Evaluation of pelt traits in Karakul sheep applying linear and threshold models

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A total of 967 animal records, of subjective trait scores, obtained between 1989 and 1990, from the control flock at the Karakul Research Station near Upington were used to evaluate 20 pelt traits in Karakul sheep, applying linear and threshold models. It seemed that categorical traits with an extended number of categories are almost continuous rather than discrete. A threshold model therefore holds no advantage over the use of a linear model. However, if the shape of the distribution is not normal, a threshold model may be preferred.

'n Totaal van 967 diere-rekords, van subjektiewe tipe klassifikasies, verkry vanaf 1989 tot 1990, van die kontrolekudde van die Karakoel Navorsingstasie naby Upington is gebruik om 20 pelseienskappe by Karakoelskape te evalueer met behulp van lineêre en drumpelwaarde-modelle. Wanneer kategoriese eienskappe met 'n groot aantal kategorieë se verspreiding byna normaal is, wil dit voorkom asof 'n drumpelwaarde-model nie 'n werklike voordeel bo 'n lineêre model vir die ontleding inhou nie. As die verspreiding egter nie na aan normaal is nie, kan 'n drumpelwaarde-model moontlik meer aanvaarbaar wees.

Keywords: heritabilities, Karakul sheep, pelt traits, linear and threshold models

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Introduction

Economically important pelt traits in Karakul sheep are normally evaluated subjectively by the allocation of scores (Anonymous, 1982). The method of scoring has recently been revised and refined in the Upington control flock making it more useful for selective breeding purposes. As with other subjective scores in livestock, the best method of analyses for these traits is controversial (Harvey, 1982; Randall, 1993; Schoeman & Albertyn, 1993). Another important question is whether such scores should be treated as ordinary polygenic or as threshold traits. It is generally excepted that they are polygenic. The estimation of genetic parameters and breeding values for these traits is pertinent.

No better method of assessing quality in Karakul pelts presently exists than subjective scoring. This system will most probably still be used for a long time. Modelling should ideally be done by judiciously studying and applying biological principles and not by randomly using different models and then selecting the one yielding results to the best of one's liking. Although the authors support an ordinary polygenic approach to subjective scores a threshold model could be more effective in analysing traits with very few recorded classes and very poor distributions. These traits are not threshold traits from a genetic point of view but merely analysed by threshold procedures The aim of the study was to investigate this approach.

Material and methods

Data from the control flock at the Karakul Research Station near Upington were used in this study. The flock consists of 200 ewes and was established in 1963. Rams constituted about 20% of the breeding flock. The rams were kept in two age groups (18 and 30 months). Half of the rams were replaced each year. Replacements for both rams and ewes were chosen at random. Every second ewe and fourth ram lamb was taken as replacement. Animals with serious body defects were not considered as replacements. Ewes were kept in the flock until seven years of age, but infertile and subfertile ewes were removed earlier. To ensure minimum inbreeding no close relatives were mated. Three mating seasons were applied during January/February, May and August for a period of 34–51 days depending on the time of the year. Handmating or controlled group-mating was practised where possible. Pregnant ewes were kept in confinement to ensure positive identification of lambs born and to ensure that all relevant data were collected within 36 h after birth. The control flock experiment was terminated at the end of 1994.

Only 976 complete records, obtained between 1989 and 1994 inclusive, were available since a new scoring system was introduced in 1989. All 20 traits scored were included in the analysis. The three main economically important pelt traits are pattern, curl development and hair quality. Skin thickness is considered as a secondary trait (Nel, 1966). All these traits and their different components, with the exception of curl type (scale 1–10), were scored on a scale of 2–8. This means that 5 was taken as the mid value, 4 and 6 as the lower and higher values and 2 and 8 as the minimum and maximum values.

For the linear model analyses, non-genetic effects were tested for inclusion in the fixed part of the model using the General Linear Model (GLM) procedure of SAS (SAS, 1991). The effects tested were year of birth (6 levels), season (3 levels), sex (2 levels), birth status (2 levels) and age of dam (8 levels). It was found that all the pelt traits, except brittle hair (body), were significantly ($p < 0.05$) affected by all these factors. Variance components and resulting heritabilities were estimated using the Derivative Free Restricted Maximum Likelihood (DFREML) program developed by Meyer (1995). The following univariate model was fitted:

$y = Xb + Za + e$

Where

y = vector of observed traits of animals,
b = vector of fixed effects (year of birth, season, sex, birth status and age of dam)
a = vector of direct additive genetic effects
X, Z = the corresponding incidence matrices relating the effects to y and
e = the vector of residuals

For the threshold analysis, a non-linear (CATMOD) procedure from the SAS package was used to test the same non-genetic effects. Results were much the same as those from the least-squares analyses. All the pelt traits were significantly affected ($p < 0.05$) by the fixed effects included. Variance components were estimated by means of the method proposed by Gianola & Foulley (1983) for threshold traits and utilised in the set of programs developed by Konstantinov (1995)(GFCAT). The following model was used:

$\mu = X\beta + Zs$

where

μ = vector of underlying means

β = vector associated with the fixed effects (year of birth, season, sex, birth status and age of dam)

s = vector of sire effects and

X, Z = design matrices

Heritability estimates applying the two different models can strictly speaking not be compared since a linear model is based on the observed scale whereas a threshold model utilises the underlying scale. If reasonably large differences in the estimates exist, it could, however, have serious practical implications and make a comparison, albeit theoretically dubious, of great practical value. In the case of variance components, however, a comparison is truly impossible. With the present threshold analysis, sire and not animal additive variance was estimated, the error variance was set to unity and all solutions were expressed in units of residual standard deviations of the underlying variable.

Results and discussion

The heritability estimates from both the linear and threshold analyses are presented in Table 1.This is the first study done on Karakul pelt traits using a threshold model, thus there are no other values

Table 1 Heritability estimates from linear and threshold analyses

Trait	Linear	± S.E.	Threshold	Skewness	Kurtosis	No of classes
Pattern score	0.337	0.008	0.128	0.17	1.75	7
Rib	0.425	0.007	0.188	0.20	-1.09	8
Moiré	0.222	0.006	0.163	2.48	5.02	4
Lyre	0.266	0.008	0.149	2.71	8.71	6
Waviness	0.416	0.008	0.112	1.56	2.56	6
Silkiness	0.159	0.006	0.012	4.97	25.85	4
Skin thickness	0.443	0.007	0.277	–0.74	0.48	8
Curl development	0.676	0.005	0.673	9.06	–0.81	8
Curl breadth	0.499	0.006	0.430	0.26	0.97	8
Vertical pattern	0.344	0.008	0.312	0.10	–0.05	7
Metallic/gloss	0.484	0.007	0.418	–0.04	–0.75	8
Dullness	0.443	0.007	0.495	–0.14	–0.42	6
Hair thickness	0.424	0.007	0.449	–0.78	0.97	7
Hair quality score	0.384	0.006	0.663	–0.30	0.50	7
Bandedness	0.322	0.006	0.413	0.92	–0.35	8
Straight hair	0.390	0.007	0.571	2.03	3.47	7
Hair length	0.534	0.006	0.616	0.25	–0.46	6
Brittle hair	0.408	0.006	0.721	2.61	0.04	8
Hair stiffness	0.541	0.006	0.680	0.24	–0.44	5
Lustre	0.450	0.006	0.584	0.17	0.05	6

in the literature for comparison. For the linear animal model, heritabilities were estimated as $h^2 = \sigma_a^2/(\sigma_a^2+\sigma_e^2)$. For the threshold sire model σ_e^2 was set to unity. Thus, $h^2 = 4\sigma_s^2/(1 + \sigma_s^2)$. It is also important to note that heritabilities for threshold models are estimated on the underlying normal distribution, otherwise each category would have its own heritability. This implies that the estimated heritabilities are in fact not the real heritability.

Heritability estimates obtained from the threshold model varied more (0.012 to 0.721) than those from the linear model (0.159 to 0.676). It is obvious that the differences in estimates applying the two different models is largely influenced by the distribution of the trait. Although it cannot be generalised, a large departure from normality generally led to larger differences in estimated values. Lower estimates were also obtained with the threshold model for traits with a small number of classes.

Conclusions

Threshold traits, by definition, have an underlying continuous variation but are expressed on a discontinuous (categorical) scale. It is argued that in the case of most subjective scores with more than two categories, the continuous variation is not underlying but in fact fully or partially expressed. The authors are therefore of the opinion that these traits can be considered as ordinary polygenic traits since they do not fit the description of threshold traits. It is, however, not possible for the human eye to observe small differences in the expression of the trait. They thus agree with Harvey (1982) that a least squares analysis of discrete variables is valid if these values scored are an indication of quantitative differences between classes.

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