Original Report

Additive genetic and error variance components for conformation and coat traits in arctic fox *Alopex lagopus* (L.)

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Abstract

Records of 3782 arctic foxes were used for estimation of additive genetic and error variance components for conformation and coat traits. Body size (BS), colour type (CT), colour purity (CP), coat density (CD), hair length (HL), general appearance (GA) and total score (TS) were analysed. The variance components were estimated by the Restricted Maximum Likelihood (REML) method with a univariate animal model. Since data exhibited skewed distribution (skewness ranged from 0.0110 for CP to −3.8631 for TS) the probit transformation was applied. Both transformed and untransformed data were used for the estimation of variance components. Transformation of the data resulted in reduced estimators of variance components, and in consequence, lower heritability estimates for studied traits were obtained (heritabilities ranged from 0.266 for GA to 0.533 for HL).

Key words: arctic fox, animal model, heritability, probit transformation, variance components

Introduction

In fox populations evaluation of conformation and coat traits is done subjectively on a discrete scale. Although the point scale which is used for evaluation of each conformation trait is diversified (see Table 1), the judges mainly score the highest points or zero. This disadvantage of subjective evaluation leads to non-normality of scores distribution.

Arbitrarily assigned scores introduce a large amount of measurement error, which appear as environmental variance if components of variance are estimated (*Falconer and MacKay, 1996*). Since conformation and coat traits of foxes are recorded in points, the data should be transformed before they are subjected to statistical analyses. Transformation improves the properties of the data by removing the variance due to measurement error.

When estimating heritability the respective variance components have to be used. The commonest method of estimating variance components in the context of unbalanced data is the Restricted Maximum Likelihood (REML), which was introduced by Patterson and Thompson (1971). REML is often preferred to maximum likelihood estimation because it takes account of the loss of degree of freedom in estimating the mean and produces unbiased estimating equations for the variance parameters (*Smyth and Verbyla, 1996*). However, REML requires normally distributed *data (Besbes et al., 1993*). Logarithmic or Box-Cox data transformation is usually applied to approach normality (*Boldman and Freeman, 1990; Koerhuis and McKay, 1996; Strabel and Szwaczkowski, 1997*).

Fox conformation and coat traits are measured/evaluated qualitatively rather than continuously and for this type of traits the probit transformation, which arose from the need to analyse qualitative variables, has been shown to be well *suited (¯uk, 1989).*

The aim of the present study was to estimate additive genetic and error variance components for conformation and fur traits in arctic fox. Moreover, the effect of the data transformation on the magnitude of estimated heritabilities and their standard errors was investigated.

Material and methods

Data comprised 3782 records of arctic foxes kept in the pedigree farm in Œniaty (Poland). The data were collected in a data base of the LISY computer system (*Chudoba et al., 1988*). Only records with complete information on each animal were taken into account during statistical analyses. The following traits were studied: body size (BS), colour type (CT), colour purity (CP), coat density (CD), hair length (HL), general appearance (GA) and total score (TS). Since evaluation of fox conformation is done subjectively on a discrete scale, each unitrait data set was examined according to its skewness of distribution. Statistical description of the data is presented in Table 1. A detailed description of the data set and a structure of the studied fox population has been presented by Wierzbicki et al. (2000).

Table 1. Scales of conformation scores, means, standard deviations (SD) and skewness coefficients of studied traits

Trait	Scale of conformation scores	Mean	SD	Skewness
Body size	0-3	2.743	0.511	-1.8724
Colour type	0-6	5.638	0.844	-2.2620
Colour purity	0-6	4.747	1.060	0.0110
Coat density	0-6	5.276	0.639	-0.8541
Hair length	0-6	5.513	0.625	-1.1956
General appearance	0-3	2.921	0.272	-3.2526
Total score	0-30	26.816	1.995	-3.8631

Since the data sets exhibited strongly skewed distribution they were transformed into normally distributed ones. The probit transformation according to procedure described by ¯uk (1989) was employed.

The variance components were estimated using the Restricted Maximum Likelihood (REML) with a following univariate animal model:

$$y_{ijk} = \mu + r_i + p_j + a_{ijk} + e_{ijk} \ ,$$

where:

y_{ijk} = observation,
μ = overall mean,
r_i = fixed effect of year,
p_j = fixed genetic effect of colour variety,
a_{ijk} = random additive genetic effect,
e_{ijk} = random error.

In order to investigate the effect of data transformation on the magnitude of heritability estimates, the variance components for the studied traits were estimated using the original and transformed data. Heritability was calculated according to the following formula:

$$\hat{h}^2 = \hat{S}_a^2 / \hat{S}_a^2 + \hat{S}_e^2 \ ,$$

where $\hat{S}_a^2$ and $\hat{S}_e^2$ are additive genetic and error variance components, respectively.

All statistical analyses were performed using the SAS computer package (1990).

Results and discussion

Table 1 shows the skewness coefficients for the unitrait data sets. All traits (except CP) exhibited markedly skewed distributions. The strongest deviation from a normal distribution was computed for TS and GA (-3.8631 and –3.2526, respectively) followed by CT (-2.2620). The distribution of scores for CP was very close to normal (0.0110).

The additive genetic and error variance components estimated using both untransformed and trans-

formed data are shown in Table 2 and Table 3, respectively. For each trait analysed the probit transformation decreased the variance components estimates. The additive genetic variance components derived from original data ranged from 0.018716 for GA to 2.742427 for TS (Table 2), whereas after data transformation they ranged from 0.000360 for GA to 0.018268 for CP (Table 3). The error variance components were also reduced. Before transformation the highest estimate of the error variance was found for TS (2.813317) and the lowest for GA (0.061128), while after transformation they were reduced to 0.009196 and 0.001236, respectively. Generally, the data transformation caused a substantial reduction of the variance estimates.

Table 2. Additive genetic ($\hat{S}_a^2$) and error ($\hat{S}_e^2$) variance components for studied traits before data transformation

Trait	$\hat{S}_a^2$	$\hat{S}_e^2$
Body size	0.134544	0.157118
Colour type	0.355840	0.443695
Colour purity	0.828168	0.666032
Coat density	0.206908	0.308439
Hair length	0.471104	0.269800
General appearance	0.018716	0.061128
Total score	2.742427	2.813317

Strabel and Szwaczkowski (1997) estimated variance components for test day milk traits in cattle and found that the Box-Cox transformation resulted in lower estimates of the additive genetic, permanent environmental and error variance components. In a study on genetic and environmental effects on a temperament score in beef cattle, Hearnshaw and Morris (1984) stated that a logarithmic transformation of the data equalised the variance of scores, but did not affect the results.

Also Jakubczak (2000), who carried out the study in a population of silver fox, stated that the Box-Cox transformation did not change markedly the variance components. In contrast, Boldman and Freeman (1990) found that logarithmic transformation did not stabilise the additive genetic and environmental variances for milk yield. Furthermore, they stated that the environmental variances for transformed yields decreased as production level increased.

Table 3. Additive genetic ($\hat{\boldsymbol{S}}_a^2$) and error ($\hat{\boldsymbol{S}}_e^2$) variance components for studied traits after data transformation

Trait	$\hat{\boldsymbol{S}}_a^2$	$\hat{\boldsymbol{S}}_e^2$
Body size	0.003263	0.008069
Colour type	0.002548	0.004894
Colour purity	0.018268	0.018906
Coat density	0.008172	0.018584
Hair length	0.002356	0.002060
General appearance	0.000360	0.001236
Total score	0.005488	0.009196

Table 4. Heritability ($\hat{h}^2$) and approximate standard errors of the estimators (*SE*) of studied traits before (BT) and after (AT) data transformation

Trait	BT		AT	
	$\hat{h}^2$	*SE*	$\hat{h}^2$	*SE*
Body size	0.461	0.055	0.288	0.047
Colour type	0.445	0.054	0.342	0.049
Colour purity	0.554	0.059	0.491	0.056
Coat density	0.401	0.052	0.305	0.048
Hair length	0.636	0.062	0.533	0.058
General appearance	0.234	0.045	0.226	0.044
Total score	0.494	0.056	0.374	0.037

Table 4 shows the heritability estimates of conformation and coat traits. Heritabilities derived from the original data ranged from 0.234 for GA to 0.636 for HL and they were higher than those estimated using transformed scores. After transformation all heritability estimates decreased ranging from 0.226 for GA to 0.491 for CP. Standard errors of estimates were slightly (BS, CT, CP, CD, HL, GA) or significantly (TS) lower after transformation. The heritability estimates obtained after the data transformation were within the range (except BS) of those estimated by Filistowicz et al. (1999) who carried out the study in a population of silver fox. The authors applied the normal probability scale transformation and derived heritabilities ranging from 0.168 for CP to 0.374 for TS.

Buddenberg et al. (1989) found that the transformation to the probit scale decreased the heritability estimates of pregnancy rate estimated for beef cattle. Boldman and Freeman (1990) used REML with a sire and nested-cow model for estimation of variance components and stated that heritability estimates were not significantly changed by logarithmic transformation of yields. The same conclusion was drawn by Jakubczak (2000) who found that the Box-Cox transformation of scores did not affect markedly heritability estimates for coat traits in silver fox.

Becerril et al. (1994) carried out research on transformation of measurements of percentage of white coat colour for Holstein cattle. The authors found that heritability estimates for percentages of white coat colour, estimated using DFREML with an animal model were higher after the Box-Cox transformation and they had lower standard errors.

Conclusions

The probit transformation of the data set resulted in lower heritabilities and slightly lower standard errors of estimates. Decreased standard errors were the consequence of a reduction of error variance estimates. However, the data transformation led to a substantially smaller additive genetic variance components resulting in lower heritability estimates.

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