Utilization of pedigree breeding values for selection against hip and elbow dysplasia in different dog breeds

K.F. Stock, M. Dammann, A. Heine, J. Engler, O. Distl

Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, 30559 Hannover, Germany (Correspondence: Kathrin-Friederike.Stock@tiho-hannover.de)



Objective

Comparative assessment of the predictive value of pedigree breeding values (pBV) for important skeletal diseases in the dog, indicating the opportunities of pBV-based planning of matings

Background

- high prevalences of canine hip dysplasia (CHD) and elbow dysplasia (ED) in many dog breeds
- relevant genetic determination of HD and ED (h² = 0.2-0.4) in German shepherd dog (GSD), Labrador retriever (LR), German Drahthaar (GD) and Rottweiler (RO)
 - limited success of mass selection \rightarrow use of breeding values for selection of breeding animals and / or choice of mating partners

Material and methods

- results from radiographic screening for CHD (DSH, LR, GD) and ED (RO)
- genetic evaluation without own phenotype information (prediction of pBV) using Best Linear Unbiased Prediction (BLUP1) or Gibbs sampling (GS2)
- test of relationship between phenotypes and pBV (proportion of phenotypic variance explained by pBV = predictive value of pBV)

Conclusions

- no reliable prediction of HD and ED phenotypes by pBV
 - → limited efficiency of pBV-based planning of matings
- need for improving genetic evaluation for skeletal health
 - → revision of phenotype recording practices (e.g. minimum proportion of examined progeny as premise for prolonged breeding use)

German shepherd dog

CHD information on 184,489 dogs born 1985-2007 CHD grades: 60.7% A, 23.7% B, 15.6% C-E genetic evaluation: BLUP with $h^2 = 0.2$ and 200,853 animals in relationship matrix (4 generations)

 $y_{iik} = \mu + BMONTH_i + a_i + e_{iik}$



Labrador retriever

CHD information on 2,867 dogs born 2000-2004 CHD grades: 64.8% A, 18.8% B, 16.4% C-E genetic evaluation: BLUP with $h^2 = 0.4$ and 6,310 animals in relationship matrix (8 generations)

 $y_{ijklmnop} = \mu + b_1 AGE_i + b_2 AGE_i^2 + b_3 IBC_i + b_4 IBC_i^2 + SEX_k$ $+BYEAR_{l} + dam_{m} + vet_{n} + a_{o} + e_{ijklmnop}$





German Drahthaar

CHD information on 7,303 dogs born 1995-2005 CHD grades: 70.0% A, 19.4% B, 10.6 % C-E genetic evaluation: GS with 11,009 animals in relationship matrix (4 generations); $h^2 = 0.29 \pm 0.04$

 $+dam_1 + kennel_m + vet_n + a_o + e_{ijklmnop}$





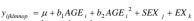
Results

- possible prediction of pBV, i.e. genetic evaluation on the basis of radiographic information on ancestors, in all dog breeds considered
- only 3-4% of the phenotypic variance of skeletal diseases explained by pBV (across breeds, diseases and methods of pBV prediction)

Table 1: Predictive value of pBV for CHD and ED in different dog breeds

Dog breed	Disease	r²
German shepherd dog	CHD	0.031
Labrador retriever	CHD	0.044
German Drahthaar	CHD	0.025
Rottweiler	ED	0.025

r² = proportion of explained phenotypic variance





ED information on 2,386 dogs born 1997-2005 ED scores: 68.5% ED0, 31.5% ED1-ED3 genetic evaluation: BLUP with h2 = 0.18 and 4,548 animals in relationship matrix (4 generations)

 $y_{iiklmnop} = \mu + b_1 AGE_i + b_2 AGE_i^2 + SEX_i + POS_k + FLEX_1$ $+dam_m + vet_n + a_o + e_{iiklmnon}$



1) Pest4.2 - Groeneveld E. (1990) PEST User's Manual. Institute for Animal Science and Animal Husbandry. Federal Agricultural Research Centre, Mariensee / Neustadt, Germany.

2) MTGSAM - Van Tassell CP, Van Vleck LD (1996). Multiple-trait Gibbs Sampler for Animal Models: Flexible programs for Bayesian and likelihood-based (co)variance component inference. J Anim Sci 74: 2586-2597.

