COMPARISON OF GENETIC PARAMETERS OBTAINED FROM AN ORDINAL CANINE HIP PHENOTYPE DATA SET BY LINEAR AND ORDINAL ANALYSES

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SUMMARY

Many traits upon which selection may be desired are categorical traits recorded on an ordinal scale. Due to the relative ease and accessibility of linear analysis, researchers often set aside the categorical nature of these data sets and analyse them on the observed scale. Canine hip dysplasia is a common developmental disorder of the canine coxofemoral joint which results in significant pain and dysfunction in many affected animals. It is a multifactorial disease and genetic control is highly desirable. The hip dysplasia records used most commonly for selection in Australia comprise nine, radiographically assessed, ordinal traits with varying distributions, scored on each side of a dog's hips. Hip dysplasia and pedigree records from 13124 German Shepherd Dogs were analysed to compare heritability estimates and estimated breeding values obtained by analysing original or log-transformed scores with those obtained using ordinal logistic regression as well as binary logistic regression at each possible cut-point. All models incorporated the same fixed and random effects including pedigree structure. The results demonstrate that the ability of linear models to predict results of ordinal traits is variable and appears to be related to the distribution of the scores. It is therefore recommended that, where practical, the categorical nature of ordinal traits be accounted for in calculation of estimated breeding values and heritability estimates, particularly when the distributions of traits demonstrate significant skewness.

INTRODUCTION

Many important traits in animal breeding are recorded using discrete categories which have a natural order. Often these categories are assigned numerical labels based upon their order, and the categorical nature of these traits is often ignored when the traits are being analysed for use in a selection program. This could potentially lead to inaccuracies in the evaluation of the suitability of candidates for breeding and compromise the success of selection programs.

Selection against the multifactorial developmental joint disease, canine hip dysplasia (CHD), in Australia has traditionally followed the UK in the use of a hip score phenotype. This phenotype is based on radiographic examination of the dog's hips in young adulthood (typically around 19 months). Nine radiographic traits from each hip are each assigned a numerical score between the best (0) and worst (5 for one trait; 6 for the other traits). The nine scores for each hip are then added together to give a total for that hip, and the scores for left and right hip are then added together to give each dog a score between the ideal (0) and the worst (106). Selection advice is typically based on either the total score or the score of the worse hip, neither of which takes into account the ordinal nature of the data, nor the potential for underlying differences of distribution in each of the nine radiographic traits (Lawson 2000; Wood *et al*. 2004).

In this study we evaluate the extent to which the nine radiographic traits have similar distributions and compare heritability estimates and estimated breeding values (EBVs) calculated from the original and log-transformed data and from ordinal logistic regression as well as binary logistic regression at each possible cut-point.

MATERIALS AND METHODS

Data. A total of 13124 hip dysplasia scores collected from Australian registered German Shepherd Dogs (GSDs) born between 1980 and 2004 were collected and matched to pedigree information. The depth of pedigree information available for each dog with a record was variable, depending on when the dog was born and how recently its ancestors were imported into Australia. In addition, the animal's sex, age at radiography and year of birth were collected. Two ordinal scores (one from each hip) were available from each animal for each of the nine traits, resulting in 26248 scores for each trait.

Analysis. Genstat 10 was used to calculate the skewness of the distribution of the raw and log-transformed scores for each trait. ASReml 2 and beta versions of ASReml 3 were used to estimate the variance components and to calculate EBVs by fitting mixed models using residual maximum likelihood (REML) techniques (Gilmour *et al.* 2006). Models included fixed effects for gender, age (in months) at which radiography for scoring was undertaken, year of birth and hip (left or right). Random effects were a pedigree effect (additive genetic effect) and a permanent environmental effect to account for non genetic similarity in the left and right hip score of each dog. A linear model was fitted using untransformed (uLIN) and log-transformed scores (tLIN) for each of the 9 traits. A binary model (BIN) was fitted at each feasible cut-point for each of the traits. Finally, a multi-threshold model (ORD), which required the use of ASReml 3, was fitted for each trait, using as many thresholds as the program was able to include and reach a solution. Heritability estimates were obtained from ASReml for each analysis. Correlations between EBVs calculated by different methods were estimated using R software.

RESULTS

Distribution: All nine traits demonstrated positive skew, with traits 1 through 3 showing less skewness than traits 4 through 9 (see Figure 1). Log transformation decreased the skewness in all traits except trait 2, although some remained very significantly skewed (See Table 1).

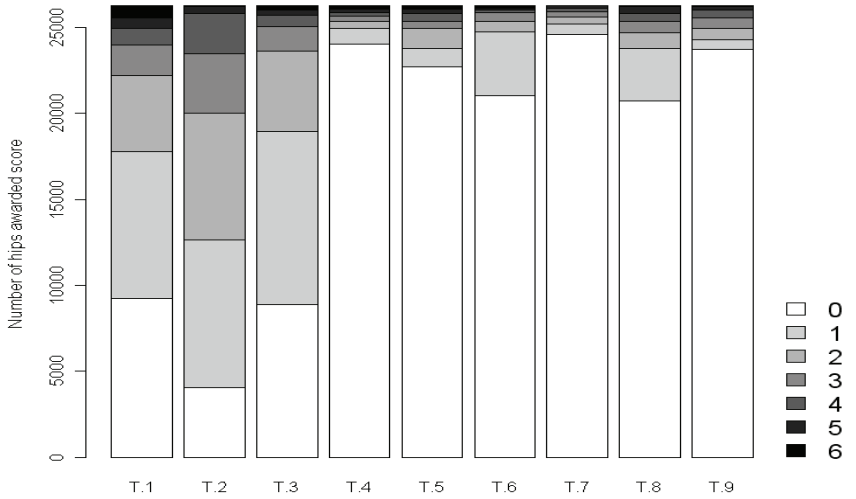

Figure 1: Distribution 26248 ordinal scores (from 13124 dogs) awarded for each of nine hip dysplasia traits.

Heritability Estimates: Heritability estimates are shown in Tables 1 and 2. Table 1 demonstrates that linear methods can result in estimates which are significantly different from estimates obtained using a multi-threshold analysis. Transformation appears generally to increase the similarity between linear and multi-threshold estimates, although the estimates may remain significantly different, e.g. for T.7 which remained very skewed despite the transformation. There does not seem to be a particular binary cut point that results in heritability estimates similar to that of the multi-threshold analysis.

Table 1. Heritability estimates plus standard errors for ordinal scores of nine radiographic traits analysed using raw and log-transformed linear analyses and a multi-threshold analysis (and skewness parameters for the score distribution)

Trait	Untransformed linear analysis	Log-transformed linear analysis	Multi-threshold ordinal analysis
T.1	0.30 ± 0.02 (1.45)	0.27 ± 0.02 (0.08)	0.26 ± 0.02
T.2	0.29 ± 0.02 (0.56)	0.23 ± 0.01 (-0.72)	0.25 ± 0.01
T.3	0.33 ± 0.02 (1.51)	0.26 ± 0.02 (-0.03)	0.27 ± 0.02
T.4	0.24 ± 0.02 (4.81)	0.18 ± 0.02 (3.54)	0.16 ± 0.02
T.5	0.27 ± 0.02 (3.47)	0.24 ± 0.02 (2.49)	0.24 ± 0.02
T.6	0.28 ± 0.02 (3.73)	0.22 ± 0.02 (1.99)	0.25 ± 0.02
T.7	0.40 ± 0.02 (5.13)	0.32 ± 0.02 (4.05)	0.24 ± 0.03
T.8	0.28 ± 0.02 (2.98)	0.26 ± 0.02 (1.87)	0.24 ± 0.02
T.9	0.21 ± 0.02 (3.70)	0.19 ± 0.02 (3.02)	0.21 ± 0.03

Table 2. Heritability estimates for nine ordinally scored radiographic traits obtained by binary logistic regression using different score cut points to define the outcome variable

	0and1	1and2	2and3	3and4	4and5	5and6
T.1	0.21[sd]	0.21[sd]	0.23	0.25	0.27	0.27
T.2	0.16[sd]	0.20[sd]	0.27	0.28	0.35	0.18
T.3	0.18[sd]	0.24	0.27	0.28	0.30	0.37
T.4	0.14	0.24	0.23	0.28[sd]	0.33[sd]	0.35
T.5	0.23	0.24	0.25	0.25	0.30	0.39
T.6	0.22	0.22	0.22	0.32	0.40	0.30
T.7	0.24	0.24	0.23	0.24	0.27	-
T.8	0.21	0.21	0.20	0.20	0.30	0.30
T.9	0.21	0.17	0.18	0.26	0.35	0.32

[sd] Significantly different ($P < 0.05$) from multi-threshold ordinal estimate

Estimated Breeding Values: The relationship between the skewness of the scores and the correlation between EBVs obtained by the ORD and uLIN analyses and those obtained by the ORD and tLIN analyses is shown in Figure 2. It demonstrates a clear trend for the utility of linear analyses to decrease as skewness increases.

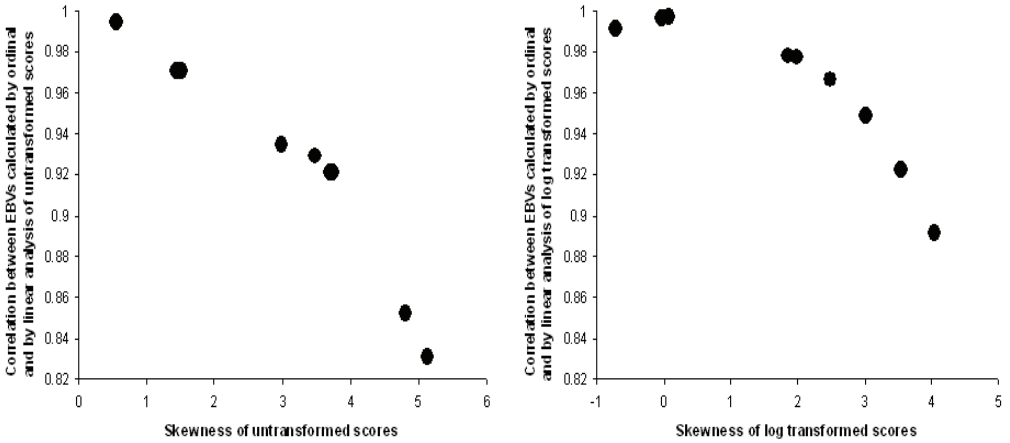

Figure 2: Relationship between the skewness scores and the correlation between EBVs calculated by linear and multi-threshold methods for untransformed linear scores (left) and log transformed linear scores (right).

DISCUSSION

The results show that while calculation of EBVs and heritability estimates for ordinal scores using linear mixed models may result in reasonable estimates in some cases, there may also be appreciable differences in the results. Analysis of this real data set showed that a log transformation resulted in heritability estimates more similar to those estimated by multi-threshold procedures. For one especially skewed trait, however, the result remained significantly different. The binary model heritability estimates were not demonstrably better than the transformed linear model estimates. The correlation between EBVs from linear and multi-threshold models showed a strong negative association with skewness. While correlations for traits with minimal skew were very good, further work is needed to assess the extent to which there might be individual animals for which substantially different EBVs are obtained from the two approaches; and the effect which this may have on the effectiveness of a selection program. It is therefore recommended that when calculating EBVs and heritabilities for ordinal traits, a multi-threshold model be implemented using an ordinal logistic mixed model. If linear models must be used, then a correction for skewness appears to be advantageous.

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