



Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

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Genetic parameters affecting leg length, leg weakness, hip- and elbow conformation in domesticated dogs, in comparison with pigs

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Department of Animal Breeding and Genetics

476

Uppsala 2015

Examensarbete, 15 hp
– Bachelor Thesis (Literature study)

Agriculture Programme
– Animal Science



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Genetiska parametrar som påverkar benlängd, bensvaghet, höft och armbågsledskonformation hos domesticerade hundar, i jämförelse med gris

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Credits: 15 hp

Course title: Kandidatarbete i husdjursvetenskap

Course code: EX0553

Programme: Agronomprogrammet–Husdjur

Level: Grund, G2E

Place of publication: Uppsala

Year of publication: 2015

Cover picture: Victoria Ekenberg

Name of series: Examensarbete / Swedish University of Agricultural Sciences,
Department of Animal Breeding and Genetics, 476

On-line publication: <http://epsilon.slu.se>

Keywords: Dog, canine, pig, conformation, genetic parameters, leg weakness, leg length, hip dysplasia, elbow dysplasia, chondrodysplasia, osteochondrosis

Nyckelord: Hund, gris, konformation, genetiska parametrar, bensvaghet, benlängd, höftledsdysplasi, armbågsledsdysplasi, chondrodysplasi, osteochondrosis

Sammanfattning

Denna litteraturstudie sammanfattar genetiska parametrar för benkonformation hos hund (*Canis lupus familiaris*). Detta för att undersöka ifall selektiv avel är användbart till att förbättra hundars hälsa och välfärd med avseende på fyra ben konformationer; benlängd, bensvaghets, höftled och armbågsledskonformation. Summerade genetiska parametrarna hos hund jämförs sedan med genetiska parametrar hos gris (*Sus scrofa*). Av de fyra konformationerna så är höft och armbågsleds konformation mest studerade hos hund, dessa är inte lika utförligt studerade hos gris. På gris så är bensvaghets mest välstuderat. Benlängd finns studerat hos både gris och hund, dock är dessa studier huvudsakligen fokuserade på orsakande gener och inte genetiska parametrar. En positiv korrelation mellan höft och armbågsleder finns. Även en brant och svag karled hos gris har associerats till sämre armbågsled, detta indikerar att tester för detta bör göras även hos hund. Sammanfattningsvis så behövs det mer forskning om korrelationer mellan dessa egenskaper, även mer forskning om benlängd och bensvaghets behövs. Göras detta kan selektiv avel användas för att förbättra renrasiga hundars benkonformation och välfärd.

Abstract

Genetic parameters for four leg conformation traits in dogs (*Canis lupus familiaris*) are in this literature review summarized to investigate whether selective breeding could be useful to improve purebred dogs' health and welfare. The four traits are leg length, leg weakness, hip joint and elbow joint conformation. When summarized, the genetic parameters are compared with genetic parameters affecting in pigs (*Sus scrofa*). Of the four traits, hip and elbow conformations were mostly studied in dogs. However, these traits were not widely studied in pigs. In pigs the most studied trait was leg weakness. The trait leg length is studied in both species, however, these studies mainly focuses on causative genes and not genetic parameters. A positive correlation was found between hip and elbow joint conformation in dogs. In pigs, a steep and weak forearm pastern was associated with a worse elbow score, indicating that this should also be tested in dogs. In conclusion more research on correlations between these four traits and on leg length and leg weakness traits needs to be done in dogs. If this is done selective breeding can be used effectively to improve purebred dogs' leg conformation and welfare.

Introduction

Recording health problems in dog (*Canis lupus familiaris*) breeds is important in order to improve health status of all breeds. With this recording of health problems kennel clubs, such as the Swedish Kennel Club, aim to decrease heritable diseases (SKK, 2014). The worldwide canine organization Fédération Cynologique Internationale (FCI) also work to improve the health status in purebred dogs. One of FCI: s goals for dog breeding is to make sure that breeders use functionally healthy individuals with both a conformation and mentality that is typical for the breed (FCI, 2010). Common joint health issues in dogs are for instance hip and elbow dysplasia, and especially fast growing, large breeds and heavy dogs seem to be affected (SKK, 2014; Guthrie & Pidduck, 1990). This literature review will focus on how a good functionality can be achieved by selective breeding in four leg conformation traits: leg length, leg weakness, hip joint and elbow joint conformation. Figure 1 displays the basic dog anatomy to help understand which dog parts that are discussed in the literature review later.

Traits with a continuous variation, such as length and other variable conformation traits are thought to be governed by a large number of genetic factors, environmental factors and their interactions. These so-called complex traits are often referred to as quantitative traits (Griffiths *et al.*, 2012). To assess whether selective breeding for a trait can be useful genetic parameters such as heritability, inbreeding and correlations between traits will be reviewed. Known causative gene mutations will also be reviewed. When the genetic parameters have been reviewed, the leg conformation traits in dogs will be compared with research made on pig (*Sus scrofa*) leg conformation. The main purpose is to investigate whether it is possible to improve purebred dogs' leg conformation through selective breeding, and in the long run, aid the animal welfare.

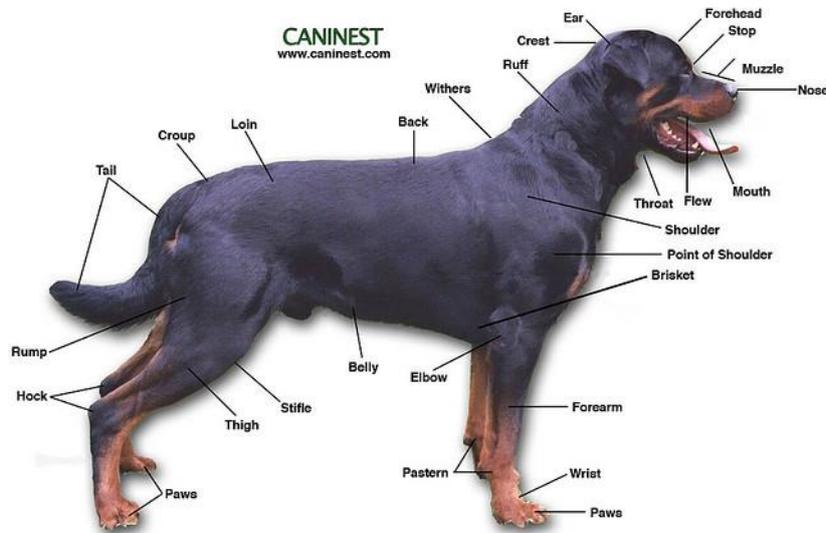


Figure 1. Basic dog anatomy (Caninest, 2010).

Literature Review

Leg length

The leg phenotype chondrodysplasia, see figure 2, is associated with very short legs in at least 19 dog breeds. Some of the breeds associated with chondrodysplasia are the Corgi and the Basset hound (Parker *et al.*, 2009). The inherited phenotype of chondrodysplasia affects cartilage growth and gives a disproportionately small stature, hence the short legs (Horton *et al.*, 2007). In three larger dog breeds, Chesapeake Bay retriever, Newfoundland and Nova Scotia Duck Tolling Retriever, a phenotype similar to chondrodysplasia has been observed. This phenotype has similar characters of a short stature and bowed, thickened forearms, but less severe than chondrodysplasia (Young *et al.*, 2006).



Figure 2. Corgi with chondrodysplasia (Sannse, 2003).

Chase et al. (2002) used principal component (PC) analysis to investigate the genetic basis of skeletal traits. PC analysis can be used to reduce a large number of variables into a few PCs to facilitate analysis of high dimensional measured data. PC analysis is both descriptive and dimension reducing and has been found useful when identifying sources of variation for different anatomical traits (Jolliffe, 2002). The metrics of the leg length could with PC analysis be connected with the tested PC3 in dogs. In this tested PC3 they could identify a quantitative trait loci (QTL) marker, FH3771, which had a heritability of 0.24 (Chase *et al.*, 2002). Parker et al. (2009) tested if chondrodysplasia can be associated with a retrogene that is coding for the fibroblast growth factor four (*Fgf4*). It is hypothesized that breed defining traits, such as chondrodysplasia, would be exposed to a strong selective pressure. Therefore, high homozygosity is to be expected around the chondrodysplasia mutation in the tested dogs with this morphological feature. Only seven of the 175 tested chondrodysplastic dogs were heterozygous for the tested *Fgf4* insertion, while this insertion was not found in 204 tested dogs with medium to long legged phenotypes. *Fgf4* could certainly be associated with chondrodysplasia, but no further tests were made to show whether its position or content is causative for this morphological feature (Parker *et al.*, 2009). In pigs, the *Fgf4* gene has been suggested to have a paracrine (cell to cell) signaling effect to the trophectoderm in the embryo and to initiate the elongation process in embryos (Valdez Magana *et al.*, 2014). Another gene, the *COL10A1* gene has in dogs been shown to not cause skeletal dysplasia/chondrodysplasia (Young *et al.*, 2006). In comparison with pigs, it is reported that dwarfism and skeletal defects are partly caused by a dominant mutation present in the *COL10A1* gene (Nielsen *et al.*, 2000).

In a study on Portuguese water dogs Chase et al. (2002) found two different QTL markers, FH2295 and FH2587, which regulate systems that control skeletal growth. Analysis of these two QTL showed that the tested traits were associated with one or the other QTL in 91 % of all tested skeletal traits. However, these two QTL do not only affect the leg length, but many other skeletal traits (Chase *et al.*, 2002). Another major determinant which has been shown to give small size in dogs is a specific allele of the *IGF1* gene. The intense artificial selection when breeds were formed has in small breeds left a signature around the *IGF1* gene. This allele was identified by Sutter et al. (2007) and the fact that it could be identified without doing a genetic cross and instead using centuries of dog breeding, highlights the usefulness of canine genetics in understanding other morphological traits in mammalian species (Sutter *et al.*, 2007). Also a

specific genotype of the IGF1 gene has in pigs been suggested to cause smaller size, however, further studies on a bigger population are needed to verify this result (Yue *et al.*, 2014).

Hips

To measure a hip phenotype Todhunter *et al.* (1999) suggests that at least two trait components should be looked at: cartilage-bone conformation and hip joint laxity (distraction index) (Todhunter *et al.*, 1999). A common inherited developmental disease trait in dogs is hip dysplasia (HD). The trait is characterized by hip laxity, incongruity of the femoral head (ball) and acetabulum (socket) or subluxation in the affected hip, see figure 3 (Todhunter *et al.*, 2005; Todhunter *et al.*, 1999).



Figure 3. Position of femoral head and acetabulum in hip joint (School of Veterinary Medicine and Science University of Nottingham, 2011).

To assess hip conformation different scoring methods are used. Currently there are three hip joint scoring methods that are most commonly used. The Orthopedic Foundation for Animals (OFA)-, the British Veterinary Association/The Kennel Club (BVA/KC) - and the FCI method (Fluckiger, 2008).

The FCI scoring method for different hip joint conformations is used worldwide and based on radiographic screening. FCI screening is done from 12 months of age and hips are scored on a five grade scale ranging from A, where the hip is considered normal, to the score E which indicates severe hip dysplasia. At two years of age dogs can be officially scored with the OFA method. OFA has a 7 point system that divides the scored dogs into two groups, one with healthy non-dysplastic hips and the other with dysplastic hips. Both of these groups have 3 grades each where excellent, good and fair are those with no HD present. This method is also based on radiographic screening, but the owner can choose to not make the scoring result public. The third method, BVA/KC also uses radiographic screening. Apart from the other methods BVA/KC mainly focuses on nine different morphological features when grading a hip. Each feature is scored from 0 – 6, where 0 is the best and 6 the worst feature conformation. Finally these scores are summed, with a maximum of 53 for each hip and 106 for both hips. BVA/KC recommends that only individuals with < 5 points per hip and a maximum of < 10 for both hips should be used in breeding (Fluckiger, 2008).

Zhang *et al.* (2009) tested whether dividing the hip joint trait into four different traits affecting HD could more effectively improve the HD status in dog breeds. They concluded that a single

hip joint radiograph does not provide enough information on the hip trait. Instead, to best value a dogs genetic potential a combination of four different hip joint conformations should be used (Zhang *et al.*, 2009).

Different factors affecting hip conformation have been suggested. The effect of sex, birth year, birth season, birth year x birth season interaction, age at screening, experience of the x-raying veterinarian and panelist were found to be significant in a Finnish study (Maki *et al.*, 2000). Krontveit *et al.* (2010) notes that there are divided opinions whether sex influences the HD value, however, in this study sex was not significant. Zhang *et al.* (2009) found the effect of sex to be minimal on the hip joint trait. They also summarized estimated effects on hip joint traits and concluded that the effect of breed had the largest effect on all their four tested hip joint traits (Zhang *et al.*, 2009). Krontveit *et al.* (2010) also tested the effect of breed, which had a significant effect on the odds of getting HD. In this study the largest breeds, Newfoundland and Leonberger had highest occurrence, and the smaller Labrador Retriever had a lower occurrence (Krontveit *et al.*, 2010).

Calculated mean values in table 1 are scored with an older FCI method where score 1 represents the borderline cases with grade B according to the new FCI grading system. This older method used scores from 0 – 5 with 5 representing hip score E (Maki *et al.*, 2000). Means ranged between 1.54 in Rottweiler to 1.981 in Estrela Mountain Dog. In the same Rottweiler population as above 1.6 % were scored with HD E, see table 1. The Estrela Mountain Dogs had 17.4% with score E. However, in the Estrela Mountain Dogs no screening program for the breed exists. Silvestre *et al.* (2007) suggests it might be the reason why they have a higher frequency of dogs with low FCI hip scores (E) (Silvestre *et al.*, 2007). Heritability estimates for HD ranged between 0.20 in Rough Collie to 0.58 in Rottweiler, all values are presented in table 1. Also in table 1, the estimated additive genetic variances are presented, they ranged from 0.15 in Rough Collie to 0.87 in Estrela Mountain Dog.

Table 1. Heritability (h^2) additive genetic variance estimates (σ_a^2), mean values and score E percentage for HD

h^2	σ_a^2	Mean value	Score E %	Breed	Reference
0.20	0.15	-	-	Rough Collie	Maki <i>et al.</i> (2002)
0.24	0.26	-	-	German Shepherd	Maki <i>et al.</i> (2002)
0.26	0.31	-	-	Labrador Retriever	Maki <i>et al.</i> (2002)
0.29	0.33	-	-	Golden Retriever	Maki <i>et al.</i> (2002)
0.37	0.49	-	-	Bernese Mountain Dog	Maki <i>et al.</i> (2002)
0.38	0.46	-	-	Rottweiler	Maki <i>et al.</i> (2002)
0.38	0.15	1.54	1.6 %	Rottweiler	Malm <i>et al.</i> (2008)
0.41	0.37	-	-	Finnish Hound	Maki <i>et al.</i> (2002)
0.42	0.24	1.65	3.6 %	Bernese Mountain Dog	Malm <i>et al.</i> (2008)
0.58	0.75	1.07	1.95 %	Rottweiler	Maki <i>et al.</i> (2000)
0.38	0.87	1.981 (right hip only)	17.4 %	Estrela Mountain Dog	Silvestre <i>et al.</i> (2007)

A complex inheritance pattern is coupled to HD (Todhunter *et al.*, 2005). HD is also said to have a polygenic (controlled by > 2 genes) occurrence (Maki *et al.*, 2001). In another study by Maki *et al.* (2004) the mode of inheritance for HD was found to be quantitative with a major gene in combination with several minor genes (small effect by its own, contributing to the polygenic occurrence) affecting the HD trait (Maki *et al.*, 2004).

One tested gene for HD is the FBN2 gene. Friedenberget al. (2011) tested whether a mutation in FBN2 influenced the appearance of HD in dogs. The test concluded that FBN2 gene expression was higher in dysplastic hips in the joint capsule (Friedenberget al., 2011). In a study on crossbreeds (Labrador Retriever – Greyhound) Todhunter *et al.* (2005) have found QTLs from Greyhounds that could be conferred to protecting against HD in dogs.

Elbow

Elbow osteochondrosis or dysplasia (ED) is a painful condition that often gives rise to elbow lameness. ED can arise as early as at six weeks age, but mostly appears between the age of four and eight months. The occurrence of the ED phenotype can be diagnosed with radiographic screening (Guthrie & Pidduck, 1990). ED grading done by the International Elbow Working Group (IEWG) protocol has a score system from 0 to 3. Normal and borderline ED is represented by the score 0, and slight, moderate and severe ED is represented by the scores 1, 2 and 3 (Malm *et al.*, 2008; Maki *et al.*, 2000).

Elbow mean values presented in table 2 ranged from 0.6 in Rottweiler to 1.45 in another Rottweiler population, the IEWG grading system was used to score the elbows. A significant difference in the Finnish Rottweiler population has been found between male and female dogs, with females having slightly better ED than males. Practically, this difference is not that large, only 0.18 score points (Maki *et al.*, 2000). In another study, on Labrador retrievers, a significant difference between the sexes was found, where ED occurrence in males in this population was 1.25 % and in females 0.57 %. (Guthrie & Pidduck, 1990).

Heritability estimates for ED ranged between 0.10 in Labrador Retriever to 0.77 in another Labrador Retriever population, however, the last value only represents males. All values are presented in table 2. The heritability estimation of 0.77 is very high, but Guthrie and Pidduck (1990) suggests that it might be overestimated. Overestimation might be due to the usage of sibling data and thus, the scored individuals have at least partly shared the same environment and in this study no other first-degree relatives (parent, offspring of affected individual) could be used to overcome this problem (Guthrie & Pidduck, 1990). Additive genetic variances are also presented in table 2, and they ranged from 0.03 in Labrador Retrievers to 0.17 in Rottweiler. Guthrie and Pidduck (1990) states that the high heritability of ED indicates that strong selective breeding will have a significant role in the prevention of ED. Four guidelines for the selective breeding are also suggested to prevent ED. Firstly, all ED affected dogs should be excluded from breeding. Secondly, do not use sires and dams in breeding again after they have produced ED affected dogs. Thirdly, siblings to affected dogs should not be used in breeding. And finally, never breed on offspring from affected dogs (Guthrie & Pidduck, 1990).

Table 2. Estimated heritability (h^2), additive genetic variance (σ_a^2) and mean values for ED

h^2	σ_a^2	Mean	Breed	Reference
0.10	0.03	-	Labrador Retriever	Maki <i>et al.</i> (2002)
0.15	0.04	-	German Shepherd	Maki <i>et al.</i> (2002)
0.17	0.11	-	Bernese Mountain Dog	Maki <i>et al.</i> (2002)
0.26	0.08	-	Golden Retriever	Maki <i>et al.</i> (2002)
0.31	0.15	0.60	Rottweiler	Maki <i>et al.</i> (2000)
0.34	0.11	1.45	Rottweiler	Malm <i>et al.</i> (2008)
0.37	0.17	-	Rottweiler	Maki <i>et al.</i> (2002)
0.38	0.14	1.38	Bernese Mountain Dog	Malm <i>et al.</i> (2008)
0.45	-	-	Labrador Retriever (female)	Guthrie and Pidduck (1990)
0.77	-	-	Labrador Retriever (male)	Guthrie and Pidduck (1990)

Guthrie and Pidduck (1990) looked at siblings to dogs affected by ED. They found a higher ratio of ED occurrence in the siblings than in the overall population. However the ratio was lower than expected to assume a simple unifactorial inheritance mode and therefore the multifactorial mode of inheritance is suggested. Thus ED is not only affected by additive gene effects but also by environmental effects (Guthrie & Pidduck, 1990). Maki *et al.* (2002) tested the mode of inheritance for ED and found no difference in the mode of inheritance between sexes and thus, both selected parents will contribute equally to their progeny. Furthermore, no sex-linked or mitochondrial inheritance has been verified (Maki *et al.*, 2002).

Leg weakness

In a study on blue fox Kempe *et al.* (2010) used the carpal joint angle, the pastern, to evaluate leg weakness phenotype in the forearm, see figure 1 (Kempe *et al.*, 2010). In pigs leg weakness phenotypes can be associated with osteochondrosis (de Koning *et al.*, 2012; as reviewed by Korwin-Kossakowska *et al.*, 2013). The leg weakness traits in a study on pigs by Serenius *et al.* (2001) were divided into five different leg traits. These conformations were in the forearm, buck-kneed, small inner claws and legs turned out. In the hind leg it included the conformations small inner claws and an upright hind leg pastern. Heritability for these five different leg weakness traits were estimated in two different pig breeds, Finnish Landrace and Large White. The estimates ranged between 0.02 to 0.19, with upright hind pastern having the smallest estimate and buck-kneed the highest (Serenius *et al.*, 2001). In a later study buck-kneed had a heritability of 0.11 in Finnish Landrace (Serenius *et al.*, 2004).

When grading the wrist in blue fox, a five grade scale was used. Five was considered as excellent wrist conformation and the score 1 as very poor wrist angle. In this study only 8.3 % of the foxes scored good (4) or excellent (5), and as many as 67.3 % had the wrist conformation very poor (1) or poor (2) and the mean score value in the tested population for wrist conformation was as low as 2.1. Kempe *et al.* (2010) estimated the heritability for wrist conformation to 0.25. Also a heritability estimate on body condition score could be done, and was estimated to 0.30. Thus, implying that these two traits have a genetic background (Kempe *et al.*, 2010).

De Koning *et al.* (2012) found associations linking the hind leg osteochondrosis score with the forearm conformation and vice versa. This suggests that the leg conformation might influence body weight distribution between forearm and hind leg. Therefore, leg conformation traits might not only be limited to influence osteochondrosis score in the affected legs, but also to unaffected legs (de Koning *et al.*, 2012). Morgan *et al.* (1999) studied the incidence of osteochondrosis and joint dysplasia in Labrador Retrievers. They looked at the prevalence of osteochondrosis in the hock, stifle, and shoulder and for dysplasia in the hip and elbow. Of all tested 1018 dogs, 24.6 % were affected in one site, 6.7 % in two sites and 1.2 % were affected in three sites. When looking only at the affected dogs, the occurrence of one affected anatomical site in combination with another one of the tested anatomical sites, had frequencies varying from 56.2 % in the hock to 31.6 % in the shoulder (Morgan *et al.*, 1999). A study using computed tomography scanning, to estimate osteochondrosis for different joints in pigs, has shown medium to high favorable correlations. These correlations are between single joint traits and the tested total osteochondrosis score in the pig. Also the total osteochondrosis score had higher heritability estimate than the joint traits on its own. Which implies that selection for an improved total osteochondrosis score would be the most effective way to decrease leg weakness in pig (Aasmundstad *et al.*, 2013).

Correlations

One correlation showed by Chase *et al.* (2002) within the Portuguese Water Dog breed is that the length of the skull and legs is inversely correlated with the width of the skull and skull height. It is easily illustrated when looking at other breeds, for example the typical characteristics of a Greyhound and a Pitbull. The Pitbull has short legs and a broad robust head whilst the Greyhound has long legs and a long, slim head (Chase *et al.*, 2002).

Maki *et al.* (2000) showed a positive and moderate correlation between hip and elbow dysplasia in a population of Finnish Rottweiler dogs. The phenotypic correlation was estimated to 0.24 and the genetic correlation between these two traits to 0.37. Due to these positive correlations Maki *et al.* (2000) assumed that selection against one trait will also improve the other. Malm *et al.* (2008) also provided evidence that a genetic correlation between ED and HD exists, however these correlations were much weaker. In the Swedish Rottweiler population, a positive genetic correlation of 0.23 was found and in The Bernese Mountain Dog population a much smaller positive correlation was found, 0.06 (Malm *et al.*, 2008). In comparison, when studying pig's forearm conformation. A steep and weak forearm pastern (see figure 1), has been associated with worse osteochondrosis/dysplasia score in the elbow joint (de Koning *et al.*, 2012).

Also correlations between foreleg wrist laxity and other traits have been found in blue fox by Kempe *et al.* (2010). This leg weakness trait was correlated with grading size, body weight, daily gain and body condition score. The genetic correlation between these traits were moderately unfavorable, i.e. negative, and ranged between - 0.40 to - 0.50. They also found a negative phenotypic correlation between these traits, - 0.28 to -0.41. From this Kempe *et al.* (2010) concluded that foreleg wrist laxity, high body weight, fast growth rate, large grading size and fatness might be connected. A study on pigs got results supporting this, with computed tomography scanning they studied genetic correlations to weight gain in specific age intervals.

They showed an unfavorable genetic correlation, - 0.74, between the total sum of found osteochondrosis, i.e. leg weakness, in the pig and an high early growth (days until 30kg) (Aasmundstad *et al.*, 2013).

Inbreeding

When breeding for hip traits, the inbreeding coefficient must be considered. Inbreeding coefficients can be estimated with the help of known pedigree information and when this is estimated for all individuals, inbreeding coefficients can be estimated for the progeny before mating. This way estimated breeding values coupled to hip traits, or other traits, can improve a populations hip joint conformation with a durable approach (Zhang *et al.*, 2009).

The inbreeding trend and the average inbreeding coefficient have been found by Maki *et al.* (2001) to steadily increase in a closed Finnish Hound population during the period of 1951 to 1998. During the same time period, an increase could also be seen in four other dog breeds, but these populations differed from the Finnish Hound as they were open populations. In these four breeds a change in the inbreeding coefficient was detected, from 1982 to 1986 it decreased. It was suggested that when including imported dogs with incomplete pedigrees, or other individuals with incomplete pedigrees, they falsely decrease the populations inbreeding coefficient (Maki *et al.*, 2001).

Maki *et al.* (2001) also found that the within breed distribution of the progeny number per sire and dam was significantly skewed. Of six tested dog breeds all were skewed to the sires favor. Thus a small number of sires are favored when selecting the next generation. Skewed selection might increase the inbreeding, therefore to avoid excess inbreeding a more equal selection distribution between the sexes should counteract this (Maki *et al.*, 2001)

Discussion

The trait leg length, looking at only the length of the legs, seems to be mostly associated with chondrodysplasia in short legged dog breeds (Parker *et al.*, 2009). However chondrodysplasia seems to be present not only in small breeds, as in the Corgi, but also in larger breeds, as in the Nova Scotia Duck Tolling Retriever and in the Newfoundland (Young *et al.*, 2006). The information that also a few larger breeds are affected by chondrodysplasia makes me wonder whether these bigger heavier dogs would suffer more from this condition than smaller breeds. When looking at heritability of the chondrodysplasia leg trait no studies were found that describe heritability for chondrodysplasia within breeds. One reason might be that in the most frequently tested breeds for chondrodysplasia the entire breed expresses this phenotype (as in Corgi) and as Parker *et al.* (2009) states, homozygosity is to be expected for this trait. So therefore heritability estimates for chondrodysplasia might seem redundant. Still, Chase *et al.* (2002) estimated heritability for a QTL that they coupled to overall leg length, but since other studies with heritability estimates have not been found for the leg length traits it is hard to validate this estimation.

Studies have shown that several genes seems to affect leg length in dogs, some of these are *FH3771* (QTL marker), *Fgf4*, the *IGF1* gene that give overall small size, and also two different QTLs that control the regulation of overall skeletal growth (Parker *et al.*, 2009; Sutter *et al.*,

2007; Chase *et al.*, 2002). When comparing these affecting genes with pig, some difference between them were found. *Fgf4* is in pigs at least coupled to embryo elongation (Valdez Magana *et al.*, 2014) but no further studies have been found that couple it specifically to leg length. The *IGF1* gene has recently been suggested to also cause small size in pigs (Yue *et al.*, 2014), thus, validating this gene also in dogs. One big difference between causal genes in dogs and pigs is the *COL10A1* gene that in pigs causes skeletal defects and dwarfism (Nielsen *et al.*, 2000), but in dogs this gene has been found to not cause skeletal dysplasia/chondrodysplasia (Young *et al.*, 2006). From the studies read, the conclusion drawn is that it is not yet proven which the exact causative genes for leg length are. Also further studies could be done to measure length variation and health effects of different leg lengths. Thus estimations of genetic parameters for this trait would be possible to calculate. So that further evaluation on how the leg length truly affects breeds functional health can be done.

The trait hip conformation, and especially HD, seems to be largely studied in dogs. In dogs it seems to be mostly larger dog breeds, such as German Shepherd, Rottweiler, Labrador Retriever, that are noticeably affected and therefore studied (Malm *et al.*, 2008; Silvestre *et al.*, 2007; Maki *et al.*, 2004; Maki *et al.*, 2002; Maki *et al.*, 2001; Maki *et al.*, 2000). No studies have been found that test the hip conformation or estimate genetic parameters for HD in pigs. One reason why this has not been done in pigs, might be that pigs are mostly kept as production animals and dogs mostly as companion animals. Also since the dog has a longer lifespan than a pig, it might give this type of health problem more time to develop in dogs. Since the three most common diagnostics for HD is by radiograph in dogs (Fluckiger, 2008), which might be expensive, it would be too expensive to test pigs in production or even breeding pigs, and therefore it's not implemented in to pig production systems. However, lately computed tomography have been used to study osteochondrosis in other joints in pig (Aasmundstad *et al.*, 2013), so this technique could also be used to study HD in pigs. Different grading methods and techniques seem to exist on how to best asses a dog's hip breeding value (Zhang *et al.*, 2009; Fluckiger, 2008). Still Zhang *et al.* (2009) might be onto a good solution when suggesting to divide the HD trait into four different measurable traits to improve the hip status more effectively in breeds. Thus improving the hip health faster in dog breeds (Zhang *et al.*, 2009).

When comparing studies from Silvestre *et al.* (2007) with Maki *et al.* (2000) and Malm *et al.* (2008) mean values in tested breed populations for HD conformation seems to show that populations with existing screening programs for HD have better HD status in the population. One study has shown that the effect of breed has the largest effect on the hip joint trait (Zhang *et al.*, 2009) which might be true since also Krontveit *et al.* (2010) have found the occurrence of HD to be significant between breeds. This might also be true since Todhunter *et al.* (2005) have found QTLs present in Greyhounds, but not in Labrador Retrievers, that could be protective against HD. Other studies have tested the effect of sex, were Maki *et al.* (2000) found the effect to be significant, Zhang *et al.* (2009) found the effect of sex to be minimal and Krontveit *et al.* (2010) found it to be not significant. However since sex has been found to be significant in the ED trait (Maki *et al.*, 2000; Guthrie & Pidduck, 1990) and ED and HD have been found to be positively correlated (Malm *et al.*, 2008; Maki *et al.*, 2000), maybe the sex still might influence the HD trait even though studies have shown different results.

From the articles read, the true inheritance pattern of HD seems to not yet be fully established. Studies at least agree that HD has a complex polygenic inheritance pattern and maybe also involves a major gene (Todhunter *et al.*, 2005; Maki *et al.*, 2004; Maki *et al.*, 2001). No final conclusion on the exact causative HD genes have been found. However, the *FBN2* gene has been found to at least influence the occurrence of HD (Friedenberg *et al.*, 2011), and as mentioned before QTLs have been found that seems to protect against HD (Todhunter *et al.*, 2005). When comparing heritability estimates they ranged between 0.2 – 0.58 between different breeds and different breed populations, see table 1. These moderate to high heritability estimates imply that selective breeding could be efficient to improve the hip joint conformation. Also quite high additive genetic variances have been estimated, ranging from 0.15 – 0.87 (table 1), which also is positive and imply the same as above. In conclusion the hip conformation can be improved with selective breeding, however, a valid phenotypic scoring is important.

Elbow conformation in dogs is, as hip conformation, also scored by radiographic screening (Guthrie & Pidduck, 1990). For the trait ED a study by de Koning *et al.* (2012) looked at elbow conformation in pigs and in comparison with when dogs are tested, no radiographic screening were used. They also concluded that in pigs a steeper forearm pastern conferred to a worse ED score (de Koning *et al.*, 2012). No studies on dog, that connect other leg conformations traits to worse ED score have been found, however it would be a good thing to research in both the ED and HD trait on dogs. Mainly this should be done to prevent breeding for the wrong exterior traits in dogs, which without the knowledge of how they are associated with each other, might worsen the ED and HD traits.

Heritability estimates for ED in dogs ranged from 0.1 to 0.77 in different breed populations, see table 2, however the highest estimates are by Guthrie and Pidduck (1990) suggested to be overestimated. When looking at all estimated values this might be true, since at least the one for Labrador retriever males are much higher than the rest. Also another study has showed a very low estimated value in the same breed but another population. Thus maybe a more accurate heritability range might be 0.1 to 0.38, see table 2. As in HD the moderately to high heritability estimates suggests that selective breeding will have a significant role in improving ED in the tested populations. This is also supported by Guthrie and Pidduck (1990). They also suggested four guidelines to improve ED with selective breeding that seem reasonable. However, inbreeding and other breed qualities must be taken into account also. Especially inbreeding might be of importance, since the inbreeding trend has increased steadily in several dog populations (Maki *et al.*, 2001).

The inheritance mode seems to be clearer in ED, as compared to what was concluded earlier in HD, and a multifactorial inheritance is suggested to affect ED (Guthrie & Pidduck, 1990). Maki *et al.* (2002) found no evidence that contradicts this, thus it might be accurate. So therefore both environmental and additive gene effects affect the ED trait (Guthrie & Pidduck, 1990). However the summarized additive genetic variances, in table 2, are quite low, ranging from 0.03 – 0.17, and this might obstruct the genetic progress, slowing it down, due to the largely affecting environmental factor that might be hard to control.

When looking at leg weakness, no research on genetic parameters in dogs were found. A book was found summarizing clinical signs for osteochondrosis in different joints, i.e. leg weakness, though no summarized genetic parameters (Morgan *et al.*, 2000). Another study by Morgan *et al.* (1999) looked at the occurrence of osteochondrosis but did also not estimate genetic parameters. In another canine species, the blue fox, Kempe *et al.* (2010) researched foreleg wrist weakness. The heritability for the leg weakness trait in the wrist was estimated to 0.25 and this imply that the trait has a genetic background (Kempe *et al.*, 2010). It is strange so few studies have been found on this trait in dogs, mainly because my own experience tells me that there are phenotypic differences within and between breeds for the leg weakness trait. Since both the blue fox and the dog is canine species, future research on dogs might give a similar result. More studies have been done on leg weakness traits in pigs. When comparing heritability estimates for pigs with blue fox, the heritability is lower in pigs than in blue fox. In the studies on pigs both foreleg and hind leg weakness were studied, and the ones getting a higher heritability were those present in the foreleg. So when only comparing the foreleg heritability between blue fox and pig, the difference is much smaller (Kempe *et al.*, 2010; Serenius *et al.*, 2004; Serenius *et al.*, 2001).

Research on pig has also shown that one leg conformation trait in for example the forearm, might influence the leg weakness in the hind leg, since the body weight distribution might be affected by one bad leg conformation (de Koning *et al.*, 2012). Two studies have been found that support this theory. In the first, the high occurrence of dogs with more than one tested joint that is affected with osteochondrosis/dysplasia might support this, however, only a few dogs are affected of osteochondrosis in this study (Morgan *et al.*, 1999). So a study on a bigger number of affected dogs are needed to confirm this connection. The second study also supports the importance of looking at osteochondrosis in combined/different traits because of the medium to high correlations between the total osteochondrosis score and the single joints tested. Also the suggestion that selecting for total osteochondrosis score instead of single scored joints, to more effectively decrease leg weakness in the population, might support this theory (Aasmundstad *et al.*, 2013). However, more research are needed to verify this, and to understand truly how the bodyweight distribution affects leg weakness.

In conclusion, the traits reviewed are all skeletal disorders. Thus, they all might be connected, and both directly and indirectly affect each other. Since there seems to be variation within the traits, and moderate to high heritability estimates present in several traits, selective breeding could be used to improve these traits. Still, more research is needed to be sure that the most effective and sustainable breeding programs are used for dogs. In dogs the traits HD and ED seem to be more thoroughly researched than the leg length and leg weakness traits. When comparing this with pigs, of the four traits reviewed, the leg weakness trait seem to be mostly researched in pigs. Finally after reading these articles I conclude that these four traits are connected, and the connections between these traits might be the key to attain the best possible health and welfare in dogs. Therefore, the most important thing to study further is the connections between them.

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