The genetic correlation between scapula shape and shoulder lesions in sows¹

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ABSTRACT: Shoulder lesions and body condition of sows at weaning have both environmental and genetic causes. The traits can be scored at farm level, and following recording, the traits can be included in the breeding goal and directional selection can be applied. However, to further increase the genetic progress of these traits, it is advantageous to develop indicator traits on the selection candidates (test boars or gilts, not yet exhibiting the phenotype themselves). It has previously been suggested that the scapula morphology and the spine of scapula might be a key factor for the sow to develop shoulder lesions. In this study, we developed 11 novel traits describing the morphology of the shoulder blade based on computed tomography images from scanned test

boars. These traits include the area, length, width, height, and volume of the shoulder blade as well as 6 traits obtained from principal component analysis, describing 80% of the variation observed for the scapula spine profile. The analyzed traits have moderate to high heritability (h^2 from 0.29 to 0.78, SE = 0.06), low to medium genetic correlations with shoulder lesions (up to 0.4, SE = 0.1), and body condition scoring at weaning (up to 0.25, SE = 0.1). These novel phenotypes can now be recorded automatically and accurately prior to selection of the AI boars. If such recordings are included in multivariate genomic selection models, it is expected to improve the genetic progress of shoulder lesions and body condition score by weaning.

Key words: computed tomography, genetic correlations, pig, principal component analysis, scapular shape, shoulder lesion

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INTRODUCTION

One of the challenges in pig production is the development of shoulder lesions (SL) in lactating sows (Herskin et al., 2011). The development of SL is affected by mechanical stress in the soft tissue between solid surface and the scapular spine for an extended period. Blood vessel compression in the tissue around the tuber of the scapular spine results in insufficient blood circulation, necrosis, and subsequently ulceration (Herskin et al., 2011). In addition to pain (Larsen et al.,

2015), SL can act as an entrance for pathogens causing infections and thus result in antibiotic treatment and economic loss (Reese et al., 2005; Bonde et al., 2007; Herskin et al., 2011). The prevalence and severity of SL are affected by environmental factors, such as feeding, flooring, temperature, and humidity (Reese et al., 2005; Zurbrigg, 2006; Bonde et al., 2007). The genetic basis for SL is complex. Simultaneous selection for improving maternal traits, such as litter size and piglet growth, and breeding for leaner animals have reduced the fat reserves of lactating sows (Lundeheim et al., 2014). As the fat layer might work as a protecting layer between the skin and the bones, keeping a satisfactory body condition is important to reduce SL risk (Lundgren et al., 2012). It has previously been investigated whether the scapular shape affects the risk of getting SL

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(Agerley, 2007; Billström, 2007). However, these were carcass studies, and the size of the data set evaluated may have been too limited to observe any relationship.

Here, computed tomography (CT) images from test boars are utilized and traits are developed to quantify the scapular shape. Heritabilities for these new traits are estimated as well as genetic correlations with SL and body condition score (BCS). The aim of the study was to quantify the scapular shape effects on SL and BCS observed on sows by weaning.

MATERIALS AND METHODS

Animals

The animals in this study were purebred Landrace and originated from the Norsvin-breeding nucleus and multiplier herds. All phenotypes described were part of the routine collection in the breeding program and conducted in accordance with the laws and legislations for keeping the pigs in the country where recordings were made.

Sows. The 65,729 sows in this study were Norsvin Landrace, raised in more than 50 nucleus herds in Norway, Lithuania, Finland, Sweden, Spain, and the United States. The protocols for scoring were the same in all countries and close genetic ties between the subpopulations were ensured by the supply of semen from elite-boars in Norway. Shoulder lesions and BCS for individual sows at weaning were recorded according to the protocol developed by Norsvin and Animalia (Animalia, 2016). The assessment protocol builds on the article by Jensen (2009), where the lesions are scored on the side with most severe SL, from 0 (no ulceration) to 4 (spina scapula protruding through the skin). The assessments were done by the herdsmen and entered into the sow management system. Only data from the first parity of sows were included in the analysis.

Boars. The 2,393 Landrace test boars in this study were CT scanned as part of the Topigs Norsvin genetic program as described in detail by Aasmundstad et al. (2013). These purebred boars were born and raised to 25 to 30 kg in different nucleus herds located in Norway before they were sent to the boar testing station. The test includes feed and weight recordings, score for conformation traits, and CT scanning at the end of the test (at 120 kg) as described by Gjerlaug-Enger et al. (2012).

Virtual Dissection and Aligning of Objects

As in Kongsro et al. (2017), the full skeleton of in vivo pigs was identified by applying a threshold value of 200 Hounsfield units to the CT scans (Fig. 1). Thereafter, the shoulder blades were identified, extracted (Gangsei and Kongsro, 2016), and aligned based on image moment invariants (Hu, 1962). Each shoulder blade was centered based on its mass center, scaled based on its length, and rotated based on its eigenvectors, see Gangsei et al. (2016) for details. Eigenvectors are per definition orthogonal to each other. The first eigenvector of the shoulder blade was parallel to the spine of scapula (x-axis Fig. 2a and b), and the length was measured along this axis. The second eigenvector points in the direction of second most distribution of mass (y-axis Fig. 2a and x-axis Fig. 2c), and the third vector is orthogonal to the first two (y-axis Fig. 2b and c).

Phenotypes from Scapula

The following measures were registered from CT-scanned animals:

- The volume measured in cubic centimeter; length (x-axis Fig. 2a), maximum width (y-axis Fig. 2a), and maximum thickness (y-axis Fig. 2b), all measured in millimeter; as well as area of scapula measured in square centimeter in the plane spanned by first $\times$ second eigenvector (Fig. 2a).
- The profile of the scapula, which gives the thickness measured in millimeter for the thickest point along the main direction of distribution of mass, indicated as red dots from left to right of Fig. 2a and with values visualized in Fig. 3.

For each animal, these traits were registered for the left and the right shoulder blades independently.

Figure 1. Pig skeleton with scapula highlighted, reconstructed based on CT imaging.

Figure 2. The shape of the scapula from 3 different views: (a) the first (along the x-axis) vs. second (along y-axis) eigenvector, (b) the first (along x-axis) vs. third eigenvector (along y-axis), and (c) the second (along x-axis) vs. the third eigenvector (along y-axis). The units of the axes are scaled to the length of the scapula along the first eigenvector. The colors indicate the number of pixels in the direction not shown in each of the views. The red dots in (a) correspond to the column with maximum thickness along the third eigenvector, going from row 1 to 100 along the first eigenvector (x-axis in the panel).

Figure 3. The thickness profile vector of the shoulder blades. Each line corresponds to one animal and measures the thickness of the scapula along the first eigenvector from the joint between scapula and humerus (pos 0), over the spine of scapula and to the medial border (pos 100).

Three datasets were generated, one for the left, one for the right, and one for the average of the 2 shoulder blades. To get rid of noise due to segmentation in the datasets, 2.5% of the observations in each dataset were classified as outliers, using Mahalanobis distance (Mahalanobis, 1936) based on principal components of the profile vector.

The thickness profile vectors (Fig. 3) are 100-dimensional; however, measurements of neighbor points are highly correlated. To obtain a manageable number of uncorrelated traits for genetic analysis, a principal component analysis (PCA) (MATLAB R2017b, 2017) was performed on the “cleaned” profile vectors and the PCA scores were used as phenotypes. All of the thicknesses traits

Figure 4. Cumulative phenotypic variance explained by adding principal components. The red line corresponds to the full dataset, averaged over left and right scapula, while green and blue dotted lines correspond to the left and right scapula datasets, respectively.

were measured in millimeters in the profile vectors, and consequently, there was no need to scale the data. By default, this PCA centers the data before performing singular value decomposition and the centering provides the average profile vectors for each of the datasets (Fig. 4). To avoid mixing negative phenotypes from PCA analysis and indicators for missing values (which is “-9” in the genetic analysis), the smallest value observed was added from all PCA scores, so all values observed were positive.

Genetic Analysis

Each of the traits from the CT-scanned animals was used in multitrait BLUP animal models together with SL and BCS at weaning from the sows' first parity. The CT traits, which includes volume, length, width, height, and area of the scapula as well as PCA traits, were modeled as follows:

$$\text{CTtraits}_{ijklm} = \text{HY}_i + \text{BM}_j + \text{PN}_k + \beta \times \text{LW}_l + a_m + e_{ijklm}$$

The fixed effects included in the model for the traits recorded based on CT images were birth herd-year (HY) of the boar, birth month (BM), and parity number of the dam of the sow (PN). The boar's phenotype for live weight at scanning date (LW) was included as a fixed regression. The additive genetic effect of the animal (a_m) and the residual (e_{ijklm}) were included as random effects. Number of levels for HY was 152, for BM it was 12, and for PN it was 4.

SL and BCS registered at weaning of the first litter were analyzed as follows:

$$\text{SL / BCS}_{ijkl} = \text{HY}_i + \text{SEA}_j + \text{WEAN}_k + a_l + e_{ijkl}$$

The fixed effects included in this model were HY, season (SEA), and number of weaned piglets (WEAN). Number of levels for HY for SL was 749 and for BCS it was 705. Number of levels for SEA was 4 and for WEAN it was 28 for both traits. The additive genetic effect of the animal (a_l) and the residual (e_{ijkl}) were included as random effects. The (co)variance estimates were obtained from 3-variate genetic models where SL and BCS at weaning from the sow data were modeled together with each of the boar CT traits (one at a time) using the DMU software (Madsen and Jensen, 2013). Including more than one PCA in multitrait models together with SL and BCS resulted in convergence problems. Hence, 3-variate models were used.

RESULTS

Descriptive Statistics

Descriptive statistics for the traits are shown in Table 1. The CT traits in this table represent the dataset where the phenotypes are calculated as a mean of the 2 shoulder blades. Corresponding tables where the CT traits are based on the right and left shoulder blades independently are in Supplementary Tables S1 and S2. All the traits registered from the CT images (volume, area, length, width, height, and PCAx) and BCS seem to be normally distributed, while SL has quite a skewed distribution with about 80% of the animals having the phenotype 0 (Table 1).

Principal Components

The profile of the scapular spine is defined as a vector of depths for each animal (Fig. 2). As there is a lot of covariance between neighboring points, a PCA summarizes the main axis of variation. As showed in Fig. 4, a few principal components can explain a large degree of the phenotypic variation. The first 6 principal components explain approximately 80% of the variation (Fig. 5) and were selected for further analysis. The subsequent principal components fluctuate more, were hard to interpret, and were omitted for the rest of the analyses. In addition to the principal components, the

Table 1. Descriptive statistics of the traits in the full dataset in a study of scapula traits and shoulder lesions in purebred Norwegian Landrace pigs

Trait ¹	Mean	SD	Minimum	Maximum	N ²
Area, cm ²	140.4	8.1	112.0	182.9	2,333
Volume, cm ³	171.3	15.6	126.0	240.6	2,333
Length, mm	172.2	5.5	153.3	197.3	2,333
Width, mm	131.5	4.4	113.8	147.5	2,333
Height, mm	59.4	3.6	46.9	79.6	2,333
PCA1	62.1	16.7	0	118.9	2,333
PCA2	41.3	12.8	0	88.8	2,333
PCA3	54.3	9.4	0	81.9	2,333
PCA4	41.9	7.6	0	65.3	2,333
PCA5	22.9	6.2	0	52.8	2,333
PCA6	22.6	5.6	0	41.3	2,333
SL	0.2	0.6	0	4	65,729
BCS	4.2	0.9	1	9	64,264

¹Scapula area measured in the plane spanned by first × second eigenvector; scapula volume; the scapula length, width, and height (the extent of scapula along first, second, and third eigenvectors, respectively); PCA = principal components of the profile of the scapula; SL = shoulder lesions; BCS = body condition score.

²N = number of animals with trait recorded.

PCA provides the mean, which represents the population's average thickness profile for the scapula. The thickness of the right scapula was a slightly higher than for left (see Fig. 6). For the spine of the scapula (pos = 60, Fig. 6), the average thickness was about 2 mm greater for right shoulder blades than for left shoulder blades. Similarly, this was observed for the height phenotype in the descriptive statistics (Supplementary Tables S1 and S2).

Principal component coefficients based on mean compared to left or right scapula were similar both in proportion of explained variance and in geometric description (results not shown here). For the full dataset, the first 6 principal component coefficient vectors (Fig. 5) explain 34%, 20%, 11%, 7%, 5%, and 4% (79% all together) of the observed variance. If the PCA scores are multiplied by their respective coefficient vectors and then added to the population average (Fig. 5), then it is possible to restore the original phenotypes (Fig. 3). Figure 7 shows a partial restoring, using the 6 first principal components.

Genetic Parameters

The heritabilities for the scapula traits vary from moderate (0.29) to high (0.78) (Table 2), while SL and BCS had heritabilities equal to 0.18 and 0.19, respectively. The average trait heritability

Table 2. Heritability estimates ($\pm$ SE) for the traits from the CT-scanned animals from a study evaluating the relationship between scapula measures and shoulder lesions in purebred Norwegian Landrace sows

Trait ¹	Full		Left		Right	
	<i>h</i> ²	$\pm$ SE	<i>h</i> ²	$\pm$ SE	<i>h</i> ²	$\pm$ SE
PCA1	0.52	0.06	0.52	0.06	0.58	0.07
PCA2	0.63	0.06	0.59	0.06	0.63	0.07
PCA3	0.29	0.06	0.29	0.06	0.35	0.06
PCA4	0.48	0.07	0.41	0.07	0.41	0.06
PCA5	0.37	0.06	0.31	0.05	0.39	0.06
PCA6	0.50	0.06	0.54	0.07	0.44	0.06
Area, cm ²	0.57	0.07	0.71	0.07	0.55	0.07
Volume, cm ³	0.78	0.06	0.72	0.06	0.77	0.06
Length, mm	0.51	0.06	0.54	0.07	0.54	0.07
Width, mm	0.72	0.07	0.66	0.07	0.69	0.07
Height, mm	0.60	0.06	0.47	0.06	0.51	0.06
Mean	0.54		0.52		0.53	

Results for full dataset and for datasets where the left and right scapula were analyzed independently.

¹PCA = principal components of the profile of the scapula, scapula area measured in the plane spanned by first $\times$ second eigenvector, scapula volume, the scapula length, width, and height (the extent of scapula along first, second, and third eigenvectors, respectively).

Figure 5. The first 6 PCA coefficient vectors of the full dataset, averaged over left and right scapula. These vectors define the traits from the PCA. The x-axis spans the first eigenvector from the joint between scapula and humerus (pos 0), over the spine of scapula and to the medial border (pos 100).

based on the mean of the 2 shoulder blades is a little higher than for traits based on the shoulder blades from either left side or right side individually. The scapula volume had the greatest heritability among the traits from all 3 datasets. Furthermore, the area, width, length, and height as well as PCA1, PCA2, and PCA6 have relatively high heritability. For all 3 datasets, PCA3 and PCA5 had the lowest heritability.

Genetic correlations between the CT traits and SL and BCS at weaning varies from low to moderate (Table 3). The correlations with SL are somewhat stronger than those with BCS. The traits with high heritability tend to have stronger correlation with both SL and BCS than traits with low heritability. Among the traits with strongest correlation are the width of the scapula based on the full dataset, which has a genetic correlation of 0.32 with SL and -0.25 with BCS. The first 2 principal components contribute significantly to both increased SL risk and having reduced BCS. The first of the principal components scales the thickness of the scapula spine (Fig. 5), and a more prominent tubular spine is genetically correlated with greater risk for getting SL. The second principal component moves the peak of the scapula spine in the length direction (Fig. 5). A high PCA2-component moves the scapula spine toward the joint between the scapula and the humerus and reduce the probability of getting shoulder ulcers. Figure 8 compares a favorable and an unfavorable scapula profile where the (un)favorable scapula is defined by adding 1 SD of scores in (un)favorable direction (from Table 3) of the first 6 PCA components to the average scapula

Figure 6. The average thickness profile vector of the scapula for the full dataset, averaged over left and right scapula (in red), while green and blue lines correspond to the left and right scapula datasets, respectively. The x-axis spans the first eigenvector from the joint between scapula and humerus (pos 0), over the spine of scapula and to the medial border (pos 100).

thickness profile. As the principal components are data dependent, the coefficient vectors for the full, left and right datasets are different. For PCA4 and PCA5, the left- and right-hand side PCA coefficient vectors are close to 180° to each other and the corresponding genetic correlations with SL and BCS have comparable size, but opposite sign (Table 3).

DISCUSSION

This study presents new objective traits describing the scapular shape and make use of PCA to aggregate high dimensional morphology variation

Figure 7. The thickness profile vector from the first 6 principal components. Each line corresponds to one animal and is the sum of the average thickness profile vector and the score $\times$ coefficients of the 6 first PCA components. The x-axis spans the first eigenvector from the joint between scapula and humerus (pos 0), over the spine of scapula and to the medial border (pos 100).

into a manageable number of traits for genetic analysis. The scapular shape recorded on CT-scanned boars is highly heritable and has a moderate genetic correlation with both SL and BCS observed on sows.

As seen from the results, the heritability of the traits describing the scapula size and shape is generally high (above 0.5 averaged over traits). This was expected as traits related to skeletal features have been reported as highly heritable both in human (Jian et al., 2004; Havill et al., 2007; Tsagkrasoulis et al., 2017) and in livestock animals (Hintz et al., 1978; Vargas et al., 1998; Utrera and Van Vleck, 2004). However, most of such literature within livestock science focus on the bone size or phenotypes related to bone length (e.g., height or stature), and not on the bone shape.

The heritability of the different measures of the scapular shape varies considerably, from 0.29 to 0.78. This may in part be explained by the bone segmentation accuracy. The automatic segmentation algorithms do not perfectly detect border zones between bone and cartilage, so the expectation is that an improved algorithm for segmentation and identification of the bones (Gangsei and Kongsro, 2016) would increase the heritability estimates. In contrast to the Width phenotype, the accuracy of both the length and thickness phenotypes depends on an accurate dissection between cartilage and bones. In addition, for some animals, when segmenting the joint between the shoulder blade and humerus, a small part of the scapula is removed or a small piece of the humerus is added to the scapula. Most of such “noise” is removed from the dataset through the outlier detection, but remaining outliers might add some noise into the genetic analysis, and thus reduce the heritability of the length of scapula. The suboptimal joint segmentation also adds “noise” to the phenotypes describing the scapula spine shape (PCA_x). Principal component 3 (PCA3) and PCA5 are the traits describing most of the variation in this region (Fig. 6, pos: 0 to 20 along the x-axis). Therefore, these phenotypes explain a lot of the “noise,” and this results in lower heritabilities than for the other PCA traits.

The results show that different modes of the scapular shape affect the sow’s risk for getting SL. For example, animals with a wide scapula have an increased risk of getting SL, which is similar to the findings based on sow postmortem inspection (Agerley, 2007). Agerley (2007) suggested that lesions build up gradually and were not evident on the skin surface before the sows were old. Agerley also suggested that that older sows have broader

Table 3. Genetic correlations (r) $\pm$ SE between the traits from the CT-scanned animals and SL and BCS for the full dataset and for the datasets where the left and right scapula were analyzed independently

Trait 1 ¹	Trait 2 ²	Full		Left		Right	
		r	$\pm$ SE	r	$\pm$ SE	r	$\pm$ SE
PCA1	SL	0.20	0.10	0.21	0.10	0.14	0.10
PCA1	BCS	-0.17	0.10	-0.17	0.10	-0.16	0.09
PCA2	SL	-0.33	0.09	-0.41	0.09	-0.27	0.10
PCA2	BCS	0.16	0.09	0.18	0.09	0.14	0.09
PCA3	SL	0.23	0.13	0.24	0.13	0.13	0.12
PCA3	BCS	0.01	0.12	0.11	0.12	0.06	0.11
PCA4	SL	-0.01	0.11	-0.11	0.12	0.11	0.11
PCA4	BCS	-0.09	0.10	-0.06	0.11	0.07	0.11
PCA5	SL	0.28	0.11	0.19	0.12	-0.26	0.11
PCA5	BCS	0.03	0.11	-0.08	0.12	-0.10	0.11
PCA6	SL	-0.13	0.10	-0.07	0.11	-0.12	0.11
PCA6	BCS	-0.09	0.10	-0.12	0.10	-0.01	0.10
Area, cm ²	SL	0.08	0.10	0.14	0.09	0.06	0.10
Area, cm ²	BCS	-0.19	0.09	-0.23	0.09	-0.24	0.10
Volume, cm ³	SL	0.14	0.09	0.17	0.09	0.13	0.09
Volume, cm ³	BCS	-0.18	0.08	-0.18	0.09	-0.17	0.09
Length, mm	SL	-0.03	0.10	0.02	0.10	-0.09	0.10
Length, mm	BCS	-0.18	0.10	-0.25	0.09	-0.20	0.09
Width, mm	SL	0.32	0.09	0.29	0.09	0.30	0.09
Width, mm	BCS	-0.25	0.09	-0.18	0.09	-0.27	0.09
Height, mm	SL	-0.23	0.09	-0.26	0.10	-0.18	0.10
Height, mm	BCS	-0.12	0.09	-0.08	0.10	-0.16	0.10

¹PCA = principal components of the profile of the scapula; scapula area measured in the plane spanned by first $\times$ second eigenvector; scapula volume, the scapula length, width, and height (the extent of scapula along first, second, and third eigenvectors, respectively).

²SL = shoulder lesions, BCS = body condition score.

scapula. However, in the present study, the animals were approximately the same weight (120 kg) when CT scanning was performed. In addition, the weight of the animal was included in the model as a linear

Figure 8. The average (in red) vs. the favorable (in green) and unfavorable (in blue) thickness profile of the scapula based on the full dataset. The (un)favorable scapula is defined by adding 1 SD of scores in the (un)favorable direction (Table 3) of the first 6 PCA components to the average scapula thickness profile. The x-axis spans the first eigenvector from the joint between scapula and humerus (pos 0), over the spine of scapula and to the medial border (pos 100).

covariate, and the results show a significant genetic correlation between scapula Width and SL. We assume that when a sow is lying on her side, a portion of her weight is transmitted through the scapula and another portion transmitted through soft tissue. A wide scapula accumulates a greater proportion of the sow's weight than a narrow one. This weight is transmitted through the scapular spine and through the thin layer of soft tissue between the tubular of the scapula spine and the surface where the animal is lying. Keeping all other parts of the sow's morphology constant, a wide scapula may generate a greater mechanical normal stress in the tissue between the spina of the scapula and the flooring than a narrow one. The other scapular shape measures that might affect the proportion of the weight transmitted through the scapula (e.g., volume and area) tends to influence SL in the same direction, although the correlations are weaker.

The interpreting of the relationship between the morphology traits and the biomechanical phenomena is not straight forward. A high peak of the scapular spine (high PCA1) may lead to increased mechanical stress on the surrounding tissue and might also be covered by a thinner fat layer than a

shorter peak. The results indicate that a flattened scapula with reduced distance between the joint and the spine of the scapula seems to be favorable to reduce the frequency of SL and improve the BCS at weaning.

There was a significant genetic correlation between the scapular shape and the risk for the sow having low BCS by weaning. However, this correlation was smaller when compared to the correlation between SL and the scapular shape. Literature reports a strong genetic correlation between BCS and SL, which is largely explained by a thinner fat layer increasing the risk of SL (Lundgren et al., 2012; Lundeheim et al., 2014). The genetic correlation between scapular shape and BCS suggests that the causal mechanism between SL and BCS partly works in both directions. Animals that get SL due to an unfavorable scapular shape might also get a low BCS. SL causes animals to change their behavior (Larsen et al., 2015), which might lead to reduced feed intake due to pain, and might increase maintenance requirements due to damaged tissue and thus reduce available resources for production and growth (Huber, 2018). All this could again lead to the sow having a low BCS. An alternative explanation for the genetic correlation between BCS and the scapular shape is that some animals have more prominent bone structure and this might affect the manual scoring of body condition. However, because almost all the CT traits with genetic correlation to BCS also have a significant correlation to SL, it is likely that the scapular shape mainly affects SL, which in turn may affect the BCS.

Another interesting finding in this study was the asymmetry of the 2 shoulder blades. Averaged over all animals, the right scapular spine was about 2 mm thicker than the left one, which correspond to about 6% of scapula thickness. Interestingly, this finding is in agreement with Billström (2007). Such asymmetric differences are not seen among the other traits in this study. Davies et al. (1997) reported a larger prevalence of SL on the right-hand side than on the left-hand side, which might indicate that sows may prefer laying on the right shoulder. The 2 traits that are closest connected to the scapula spine height in the current study (PCA1 and Height) have opposite signs of the genetic correlation with SL, and this complicates the interpretation of the relationship between SL and the scapula spine height. The causal link between the scapula shape and SL is probably the mechanical stress in the tissue surrounding the scapular spine. Increased mechanical stress might

induce bone growth (Lieberman et al., 2003). Such a phenomenon could potentially increase the scapula spine height on the preferred laying side, due to the mechanical load of the animal's weight when laying. If the animals really have a preferred laying side, this could explain both thicker right-hand scapula and more frequent SL on the right-hand side. To enlighten these questions, SL should be recorded separately on the left-hand and right-hand sides. In addition, more knowledge is needed about bone growth and sow laying behavior.

The new traits, describing the scapula shape, have greater heritabilities than most other traits in the breeding goal. The scapula has several suspension points for tendons and muscles, and putting much weight on the shape of the scapula in the breeding goal might have undesirable consequences for the functionality of the limb. In addition, a selection for a narrower scapula might alter the weight distribution of the pig, moving more of the total weight over to the hind legs. This could possibly also hamper the movement of the pig.

As the new measures of scapular shape have indirect economic or societal value only, it is not relevant to put weight on them in the breeding goal. Therefore, these new traits will be used only as covariables to improve the prediction of SL and BCS, which are already in the breeding goal for the Norwegian Landrace, partly due to animal welfare reasons (Kanis et al., 2005).

Implications

The use of atlas segmentation based on CT scans of test boars provides detailed morphological data of Norsvin Landrace nucleus boars. Because all station-tested boars have been CT scanned during the last 10 years, new traits can automatically be obtained for all relevant paternal ancestors of the breeding pigs. The new traits obtained in this study can be recorded on the nucleus boars before selection and will therefore most likely lead to increased accuracy of breeding values and improved genetic progress for SL and BCS. Improved genetic progress for SL and BCS will lead to improved welfare in the hybrid sows sired by boars from the Norsvin Landrace population selected for the trait.

SUPPLEMENTARY DATA

Supplementary data are available at *Journal of Animal Science* online.

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