Session 07 (Poster Presentation 015)

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

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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 (h^2 = 0.2-0.4) in German shepherd dog (GSD), Labrador retriever (LR), German Drahthaar (GD) and Rottweiler (RO)
- limited success of mass selection
  → 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 (BLUP[1)]) or Gibbs sampling (GS[2)])
- 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)

$$y_{ijk} = \mu + BMONTH_i + a_j + e_{ijk}$$

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)

$$y_{ijklmnop} = \mu + b_1 AGE_i + b_2 AGE_i^2 + b_3 IBC_j + b_4 IBC_j^2 + SEX_k + BYEAR_l + dam_m + vet_n + a_o + e_{ijklmnop}$$

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 ± 0.04

$$y_{ijklmnop} = \mu + b_1 AGE_i + b_2 AGE_i^2 + SEX_j + EX_k + dam_l + kennel_m + vet_n + a_o + e_{ijklmnop}$$

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

$$y_{ijklmnop} = \mu + b_1 AGE_i + b_2 AGE_i^2 + SEX_j + POS_k + FLEX_l + dam_m + vet_n + a_o + e_{ijklmnop}$$

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	r^2
German shepherd dog	CHD	0.031
Labrador retriever	CHD	0.044
German Drahthaar	CHD	0.025
Rottweiler	ED	0.025

r^2 = proportion of explained phenotypic variance

[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.