Heritabilities For Abdominal Cryptorchidism And Umbilical Hernia In Dog

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Introduction

Cryptorchidism where one or both testes are not properly descended is caused by the interaction of genetic, epigenetic, and environmental factors (Amann and Veeramachaneni (2006)). Although many genes have been implicated in the regulation of testicular descent (Ivell and Hartung (2003); Klonisch et al. (2004); Yoshida et al. (2005)), the genetic makeup of cryptorchidism in domestic animals still is unclear (Amann and Veeramachaneni (2007)). In domestic animals the occurrence of umbilical hernias varies widely depending on species, breed and lineage (Enzerink et al. (2000); Distl et al. (2002); Petersen et al. (2008)). The mode of inheritance of umbilical hernia is likely to be complex. Several chromosome regions associated with umbilical hernia have been identified in pig (Germerodt et al. (2008); Ding et al. (2009)) and one chromosome region in cattle (Ron et al. (2004)). In animal breeding, the occurrence of cryptorchidism and umbilical hernia leads to economic loss and decreased selection potential. A better understanding of the genetics of cryptorchidism and umbilical hernia will be helpful to breeders attempting to eliminate these problems.

As both phenotypes most likely are complex traits, the goal of this study was to estimate population parameters in the dog amenable to the estimation of breeding values.

Materials and methods

Animals. The Seeing Eye Inc. provided phenotypic information on Golden Retrievers (GR), Labrador Retrievers (LR) and German Shepherds (GS), all born 1992 - 2007. These dogs were bred in three mostly closed colonies, which actually were three large families that have been under selection for over 7 generations. The phenotypes umbilical hernia (UH) and abdominal cryptorchidism, unilateral or bilateral, (AC) were established as binary traits by the organization's veterinary team, usually when the puppies returned from puppy raiser homes to begin their training. All puppies of each litter were examined with respect to UH and AC where appropriate. In most cases of the diagnosis, 76% for UH and 88% for AC, dogs were aged between one and two years. In the case of UH 1% was older than two years, the oldest being 2203 days of age, and 23% were younger than one year where the earliest diagnosis was right after birth. In the case of AC 12% were younger than 1 year, the youngest being 56 days of age. The distribution of the phenotypes is shown in table 1. Only litters with two to 11 puppies were considered.

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Table 1: Distribution of sex, UH and AC in GR, LR and GS

Trait	Status	GR		LR		GS	
		male	female	male	female	male	female
UH	all	846	751	1480	1297	1509	1484
	unaffected	841	738	1446	1243	1416	1386
	affected	5	13	34	54	93	98
AC	all	836		1434		1461	
	unaffected	800		1404		1326	
	affected	36		30		135	

Statistical analyses. The procedure LOGISTIC of the SAS 9.2 program package (SAS Institute Inc., Cary, NC, USA) was used to investigate a possible association between sex (SEX), year of birth (YEAR), season of birth (SEASON) and litter size (LITTER) with UH in GR, LR and GS. The same model without SEX was used for the analysis of AC. For all analyses with SAS, a significance level of 5% was chosen. The software iterative Bayes (iBay 1.47, http://www.lucjanss.com) was used to estimate variance components to calculate heritabilities for AC and UH, and breeding values to calculate correlations between AC and UH in GR, LR and GS.

Results and discussion

Table 2 shows the results of the logistic regression analyses.

Table 2: Significance of the effects SEX, SEASON, YEAR and LITTER on UH and AC in GR, LR and GS

	GR		LR		GS	
	UH	AC	UH	AC	UH	AC
SEX	0.02	not done	< 0.01	not done	0.60	not done
SEASON	1.00	0.39	0.64	0.59	0.03	0.61
YEAR	1.00	0.32	0.76	0.49	0.19	< 0.01
LITTER	0.85	0.31	0.03	0.64	< 0.01	< 0.01

In GR logistic regression showed no significant effect of SEASON, YEAR or LITTER on AC or UH but SEX had a significant effect on UH. The same holds true in LR with the exception that LITTER had a significant effect on UH. In GS significant effects were LITTER on AC and UH, Year on AC and SEASON on UH. The remaining effects were not significant. Although significant in GR and LR the association of SEX and UH was weak (Cramer's V = 0.05). The effect of season on UH in GS was also weak (Cramer's V = 0.06). The effect of YEAR on UH and AC in GS and on UH in LR was not considered in the Bayesian analyses as this effect most likely represents parental effects. In LR the effect of LITTER on UH was moderate (Cramer's V = 0.09). In GS the effect of LITTER on UH (Cramer's V = 0.12) and on AC (Cramer's V = 0.16) was more pronounced. In GS large litters had less and small litters more AC and UH affected puppies than expected whereas in LR no clear trend could be recognized. The occurrence of AC and UH in litters was not significantly associated in LR ($p = 0.61$) but was significant in GS (Cramer's V = 0.15, $p < 0.01$) and GR (Cramer's V = 0.10, $p < 0.01$).

The basic model for the Bayesian estimation of variance components in both traits was mean + animals + error. In models for discrete data, the error variance is fixed to 1. With the exception of YEAR, the significant effects entered the model according to table 2. Table 3 shows the heritability estimates for UH and AC obtained with the best models. For all variance estimates, zero was not included in 95% highest posterior density regions (HPD95).

Table 3: Heritabilities of UH and AC for AC in GR and LR

	GR		LR		GS	
	AC	UH	AC	UH	AC	UH
h^2	0.46	0.64	0.69	0.76	0.75	0.67
HPD95	0.17-0.69	0.36-0.83	0.46-0.82	0.58-0.85	0.52-0.86	0.39-0.86

Whether effects entered the models as fixed or as random had no impact on the estimates of the heritabilities. Although ranging from 0.46 to 0.75 for AC and from 0.51 to 0.76 in UH the heritability estimates in the three breeds did not really differ as the HPD95s were overlapping. Correlations (Table 4) were calculated as correlations between the breeding values for AC and UH obtained with the above mentioned models.

Table 4: Correlations (r) between AC and UH using the breeding values obtained with models including the same effects as mentioned in table 3

	GR N = 2211	LR N = 3107	GS N = 3218
r	0.08	0.06	0.16
CI 95%	0.04-0.12	0.02-0.10	0.13-0.20

The correlation between AC and UH was higher in GS than in GR or LR which were not different from each other.

There are only very few studies on heritabilities of AC or UH in companion animals or livestock available. In a birth cohort of 747 male Boxers a heritability for cryptorchidism was estimated to be 0.23 (Nielen et al. (2001)). Beissner (2003) estimated heritabilities of UH in German Landrace and Piétrain to be around or below 0.1. Her heritability estimates for cryptorchidism ranged from 0.06 to 0.29. The genetic correlations between UH and cryptorchidism were 0.19 in Piétrain and -0.39 in German Landrace. In her thesis Beissner (2003) points out that heritabilities of UH are rarely published because of the very low frequency of UH in pigs and because UH often is not differentiated from other hernias. These reasons probably hold true for other livestock species. In a study by Distl and coworkers (2002) frequencies of UH in different progeny groups of German Fleckvieh with at least 100 calves varied between 0.001 and 0.071. Heritabilities for UH were around 0.4 depending on size of the progeny groups included in the estimation. In comparison to the estimate of the heritability for cryptorchidism of 0.23 by Nielen and coworkers (2001) our estimates turned out rather high with a range from 0.46 to 0.75. A major part of this difference probably is due to the definition and evaluation of the phenotype. In our study only AC diagnosed by a single veterinarian team was considered whereas in the study by

Nielen and coworkers (2001) all types of cryptorchidism diagnosed either by owners or different veterinarians were included.

Conclusions

Our heritability estimates for AC and UH suggest that these disorders can be successfully addressed in a dog breeding program. The estimated correlations indicate that there may be some small overlap in the genetic background of AC and UH.

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