedness ratings for average daily gain

The average CRs for ADG in each breed are listed in Table 3. For the ADG in Yorkshire, a total of 8 herds were analyzed. The average CR between two herds ranges from 1.32 (B herd) to 28.05 (E herd). The maximum CR value was 93.44 between herds E and G, and the lowest CR value was 4.4 between herds B and G. For the ADG trait in Landrace, a total of 5 herds were used for analysis. The highest average CR was 2.50 between herds A and F, and the lowest average CR was 0.55 between herds C and H. All four herds A, B, C, and G were used in Duroc. The highest average CR was 16.14 between herds C and G, and the lowest average CR was 5.03 between herds A and C.

Connectedness ratings for number born alive

The average CRs for NBA in each breed are presented in Table 4. The same numbers of herds that were used for ADG analysis were used to analyze NBA. The minimum average CR ranged from ~0 (herd A) to 12.79 (herd E) in Yorkshire. The maximum CR was 89.38 between herds E and G, and the lowest CR value was identified between herds A and F. The highest average CR was 0.09 (herd H), and the lowest average CR was ~0 (herds A and F) in Landrace. The highest average CR for NBA ranged from 1.17 to 4.70 in Duroc. According to Mathur et al. [6], the recommended minimum average CRs for ADG and NBA are 3% and 1.5%, respectively. When these criteria for both the performance and reproductive traits are met, the EBV comparison between herds can be performed accurately. The average CR values for the Landrace herd are below this criterion, so the values for the Landrace herd were excluded in the following evaluation step.

Evaluation of connectedness ratings using prediction error variance of the difference

If two herds are highly connected, the PEVD decreases. The accuracy of the EBV is therefore greater when a pair of herds is evaluated jointly. According to Kennedy and Trus [4], the VHD is highly correlated with the average PEVD of pairwise comparisons of EBVs. Therefore, VHD can be used as an evaluation of CR. The VHDs for the Yorkshire and Duroc herds were calculated, but the VHD for the Landrace herd was not calculated due to its CR result. The PEVDs for the ADG and NBA traits in Yorkshire and Duroc breeds are shown in Tables 5, 6, 7, and 8. The tables show that the PEVD decreases as the CR increases, suggesting that the PEDV can be used as a validation indicator for the accuracy of the CR.

Based on the results, it can be observed that there are significant differences in CR between different herds for each of the evaluated breeds. For instance, in the case of the Korean Yorkshire breed, the CR between herds E and G is very high at 93.44, whereas the CR between herds B and G is relatively low at 4.4. These findings indicate that the level of genetic exchange varies among different herds, which can have implications for the reliability of genetic evaluations and breeding programs. Another important observation is the relationship between the size of the contemporary group (CG) and the accuracy of the EBVs. When the size of the CG is less than ten animals, the accuracy of the EBVs significantly decreases. Therefore, it is crucial for each CG to consist of at least 10 or more pigs to achieve higher accuracy, which ensures a sufficient sample size for more reliable genetic evaluations and breeding decisions.

Increasing connectedness is crucial for breeding programs, which can be achieved by using common sires from multiple herds or sharing genetically superior artificial insemination (AI) boars. By doing so, it becomes possible to conduct extensive genetic comparisons across herds, explore the potential for large-scale selection, and achieve greater genetic progress. The continuous supply of genetically superior pigs is directly related to the active participation of swine producers in breeding programs, who can contribute by providing their own genetically superior animals or by participating in the formation of a pool of superior AI boars. Such active involvement allows for the improvement of the national breeding program's structure, leading to increased genetic variability and connectedness. As a result, the participation of swine producers plays a crucial role in the field of animal breeding and helps foster greater genetic advancements and overall progress.

Discussion

A certain level of connectedness is needed for accurate estimated breeding value comparisons between herds. In this study, 104,380 performance data items and 83,200 reproduction data items from three different swine breeds across a total of fifteen herds were used to analyze connectedness using the CR method. The range of the CR for ADG in Korean swine herds was between 0.55 and 28.05. The ranges in the Yorkshire and Duroc breeds were deemed satisfactory with an average CR greater than 3%, while those of the Landrace breed were lower than 3%. Therefore, it is possible to compare the genetic evaluation results of the Yorkshire and Duroc herds for the ADG trait. The efforts are significantly required to improve the CR between pig herds for a national swine genetic evaluation. Increasing CR between herds primarily involves enhancing the use of common boars. Leveraging AI technology in the swine industry, boar exchange among farms, establishing pools of superior AI boars, and using AI boars with high CR can be effective strategies. Ensuring an adequate proportion of offspring from common sires is crucial, as it enables accurate comparisons of animals across different herds. Increasing the proportion of offspring from common sires can enhance genetic connectedness and reduce bias in inter-herd comparisons.

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Table 1. Number of records for ADG

Farm	Yorkshire	Landrace	Duroc
A	20,460	327	759
B	8,620	205	580
C	9,710	3,812	3,492
D	1,296	-	-
E	17,888	357	-
F	2,971	1,094	-
G	5,476	-	2,261
H	14,138	10,484	-
TOTAL	**80,559**	**16,279**	**7,092**

ADG: average daily gain

Table 2. Number of records for NBA

Farm	Yorkshire	Landrace	Duroc
A	5,127	327	759
B	2,773	205	580
C	9,710	3,812	3,492
D	1,296	-	-
E	17,888	357	-
F	2,971	1,094	-
G	5,476	-	2,261
H	14,138	10,484	-
TOTAL	**59,379**	**16,279**	**7,092**

NBA: number born alive

Table 3. Connectedness rating (CR) for ADG among herds

Herds	**Yorkshire connectedness rating (%)**			**Landrace connectedness rating (%)**			**Duroc connectedness rating (%)**		
	Mean	**Max**	**Most connected herd**	**Mean**	**Max**	**Most connected herd**	**Mean**	**Max**	**Most connected herd**
A	2.18	9.56	F	2.08	12.49	F	5.03	10.77	C
B	1.32	4.41	G	0.55	2.44	H	11.21	27.81	G
C	1.68	7.42	H	0.88	0.32	H	13.8	30.92	G
D	18.29	86.81	F	-	-	-	-	-	-
E	28.05	93.44	G	-	-	-	-	-	-
F	21.18	86.81	E	2.50	12.49	A	-	-	-
G	12.92	93.44	E	-	-	-	16.14	30.92	C
H	2.01	7.42	C	1.31	4.1	C	-	-	-

ADG: average daily gain

Table 4. Connectedness rating (CR) for NBA among herds

Herds	**Yorkshire connectedness rating (%)**			**Landrace connectedness rating (%)**			**Duroc connectedness rating (%)**		
	Mean	**Max**	**Most connected herd**	**Mean**	**Max**	**Most connected herd**	**Mean**	**Max**	**Most connected herd**
A	~0	~0	F	~0	~0	F	1.17	3.40	G
B	0.82	3.65	G	0.02	0.1	H	1.27	4.01	G
C	0.17	0.86	H	0.08	0.37	H	3.23	11.4	G
D	8.40	59.60	F	-	-	-	-	-	-
E	12.79	89.38	G	-	-	-	-	-	-
F	8.71	59.55	E	~0	~0	A	-	-	-
G	11.7	89.38	E	-	-	-	4.70	11.4	C
H	0.20	0.86	C	0.09	0.37	C	-	-	-

NBA: number born alive

Table 5. Prediction error variance of difference (PEVD) for ADG among Yorkshire herds

Herds	CR (%) > 3	PEVD
A,D	5.86	0.0024
A,F	9.56	0.0028
B,E	4.04	0.0022
B,G	4.41	0.0069
C,E	3.86	0.0017
C,H	7.42	0.0067
D,E	47.97	0.0010
D,F	86.81	0.0004
D,G	5.53	0.0059
E,F	65.86	0.0006
E,G	93.44	0.0001
E,H	7.22	0.0027

ADG: average daily gain

Table 6. Prediction error variance of difference (PEVD) for ADG among Duroc herds

Herds	CR (%) > 3	PEVD
A,B	3.53	0.00413
A,C	10.77	0.00400
A,G	5.82	0.00402
B,C	13.50	0.00462
B,G	27.81	0.00342

ADG: average daily gain

Table 7. Prediction error variance of difference (PEVD) for NBA among Yorkshire herds

Herds	CR (%) > 1.5	PEVD
B,E	2.40	0.0456
B,G	3.65	0.0762
D,E	7.39	0.0456
D,F	59.55	0.0203
E,F	9.86	0.0337
E,G	89.38	0.0048

NBA: number born alive

Table 8. Prediction error variance of difference (PEVD) for NBA among Korean Duroc herds

Herds	CR (%) > 1.5	PEVD
A,G	3.40	0.0809
B,G	4.01	0.0847
C,G	11.40	0.0469

NBA: number born alive