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DETERMINATION OF THE APPROPRIATE GENETICALLY MODEL, ESTIMATION OF BREEDING VALUES AND EVALUATION OF GENETIC TREND FOR BASICALLY REPRODUCTIVE TRAITS ON LANDRACE, YORKSHIRE PIGS

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INTRODUCTION

1.1. Rationable

In recent years, the pig breeding in our country is improving successfully, but the productivity is still limited, especially the reproductive performances of the breeding sows due to affected by many genetic and environment factors.

It, therefore, to identify the positive and negative factors affecting the reproductive performances of the sow is one of the decisive keys to improve sow fertility enhancement. Therefore, to determine the fixed factors affecting fertility is selected as one of the contents of this thesis.

From the identified influencing factors, use them to build up genetic models to find out the suitable model in our country's breeding conditions for the analysis of the component variance and estimated breeding value for reproductive traits of Landrace and Yorkshire sows raised in some hatcheries in Vietnam are the most important content of this thesis.

After identifying the appropriate genetic statistical model, estimating breed values for basic reproductive traits and SPI for Landrace and Yorkshire pigs raised at a number of hatcheries in Vietnam in order to improve reproductive productivity of the sow herd more effectively is an indispensable fundamental content in breeding work.

At the same time, through the estimated breeding value (EBV) and other genetic parameters assess the genetic trends over different periods of reproductive traits in Yorkshire and Landrace pig breeds in some breeding facilities in order to identify the currently applied selection methods to achieve propagation goal is another indispensable content in the breeding work.

It, therefore, the topic "Determination of the appropriate genetically model, estimation of breeding values and evaluation of the genetic trends for basically reproductive traits of Landrace, Yorkshire pigs" is particularly necessary in the context, there is a shortage of good breed sources for production.

1.2. Objective of study

\+ Determination of the influent level of some fixed and coveted external factors to the number born alive (NBA), number weaned (NW) and litter weaned weight (WW) traits of Landrace and Yorkshire sows reared in some breeding facilities in Vietnam

\+ Determination of the appropriate genetic statistical models used in the analysis of component variance and EBV of NBA, NW and WW traits in Yorkshire and Landrace pigs in some breeding facilities in Vietnam.

+ Estimation the EBV of NBA, NW, WW traits and SPI index for Landrace and Yorkshire sows in some breeding facilities in Vietnam.

+ Evaluation of genetic trends over different periods of NBA, NW, WW traits and SPI index in Yorkshire and Landrace breeds in some breeding facilities in Vietnam.

1.3. Scientific and practical value of thesis

Scientific value

- The thesis has determined the influent level of fixed and coveted external factors on 3 reproductive traits (NBA, NW and WW), from which genetic statistical model was built to apply in analyzing the components of variance, covariance due to the influence of direct genetics from the individual, the genetic influence from the mother, the influence of fixed externalities, the influence of permanent externalities of parity and general maternal external influences to the NBA, NW and WW, consistent with the database of Landrace and Yorkshire pig herds reared at some breeding facilities in Vietnam. From there, it is recommended to use the appropriate model to estimate the breeding value in the breeding program for these breeding facilities.
- The thesis is used as a scientific basis for the work of breeding pig selection in Vietnam.

Practical value

- The breeding value estimated of basically reproductive traits was based on the actual database of breeding stock of two pig breeding facilities in Vietnam (Binh Thang and Dabaco) to apply on selective evaluation, contributing to improve selection efficiency, genetic quality of reproductive traits in Yorkshire and Landrace pig breeds in these breeding facilities.
- The genetic trend of some reproductive traits in Yorkshire and Landrace pig breeds was evaluated in recent years to clearly recognize the effectiveness of the selection method applied in the past and thus allow breeding facilities to control properly breeding goals and the effectiveness of the current selection and genetic evaluation programs.

1.4. New contributions of thesis

The thesis is a systematic and in-series study from a set of data on reproductive performance of Landrace, Yorkshire sows that determine the fixed factors for the development of genetic statistical analysis models. Based on that, select an appropriate model for analyzing the variance of components, determine genetic factors and estimating breeding values, genetic trends of 3 reproductive traits including the number born alive, number weaned and the litter weaned weight for Landrace and Yorkshire pigs to help our country’s pig breeding systems will be more effective.

Chapter 1. LITERATURE REVIEW

The estimated breeding value (EBV) of domestic animal is defined as the additive genetic value of that animal. In fact, only phenotypic values can be measured, but we have a desire to estimate the value represented the genetic nature, which is the estimated breeding value (EBV).

The BLUP method is currently the most advanced method to allow adjustment of the combined genetic value of the animal according to fixed external influences such as crop, feeding, sex, parity and other fixed external factors. Therefore, selection through EBV is a more accurate method than previous phenotypic selection methods.

The statistical model applied in the BLUP method to estimate the breeding value of production traits in pigs is a linear model, always including fixed factors and random effect factor.

Genetic trend is the trend of changing (increasing, decreasing) for average genetic value of pig herds over the years. They show the average of the agents that influence to the trait over certain periods (Hamond, 1991; Falconer, 1993; Hans, 1993).

Chapter 2. MATERIALS, CONTENTS AND METHODS

2.1. Period and location of study

Study was conducted from 2015 to 2019 on pure Landrace and Yorkshire herd, born from 2011 to 2018 at 2 breeding facilities in North Vietnam (A facility) and North Vietnam (B facility).

In the North, the study was conducted at two breeding facilities belonging to Dabaco Nuclear Pig Breeding Company (Bac Ninh). In the south, the study was conducted at the Binh Minh pig farm (belonging to the Binh Thang Pig Breeding Development and Research Center) and a satellite breeding farm of the Binh Thang Center, the Khang Minh An farm. Both farms are located in Dong Nai province.

2.2. Contents of study

Ddetermine the fixed factors effecting to the reproductive traits of Landrace and Yorkshire sows.

Find out the optimal genetic models to be applied for analyzing the reproductive traits of Landrace and Yorkshire sows.

Estimation of breeding value for the NBA, NW and WW traits and SPI selection indices of Landrace and Yorkshire pigs.

Evaluation of genetic trend for the NBA, NW and WW traits and SPI selection index in Landrace and Yorkshire pigs reared in two breeding facilities A and B.

2.3. Objectives and study conditions

2.3.1. A facility

Pure Landrace and Yorkshire pigs in research at A facility had a scale of 650-700 sows and 140-150 sires, reared in closed cages equipped with climate control system for breeding cages (temperature, humidity and wind speed). All breeds in this facility were monitored for joint management on the same numbering system, data collection system and general management using HEOPRO-B software. Since 2015, the program of genetic evaluation, selection and breeding was started to develop and implement at the breeding facilities of Dabaco Nuclear Pig Breeding Company using BLUP method.

2.3.2. B facility

The pure Landrace and Yorkshire pigs in this study had a scale of 600-700 sows and 50-80 sires, reared in closed cages (air-conditioned, humidity) and some reared in opened cages with ventilation fan and roof cooling system as needed. Khang Minh An Pig Breeding Farm was an affiliate satellite breeding facility of Binh Thang Center

Both facilities had the same numbering system, individual pedigree management system, gilt individual productivity test system and reproductive sow data collection system. Since 2005, Binh Minh breeding facility has applied the evaluation of breed value by BLUP method in selecting pure pig herds. Since 2014, the collection, updating and management of the breeding database has been replaced by HEOMAN (Vietnam) software in both Binh Minh and Khang Minh An breeding facilities.

2.2.3. Data collection

From the available pig herds and individual data is managed and stored at breeding facilities A and B:

Data collection:

- Genealogy: sire/sow code, breed, date of birth, father code, father origin, mother code, mother origin, facility, date of elimination
- Reproductive data: sow code, date of birth, bell type, breed, parity, mating sire, mating date, date of birth, number of farrowed/dead animals, number of newborn piglets alive, weaning day, number of weaned piglets,

total weight of litter at weaning.

The data structure is presented in Table 2.1.

Table 2.1: Reproductive data structure of Landrace and Yorkshire breeding herds 2011-2018 used in genetic analysis

Breed	Index	Facility A	Facility B	Total
Landrace	Total sires (pig)	180	158	338
	Total sows (pig)	748	1,092	1,840
	Total litters (litter)	2,156	3,496	5,652
	NBA (piglets/litter)	10.63±2.94	11.02±3.62	
	NW (piglets/litter)	10.51±1.56	10.39±2.09	
	WW (kg)	72.35±15.7	67.4±16.7	
	Age of weaning (day)	23.3±2.7	25.5±2.5	
Yorkshire	Total sires (pig)	147	131	278
	Total sows (pig)	1,155	1,041	2,196
	Total litters (litter)	3,756	3,684	7,440
	NBA (piglets/litter)	11.01±3,06	11.00± 3.39	
	NW (piglets/litter)	10.61±1,71	10.34±2.03	
	WW (kg)	67.1±15,8	64.7±16.1	
	Age of weaning (day)	23.4±2,6	25.4±2.7	

2.4. Study methods and data analysis

2.4.1. Analyze the influence of a number of fixed factors to the NBA, NW and WW traits

Reproductive traits in this study, including NBA, NW and WW. Was analyzed by the model:

$$Y_{ijkhlmno} = \mu+CS_i+ND_j+NS_k+MV_g+KC_h+LĐ_l+ĐP_m+TS_n+e_{ijkghlmno}$$

Where, Y is the observation of the o^{th} *sow farrowed in* i^{th} *farm (CS) with* k^{th} *year of birth of sows (ND), of the* k^{th} *year of giving birth (NS) in the* g^{th} *season of litter (MV), of* k^{th} *cage type (KC), in* l^{th} *parity (LĐ) of* m^{th} *service sire (ĐP), of* n^{th} *weaning age (TS);* μ*: is the unknown constant;* $e_{ijkghlmno}$ *is the random error associated with an observation on the* $ijkghlmno^{th}$ *pig.*

The fixed factor analyzes influencing the three reproductive traits studied were analyzed using SAS statistical software (Version 9.00).

2.4.2. Estimate the component variance and genetic coefficient of the NBA, NW and WW traits

Use different mixed animal models with fixed influencing factors cage type (α), parity (β), weaning age (γ), Herd*Year*season (HYS) and different random maternal factors (L), maternal general background (C) and maternal inheritance (M) on the same database to estimate component variance and genetic coefficients. The model is presented as follows:

Model 1 (MD1): $Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + a_m + L + e_{ijklmn}$
Model 2 (MD2): $Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + a_m + C + e_{ijklmn}$
Model 3 (MD3): $Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + a_m + L + C + e_{ijklnm}$
Model 4 (MD4): $Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + a_m + L + M + e_{ijklmn}$
Model 5 (MD5): $Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + a_m + L + C + M + e_{ijklmn}$

The component variance and genetic factors of the NBA, NW and WW traits were estimated by REML (Restricted Maximum Likelihood) method on VCE6 genetic statistics software (Groeneveld *et al*., 2010).

Criteria for selecting the most appropriate genetic statistical model are models that simultaneously have: 1) The model has the SE value of the coefficients smaller than the average when estimating the component variance and the corresponding coefficients of and 2) The total value of the coefficients of the L, C and M influences is the largest value of the genetic coefficient for NBA, NW and WW traits in both Landrace and Yorkshire breeds reared in Facility A and B.

2.4.3. Estimation of the breeding value for the NBA, NW and WW traits and SPI index

After obtaining an appropriate statistical genetic model in the estimation of the component variance and genetic coefficients, that model will be used to estimate the breeding value.

Statistical model with fixed influencing factors is followed:

$$Y_{ijklmn} = \mu + \alpha_i + \beta_j + \gamma_k + HYS_l + L + C + a_m + e_{ijklmn}$$

Where, μ: is the unknown constant; cage type (α), parity (β), weaning age (γ), HYS and different random contexts (permanent parity (L), general maternal factors of the mother (C); $e_{ijkghlmn}$ is the random error associated with an observation on the ijkghlmnoth pig.

Breeding values of NBA, NW and WW traits were estimated by BLUP (Best Linear Unbiased Prediction) using PEST genetic statistics software (Groeneveld, 2006).

The accuracy of the estimated breeding values was calculated using the following formula of Mrode (1996):

$$\mathbf{r_{A\tilde{A}}} = \sqrt{1-(PEV/\sigma_A)}$$

In which, $r_{A\hat{A}}$: *Accuracy of the predicted breeding values*
σ_A: *Additive genetic variance*
PEV: Variance of predicted variance (estimated with the same value of each individual by PEST software)

The SPI selection index for sire and sow herds of Landrace and Yorkshire breeds was used as follows:

$$SPI=100+ {}^{25}/_{SD}*(3{,}09*EBV_{NBA}+1{,}72*EBV_{NW}+0{,}27*EBV_{WW})$$

2.4.4. Evaluation of genetic trand forthe NBA, NW and WW traits and SPI selection index

The genetic trend of traits is included NBA, NW and WW and selection index of reproductive sows (SPI). Average genetic improvement is calculated by the following equation:

$$y = bx + a$$

Where: y is the average breeding value of the study trait of the individual groups born in the same year, a is constant, x is the year of birth of the individual groups, and b is regression coefficient - is the increase of the breeding value year.

Chapter 3. RESULTS AND DISCUSION

3.1. The effects of some fixed factors on the NBA, NW and WW traits

For Landrace herds, the factors of born and seasonal year were all influenced to NBA, NW and WW traits with probability levels from P<0.05 to P<0.001;

The NW and WW traits are significantly influenced by weaning age (P<0.001). Meanwhile, parity factors only were influenced NBA trait (P<0.001). Cage type factors were influenced to NW and WW traits with probability P<0.01-P<0.001. The sire factor did not influence to all three reproductive traits in this study

For Yorkshire herds, the sire factor was not influenced to all three reproductive traits including NBA, NW and WW. Cage type factors only influenced to NBA trait (P<0.01). While other factors such as breeding stock, year of born, year of laying farrowing, season, parity and weaning age all influenced the reproductive traits of NBA, NW and WW with differences in significantly (P<0.05-P<0.001).

Table 3.1: Influence of some factors on NBA, NW and WW traits

Breed	Study traits	Number of farrowing (n)	Influent factors							
			Facility	Year of born of sow	Year of birth giving	Season	Litter	Cage type	Mating sire	Age of weaned
Landrace	NBA	5,652	ns	ns	*	**	***	ns	Ns	-
	NW	5,652	**	***	**	***	ns	**	Ns	***
	WW	5,652	***	*	***	***	ns	***	Ns	***
Yorkshire	NBA	7,440	**	*	***	**	***	**	Ns	-
	NW	7,440	**	*	**	*	**	ns	Ns	***
	WW	7,440	***	**	***	***	***	ns	Ns	***

*Note: -: no testing; ns: P>0,05; *: P<0,05; **: P<0,01; ***: P<0,001*

3.2. Estimation of component variance and genetic coefficients for the NBA, NW and WW traits

3.2.1. For Landrace breeding herds at facility A

For the NBA trait in Landrace herd at facility A, MH3 was more suitable because the genetic coefficient of the NBA trait in MH3 was 0.111 but the total coefficients c^2 and l^2 was 0.069, equal to 61% of the genetic coefficient.

For NW traits on the Landrace breeding herd at facility A, the overall external maternal coefficient (c^2) of this trait was very small at facility A (0.003-0.021). In MH1, the l^2 coefficient was the highest value (0.046) compared to other MH. Therefore, in analyzing the genetic statistics of NW traits for facility A, MH1 model was more suitable.

Although the l^2 coefficient of MH3 was higher than MH1, the SE value of c^2 was higher than the average. Therefore, like the NBA and NW traits, when analyzing separate genetic statistics for the WW trait in the Landrace herd at facility A, consider the permanent effect of parity needed and then MH1 model would be more suitable

3.2.2. For Landrace breeding herds at facility B

For NBA trait of Landrace herd at facility B, the statistical analysis model of MH3 for Landrace herd was more suitable at facility B. The reason, MH3 was more suitable because the l^2 value and c^2 coefficients MH were equal or greater than their respective values of other MH.

MH2 or MH3 model was suitable in the case of statistical analysis of NW traits in Landrace herd at facility B because the c^2 value of these two MH was large (0.085).

For the WW trait in the Landrace herd at facility B, in case of analyzing genetic statistics, the MH1 model would be more suitable on the same trait.

Thus, in Landrace herd, analysis results on reproductive data of two breeding A and B facilities in this study showed that the value of the genetic coefficient of NBA, NW and WW traits was low and there was a significant difference between facility A and facility B. This result was consistent with many claims (Hamann *et al*, 2004; Arango *et al*, 2005; Imboonta *et al*, 2007; Nguyen Huu Tinh *et al*, 2010; 2012; 2018). In most cases, the maternal genetic influence was negligible for the traits studied in both farms (except for the WW trait). The permanent external effect of parity (L) was greater in base herd A, but smaller in facility B.

3.2.3. For Yorkshire breeding herds at facility A

The genetic factor of MH3 was the second highest after MH2.

However, in MH3, the c^2 value was equal to MH2 but the of c^2/h^2 ratio in MH2 was lower than MH3. Therefore, the MH3 model can be applied in the statistical analysis of NBA trait in Yorkshire herds at facility A.

For NW trait in Yorkshire herd at facility A, the genetic coefficient value of this trait in Yorkshire herd at facility A was very low and not significant difference between the statistical models in the current study (0.056-0.090). Although the genetic coefficient of MH5 was the lowest out of 5 MHs, the c^2 coefficient was equal to 98.21% of the genetic factor. Besides, in MH3 and MH5, the external factor was a lower value than the other three MHs. Thus, in the genetic statistics of NW traits in Yorkshire breeding herds at facility A, the use of model MH3 or MH5 were appropriate.

For the WW trait in Yorkshire herd at facility A, the heritability of this trait in Yorkshire herd at facility A was very low (0.014–0.075) in all 5 statistical models. Both l^2 and c^2 coefficients of MH3 was higher than or equal to other MH3, the e^2 value of MH3 was lowest (0.807). On other hand, in 5 study models, MH3 model will be more suitable for genetic analysis of this trait in Yorkshire breeding herds at facility A

3.2.4. For Yorkshire breeding herds at facility B

Genetic coefficients of NBA trait in Yorkshire herd at Facility B were hardly changed between the 5 statistical analysis models in the current study (0.206-0,214). Thus, for the NBA trait in Yorkshire herds at Facility B, only the overall external influence of the dam was relatively significant (0.025). MH2 was the unique MH without SE value above the average at l^2, c^2 and m^2. Therefore, the MH2 model can be applied in statistical analysis of this trait in Yorkshire breeding stock at facility B.

For NW trait in Yorkshire herd at facility B, the l^2, c^2 coefficient values of MH3 was higher than or equal to other MHs; e^2 value was the second lowest compared to the other MHs. Thus, just like at facility A, for the NBA trait in Yorkshire breeding herds at facility B, the use of the MH3 model will be appropriate, as this model included the permanent effect of parity and the overall influence of the dam.

For the WW trait in Yorkshire herd at facility B, the genetic coefficient of this trait in Yorkshire herds at facility B was low (0.085-0.125) in all 5 statistical models. The l^2, c^2 coefficient values of MH3 was higher than or equal to other MHs; c^2 value was lowest compared to the other MHs (except MH5). Thus, the use of the MH3 model would be appropriate for a single trait analysis, as this model was considered both the permanent effect of parity and the overall effect of the dam.

Thus, depend on each trait, each breed and each facility that will give suitable different statistical models.

However, here, suitable general model for all three traits (NBA, NW and WW) was given in two Landrace and Yorkshire breeds reared at facility A and B according to the criteria in the methodology. Results were shown in table 3.14. According to Table 3.14, the model that was most appropriate for all three NBA, NW and WW traits in Landrace and Yorkshire pigs raised in facility A and facility B, MH3 was selected to estimate the breeding value for these traits.

Table 3.14: Selection of appropriate statistical models for three traits of NBA, NW and WW in L and Y breeds reared at facility A and B

Criteria Breed, facility		The SE value of the coefficient was smaller than the average value of the corresponding coefficient					Sum of the largest l^2, c^2, m^2 coefficients				
		MH1	MH2	MH3	MH4	MH5	MH1	MH2	MH3	MH4	MH5
L A	NBA	x		x					x		
	NW	x		x			x				
	WW	x	x					x			
L B	NBA		x	x					x		
	NW		x					x			
	WW	x	x	x					x		
Y A	NBA	x	x	x					x		
	NW	x	x	x					x		
	WW	x	x	x		x					x
Y B	NBA		x					x			
	NW	x	x	x					x		
	WW	x	x	x					x		

Genetic coefficients of NBA, NW and WW traits of Landrace, Yorkshire pig breeds reared at facility A and facility B when analyzed according to model 3 were presented in Table 3.15.

Table 3.15: Genetic coefficients of NBA, NW and WW traits in both L and Y breeds reared at facilities A and B according to MH3

Traits	Landrace		Yorkshire	
	Facility A	Facility B	Facility A	Facility B
NBA	0.113±0.034	0.125±0.016	0.179±0.018	0.211±0.018
NW	0.033±0.017	0.017±0.007	0.075±0.010	0.058±0.014
WW	0.028±0.021	0.071±0.015	0.032±0.011	0.088±0.018

3.3. Estimation of breeding value for the NBA, NW and WW and SPI selection index

3.3.1. Estimation of breeding value for the NBA

The accuracy of the breeding values from the average values to the relatively high value level for the sire herds, from 0.477 to 0.730 (table 3.16) and high value level for the sow herds, from 0.623 to 0.765 (table 3.17) in both same and both facilities.

Table 3.16: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sire herds for NBA in Jan 2019

Facility	Breeding level	Landrace sire herd			Yorkshire sire herd		
		Number of sires	EBV_{NBA} (Mean±SD)	Accuracy level	Number of sires	EBV_{NBA} (Mean±SD)	Accuracy level
A	Top5%	5	1.160±0.253	0.498	3	1.875±0.025	0.477
	Top10%	9	1.013±0.250	0.504	5	1.841±0.049	0.497
	Top25%	23	0.683±0.266	0.486	13	1.278±0.570	0.519
B	Top5%	2	1.381±0.184	0.621	1	1.488	0.730
	Top10%	5	0.980±0.383	0.537	3	1.202±0.404	0.687
	Top25%	8	0.800±0.394	0.577	5	0.945±0.312	0.574

Table 3.17: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sow herds for NBA in Jan 2019

Facility	Breeding level	Landrace sow herd			Landrace sow herd		
		Number of sows	EBV_{NBA} (Mean±SD)	Accuracy level	Number of sows	EBV_{NBA} (Mean±SD)	Accuracy level
A	Top5%	13	1.799±0.462	0.667	20	2.160±0.398	0.712
	Top10%	25	1.555±0.422	0.666	40	1.780±0.481	0.699
	Top25%	62	1.132±0.450	0.623	89	1.334±0.533	0.699
B	Top5%	21	1.943±0.262	0.757	9	2.100±0.457	0.765
	Top10%	42	1.700±0.311	0.749	18	1.771±0.564	0.721
	Top25%	105	1.262±0.429	0.727	46	1.270±0.508	0.646

In sire herds (Table 3.16), for comparing the Top5%, Top10% and Top25% individual groups between the two breeds, the average breeding value of the corresponding groups in Landrace herds was lower than in Yorkshire breeds in both facilities A and B. The average breeding value of the Top5% group at facility A and facility B were +1.160 and +1.381 piglets/litter in Landrace breeds and +1.875 and +1.488 piglets/litter in Yorkshire breeds.

The different level in the average EBV between Top5% and Top10% group in facility A was not significant in both Landrace and Yorkshire breeds, respectively, 1.160 compared to 1.013 piglets/litter in Landrace breed and 1.875 compared to 1.841 piglets/litter in Yorkshire breed. In contrast, for the sire herds at facility B (Table 3.16), the average breeding values of these two groups were a significantly different compared to the facility A, corresponding to 1.381 compared to 0.980 piglets/litter in Landrace breed, and 1.488 compared to 1.202 piglets/litter in Yorkshire breeds.

It is indicated that the variation level of the genetic variance in the sire herds at facility B was higher than that at facility A. For breeding sires, selection of setting up the nucleus herd to continue breeding instead of the next generation were usually very small, so selection of breeding sires in Top10% at facility B would be more convenient than at facility A.

The average EBV in NBA traits of Top5%, Top10% and Top25% sow herd were all higher than the corresponding Top in sires of Landrace and Yorkshire breeds reared at facility A and facility B. Such results obtained from the size of the sow selection were much larger than that of the sires.

In the sow herds (table 3.17), the difference of the average EBV in NBA traits between the best individual Top5% and Top25% groups was much larger in both Landrace and Yorkshire breeds in both A and B facilities. Corresponding to 1.799-1.943 compared with 1.126-1.132 piglets/litter in Landrace and 2.100-2.160 compared to 1.270-1.334 piglets/litter in Yorkshire.

3.3.2. Estimated breeding value for NW

The accuracy value of EBV in sires (Table 3.18) was mostly below the average (0.434-0.481), except for Yorkshire sires at facility B that were above average (0.50-6-0488). Whereas in the sows (Table 3.19), the accuracy value of the breeding values was estimated to be relatively high (0.564-0.6666) in both breeds and both facilities.

As shown in table 3.18, in the Landrace sires, the average EBV among the 5%, Top10% and Top25%groups was 0.411; 0.371 and 0.234 piglets/litter (facility A) and 0.342; 0.253 and 0.203 (facility B). Similarly, in Yorkshire sires, the average EBV between these three groups was 0.697 0,674 and 0,501 piglets/litter at facility A and 0,526; 0.471 and 0.371 piglets/litter in facility B, respectively. Obviously, the small difference between the three groups will be a major obstacle for genetic improvement selection in Landrace and Yorkshire sires in this study.

Table 3.18: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sire herds for NBA in Jan 2019

Facility	Breeding level	Landrace sire herd			Yorkshire sire herd		
		Number of sires	EBV_{NBA} (Mean±SD)	Accuracy level	Number of sires	EBV_{NBA} (Mean±SD)	Accuracy level
A	Top5%	5	0.411±0.076	0.471	3	0.697±0.020	0.434
	Top10%	9	0.371±0.072	0.455	5	0.674±0.035	0.452
	Top25%	23	0.234±0.105	0.439	13	0.501±0.182	0.481
B	Top5%	2	0.342±0.096	0.453	1	0.526	0.648
	Top10%	5	0.253±0.099	0.465	3	0.471±0.078	0.563
	Top25%	8	0.203±0.101	0.479	5	0.371±0.102	0.506

Table 3.19: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sow herds for NBA in Jan 2019

Facility	Breeding level	Landrace sow herd			Landrace sow herd		
		Number of sows	EBV_{NBA} (Mean±SD)	Accuracy level	Number of sows	EBV_{NBA} (Mean±SD)	Accuracy level
A	Top5%	13	0.626±0.110	0.619	20	0.780±0.164	0.653
	Top10%	25	0.538±0.126	0.578	40	0.655±0.174	0.650
	Top25%	62	0.402±0.143	0.564	89	0.501±0.185	0.650
B	Top5%	21	0.545±0.119	0.666	9	0.629±0.100	0.651
	Top10%	42	0.463±0.119	0.659	18	0.540±0.119	0.634
	Top25%	105	0.345±0.126	0.636	46	0.402±0.135	0.577

Compared to sire herds, the difference of estimated breed value between the Top5%, Top10% and Top25% groups was higher than in the sow herds (Table 3.19). The results showed that in the Landrace sow herds, the average EBV among the three groups including Top5%, Top10% and Top25% were 0.626; 0.538 and 0.402 piglets/litter (facility A) and 0.545; 0.463 and 0.345 (facility B), respectively. In Yorkshire sow herds, the average EBV between among three groups was 0.780, 0.655 and 0.501 piglets/litter at facility A and 0,629; 0.540 and 0.402 piglets/litter facility B, respectively. However, the sows usually were selected to replace the herds at the ratio: 15-20%, higher than the sire herds (2-5%), so the genetic improvement was calculated. This condition used by selection will also be more difficult than the NBA traits

3.3.3. Estimated breeding value for the weaned litter weight

Estimated results show that in each facility, the average EBV of the weaned litter weight (WW) trait also was not significantly different among the Top5%, Top10% and Top25% groups in both breeds, in both sire herds (Table 3.20) and sow herds (Table 3.21). However, the average EBV of this trait was significantly different between the two facilities A and B by each group of Top5%, Top10% and Top25% individuals.

Regarding to the accuracy of the average estimated breeding values of the WW trait for the sire herds (Table 3.20) was relatively low at facility A (0.332-0.369) and medium at facility B (0.473-0.559) in both facilities. Similarly, the sow herds had a low medium at facility A (0,404-0,508) and had a relatively medium at facility B (0,540-0,674) for both breeds.

Table 3.20: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sire herds for WW in Jan 2019

Facility	Breeding level	Landrace sire herd			Yorkshire sire herd		
		Number of sires	EBV$_{WW}$ (Mean±SD)	Accuracy level	Number of sires	EBV$_{WW}$ (Mean±SD)	Accuracy level
A	Top5%	5	1.926±0.149	0.369	3	1.159±0.181	0.322
	Top10%	9	1.681±0.316	0.352	5	1.085±0.171	0.346
	Top25%	23	1.183±0.380	0.327	13	0.898±0.191	0.348
B	Top5%	2	3.836±0.261	0.482	1	6.394	0.473
	Top10%	5	3.571±0.276	0.513	3	5.884±0.722	0.559
	Top25%	8	3.081±0.714	0.501	5	4.174±1.824	0.496

In Table 3.20, for Landrace sire herds, the average EBV among the Top5%, Top10% and Top25% groups was 1.926, 1.681 and 1.183 kg/litter at facility A and 3,836; 3,571 and 3,081 at facility B, respectively. Similarly, for Yorkshire sire herds, the average EBV among between these three groups was 1,159; 1,085 and 0,898 kg/litter at facility A and 6,394; 5,884 and 4,174 kg/litter at facility B. Thus, the average EBV of Landrace and Yorkshire sires at facility B was always higher than that of facility A by individual Top5%, Top10% and Top25% groups.

In Table 3.21 show that for Landrace sow herds, the average EBV among these three groups was 2,865; 2,432 and 1,742 kg/litter at facility A and 5,330; 4,580 and 3,379 kg/litter at facility B, respectively. For Yorkshire sow herds, the average EBV among these three groups was 2,732; 2,372 and 1,773 kg/litter at facility A and 5,475; 4,869 and 3,854 kg/litter at facility B.

Similarly, the average EBV of the breeding sire herds at facility B was always higher than that of facility A by individual Top5%, Top10% and Top25% groups.

Table 3.21: Average breeding value of Top5%, Top10%, Top25% of the best individuals in L and Y sow herds for WW in Jan 2019

Facility	Breeding level	Landrace sow herd			Yorkshire sow herd		
		Number of sows	EBV_{WW} (Mean±SD)	Accuracy level	Number of sows	EBV_{WW} (Mean±SD)	Accuracy level
A	Top5%	13	2.865±0.484	0.459	20	2.732±0.476	0.507
	Top10%	25	2.432±0.599	0.456	40	2.372±0.499	0.507
	Top25%	62	1.742±0.700	0.404	89	1.773±0.658	0.508
B	Top5%	21	5.330±1.097	0.674	9	5.475±0.410	0.582
	Top10%	42	4.580±1.093	0.641	18	4.869±0.695	0.540
	Top25%	105	3.379±1.241	0.620	46	3.854±1.000	0.552

In case of considering in the same facility and the same breed, the difference in the average EBV of the WW trait among three individual groups (Top5%, Top10% and Top25%) was relatively low. Corresponding to facility A, the difference in the average EBV among the three individual groups was 0.743-1.1123 kg /litter on Landrace breed; 0.261-0.959 kg/litter on Yorkshire breeds. Meanwhile, the difference in average EBV among the three individual groups was higher than that of facility A, from 0.755 to 0.951 kg/litter (Landrace); 1,621-2,220 kg/litter (Yorkshire). The average EBV of the breeding sows at facility B was always higher than that of at facility B A by individual Top5%, Top10% and Top25% groups in both Landrace and Yorkshire breeds.

From the results of this study, it can be seen that the selection for genetic improvement of the WW trait will face many difficulties, especially for facility A and for breeding sires in both Landrace and Yorkshire breeds.

In comparation between the two facilities, the genetic variation level among individual Top5%, Top10% and Top25% groups for the WW trait was relatively different. The variation level was very low in facility A and was much higher in facility B. The reason may be that facility A has applied a continuous transfer procedure between farrowing litters during the weaning period to increased homogeneity among piglets during weaned period. In contrast, in facility B, the piglet transplantation process was only carried out in some special cases, such as sows died, disease or milk losing due to some reasons can not continue rearing piglets but definitely to transfer to sows that rearing other piglets. Therefore, for facility A herds, the continuous transplanting process was applied during the weaning period as in this study, selection for WW trait will not bring about genetic improvement and may ignore this trait in selective index.

3.3.4.SPI selection index based on the estimated breeding value of the NBA, NW and WW

By combining the three reproductive traits for both Landrace and Yorkshire in this study, including NBA, NW and WW into the selection index (SPI) of the reproductive sows, individuals with an SPI index higher than 100 were considered higher genetic potential than the average for the entire breeding herd.

Table 3.22: Average EBV of Top5%, Top10%, Top25% of the best individuals in L and Y sire herds based on SPI index in Jan 2019

Facility	Breeding level	Landrace sire herd		Yorkshire sire herd	
		Number of sires	SPI index (Mean±SD)	Number of sires	SPI index (Mean±SD)
A	Top5%	5	147.23±10.42	3	163.57±0.79
	Top10%	9	141.52±10.03	5	162.24±1.90
	Top25%	23	127.29±10.07	13	143.14±19.21
B	Top5%	2	143.55±10.31	1	149.37
	Top10%	5	130.67±13.07	3	142.05±10.35
	Top25%	8	124.10±13.80	5	133.27±9.79

For sire herds (Table 3.22), due to the limited herd size (140 Landrace sires and 80 Yorkshire sires in both A and B facilities), the difference in the average value of the SPI index between the two the Top5% and Top10% groups was relatively low, respectively, in Landrace breed, 147.23 points compared to 141.52 at facility A and 143.55 points compared to 130.67 at facility B; in Yorkshire breed, 163.57 points compared to 161.24 at facility A and 149.37 points compared to 142.05 at facility B. Even the difference in SPI value between Top5% and Top25% was not high. Similar in Landrace breed, 147.23 points compared to 127.29 (facility A) and 143.55 points compared to 124.10 (facility B); in Yorkshire breed, 163.57 points compared to 143.14 (facility A) and 149.37 points compared to 133.27 (facility B).In other hands, the difference in SPI value among individuals in the Top25% group was not high. The reason is that the difference was not high because the number of sires was small and they have been rigorously selected so the quality was quite similar.

Therefore, the selection for genetic improvement for sires in this study will certainly face many difficulties and require selection programs in longer time.

Table 3.23: Average EBV of Top5%, Top10%, Top25% of the best individuals in L and Y sire herds based on SPI index in Jan 2019

Facility	Breeding level	Landrace sow herd		Yorkshire sow herd	
		Number of sows	SPI index (Mean±SD)	Number of sows	SPI index (Mean±SD)
A	Top5%	13	171.27±17.77	20	172.26±13.70
	Top10%	25	162.00±16.13	40	159.91±15.86
	Top25%	62	145.57±17.40	89	145.33±17.37
B	Top5%	21	162.29±10.62	9	159.38±10.09
	Top10%	42	153.64±11.82	18	149.28±12.72
	Top25%	105	140.07±13.83	46	136.44±13.33

In contrast, in the sow herds, selection for sow herds at the time of the survey with 880 Landrace sows and 580 Yorkshire sows in both facilities, the difference in SPI values between Top5% and Top25% was relatively high, corresponding to 25.7 points (facility A); 22.2 points (facility B) in the Landrace breed and 26.93 points (facility A); 22.94 points (facility B) in Yorkshire breed (table 3.23).This indicates that the genetic variation among individuals in the Top25% group of the breeding stock was relatively high. The reason for this is that the difference was higher than that of sires because the selection rate in sows was higher, so the homogeneity level in the selection group was not as high as in sires. Therefore, it is easier to improve the three reproductive traits including NBA, NW and WW in Landrace and Yorkshire sows in the current study based on SPI selection index than sires.

However, for the entire breeding herd, the annual genetic improvement depend largely on the selection for sires, because a sire can mate with hundreds of sows and produce thousands their offsprings. Therefore, for the two pig breeding facilities in this study, it is necessary to expand the linkage, exchange genetic resources with other breeding facilities to increase the size of the selective breeding herd. At the same time, applying the genetic evaluation process to link the breeding facilities to compare and detect individuals with excellent genetic potential, continue to propagate and quickly spread genetic improvement to the entire breeding herd. .

3.4. Evaluation of genetic trend for NBA, NW and WW and SPI index

3.4.1. Genetic trend for the NBA, NW and WW in breeding herd at facility A

At facility A, the results of the analysis of the genetic trend for NBA, NW and WW traits for Landrace and Yorkshire pig herds are shown in Figure 1 and Figure 2. As mentioned above, from before 2015, The breeding herds at facility A has been applied a selection method based on evaluating individualphenotype

Therefore, the genetic change in the period of 2011-2015 was very slow and erratic up and down over the years in all three reproductive NBA, NW and WWtraits, especially in Yorkshire breeds. It is clear that the selection method based on theselective efficiency ofproductivity (phenotype) evaluation in the individuals was not high, the average EBV of the breeding herds was varied abnormally and there was no genetic improvement for NBA and WW traits in both Landrace (Figure 1) and Yorkshire (Figure 2).From 2015 to the reporting time, the breeding herds at facilityA has been started to apply on SPI and MLI selection index. However, the SPI index also included only two reproductive traits in the selection index, that was, NBA and BW 21 days age/litter. Meanwhile, MLI index out of the above two reproductive traits, there was also the characteristic of back fat thickness and age of 100kg. Therefore, at this stage, the NBA traits tended to improve clearly and quite consistently over the years.Over the three years, from 2015 to 2018, the NBA traits improved a total of 0.2 piglets/litter in the Landrace herd (Figure 1) and 0.17 piglets/litter in the Yorkshire herd (Figure 2). For the WW trait, the improvement trend was very fast in the Landrace herds (Figure 1), but tends to decrease in the Yorkshire herds (Figure 2).

This may be explained by the direct selection trait at the weight of 21 days age but not WW, so it is possible that variation in weaning age have influenced the selection trait. The less varied the weaning age between the farrowings and the closer to the selected age at 21 days of age, the more direct in selection of bodyweigh at 21-day can result in a improvement in the WW trait. Continuous transfer (interval of 3-5 days/time) among litter that have been applied at facility A may also be the cause of the genetic improvement failures forWW traits in these two breeding herds.

For the NW trait, the results of Graphs 1 and 2 show that, in the period 2015–2018, the trend of this trait was indicated a certain genetic improvement in both Landrace breeding herds (0.06 piglets/litter) and Yorkshire (0.02 piglets/litter). Although this was not a selective trait, the genetic improvement of NW trait in these two herds at facility A was still achieved at a certain level. This can only be explained by the positive genetic correlation between these two traits at a relatively tight level in the Landrace herd and at a definitely tight level in the Yorkshire herd (Nguyen Huu Tinh *et al*, 2018).

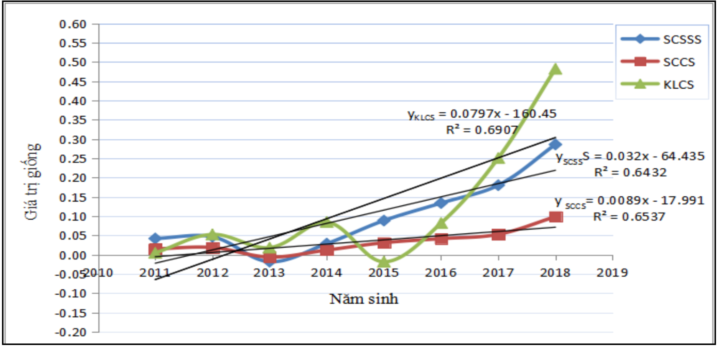

Figure 1: Genetic trend of NBA, NW and WW traits in L breed at facility A

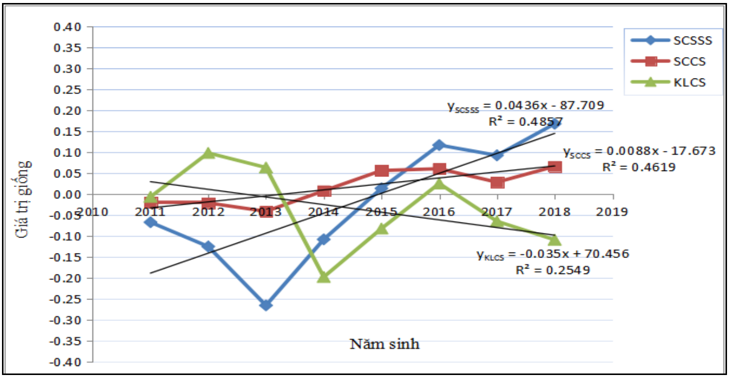

Figure 2: Genetic trend of NBA, NW and WW traits in Y breed at facility A

In the current study, overall view of the two breeds for the period 2011-2018 at facility A, genetic trend of all three traits was surveyed in Landrace and Yorkshire breeds tended for improvement, except for WW in Yorkshire herds, especially for NW traits. In Landrace breed herds, the yearly average genetic improvement of NBA, NW and WW traits was 0.032 piglets/litter, 0.0089 piglets/litter and 0.0797 kg/piglet, respectively.

Therefore, for Landrace and Yorkshire breeding herds at facility A, it is necessary to continue applying the selection method based on the breeding value, meanwhile supplementing the NW trait to the selection index so that the genetic improvement of this trait was as high as NBA trait. Whereas, for the WW trait, because the actual transfer process can greatly influence to the accuracy of the same values of this trait, it may be considered this trait is not include in the selection index, to reduce statistical complexity and possibly accelerate the rate of genetic improvement of other reproductive traits.

3.4.2. Genetic trend of NBA, NW and WW in breeding herd at facility B

For breeding herd at facility B, from 2010, the selective indexes was applied on the estimated breeding value by BLUP method, in which there were two reproductive traits: NBA and body weight at 21 days age/litter included in the selective index. By 2016, NW traits was continuedadding to the selection index for these two breeds. Therefore, compared tofacility A, the two breeds of Landrace and Yorkshire at facility B tended to improve their genetics more regularly in both NBA and NW traits during 2011-2018.

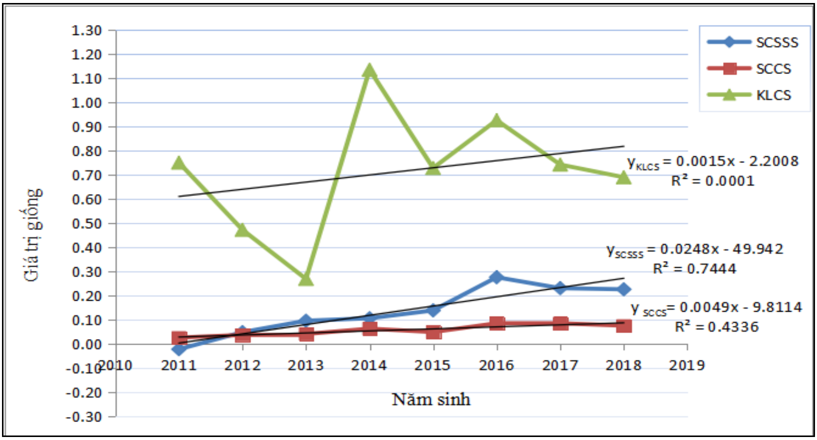

Figure 3: Genetic trend of NBA, NW and WW traits in L breed at facility B

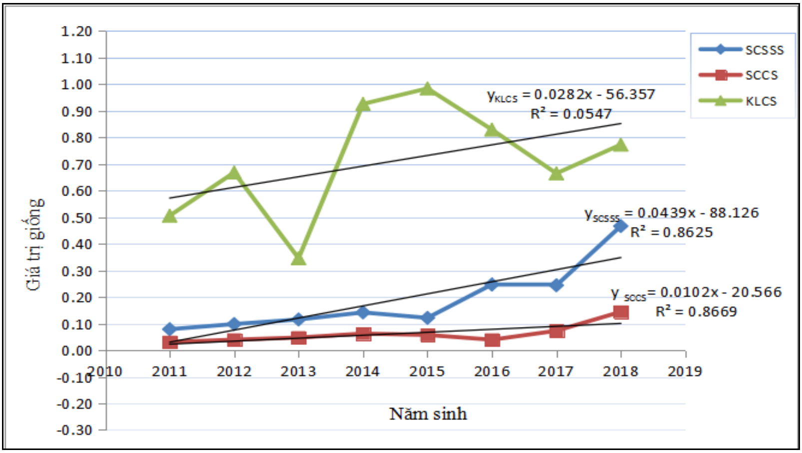

Figure 4: Genetic trend of NBA, NW and WW traits in Y breed at facility B

Particularly, WW traits, although there was still a tendency to improve, these improvements were not steady but up and down erratically over the years. Therefore, the determination coefficient (R2) of the linear regression line for the WW trait was very low in both surveyed breeding herds (0.0001-0.0547).In Landrace breeds, the total genetic improvement of NBA, NW traits in the period of 2011-2018 was 0.30 piglets and 0.04 piglets/litter and the average annual was 0.0248 piglets/litter; 0.005 piglets/litter, respectively. This shows that the selective efficiency of NBA trait was better than that of NW trait because the NW trait was influenced by environmental factors more seriously than NBA.

Thegenetic improvement of Yorkshire breeding herds was higher than that of the Landrace herd. In the period of 2011-2018, genetic improvement of NBA, NW traits in Yorkshire breeding herds at Facility B was 0.40 piglets/litter and 0.10 piglets/litter, respectively, an anual average was 0.044 piglets/litter and 0.01 piglets/litter.

This result also shows that the selective efficiency based on EBV by the BLUP method was remarkable and needed to be maintained, especially forboth NBA, NW traits. Particularly, the WW trait consideredwas not needed to be included in the selective index if the transferring process was regularly conducted among farrowings

3.4.3. Genetic trend of SPI selective index for breeding herds at facility A and facility B

In chart 5, for breeding herd at facility A, before 2015, by the application of selective evaluation based on the individual's phenotype, the genetic improvement of the SPI index was improved poorly over the period of 2011–2015 and improvement tend was irregularly, especially in Yorkshire breeding herd. The SPI index was increased from 101.6 to 103.3 points in the Landrace breeding herd and from 97.8 to 101.0 points in the Yorkshire breeding herd.

In the period of 2015-2018, by the application of a selective index based on the EBV of the NBA and BW at 21 days age, the genetic improvement of the SPI index also was improved markedly in both breeding herds at facility A. After 4 years, the SPI index was increased from 103.3 to 112.1 points in the Landrace herd and from 101.0 to 105.3 points in the Yorkshire breed. To sum up from 2011 to 2018, the SPI index was increases an average of 1.26 points every year with a coefficient of 0.66 in the Landrace herd and 1.18 points in the Yorkshire breed with a coefficient of 0.45.

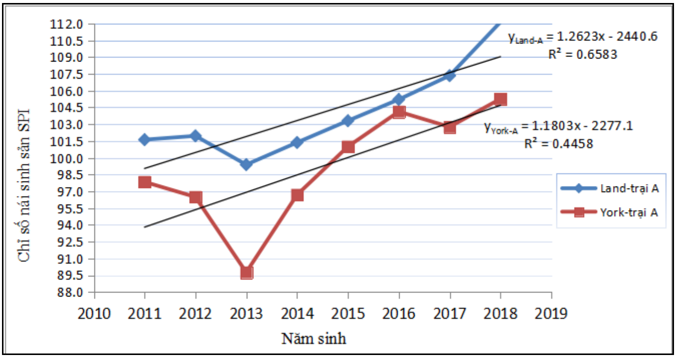

Figure 5: Genetic trend to SPI productive sow index in L, Y at facility A

In figure 5, for breeding herd at facility B, by the application of selective index based on EBV from 2010, so since 2011, the average SPI index of Landrace and Yorkshire herds was higher than 100 points. Since 2016, the NW trait has been added to the SPI index, the GT of this index also gained certain changes. In the Landrace herd, the value of the SPI was increased rapidly in 2016 but then decreased again. While in Yorkshire breeds, the value of the SPI index was increased strongly in 2018 (reached 113.5 points). This is entirely consistent with most breeding programs by adding new traits to selection, the genetic improvement achieved in the first few years was very limited (NSIF, 2001). Thus, for the breeding herd at facility B, the average for the period from 2011 to 2018, the SPI index of the two breeds of Landrace and Yorkshire was increased by 0.783 and 1,225 points/year respectively with a determination coefficient of 0.60-0.89.

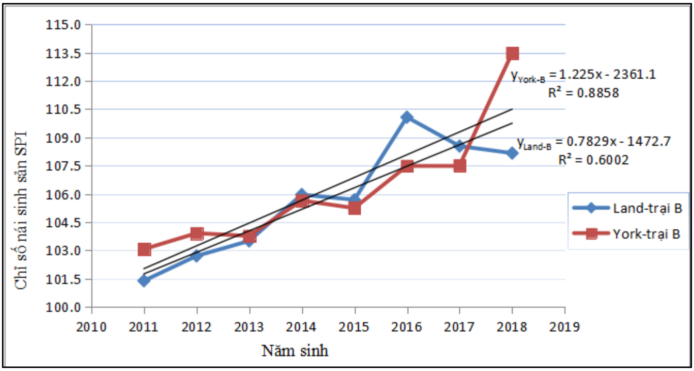

Figure 6: Genetic trend to SPI productive sow index in L, Y at facility B

CONCLUSIONS AND RECOMMENDATIONS

1. Conclusions

The annual fixed and seasonal factors all influenced the three traits of NBA, NW and WW with P levels from P<0.05 to P<0.001, the weaned age cohort had a significant influence on the traits of NBA, NW and WW (P<0.001); Mating factor did not influenced to all three traits in the two landraces and Yorkshire breeding herd at facility A and facility B. The parity factor influenced all three traits at P<0.01-P<0.001 in Yorkshire, but only influenced NBA trait (P<0.001) in Landrace. Housing type factors influenced NW and WW traits with P<0.01-P<0.001 for Landrace; Only influenced NW trait (P<0.01) for Yorkshire.

Model 3 was selected as the most appropriate model for simultaneous genetic analysis for all three traits: NBA, NW and WW on two Landrace and Yorkshire breeds in both facility A and B. Model 3 included factors such as housing type, parity, piglet weaned age, HYS, permanent parity effects, overall maternal effects and maternal genetic effects on genetic analysis

In facility A and B, the difference in average EBV of NBA, NW and WW traits between Top5% and Top10% in Landrace and Yorkshire sires was relatively low and would be difficult in the selective genetic improvement of these traits; while in the sow herd, the difference in mean breeding values between the Top5% and Top25% groups was higher to indicate that it would be easier to genetic improvement of these reproductive traits in the sows. The application of selective SPI indexs based on EBV for some reproductive traits in Landrace and Yorkshire breeders at facility A (from 2015) and facility B (from 2010) was properly improved in genetic.

Among three traits in this study, the NBA had a more regular positive genetic trend and annual genetic improvement with 0.025-0.032 piglets /litter/year in the Landrace herd and 0.044 piglets/litter/year in the Yorkshire herd.

2. Recommendations

Need to periodically analyze and check the level of genetic influence from dam line to get a timely adjustment to the appropriate statistical model in genetic evaluation programs selected for reproductive traits.

For the Landrace and Yorkshire breed herds in facility A and facility B currently, need to consider selective trait, especially in the total weigh of weaed piglets, in accordance with management conditions, technical procedures. selection of hatcheries to achieve the highest possible selective efficiency

Facilities with high crossfostering, do not need to estimate genetic value for NW trait and do not include this trait in the selectivity index.

Pig breeding facilities in Vietnam, especially, grand – grandparent, grandparent breed need to expand linkages and exchange genetic resources with other breeding facilities to increase the selective sire herd, meanwhile detect and disperse individuals with excellent genetic potential to the entire breeding herd. Other while, uniform management and a four-level pyramid breeding model building are necessary to rapidly increase genetic improvement.

PUBLISHED PAPERS RELATED TO THE THESIS

1. Tran Thi Minh Hoang, Nguyen Huu Tinh and Nguyen Van Duc. 2019. *Estimation of direct and maternal genetic, common and permanent environmental effects for litter traits in Landrace and Yorkshire pigs***.** Journal of Animal Husbandry Sciences and Technics, 251(11.19): 12-18.

2. Tran Thi Minh Hoang, Nguyen Huu Tinh and Nguyen Van Duc. 2019. *Genetic trends of reproductive traits in Landrace and Yorkshire breeds*. Journal of Animal Husbandry Sciences and Technics, 251(11.19): 19-24.

3. Tran Thi Minh Hoang, Nguyen Huu Tinh and Nguyen Van Duc. 2019. *The breeding values of reproductive traits in Landrace and Yorkshire pigs*. Journal of Animal Husbandry Sciences and Technics, 252(12.19): 02-08.