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Genetic analyses of heart- and lung volume and correlations to mortality in pigs

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Animal breeding and genetics

Forord

Denne masteroppgaven markerer slutten på mitt fem år lange studieløp ved Norges miljø- og biovitenskapelige universitet. Det var interessen for gris og svineavl som var bakgrunnen for at jeg valgte å studere husdyrvitenskap. Jeg setter derfor stor pris på at jeg fikk skrive nettopp denne oppgaven om et så spennende og aktuelt tema innen svineavl.

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Abstract

The occurrence of sudden cardiac death in pigs (*Sus scrofa domestica*) is a known problem. Sudden death of pigs causes economic consequences for the farmers and is a challenge for animal welfare. Compared to the wild boar, which is the ancestor of the domestic pig, the size of the heart of the domestic pig has decreased in relation to body weight. It is conceivable that this causes an insufficiency of the cardiovascular system. As the heart size has decreased, it is also conceivable that the size of the lungs, which is located in the thoracic cavity together with the heart, has decreased as well. A decreased lung size could affect the oxygen supply. This will most likely not benefit an already insufficient cardiovascular system. Hypertrophic cardiomyopathy (HCM) is a heritable condition defined by the presence of an increased left ventricular thickness and can cause sudden cardiac death. If HCM occurs in pigs and this condition is aggravated by an insufficiency of the cardiovascular- and respiratory system, it would be in interest to find out if heart- and lung volume are traits possible to breed for. The aim of this thesis is therefore 1) To estimate genetic parameters for heart- and lung volume in pigs and the genetic trend for these. 2) To determine if there is a genetic correlation between heart- and lung volume and mortality in pigs.

The data used in this thesis was obtained by Norsvin and Topigs Norsvin and consists of data of heart- and lung volumes of 5 430 and 5 464 purebred Landrace and Duroc boars, and data of mortality of 202 233 and 6 812 purebred individuals of Landrace and Duroc. The data of heart- and lung volume was obtained by CT-images of the boars. The data of mortality are registrations of individuals who have died by themselves in the period from weaning to finishing. Genetic parameters and genetic correlations were calculated for heart volume, lung volume and mortality. Genetic trends were investigated for heart- and lung volume.

Heritabilities ranging from 0,313 – 0,402 was found for heart- and lung volume for both breeds. There was a positive genetic correlation between heart- and lung volume for Duroc. A small positive genetic correlation was found between heart volume and mortality for Landrace. Mortality was not analysed for Duroc because of a too small dataset. A decreasing genetic trend for heart- and lung volume was found for both breeds. To conclude: there is a genetic variation in heart- and lung volume for both the breeds and the genetic trend for these traits should therefore be possible to change by selection. It is conceivable that heart and lung volume for Duroc, to some extent, changes together. The positive correlation between heart volume and mortality for Landrace indicates that relatives of pigs with genetically bigger hearts at CT-scanning tends to have higher mortality. Further research should be conducted.

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Introduction

It is found that the size of the heart relative to body weight for the modern pig (*Sus scrofa domestica*) has decreased (Niewold et al., 2000; van Essen, 2017). The wild boar, which is the ancestor of the modern pig, has a relative heart to body weight of 0,6% (Giuffra et al., 2000; Niewold et al., 2000). This relative weight has decreased significantly for the modern pig, especially during the last century, when the modern fattening pig had reached a relative heart weight of 0,3% of its body weight, measured at the same weight as the wild boar (Niewold et al., 2000). Other changes in the cardiovascular system and its components have also occurred due to domestication and selection of animals in the pig breeding. The blood volume and the haemoglobin level have also decreased in relation to body weight (Niewold et al., 2000; Van Essen et al., 2018). Selection on economical traits like growth rate, feed utilization and muscle development has with time led to remarkable differences in body composition, anatomy and physiology in the pig (van Essen, 2017).

Changes like these can cause an increased risk of insufficiency of the cardiovascular system (Niewold et al., 2000; van Essen, 2017). A well-functioning cardiovascular system is vital for all animals. The cardiovascular system and the blood's main task in the body is transportation of nutrients and oxygen (Sjaastad et al., 2016). The blood transports numerous of vital substances around in the body to the different organs and tissues. Among these substances is oxygen from the lungs (Sjaastad et al., 2016). If the size of the heart is too small in relation to the body, this can lead the heart to exceed its physiological limits while trying to serve the organs and tissues with vital substances such as oxygen (Zurbrigg, 2018). The heart will then have to compensate by pumping faster to be able to serve the body with a sufficient amount of blood. When the heart muscle have to work harder, this can with time lead to changes in the muscle tissue (Zurbrigg, 2018). The muscle cells might grow bigger and the heart walls might become thicker. A condition where the left ventricle of the heart muscle is thickened is called hypertrophic cardiomyopathy (HCM). HCM is defined by the presence of increased left ventricular wall thickness that is not solely explained by abnormal loading conditions (Elliott et al., 2014). The condition can in some cases prevent a normal blood flow and lead to heart failure (Elliott et al., 2014; Simpson et al., 2017). Although, HCM does not always cause any trouble, it can cause heart failure if the individual is exposed to stress or unusual physical activity. In other cases, it can cause heart failure without any obvious influencing factor (Maron & Maron, 2013).

It is a known problem that sudden death as a consequence of heart failure in pigs can occur (Fallavollita et al., 2005; Johnson et al., 2013; Zurbrigg, 2018). A pig's reaction to stress is usually a flight-response (Manning, 2012; van Essen, 2017). This response to stress requires an increase of oxygen transported to the skeletal muscles so that the animal can run away fast. To supply the body with the extra oxygen the heart rate increases and the breathing becomes more rapid (Manning, 2012; van Essen, 2017) This requires an adaption of the cardiovascular system that might become too much for animals with a limited functioning of the cardiovascular system and heart failure may occur (van Essen, 2017; Zurbrigg, 2018). The body's reactions to stress are mostly attempts to restore balance of the metabolism, homeostasis (Manning, 2012). The flight response is not the only thing that affects the homeostasis. Anything disturbing the balance of the metabolism requires an adaption of the cardiovascular system and can be a stress factor in the body. There are many examples of stressors that can cause this reaction for a pig, like heat or cold, mixing with new individuals, transportation, weaning and disease (Hicks et al., 1998; Manning, 2012). It is not determined that heart failure that occurs in pigs is caused by HCM or HCM alone. But there are findings that suggests that hearts with features similar to HCM increases the chance of heart failure under stressful circumstances (Zurbrigg, 2018).

Hypertrophic cardiomyopathy is known as a heritable condition for humans, cats, dogs and also some other species (Burch & Blair, 1999; Simpson et al., 2017). In humans, over 50% of all cases of HCM are inherited (Burch & Blair, 1999; Maron & Maron, 2013). Inherited HCM is caused by mutations encoding for sarcomeric and sarcomere related proteins. There is found more than 1400 mutations in 11 or more genes that causes HCM (Lin et al., 2003; Maron & Maron, 2013). These mutations lead to changes in the structure of the muscle cells of the heart and affects the hearts' ability to contract properly (Maron & Maron, 2013). It is also found a heritable form of HCM in pigs (Simpson et al., 2017). A study of cardiac morphology including measurements of the factors characterizing HCM suggested that a genetic variation in cardiac morphology might exist in pigs (Huang et al., 2001). Another study investigated if heritable cardiac conditions could be associated with histological lesions found in pig hearts of pigs that died during transport. This study concluded that pigs with limited ability for cardiac compensation could be predisposed to die during transport because of the stress and exertion this can cause for a pig (Zurbrigg, 2018).

The decrease in relative heart size in the modern pig is a fact (Niewold et al., 2000). It is conceivable that the relative size of other organs, such as the lungs, that are located in the

thoracic cavity together with the heart, has decreased as well. The main task of the respiratory system is ventilation and gas exchange of oxygen from the air and carbon dioxide from the cells in the body (Sjaastad et al., 2016). As oxygen is transported into the lungs through the airways, carbon dioxide, which is a waste product from the cells, is transported out (Sjaastad et al., 2016). The lungs consist of the left and the right primary bronchus which branches into smaller bronchi which then again branches into even smaller bronchioles. At the end of the bronchioles there are clusters of small sacs, called the alveoli. It is between the walls of the alveoli and the surrounding capillaries the gas exchange happens by diffusion. There are millions of alveoli in the lungs creating an enormous surface area for the gas exchange to happen (Ochs et al., 2004; Sjaastad et al., 2016). The size of this surface area is essential for the diffusing capacity of the lungs and the number of alveoli is therefore an important factor for the lung function (Ochs et al., 2004). One study found that, in humans, the number of alveoli is closely related to the size of the lungs. Lungs with greater volume had a considerably larger number of alveoli, with the mean size of one alveolus being rather constant (Ochs et al., 2004).

As mentioned, the pig's flight-response to stress requires more oxygen to the body (Manning, 2012; van Essen, 2017). If the size of the lungs is smaller than what they are supposed to in relation to the body, it is conceivable that this can affect the oxygen supply as the diffusing capacity will decrease (Ochs et al., 2004). More rapid breathing because of stress can cause hyperventilation. This is also an attempt by the body to maintain the homeostasis (Manning, 2012). Hyperventilation can cause acute acidosis which is characterized by high blood lactate and low pH-levels in the blood, this because of insufficient oxygen-transport (Ritter et al., 2009b). It is conceivable that smaller lungs could be to disadvantage in a case of hyperventilation and acute acidosis in the blood. Acute acidosis during stress can result in the pig becoming fatigued and nonambulatory (Carr et al., 2005; Ritter et al., 2009a; Ritter et al., 2009b). The majority of fatigued pigs will recover, but some might die or remain nonambulatory (Ritter et al., 2009b). It is possible that this alone, or in combination with an insufficient cardiovascular system, is unfortunate for the pig's survival.

Survival of the pigs is a very important economical trait in the pig production (Johnson et al., 2013; Ritter et al., 2009b). The pig-farmers main income comes from delivering animals to the abattoir. In the modern pig production systems, feed represents about 70% of the total costs. The purchasing of piglets is also one of the main costs (Niemi et al., 2010; Patience et al., 2015). It is therefore a big cost for the farmer to loose animals that has been fed and raised

to provide income, especially if this happens at the last minute before slaughtering. Dead, injured and fatigued pigs are an important concern in the pig production industry both because of significant economic losses for the farmers and because of the challenge this is to animal welfare (Dalla Costa et al., 2019; Johnson et al., 2013; Ritter et al., 2009a; Ritter et al., 2009b). In 2011 yearly transport losses in the USA were estimated to 1 million pigs (1%) (Johnson et al., 2013). This includes not only dead pigs, but also nonambulatory and fatigued pigs. Nonambulatory and fatigued pigs that do not recover are economic losses for the farmers on the same level as dead ones (Dalla Costa et al., 2019; Johnson et al., 2013). This is one of the reasons why sudden death in pigs is desirable to avoid. Another reason why sudden death because of heart failure should be avoided is, as mentioned, animal welfare. A pig that is not capable to cope with its own body is not a very healthy pig. Animal welfare and health status is an important factor for the pigs' well-being, something that among other things can affect the pigs' appetite, growth and meat quality (Broom, 1986; Carr et al., 2005; Harley et al., 2012; Patience et al., 2015; Smith et al., 2019). Animal welfare is therefore also in the farmer's economical interest. At the same time, the consumers are getting more and more aware of the animal's well-being, and to meet the requirement of the consumers is also important factor in the business (Sonntag et al., 2019).

The main goal in animal breeding is to breed animals that are both healthy and gives profitability. If hypertrophic cardiomyopathy occurs in pigs and the condition is aggravated by insufficiency of the cardiovascular system and the lungs, it would be in interest to determine if it is possible to breed for heart- and lung sizes that is scaled to the size of the body. This would be beneficial for both the animal welfare and the economics in pig production. The aim of this thesis is therefore 1) To estimate genetic parameters for heart- and lung volume in pigs and the genetic trend for these. 2) To determine if there is a genetic correlation between heart- and lung volume and mortality in pigs.

Materials and Method

Animals and description of data

The data used in this thesis is provided by Norsvin and Topigs Norsvin. The data of heart- and lung volume was obtained from computed tomography (CT) scans of boars at Norsvin's testing station, Delta. Data of mortality was obtained from Topigs Norsvin's registrations of mortality of pigs from different nucleus herds in Norway, Norsvin Delta and one big American herd.

Data of hearts and lungs

At Norsvin Delta, purebred boars with potential for breeding go through a phenotype test. These boars are born and raised in different nucleus herds around in Norway and sent to Delta when they reach a body weight of 30-35 kg. The test starts at 40 kg and ends when the boar reaches 120 kg of body weight. At the end of the test, at approximately 120 kg, the boars get CT-scanned. These images were used to obtain the data of heart- and lung volume.

The work of obtaining data of heart- and lung volume from the CT-images was performed by Øyvind Nordbø, Norsvin SA. Heart- and lung volumes was obtained by extracting the area which contained heart and lungs in the CT-images, using convolutional neural networks (cnn). The CT-scan of a pig consists of about 1200 transversal images. First, images containing the thorax was classified (approximately 300 images), then only images containing the heart and lungs were classified as the thorax using a classification cnn. These images were the ones that got analysed further. This was done by first marking the area containing the heart and then the area containing both heart and lungs. Then, the voxels belonging to the common heart and lung area, with a Hounsfield unit below -400 (measurement of the reflection of the material to the radiation, below -400 is air/gasses), were classified as lungs, voxels belonging to the heart were classified as heart, while the remaining voxels were classified as background. These three classes were used for training a segmentation cnn. Areas belonging to the heart and lung classes were summed for and constitute volume estimates of the heart and the lungs were subsequently scaled to milli litres (Nordbø, 2021).

The phenotypes generated describes the total volume (ml) of the heart and the lungs. Heart- and lung volume relative to body weight (relative volume) was calculated by dividing the total volume (ml) of the hearts and lungs obtained from the CT-images (absolute volume) by the individuals body weight at CT-scanning.



Figure 1 is showing how the manual annotation of the lungs and the heart is done. The green polygon circles both the lungs and the heart, and the red polygon circles only the heart. (Nordbø, 2021).

The boars at Delta were housed in pens of 12 individuals (After year 2020 this was changed to 11 individuals in each pen, but all data is of animals born before 2020) and share pen with the same individuals through the whole test. The boars consist of the breeds Norwegian Landrace and Duroc. Approximately 1600 Duroc boars and 1400 Norwegian Landrace boars are tested at the station each year. The dataset of heart- and lung volume consisted originally of 5485 Duroc boars and 5457 Norwegian Landrace boars born from 2011 - 2019. A few observations were removed from the dataset due to outlying values. To remove unlikely values, all observations with heart volume less than 500ml were removed from the dataset. This resulted in ten removed observations from the Duroc dataset and two removed observations from the Landrace dataset. There were no outliers due to lung volume. The data of the two breeds were analysed separately. When the analyses were run, animals with any lack of information in the datasets were removed from the analysis. This resulted in 5430 animals in the analyses for Landrace, and 5464 animals in the analyses for Duroc.

Data of mortality

The data of mortality consists of two different datasets. The first one containing data of mortality from both Norsvin Delta and the nucleus herds in Norway delivering boars to Norsvin Delta (dataset of mortality N). This means that the animals in this dataset that have not been sent to Delta are siblings or other close relatives of the boars at Delta. These animals consist of boars, sows and castrates. This data consists originally of 60 303 individuals of Landrace and 8 612 individuals of Duroc from 27 and 7 different herds, respectively. The individuals are born from year 2011-2019.

The second dataset of mortality consists of the same animals as in the first dataset in addition to animals from one big American herd (dataset of mortality N + US). These two datasets of mortality were treated separately to see the impact of the American herd on the results. This full dataset consists of 202 233 observations and were only made for the Landrace breed. These animals were also born from year 2011 to 2019.

The registrations of death are of animals who have died by themselves during the period of weaning to finishing. The period of weaning to finishing corresponds to the test period for the boars at Delta.

Data treatment

All the analyses were done separately for each breed and all the datasets were therefore divided into two, one for each breed. There were used three different combinations of datasets for the different analyses for each breed. The three combinations of datasets that were used were: the dataset of heart and lungs alone, the dataset of heart and lungs merged with the dataset of mortality N, and the dataset of heart and lungs merged with the dataset of mortality N+US. The last one was, as mentioned, only made for Landrace. This makes a total of five different datasets. This and other necessary calculations and preparations of the datasets were done using R-4.0.4 and RStudio version 1.4. 1106.

Descriptive statistics

Table 1 is showing the fixed effects for the five different datasets separately. Fixed effects included in the analyses of hearts and lungs alone are a combination of herd and year of birth (Herd year of birth), month of birth, the parity of the dam and their group at Delta (group) where one group corresponds to the individuals sharing pen. Fixed effects included in the analyses for mortality are sex code (sow, boar, castrate and unknown), a combination of herd year and season of birth and group at the nursery (Hys + class at nursery) and biological litter. All the models used for the analyses are based on the models used for routine genetic evaluations in Norsvin and Topigs Norsvin, which are the reason for choice of fixed effects included in the models.

Table 1: Fixed effects for the five datasets shown separately for each dataset. For each fixed effect for each breed: number of observations (N), number of groups (No. of groups), the mean, minimum number (min) and maximum number of individuals in one group (max.).

Fixed effects	Landrace					Duroc				
	N	No. of groups	No. per group			N	No. of groups	No. per group		
			Mean	Min.	Max			Mean	Min.	Max
Dataset of heart and lungs										
Herd year of birth	5430	230	23,61	1	106	5464	64	85,38	3	400
Month of birth	5430	12	452,5	333	574	5464	12	455,33	294	613
Parity of dam	5430	3	1810,00	540	3739	5464	3	1821,33	513	3612
Group	5430	655	8,29	1	12	5464	749	7,30	1	12
Dataset of mortality N										
Sex code	60303	4	15075,75	11	30272	6812	4	1703,00	1	4317
Hys + class at nursery	60303	689	87,52	1	558	6812	121	56,30	1	302
Litter ID	60303	7868	7,66	1	19	6812	1533	4,44	1	12
Dataset of mortality N+US										
Sex code	202233	4	50558,25	3622	109492	-	-	-	-	-
Hys + class at nursery	202233	730	277,03	1	5259	-	-	-	-	-
Litter ID	202233	24251	8,34	1	22	-	-	-	-	-

Table 2 is showing traits and regression variables included in the five different datasets.

Traits from the heart and lungs dataset are absolute heart volume, absolute lung volume, heart volume relative to body weight and lung volume relative to body weight. Weight at CT-scanning were included in the models of heart and lungs as a fixed regression. The trait from the datasets of mortality is mortality. Mortality is registered as a binary trait where dead animals are registered with code 1 and survived animals are registered with code 0. Age at nursery were included as a fixed regression for the models of mortality.

Table 2: Traits and regression variables included in the five datasets shown separately for each dataset. Absolute heart- and lung volume (ml), relative heart- and lung volume (ml/ kg body weight at CT), Weight at CT (kg), mortality (dead=1, survived = 0) and age at nursery (days). For each variable and for each breed: number of observations (N), mean, minimum value (min.), maximum value (max) and standard deviation (S.D.).

	Landrace					Duroc				
	N	Mean	Min.	Max	S.D.	N	Mean	Min.	Max	S.D.
Dataset of hearts and lungs										
Absolute Heart volume	5430	1100,20	586,90	2034,50	127,22	5464	1153,90	503,90	1778,80	131,61
Absolute Lung volume	5430	3662,50	808,30	6618,70	631,84	5464	2293,00	1086,00	5120,00	470,96
Relative Heart volume	5430	9,00	4,70	16,80	1,01	5464	9,46	4,10	14,53	1,06
Relative Lung volume	5430	29,80	7,20	57,10	5,15	5464	24,54	8,94	42,07	3,90
Weight at CT	5430	122,80	101,90	142,30	3,54	5464	122,00	98,70	139,60	3,48
Dataset of mortality N										
Mortality	60303	0,02	0	1	-	6812	0,02	0	1	-
Age at nursery	60303	33,99	0,00	132,00	NA	6812	33,61	1,00	64,00	5,32
Dataset of mortality N+US										
Mortality	202233	0,02	0	1	-	-	-	-	-	-
Age at nursery	202233	24,87	0,00	132,00	NA	-	-	-	-	-

Statistical analyses

The statistical analyses were performed using DMU version 6, release 5.2, a package for analysing multivariate mixed models (Madsen & Jensen, 2013). 14 different analyses were run. For each run, one data file and one corresponding pedigree file were used in addition to a parameter file for each analyse. The pedigree included all the individuals with observations and 5 generations of ancestors. All individuals in pedigree are born from 2003 to 2019.

The analyses that were done and the models used were as following:

- 1) Bivariate models for analysing absolute heart- and lung volume.

These models were used for analysing the absolute heart- and lung volume for Landrace and Duroc.

The models:

$$HV_{ijklm} = HY_i + MB_j + PD_k + G_l + PID_m + \beta^*x + e_{ijklm}$$

$$LV_{ijklm} = HY_i + MB_j + PD_k + G_l + PID_m + \beta^*x + e_{ijklm}$$

2) Bivariate models for analysing heart- and lung volume relative to body weight.

These models were used for analysing heart- and lung volume relative to body weight for Landrace and Duroc.

The models:

$$RHV_{ijklm} = HY_i + MB_j + PD_k + G_l + PID_m + e_{ijklm}$$

$$RLV_{ijklm} = HY_i + MB_j + PD_k + G_l + PID_m + e_{ijklm}$$

Where (for model 1 and 2):

HV_{ijklm} = Heart volume (Landrace: $ijklm = 1, \dots, 5430$. Duroc: $ijklm = 1, \dots, 5464$)

LV_{ijklm} = Lung volume (Landrace: $ijklm = 1, \dots, 5430$. Duroc: $ijklm = 1, \dots, 5464$)

RHV_{ijklm} = Relative heart volume (Landrace: $ijklm = 1, \dots, 5430$. Duroc: $ijklm = 1, \dots, 5464$)

RLV_{ijklm} = Relative lung volume (Landrace: $ijklm = 1, \dots, 5430$. Duroc: $ijklm = 1, \dots, 5464$)

HY_j = Fixed effect of herd year of birth (Landrace: $i = 1, \dots, 230$. Duroc b: $i = 1, \dots, 64$)

MB_j = Fixed effect of month of birth (Landrace and Duroc: $j = 1, \dots, 12$)

PD_k = Fixed effect of parity of the dam (Landrace and Duroc: $k = 1, 2, 3$)

G_l = Random effect of group number at Delta (Landrace: $l = 1, \dots, 655$. Duroc: $l = 1, \dots, 749$)

PID_m = Additive genetic effect of pig ID (Landrace: $m = 1, \dots, 595$ 639. Duroc: $m = 1, \dots, 155$ 772)

β = Regression coefficient for weight at CT scanning (x)

e_{ijklm} = Residual error (Landrace: $ijklm = 1, \dots, 5430$. Duroc: $ijklm = 1, \dots, 5464$)

3) Univariate model for analysing mortality of Landrace.

This model was used for analysing the dataset of mortality N and the dataset of mortality N+US. Analyses of mortality were not run for Duroc because of limitations due to the low number of dead animals in the dataset.

The model:

$$M_{ijkl} = SC_i + HYSN_j + LID_k + PID_l + \beta * x + e_{ijkl}$$

Where:

M_{ijkl} = Mortality from weaning to finishing (Dataset N: $ijkl = 1, \dots, 60\ 303$.

Dataset N+US: $ijkl = 1, \dots, 202\ 233$)

SC_i = Fixed effect of sex code (Dataset N and Dataset N+US: $i = 1, 2, 3, 4$)

$HYSN_j$ = Fixed effect of herd year and season of birth and class at nursery (Dataset N: $j = 1, \dots, 689$. Dataset N+US: $j = 1, \dots, 730$)

LID_k = Random effect of litter ID (Dataset N: $k = 1, \dots, 7868$. Dataset N+US: $k = 1, \dots, 24251$)

PID_l = Additive genetic effect of pig ID (Dataset N: $l = 1, \dots, 78\ 335$. Dataset N+US: $l = 1, \dots, 222\ 666$)

β = Regression coefficient for age at nursery (x)

e_{ijkl} = Residual error (Dataset N: $ijkl = 1, \dots, 60\ 303$. Dataset N+US: $ijkl = 1, \dots, 202\ 233$)

4) Bivariate models for analysing mortality and heart- and lung volume of Landrace.

Bivariate analyses were run with the model of mortality for both the N dataset and the N+US dataset in combination with all the different models for heart volume and for lung volume. Resulting in eight different analyses. In these analyses, the residual covariance was fixed at zero since observations of heart and lungs and the observations of mortality were made of different animals. Since the CT-scanning happens at the end of the test at the testing station, all the individuals in the dataset of heart and lungs will be registered as survived (code 0). There is therefore no overlap between animals registered as dead (code 1) in the datasets of mortality and the individuals in the dataset of heart and lungs.

Calculation of genetic trends

Genetic trends of absolute heart- and lung volume and relative heart- and lung volume were calculated using the estimated breeding values from the DMU-analyses. The mean of the breeding values per year (birth year of the individuals) were computed. To make it easier to compare the trends across traits and breeds, the mean breeding values per year were then scaled according to the genetic standard deviation of the respective traits. This was performed in R and RStudio. Plots of the genetic trends were made with Microsoft Excel.

Results

Genetic parameters for Landrace

The results of all the analyses run for Landrace are given in **Table 4**. The estimated heritabilities (h^2) range from 0,335 to 0,362 for the absolute heart- and lung volumes and those relative to body weight. The variance components have relatively small standard errors compared to their values. This gives an indication of reliable heritabilities. The heritabilities of mortality are rather small for both the N-dataset and the N+US-dataset, with heritabilities of 0,008 and 0,011, respectively. This reflects the small additive genetic variances for mortality.

There is a small positive genetic correlation between absolute heart- and lung volume, and between relative heart- and lung volume. There is no significant difference between the correlations of absolute volume and the volume relative to body weight for either heart volume or lung volume. The standard errors for these correlations are bigger than the correlations themselves, this indicates that there is a low accuracy for the correlations. In the end, none of the correlations between heart and lung volume are significantly different from zero.

The genetic correlations between the two measurements of heart volume and mortality in the dataset of mortality N show positive values with values of 0,347 and 0,349. The standard errors for these correlations are relatively high. Between mortality in the dataset N+US and the two measurements of heart volume, the genetic correlations are lower and with standard errors almost as high as the correlations themselves. All the genetic correlations between lung volume and mortality are very small and mostly not significantly different from zero, with standard errors larger than the correlations. The correlations between mortality in the N+US dataset and lung volume show negative values.

Table 3: Results of the analyses run for Landrace. To the left there is a table of heritability (h^2), genetic variance (σ_g^2) and residual variance (σ_e^2) for the absolute heart- and lung volume, the heart- and lung volume relative to body weight and mortality. To the right there is a correlation matrix showing the genetic correlations between absolute heart- and lung volume, relative heart- and lung volume and mortality in the upper diagonal (green). In the lower diagonal (blue) the residual correlations are found. Standard errors (S.E.) are given in the brackets below every estimate. “-“ = not analysed.

Landrace									
Heritabilities and Variances (S.E.)				Genetic Correlations (S.E.)					
	h^2	σ_g^2	σ_e^2	Heart volume	Lung volume	Relative Heart volume	Relative Lung volume	Mortality N	Mortality N+US
Heart volume	0,362 (0,041)	5580,354 (706,416)	9650,733 (540,558)	1	0,082 (0,089)	-	-	0,347 (0,150)	0,174 (0,117)
Lung volume	0,335 (0,030)	121224,052 (15398,500)	227971,598 (11955,300)	-0,078 (0,039)	1	-	-	0,037 (0,157)	-0,044 (0,118)
Relative Heart volume	0,356 (0,040)	0,365 (0,047)	0,646 (0,036)	-	-	1	0,073 (0,090)	0,349 (0,151)	0,171 (0,118)
Relative Lung volume	0,337 (0,038)	8,248 (1,043)	15,497 (0,811)	-	-	-0,659 (0,038)	1	0,027 (0,157)	-0,102 (0,190)
Mortality N	0,008 (0,003)	0,00019 (0,00007)	0,02304 (0,00014)	-	-	-	-	1	-
Mortality N+US	0,011 (0,002)	0,00018 (0,00003)	0,01701 (0,00006)	-	-	-	-	-	1

Genetic parameters for Duroc

All results from the analyses run for Duroc is given in **table 5**. The estimated heritabilities (h^2) range from 0,313 to 0,402 for both the measurements of heart- and lung volume. The estimated heritabilities is generally a little lower for heart volume and a little higher for lung volume, than for the Landrace breed. Also here, as for the Landrace breed, all the variance components have relatively small standard errors compared to their values, which indicates reliable heritabilities.

There is a significant ($p > 0,05$), positive genetic correlation between heart and lung volume with a correlation of 0,337, and between relative heart and lung volume with a correlation of 0,343. There is no significant difference between the genetic correlations of the two measurements of heart- and lung volume. The standard errors of all the correlations are small compared to their values. This indicates more accurate estimations of correlations for the Duroc breed than for the Landrace breed.

Table 4: Results of the analyses run for Duroc. To the left there is a table of heritability (h^2), genetic variance (σ_g^2) and residual variance (σ_e^2) for the absolute heart- and lung volume and the heart- and lung volume relative to body weight. To the right there is a correlation matrix showing the genetic correlations between absolute heart- and lung volume and relative heart- and lung volume in the upper diagonal (green). In the lower diagonal (blue) the residual correlations are found. Standard errors (S.E.) are given in the brackets below every estimate. “-“ = not analysed.

Duroc							
Heritabilities and Variance (S.E.)				Correlations (S.E.)			
	h^2	σ_g^2	σ_e^2	Heart volume	Lung volume	Relative Heart volume	Relative Lung volume
Heart volume	0,313 (0,034)	5238,883 (639,229)	11439,963 (509,728)	1	0,337 (0,073)	-	-
Lung volume	0,399 (0,029)	80187,236 (8330,230)	115701,642 (6153,590)	0,140 (0,034)	1	-	-
Relative Heart volume	0,313 (0,034)	0,353 (0,043)	0,773 (0,034)	-	-	1	0,343 (0,074)
Relative Lung volume	0,402 (0,029)	5,584 (0,586)	8,023 (0,431)	-	-	0,149 (0,034)	1

Genetic trends

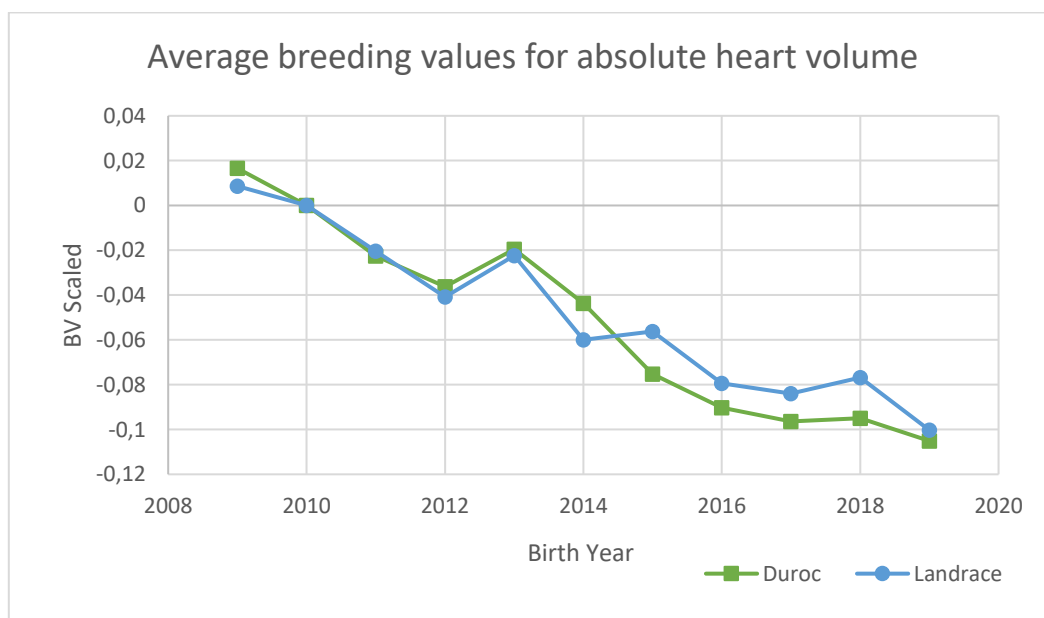


Figure 2: Mean of estimated breeding values scaled according to the genetic standard deviations (σ_g) for absolute heart volume per year, for all individuals in pedigree born from 2009 – 2019 for the heart and lung datasets.

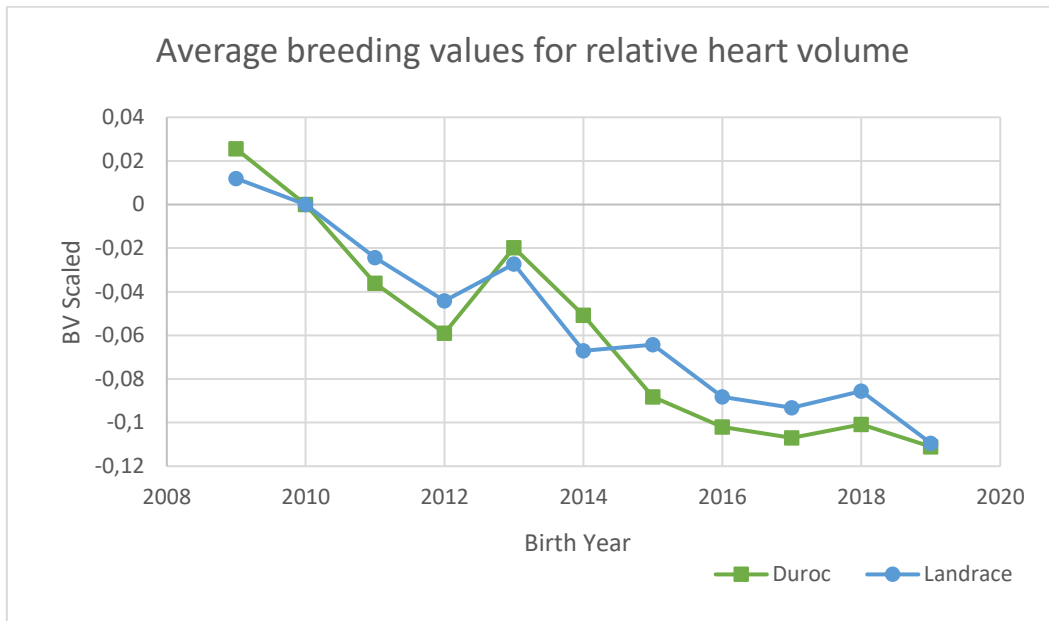


Figure 3: Mean of estimated breeding values scaled according to the genetic standard deviation (σ_g) for heart volume relative to body weight per year, for all individuals in pedigree born from 2009 - 2019 for the heart and lung datasets.

Figure 2 and **Figure 3** are showing the changes in estimated breeding values for respectively absolute heart volume and heart volume relative to body weight for both Duroc and Landrace breed, over time. The breeding values are scaled according to the genetic standard deviations (σ_g) of the respective traits (σ_g for absolute heart volume: Landrace = 74,702 and Duroc = 72,380. σ_g for relative heart volume: Landrace = 0,604 and Duroc = 0,594). The genetic trends are quite similar for both absolute and relative heart volume for both the breeds. For both figure 2 and figure 3, the Duroc generally show a little steeper trend. Thus, the Landrace breed show a curve that has a little less change over time.

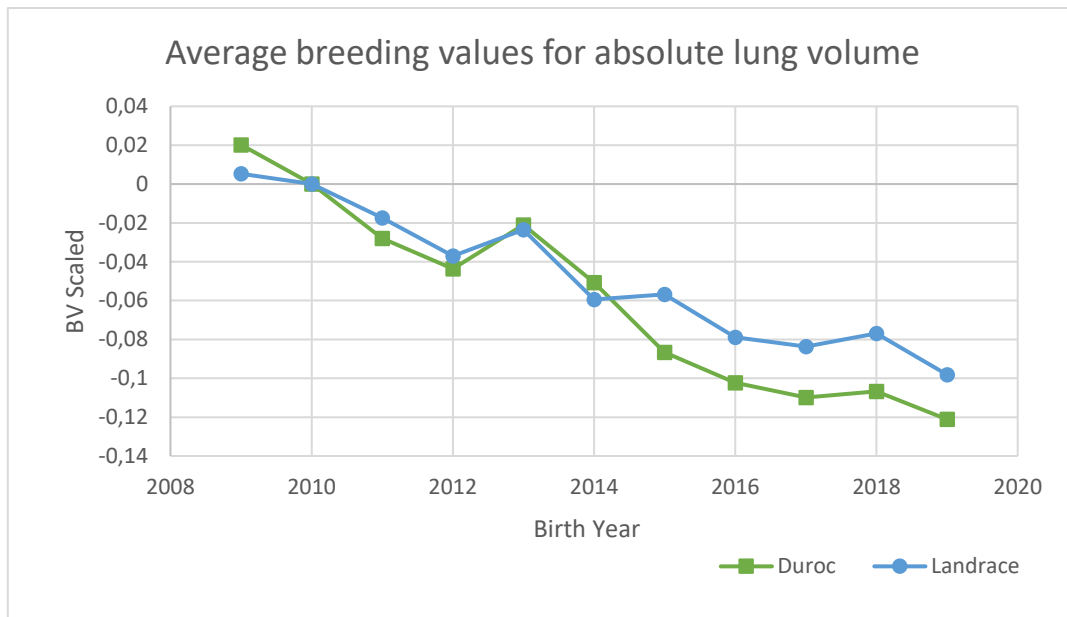


Figure 4: Mean of estimated breeding values scaled according to the genetic standard deviations (σ_g) for absolute lung volume per year, for all individuals in pedigree born from 2009 – 2019 for the heart and lung datasets.

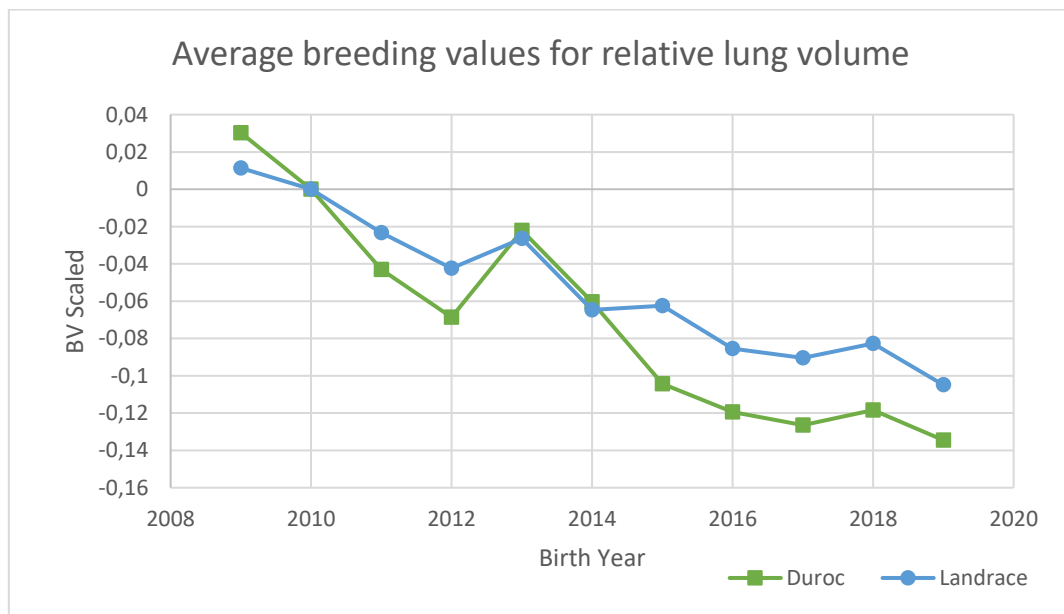


Figure 5: Mean of estimated breeding values scaled according to the genetic standard deviations (σ_g) for lung volume relative to body weight per year, for all individuals in pedigree born from 2009 – 2019 for the heart and lung datasets.

Figure 4 and **Figure 5** are showing the changes in estimated breeding values for respectively absolute lung volume and lung volume relative to body weight for both the Duroc and the Landrace breed, over time. Also here, the estimated breeding values are scaled according to

the genetic standard deviation (σ_g) (σ_g for absolute lung volume: Landrace = 348,172 and Duroc = 283,164. σ_g for relative lung volume: Landrace = 2,872 and Duroc = 2,363). Both the figures for lung volume show a similar genetic trend as the figures for heart volume. For Duroc, the changes in the curve for relative lung volume are a bit larger than for the other figures. Otherwise, the changes of the genetic trends for heart- and lung volume over time, seem to be following the same trends.

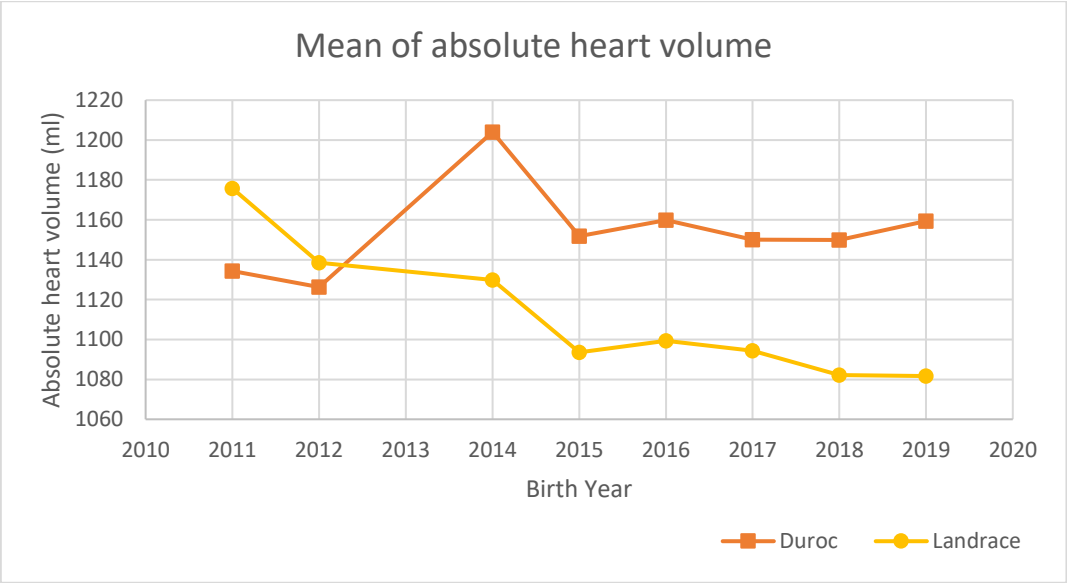


Figure 6: Mean of absolute heart volume per year of birth for Landrace and Duroc.

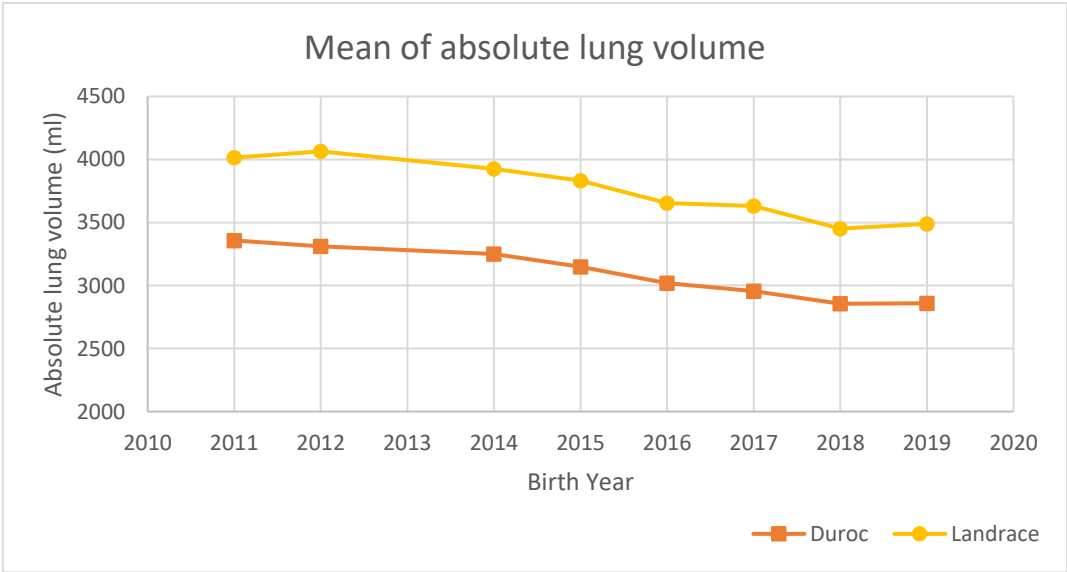


Figure 7: Mean of absolute lung volume per year of birth for Landrace and Duroc.

Figure 6 and **Figure 7** are showing the development in absolute heart and lung volume for both the breeds through the years. These figures were made to see the similarity between the genetic trends with the breeding values and the trend of the phenotypes. The same plots were also made for the relative heart- and lung volume. These are not presented, but showed the same trend as for the absolute volumes. As can be seen, the trend of the breeding values and the phenotypes for heart volume differ from each other for the Duroc breed. The heart volume has not changed a lot the last four years, but still the genetic trend is decreasing. The heart volume of Landrace and the lung volume for both Landrace and Duroc show the same trend for both the phenotypes and the breeding values.

Table 5 is showing the number of individuals with calculated breeding values per year of birth for the figures of genetic trends, and the number of individuals with observed phenotypes per year of birth for the phenotypic trends. The number of individuals with calculated breeding values shows an increase after year 2013 for Landrace and year 2014 for Duroc. The number of individuals with observed phenotypes is generally varying but with an increase after year 2015. In year 2013 there was zero individuals with observed phenotypes.

Table 5: Shows an overview of number of observations per year of birth for the figures of genetic and phenotypic trends (Figure 2, 3, 4, 5, 6 and 7).

Number of observations per year of birth for figures of genetic and phenotypic trends				
	Genetic trend		Phenotypic trend	
Birth Year	Landrace	Duroc	Landrace	Duroc
2009	487	337	-	-
2010	641	481	-	-
2011	812	611	186	197
2012	867	668	342	312
2013	791	509	0	0
2014	1353	762	589	178
2015	1181	1149	292	548
2016	1968	1549	923	895
2017	2241	1770	1212	1308
2018	1680	1208	775	703
2019	1184	1354	1136	1334
Sum	13205	10398	5455	5475

Discussion

Variance components and heritabilities

Variance components and heritability (**Table 3 and 4**) were calculated for the traits heart- and lung volume and mortality. For both breeds, the genetic variance of both absolute heart- and lung volume and relative heart- and lung volume had relatively low standard errors and the heritabilities was intermediate. The low standard errors of the variance components indicates that the heritabilities calculated are reliable. This means that it should be possible to change the genetic trends of heart- and lung volume for both breeds by selection of the wanted phenotypes.

For the trait mortality, which was only analysed for the Landrace breed, the situation was different (**Table 3**). The genetic variance of the trait mortality was low for both the datasets of mortality, which resulted in low heritabilities. As the residual variance decreased with the including of the American herd, the heritability was a little higher for the dataset of mortality N+US than it was for the dataset N. The heritability of the trait mortality calculated for the dataset N+US can also be considered more accurate than for the dataset N as the standard error for the genetic variance, and thus the heritability is lower in relation to their respective values. This means that the expanding of the dataset of mortality had a positive effect on the estimated heritability. Even though the heritability calculated for the dataset N+US seems to be reliable, it is unfortunately too low to be of any use in the breeding. These results comply with the low frequency of mortality in the datasets shown in **Table 2**. Even though more data was included in the dataset N+US, the frequency of dead animals remained the same for all the datasets of mortality. An including of data with a higher frequency of mortality would most likely have a positive effect on the heritability estimated for the trait mortality.

Genetic correlations

The genetic correlations between heart- and lung volume for the Landrace breed was positive, but low, with standard errors higher than the correlations themselves (**Table 3**). Since the correlations are not significantly different from zero, heart and lung volume for the Landrace breed does not seem to be strongly correlated. The high standard errors make these correlations inaccurate. Because of this, it is possible that the true correlations differ from these estimates. For the Duroc breed, the estimated genetic correlations were different with medium high correlations between heart- and lung volume and relatively small standard errors

(**Table 4**). Thus, the estimated genetic correlations between heart and lung volume for Duroc seems to be quite accurate. This means that the lung volume probably increases with the heart volume and the other way around. The theory that the change in body composition through domestication and selection has led to a decrease in relative volume of the lungs such as for the heart, will be strengthened by these results for the Duroc breed.

With the dataset of mortality N, the genetic correlations between both absolute heart volume and relative heart volume and mortality were intermediate and with relatively large standard errors (**Table 3**). The accuracy of these estimated correlations is therefore low, but otherwise, it looks like there could be a positive correlation between mortality and heart volume for the Landrace breed. A positive correlation between mortality and heart volume means that the mortality increases as the heart volume increases. This indicates that a big heart is not always a healthy heart. This strengthens the theory of the heart muscle growing bigger and thicker as it has to work harder to compensate for the originally small size and thus low volume. As described earlier, the volume obtained of the hearts by the CT-images describes the total volume within the outer circumference of the heart muscle. This means that both the muscle tissue and the inner volume of the heart chambers are included in this volume. With this method of obtaining heart volume, selecting for hearts with great volume could mean both selecting for healthy hearts with a great inner volume and selecting for unhealthy hearts with a large total volume, but with small heart chambers. It could be that HCM and enlarged hearts are so common among the individuals by the time they reach a body weight of 120 kg, that big hearts correspond to unhealthy hearts. The thickness of the heart muscle and the volume of the heart chambers at this age/ weight, should therefore be investigated further to be able to say anything about the healthiness of the hearts with large volumes.

For the dataset of mortality N+US, which had about 140 000 more observations, the genetic correlations between mortality and heart volume decreased. Even though the including of more data should give better estimates, the accuracy of the estimates are probably a little lower as the standard errors are larger in relation to the correlations. But as expected, the standard errors did also decrease compared to the dataset of mortality N. The differences between the estimated genetic correlations for heart volume and mortality might indicate that the environmental factors have an influence on the results. The variation of the environments the pigs have been living in is probably bigger for the dataset N+US than for the dataset N, since this data includes animals from both Norwegian and American herds.

The genetic correlations between lung volume and mortality (**Table 4**) were very low and had standard errors higher than the correlations. The accuracy of these is therefore low. The genetic correlation between the dataset of mortality N+US and relative lung volume had a negative value, which might indicate that individuals with smaller lungs is more likely to die. This would be as expected as smaller lungs is suggested to be to disadvantage when it comes to the occurrence of acidosis in stressful situations and thus survival. To find out if the death of individuals with small lungs is correlated with enlarged hearts would be in interest.

Since the analyses of mortality was only run for the Landrace breed, no genetic correlations of mortality were estimated for Duroc. One of the objectives of this thesis was to determine if there was a genetic correlation between heart- and lung volume and mortality. It is therefore unfortunate that the data was too limiting to run these analyses for the Duroc breed. It would be in interest to perform these analyses with a bigger dataset for Duroc as well. The number of nucleus herds with purebred Duroc is small. The availability of data of mortality for Duroc is therefore not as present as it is for Landrace.

Genetic trends

The estimated breeding values for both absolute and relative heart- and lung volume for both the breeds show a quite similar trend (**Figure 2, 3, 4 and 5**). The decrease in the latest years is generally a little steeper for Duroc than for Landrace. By these results, it would be logical to think that the decrease in heart- and lung volume has been more significant for Duroc than for Landrace through the years. **Figure 6** is showing that this is not the case for the measured heart volume. The negative trend in the breeding values could therefore seem to look more dramatic than what the phenotypic trend expresses. The changes in average heart volume have not been more than 20 ml from 2015 to 2019 for any of the breeds. For the years before, the changes were larger and more irregular, especially for Duroc. The number of observed phenotypes per birth year is varying (**Table 5**). This could affect the phenotypic trend as there are some years with very few observations, specifically for the years prior to 2016 and definitely for year 2013 with zero observations. This could explain the differences between the genetic- and the phenotypic trend and the irregularities of the phenotypic trends for heart volume. In addition, this could be explained by the fact that weight at CT-scanning is corrected for in the estimation of breeding values but not for the phenotypes of absolute volume. The weight at CT-scanning generally varies a little (**Table 2**) due to logistics at the testing station.

In 2017 the Norwegian Duroc was crossed with another line of Duroc, Talent. The proportion of Norwegian Duroc and Talent is varying for the individuals born after this year (from 0 – 100 %) and this has not been accounted for by the model. Both the genetic- and the phenotypic trend for Duroc after year 2017 could therefore be affected by the line proportion. Parents of these animals could also affect the genetic trend before year 2017. Genetic groups in pedigree have not been used for the analyses. In this case, this should have been done. The base population, for Duroc especially, is not homogenous as it consists of individuals of different lines. To assume that all individuals in the base population for Duroc has the same expected breeding values is therefore not realistic. Also, the animals in the base population are born across multiple years. Through these years there has been a genetic progress that could have been accounted for by the use of genetic groups in pedigree. This is applicable for both Duroc and Landrace. The use of genetic groups would probably affect the genetic trend, and the trend for Duroc could have been steeper and affected by the line proportion in a larger extent.

Since Duroc is bred to be used as a father of finishing pigs, growth, dressing percentage and meat quality is more emphasized in the breeding program for Duroc than for Landrace. The Landrace is bred to produce mother-individuals and maternal traits are therefore more emphasized for this breed. Selection for growth rate and other performance traits more emphasized for Duroc are some of the factors that may have had an impact on the change of body composition that has occurred for the pig through the years since the domestication started (van Essen, 2017). It would therefore be conceivable that the changes in heart- and lung volume was more remarkable for Duroc than for Landrace.

Data of mortality

It would have been to advantage if the datasets of mortality were bigger and included more data that were not only of Norwegian herds. In Norway, the regulations and laws of pig husbandry and transportation of animals is quite strict compared to many other countries (Forskrift om hold av svin, 2003; Forskrift om næringsmessig transport av dyr, 2012). It is for example more common with bigger herds other places in the world than in Norway. This combined with other factors in the legalisation and the practise of pig husbandry could cause differences in for example the management, housing, transportation and the handling of the pigs (Veissier et al., 2008). These are factors that could have an impact on the animal welfare and the pigs' experience of stress, something that could affect the frequency of sudden death

(Dalla Costa et al., 2019; Ritter et al., 2007). Datasets with a higher frequency of mortality would maybe have given something more to the results from the analyses of mortality. The including of the animals from the American herd in the mortality dataset for Landrace did not increase the frequency of mortality. But, the estimated correlations between mortality and the heart- and lung volume decreased. Environmental differences might have contributed to these differences in correlations.

Method for extraction of heart- and lung volume

There are some challenges connected to the method used for extraction of the data of heart and lungs used in this thesis. The reason why the method of using CT-scans is chosen is because the scanning of pigs is, as mentioned, one of the routines included in the test of the boars at the testing station. The CT-scans already contribute to a lot of different phenotype data. If the volume of hearts and lungs obtained from the scans is to be useful, this would be in grate value to the pig breeding program. The advantage of using these CT-scans for the obtaining of heart and lung data is that the boars selected for use in the breeding will have these recordings for themselves and not only for their relatives.

Distinguishing between cardiac walls and the heart chambers

One challenge associated with the method is the distinguishing between the cardiac walls (the heart muscle itself) and the heart chambers. As can be seen in **Figure 1**, the heart is showing as one big, grey area on the CT-image. It is therefore not possible to differentiate between the heart muscle itself, including the cardiac walls and the ventricles, from the heart chambers. Hypertrophic cardiomyopathy is, as mentioned, described by the presence of increased left ventricular wall thickness (Elliott et al., 2014). This, for instance, would not be possible to detect by these CT-images. The theory of the heart walls generally growing thicker because of the insufficiency of a heart that is too small in relation to the body, would probably result in bigger hearts. These hearts would show as bigger hearts with a greater volume on the CT-images, but would not be healthy hearts that is desirable to breed for. Healthy hearts with great elasticity of the heart muscle and great volume of the heart chambers, will also show as hearts with a great volume on the scans. It is therefore an important part of the process of finding out if these data of heart and lung volumes is useful, to connect the size of the heart to mortality or other traits connected to robustness. To determine if there is a correlation between heart- and lung volume would also have an important impact of the evaluation of the

healthiness of the heart. If there is a significant positive correlation between heart- and lung volume, hearts with great volume will be more likely to be big in a healthy way. As mentioned, the findings in this thesis suggests that hearts with a large volume is not necessarily a healthy one as there was a positive correlation between heart volume and mortality (**Table 3**).

Effect of the cardiac cycle and ventilation on the CT-images

Another challenge with the method for extraction of the heart- and lung volumes is that the heart and the lungs are in motion during the scan. Since the pigs are only sedated, and still alive during the CT-scanning, their hearts are beating, and their lungs are ventilating. This causes the heart and the lungs to be in different stages in their cycles during the scan.

The contractions of the heart are described as the cardiac cycle (Sjaastad et al., 2016). There are two phases in the cardiac cycle, the diastole, and the systole. One cardiac cycle then consists of one diastole and one systole. The diastolic phase refers to the relaxions of the ventricles and the systole refers to the contractions of the ventricles (Sjaastad et al., 2016). These phases will cause some continuing changes of the inner volume and the outer circumference of the heart. The phase of the heart will, to some extent, affect the size of the heart showing on the CT-images. Based on the images alone, it is not possible to determine the phase of the heart on each image. The heart volumes extracted from these CT-scans will therefore, probably, be an approximate mean of the heart's volume during a systolic and a diastolic phase.

The situation is somehow the same for the lungs as for the heart when it comes to the size showing on the CT-scans. Because of ventilation the volume of the lungs also changes during the scan. Ventilation also consists of two phases, the inspiration and the expiration (Sjaastad et al., 2016). During inspiration, the thoracic cavity expands, the lungs follow this expand and fills up with air. This causes an increase of the lung volume. During expiration, the inspiratory muscles relax and the thoracic cave, and thus the lungs, recoils. The air is pushed out of the lungs and the volume decreases (Sjaastad et al., 2016).

The challenge with the cardiac cycle can be solved with the use of electrocardiography (ECG). With the use of ECG-synchronised techniques during the scan, the motions of the heart can be corrected for (Desjardins & Kazerooni, 2004). This equipment was not available for the collection of the data used here. The correction for the respiratory motion is usually

easily done, but more difficult in this case. This is usually done by telling the patients to hold their breath for a short time, something that is hard to do with a pig.

Methods used in previous research

Others who have investigated hearts and lungs of domestic pigs have mostly done this using already dead animals or with execution. Zurbrigg (2018) did research on pigs that died during transport to the abattoir. The object of this research was to determine if cardiac weights and histological lesions on the heart were associated with the death of pigs during transport. This was done by collecting the hearts from the deceased pigs and weighing them. The hearts were also examined for lesions and thickening or dilation of the ventricles (Zurbrigg, 2018). Van Essen (2017, 2018) tested the hypothesis that cardiovascular function of the domestic pig does not comply with the laws of allometric scaling. Some of these investigations were done with open chest surgery of anesthetized pigs that were executed before hearts and lungs were taken out. The hearts and lungs were weighed and left ventricular weight were also obtained. Measurements like cardiac output, stroke volume and left ventricular end diastolic volume were also made during the surgery. Lung volume were also obtained before the execution (van Essen, 2017; Van Essen et al., 2018).

Maina and Gils (2001) did a study of the morphometric characterization of the airways and the vascular system of the domestic pig. In this study, the bronchial system and the pulmonary artery and vein were filled with silicone and casted for measurement of length and diameter. The volume of the lungs were also measured (Maina & van Gils, 2001). Similar measurements were done by Azad et.al (2016) but with the use of computed tomography (CT). The lungs were extracted from the pig and re-inflated before CT-scanning. The images were used to measure length, diameter and the angles of the branching of the bronchial system (Azad et al., 2016).

None of these methods are feasible in large scale recordings over time. They also require dead animals and would therefore not be to the same advantage as the CT-scanning which can provide data of all boars tested at the testing station. Methods like these could be used in addition to the CT-scanning to check the accuracy of the data obtained from the images.

Future research

The sufficiency of the cardiovascular system and the respiratory system is important to the economics and the animal welfare in the pig production, whether the possible insufficiency leads to death or just discomfort for the pig (Dalla Costa et al., 2019; Johnson et al., 2013; Ritter et al., 2009b; Zurbrigg, 2018). Further research on the subject should therefore be conducted. As discussed, there are methods available to probably get more accurate measurements of the heart- and lung volume from the CT-scans, as for example ECG. And as mentioned, methods requiring dead animals could be used to check the accuracy of the measurements obtained by the CT-scans to make this a more reliable method. Also bigger datasets for mortality, covering a wider range of different herds where the problem of sudden death might be more prominent, could be an option for obtaining better results on the analyses of mortality. Heart volume could also be associated with other traits showing cardiovascular stress. Mortality would most likely just show the most extreme cases. The including of animals that have symptoms but without dying, would most likely increase the frequency of animals with unhealthy hearts in a dataset.

Conclusion

The aim of this thesis was to estimate genetic parameters for heart- and lung volume in pigs and the genetic trend for these, and to determine if there is a genetic correlation between heart- and lung volume and mortality in pigs.

The genetic trend of both heart- and lung volume for Landrace and Duroc seems to be decreasing. Genetic variances and heritabilities for heart- and lung volume for both Landrace and Duroc shows that there is a genetic variance for these traits. It should therefore be possible to change the genetic trend of heart- and lung volume by selection. Positive genetic correlations between heart volume and lung volume were found for the Duroc breed. It is therefore conceivable that the size of the heart and lungs of the Duroc breed, to some extent, changes together. A positive genetic correlation between heart volume and mortality was found for Landrace. This indicates that relatives of pigs with genetically bigger hearts at CT-scanning tends to have higher mortality. Further research should be conducted with more data of mortality or other traits associated with cardiac stress. The method of obtaining data of heart- and lung volume from CT-images could be to great advantage in the breeding. More research on the data obtained by this method should therefore be conducted for a better understanding of the composition and healthiness of the hearts observed.

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