Breeding value evaluation in Polish fur animals: Estimates of direct heritability and portion of litter variation of fur coat and reproduction traits

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ABSTRACT: The study presents estimates of heritability for fur coat and reproduction traits in arctic and silver foxes kept on Polish farms. The estimates of variance components were calculated using the DFREML and single-trait animal models. Due to a discrete character of fur coat traits, they were analysed twice: (1) without normalisation of their scores distribution, (2) after the normal probability scale transformation of their scores. Linear models included random additive genetic and common litter environment effects, and fixed effects of farm × year × birth season in the silver fox or year × birth season in the arctic fox as well as the fixed effect of female age when the reproduction traits were analysed. Moreover, the estimation of variance components for fur coat traits was done by a linear model with (Model 2) or without (Model 1) inbreeding coefficients included as linear covariable. In the arctic fox accounting for inbreeding and the data transformation did not markedly influence the estimates of heritability and the portion of litter variation calculated for the fur coat traits. An inbreeding effect was negligible (except for body size – BS) likely due to the low inbred level of the arctic fox population. In the silver fox the comparison of estimates derived using 2 different linear models and 2 data sets revealed more differences than it was found in the arctic fox. Accounting for inbreeding usually led to lower estimates of heritability, mainly when heritabilities were derived from the normal probability scale-transformed data. Most of the estimates of heritability of reproduction traits were found within the range reported by other authors. However, somewhat higher heritabilities were found for litter size at birth – LSB (0.205) and litter size at weaning – LSW (0.250).

Keywords: arctic fox; fur coat; heritability; normal probability scale transformation; reproduction; silver fox

Economic success of fur production is mainly determined by the number of produced pelts and their quality. Hence, breeding programmes focus on reproductive performance (litter size at birth, litter size at weaning), and fur coat and conformation traits (skin size, fur quality, colour type) which are of economic importance.

Average litter size on a farm is a key determinant of the economic efficiency of fur production. However, this trait is unfortunately difficult to improve through selection because of its low heritability (Jakubczak, 2002; Ortega *et al*., 2002; Ślaska, 2002). Fertility is also negatively correlated with animal size (Lagerqvist *et al*., 1994). Furthermore, an increase in the litter size appears to be associated with a decrease in birth weight and survival (Haley *et al*., 1988).

The international and domestic system of selling pelts prefers skins of large sizes, high quality of hair cover and a colour type close to the required standard (Filistowicz *et al*., 1999a). The genetic improvement of these traits has proved to be an effective way of increasing the efficiency of fur production (Johannessen *et al*., 2000; Wierzbicki *et al*., 2000). Therefore, it is necessary to have reliable estimates of relationships between these traits to avoid potential negative effects of selection for production traits on the reproductive performance. Moreover, accurate estimates of (co)variance components are

needed to produce reliable predictions of breeding values (Kaufmann *et al.*, 2000).

In Poland the estimation of variance components for fur coat and reproduction traits was carried out a few times (Socha, 1996; Filistowicz *et al.*, 1999b; Wierzbicki and Filistowicz, 2002). However, the authors estimated only direct heritabilities not including in the linear models the second random effect – common litter environment.

This paper is the second part of the study on the breeding value evaluation in Polish fur animals, and presents estimates of direct heritability (h^2) and portion of litter variation (c^2) of economically important fur coat and reproduction traits in arctic and silver foxes.

MATERIAL AND METHODS

Data

Fur coat and reproduction records on silver and arctic foxes were obtained from three Polish farms. Information on fur coat traits: (1) silver fox – body size (BS), colour type (CT), colour purity (CP), coat density (CD), hair length (HL), purity of silvering (PS), general appearance (GA), total score (TS), skin length (SL); (2) arctic fox – body size (BS), colour type (CT), colour purity (CP), coat density (CD), hair length (HL), general appearance (GA), total score (TS), and skin length (SL), and reproductive performance (only in arctic fox) – litter size at birth (LSB), litter size at weaning (LSW), number of dead pups (NPD), pup weight at weaning (PW), pregnancy

length (PL), whelping age (WA) – was recorded by farmers and collected in computer data bases. The trait definitions, descriptions and full statistical analyses of the data have been given by Wierzbicki *et al.* (2004) in the first part of the study. The structure of data sets and pedigrees is given in Table 1.

Restricted Maximum Likelihood (REML), which accounts for the loss in degrees of freedom due to fixed effects in the model of analysis, has become the preferred method of analysis for animal breeding data (Patterson and Thompson, 1971). However, the REML requires normally distributed data (Besbes *et al.*, 1993). The fur coat traits are discrete ones and are graded qualitatively rather than continuously. This causes that the scores distributions have heavier-than-normal tails. Thus, the distribution of the fur coat scores in the data sets used in the study was normalised using a probit link function with

$$E(y) = \Phi(\lambda)$$

where: Φ = the normal cumulative density function
λ = the fitted value of the underlying normal scale

Then, two sets of data: (1) without transformation and (2) transformed were used for the estimation of variance components.

The fur coat traits measured on a discrete scale are theoretically better suited to nonlinear analysis. Nonlinear mixed models based on threshold theory were studied for the analysis of categorical traits (Gianola, 1982). However, the study carried out by Matos *et al.* (1997) did not show superiority of nonlinear analysis (threshold model) over

Table 1. The structure of analysed data sets

Pedigree and data structure	Silver fox	Arctic fox	
		fur coat traits	reproduction
No. of animals	9 001	5 822	7 030
base animals	1 159	687	584
with records	8 163	5 236	5 829
No. of sires	787	430	483
No. of dams	1 151	789	718
No. of years	16	13	10
No. of birth season	3	2	3
No. of breeding seasons	–	–	5
No. of farms	3	1	1

linear models as far as goodness of fit and predictive ability were concerned. Moreover, computer intensive iterative procedures are necessary to solve the nonlinear systems (Hagger, 2000). Thus, linear models were applied in this study as well as derivative-free approach which provides a flexible and powerful alternative to other REML algorithms (Meyer, 1989).

Analysis

Two single trait linear models were used for the estimation of variance components for the fur coat traits:

$$y = X_1\beta_1 + Za + Wc + e \tag{1}$$

$$y = X_1\beta_1 + X_2\beta_2 + Za + Wc + e \tag{2}$$

$$\text{with } E \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{var} \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} \sigma_a^2 A & 0 & 0 \\ 0 & \sigma_c^2 I & 0 \\ 0 & 0 & \sigma_e^2 I \end{bmatrix}$$

where:

y, β_1, β_2, a, c, e = vectors of observations, fixed effects (farm × year × birth season in silver fox or year × birth season in arctic fox), inbreeding coefficients included as linear covariable, additive genetic effects, common litter environment effects and residuals, respectively

X_1, X_2, Z, W = design matrices for fixed effects, inbreeding coefficients, additive genetic effects and common litter environment effects, respectively

σ_a^2, σ_c^2, σ_e^2 = additive genetic, common litter environment and residual variances, respectively

A = the numerator relationship matrix

I = the identity matrix

Estimates of error variance were taken as an indicator of model goodness (Sundberg, 1994).

The estimation of variance components for the reproduction traits in the arctic fox was performed by the following single trait animal model:

$$y = X_1\beta_1 + X_2\beta_2 + Za + Wc + e$$

$$\text{with } E \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{var} \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} \sigma_a^2 A & 0 & 0 \\ 0 & \sigma_c^2 I & 0 \\ 0 & 0 & \sigma_e^2 I \end{bmatrix}$$

where:

y, β_1, β_2, a, c, e = vectors of observations, fixed effects of year × birth season, fixed effects of female age, additive genetic effects, common litter environment effects and residuals, respectively

X_1, X_2, Z, W = design matrices for fixed effects of year × birth season, female age, additive genetic effects and common litter environment effects, respectively

σ_a^2, σ_c^2, σ_e^2 = additive genetic, common litter environment and residual variances, respectively

A = the numerator relationship matrix

I = the identity matrix

The inbreeding coefficient was not included in the model as linear covariable since earlier study (Wierzbicki *et al.*, 2004) did not find inbreeding in the arctic fox breeding stock.

The estimates of heritability [$h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_c^2 + \sigma_e^2)$], portion of litter variation [$c^2 = \sigma_c^2/(\sigma_a^2 + \sigma_c^2 + \sigma_e^2)$], and their approximate standard errors were estimated using the DFREML (Derivative Free Maximum Likelihood) (Meyer, 1998). A variance of the likelihood function values of less than 10^{-8} was chosen as a convergence criterion.

RESULTS AND DISCUSSION

Tables 2–5 show the estimates of heritability (h^2) and a portion of litter variation (c^2) of the arctic and silver fox fur coat traits. The parameters estimated with the use of original data (without normal probability scale transformation) are shown in Table 2 and Table 3, whereas Table 4 and Table 5 document the parameters derived using the transformed data. Furthermore, the comparison of parameters estimated with the use of the linear model without (Model 1) or with (Model 2) inbreeding coefficient as linear covariable is presented.

In the arctic fox (Table 2) the estimates of heritability and the portion of litter variation derived using Model 1 (h^2 ranged from 0.106 for GA to 0.337 for HL; c^2 ranged from 0.056 for GA to 0.169 for TS) did not differ markedly from those estimated with the use of Model 2 (h^2 ranged from 0.104 for GA to 0.335 for HL; c^2 ranged from 0.059 for GA to 0.182 for BS). The effect of the model type on estimate magnitude was clearly seen in the case of BS. Accounting for inbreeding (Model 2) led to the

Table 2. Estimates of heritability (h^2), portion of litter variation (c^2) and their approximate standard errors (s.e.), and error variances (σ^2_e) of the arctic fox fur coat traits (data set without transformation)

Trait	Model 1			Model 2		
	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e
BS	0.289 ± 0.035	0.091 ± 0.014	0.116	0.198 ± 0.002	0.182 ± 0.008	0.115
CT	0.325 ± 0.034	0.079 ± 0.014	0.270	0.315 ± 0.082	0.084 ± 0.021	0.272
CP	0.254 ± 0.032	0.151 ± 0.017	0.471	0.254 ± 0.014	0.150 ± 0.007	0.470
CD	0.197 ± 0.028	0.078 ± 0.014	0.232	0.201 ± 0.070	0.077 ± 0.002	0.230
HL	0.337 ± 0.035	0.132 ± 0.016	0.191	0.335 ± 0.033	0.134 ± 0.014	0.190
GA	0.106 ± 0.023	0.056 ± 0.011	0.509	0.104 ± 0.016	0.059 ± 0.009	0.508
TS	0.223 ± 0.030	0.169 ± 0.016	1.348	0.241 ± 0.023	0.144 ± 0.006	1.346
SL	0.229 ± 0.037	0.091 ± 0.015	0.359	0.207 ± 0.021	0.123 ± 0.016	0.149

reduction of genetic variation, and in consequence a lower h^2 for BS was estimated (0.198 vs. 0.289). On the other hand, the portion of litter variation was twice as high (0.182) as in Model 1 (0.091). This is very important information, since BS is economically the most important trait in fox breeding.

An error variance indicating the model goodness showed a similar adequacy of both models for 7 out of 8 trait analysed (residuals were almost identical). Only for SL Model 2 was better fitted ($\sigma^2_e = 0.149$) than the first one ($\sigma^2_e = 0.359$).

A comparison of estimates of heritability and portion of litter variation derived using the data without transformation (Table 2) and the transformed ones (Table 4) revealed small differences between the estimates. Pronounced differences were found for Model 2 in BS (h^2 and c^2 derived from the untransformed data were 0.198 and 0.182, respectively, whereas the same estimates derived from the transformed data were 0.233 and 0.100, respectively). The data transformation significantly reduced an error variance for CP (twice as low as before transformation) and GA and TS (three times lower than before transformation).

Generally, in the arctic fox accounting for inbreeding (Model 1 vs. Model 2) and the data transformation (Table 2 vs. Table 4) did not markedly influence the estimates of heritability and a portion of litter variation calculated for the fur coat traits. An inbreeding effect was negligible (except for BS) likely

Table 3. Estimates of heritability (h^2), portion of litter variation (c^2) and their approximate standard errors (s.e.), and error variances (σ^2_e) of the silver fox fur coat traits (data set without transformation)

Trait	Model 1			Model 2		
	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e
BS	0.081 ± 0.017	0.038 ± 0.010	0.840	0.096 ± 0.012	0.030 ± 0.009	0.824
CT	0.231 ± 0.027	0.108 ± 0.015	0.238	0.226 ± 0.019	0.121 ± 0.018	0.251
CP	0.133 ± 0.021	0.027 ± 0.009	0.174	0.141 ± 0.019	0.068 ± 0.006	0.172
CD	0.184 ± 0.023	0.080 ± 0.013	0.203	0.140 ± 0.015	0.144 ± 0.009	0.203
HL	0.239 ± 0.027	0.077 ± 0.013	0.184	0.197 ± 0.019	0.151 ± 0.019	0.187
PS	0.130 ± 0.021	0.054 ± 0.010	0.161	0.097 ± 0.010	0.070 ± 0.008	0.177
GA	0.139 ± 0.011	0.006 ± 0.017	0.178	0.183 ± 0.018	0.001 ± 0.017	0.181
TS	0.137 ± 0.024	0.081 ± 0.013	1.761	0.011 ± 0.007	0.100 ± 0.016	1.919
SL	0.348 ± 0.031	0.222 ± 0.019	3.148	0.392 ± 0.020	0.172 ± 0.007	4.961

Table 4. Estimates of heritability (h^2), portion of litter variation (c^2) and their approximate standard errors (s.e.), and error variances (σ^2_e) of the arctic fox fur coat traits (transformed data set)

Trait	Model 1			Model 2		
	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e
BS	0.291 ± 0.035	0.089 ± 0.014	0.204	0.233 ± 0.019	0.100 ± 0.011	0.217
CT	0.325 ± 0.034	0.086 ± 0.014	0.161	0.310 ± 0.029	0.086 ± 0.015	0.164
CP	0.244 ± 0.031	0.149 ± 0.016	0.242	0.202 ± 0.017	0.189 ± 0.003	0.245
CD	0.184 ± 0.027	0.083 ± 0.014	0.397	0.145 ± 0.004	0.110 ± 0.003	0.383
HL	0.333 ± 0.034	0.134 ± 0.016	0.295	0.333 ± 0.034	0.135 ± 0.017	0.295
GA	0.107 ± 0.022	0.057 ± 0.011	0.171	0.109 ± 0.013	0.097 ± 0.007	0.189
TS	0.248 ± 0.031	0.182 ± 0.017	0.425	0.261 ± 0.003	0.191 ± 0.002	0.436

SL – h^2 and c^2 were not estimated using the transformed data because the trait was measured on a metric scale and its scores had normal distribution

due to a low inbred level of the arctic fox population. According to Wierzbicki *et al.* (2004) the inbreeding coefficient in that arctic fox population in the 1980s and 1990s was markedly lower than 1%, reaching the highest level of 0.8% in 1989.

Peura *et al.* (2003) estimated the genetic parameters for fertility traits and the animal size of Finnish blue foxes. Using a single- and multi-trait animal model with 2 random effects (additive genetic and common litter environment) they found heritabilities for BS comparable to those presented in this study. Depending on the model fitted (single- or multi-trait) they reported $h^2 = 0.23$ or $h^2 = 0.27$, respectively, while in the present study the estimates

of heritability for BS oscillated around 0.2–0.3. A portion of litter variation of BS was also comparable in both studies ($c^2 = 0.11$ in the Finnish study and $c^2 \sim 0.1$ in the Polish study).

In the earlier investigation Wierzbicki (2000) studied an effect of data transformation on the variance components of fur coat traits in blue foxes. The normal probability scale transformation of the data resulted in lower estimates of heritability (ranging from 0.234 for GA to 0.636 for HL before transformation, and from 0.226 for GA to 0.533 for HL after transformation) as well as the reduction of error variance. Both types of heritability estimates (derived from transformed or not transformed data)

Table 5. Estimates of heritability (h^2), portion of litter variation (c^2) and their approximate standard errors (s.e.), and error variances (σ^2_e) of the silver fox fur coat traits (transformed data set)

Trait	Model 1			Model 2		
	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e	$h^2 \pm$ s.e.	$c^2 \pm$ s.e.	σ^2_e
BS	0.084 ± 0.027	0.042 ± 0.011	0.377	0.045 ± 0.004	0.071 ± 0.012	0.379
CT	0.215 ± 0.028	0.098 ± 0.014	0.336	0.206 ± 0.015	0.115 ± 0.012	0.349
CP	0.158 ± 0.025	0.031 ± 0.010	0.268	0.184 ± 0.022	0.028 ± 0.056	0.308
CD	0.183 ± 0.023	0.087 ± 0.014	0.339	0.097 ± 0.006	0.070 ± 0.003	0.386
HL	0.261 ± 0.027	0.070 ± 0.012	0.273	0.139 ± 0.016	0.144 ± 0.010	0.343
PS	0.135 ± 0.024	0.054 ± 0.010	0.323	0.238 ± 0.017	0.027 ± 0.002	0.303
GA	0.144 ± 0.018	0.005 ± 0.017	0.342	0.170 ± 0.019	0.003 ± 0.018	0.328
TS	0.108 ± 0.020	0.064 ± 0.011	0.560	0.119 ± 0.011	0.067 ± 0.023	0.549

SL – h^2 and c^2 were not estimated using the transformed data because the trait was measured on a metric scale and its scores had normal distribution

Table 6. Estimates of heritability (h^2), portion of litter variation (c^2) and their approximate standard errors (s.e.), and phenotypic variances (σ^2_P) of the arctic fox reproduction traits

Trait	h^2	s.e. of h^2	c^2	s.e. of c^2	σ^2_P
LSB	0.205	0.001	0.012	0.002	11.287
NPD	0.084	0.005	0.013	0.004	1.881
LSW	0.250	0.030	0.011	0.002	22.827
PW	0.027	0.057	0.031	0.190	491.40
PL	0.086	0.042	0.041	0.012	2.154
WA	0.126	0.029	0.001	0.022	21.444

were higher than those presented in this study. Higher values of heritability estimates may have been caused by differences in linear models used in both studies. In the earlier study (Wierzbicki, 2000) the model did not include uncorrelated random effect of litter environment and inbreeding coefficient as linear covariable. In the present study these two effects were included in the models, leading probably to the reduction of additive genetic variance component, and then lower heritability estimates.

The estimates of heritability and portion of litter variation of the silver fox fur coat traits are shown in Table 3 (data without transformation) and Table 5 (transformed data). The comparison of estimates derived using 2 different linear models and 2 data sets revealed more differences than it was found in the arctic fox. The accounting for inbreeding (Model 2) usually led to lower estimates of heritability, mainly when heritabilities were derived from the transformed data (Table 5). Most noticeable it is for CD (0.183 vs. 0.097) and HL (0.261 vs. 0.139). However, the error variance does not indicate clearly which of the two models is better fitted (except for SL and TS in Table 3).

In the arctic fox c^2 estimated for all fur coat traits was always lower than h^2. In the silver fox, a portion of litter variation estimated for BS ($c^2 = 0.071$, Model 2, Table 5), CD ($c^2 = 0.144$, Model 2, Table 3) and HL ($c^2 = 0.144$, Model 2, Table 5) was higher than h^2 estimated for these traits.

There is no clear indication if the normal probability scale transformation of the data changes the genetic parameters, and in which direction. For some traits (CT, TS) the estimate of h^2 is lower after transformation, for the other ones (CP, HL, PS) it is higher. Also an error variance of some traits may be substantially reduced after transformation (BS, TS) or may be noticeably larger (CD, HL, PS, GA).

In Poland the estimates of heritability of fur coat traits in the silver fox were calculated either from the sire component of variance (Filistowicz *et al.*, 1999b; Filistowicz *et al.*, 2000) or using an animal model (Wierzbicki and Filistowicz, 2002; Wierzbicki and Filistowicz, 2003).

The estimates of heritability reported by Filistowicz *et al.* (1999b) derived from the normal probability scale transformed data were somewhat higher (ranging from 0.081 for BS to 0.374 for TS) than those presented in this study. Only h^2 for BS (0.081) was almost equal to that estimated for BS in the present study (0.084, Table 5). Also Wierzbicki and Filistowicz (2002), and Wierzbicki and Filistowicz (2003) estimated higher heritabilities of fur coat traits in the silver fox than those presented in this study. Depending on the model used (single- or multi-trait) they ranged from 0.191 for PS to 0.553 for GA. However, it must be kept in mind that the linear models used in those studies did not include the effect of common litter environment, the fixed effect of farm × year × birth season as well as did not account for inbreeding. The models used in the present study included the above-mentioned effects, and should be considered as better fitted.

Generally, the estimates of heritability of fur coat traits calculated for the arctic and silver foxes were low or moderate. In an auction system of selling pelts BS is the most important skin characteristic that significantly influences the pelt price. Low (Table 3 and Table 5) or moderate (Table 2 and Table 4) estimates of heritability of that trait indicate that substantial improvement of BS can be achieved by improving the feeding regime and housing conditions.

Table 6 presents the estimates of heritability and portion of litter variation of the arctic fox reproductive traits. Out of 6 traits analysed the highest heritabilities were estimated for LSW (0.250) and

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LSB (0.205). These estimates were markedly higher than those reported by Peura *et al.* (2003), who in the Finnish blue fox estimated lower heritability for LSB. In a single-trait analysis they found $h^2 = 0.09$, while in the multi-trait analysis, depending on the number of litter (1st, 2nd or 3rd) they found heritabilities of 0.08, 0.07 and 0.03, respectively. Lower heritabilities for LSB and LSW were also calculated by Jakubczak (2002) in the Polish pastel foxes. The estimates for LSB and LSW were 0.06 and 0.026, respectively. In contrast, unexpectedly high estimates of heritability for LSB and LSW were reported by Filistowicz *et al.* (1999c), who carried out the study in the population of blue fox. In their study the estimates of heritability for LSB (0.505) and LSW (0.502) were higher than those estimated for BS (0.268) and CT (0.391).

The other reproductive traits (NPD, PW, PL and WA, Table 6) had lower estimates of heritability ranging from 0.027 for PW to 0.126 for WA. The portion of litter variation (c^2) explained from 0.1% (WA) to 4.1% (PL) of the variation in reproductive traits. Peura *et al.* (2003) reported c^2 of 2% and 39% for litter size and age at first insemination, respectively, in the blue fox.

The estimates of heritability for reproductive traits have been calculated many times in pigs (Hermesch *et al.*, 2000; Kaufman *et al.*, 2000) and sheep (Hagger, 2000). The estimates of heritability reported by the authors ranged from 0.08 through 0.114 to 0.22 for litter size, 0.02 for birth weight, 0.08 for weaning weight, and from 0.08 to 0.22 for litter weight. The portion of litter variation reported by Kaufman *et al.* (2000) ranged from 0.06 for litter size to 0.23 for weaning weight.

Most of the estimates of heritability of reproduction traits presented in this study were found within the range reported by other authors. However, heritabilities of LSB and LSW were somewhat higher, indicating that effective genetic improvement of these traits can be achieved in the arctic fox population.

CONCLUSIONS

Most of the direct estimates of heritability calculated for the fur coat traits in the arctic and silver fox were within the range or somewhat lower than those reported by other authors. A comparison of the linear models without or with the inbreeding coefficient as linear covariable revealed that ac-

counting for inbreeding did not markedly change the estimates of heritability. It can be explained by the low level of inbreeding in the Polish fox population (reported by Wierzbicki *et al.*, 2004). The normal probability scale transformation of the data, although theoretically required for the data with heavier than normal tails, did not noticeably alter ranges of the direct heritabilities in both species of fox.

The first estimates of the portion of litter variation estimated for the fur coat traits in Polish foxes indicate that the common litter environment is responsible for 0.1%–19.1% of the variation of the fur traits. The effect of the litter environment significantly influences the group of traits (CP, CD, HL) affecting the fur quality.

The reproduction traits of the arctic fox, except for LSB and LSW, were found low heritable. The estimates of the direct heritability for LSB and LSW were higher than the corresponding estimates reported in literature. The common litter environment had a more significant effect on PW than the genetic variation (however, c^2 for PW had high s.e.).

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ABSTRAKT

Hodnocení plemenné hodnoty u polských kožešinových zvířat: odhady přímé dědivosti a podílu proměnlivosti vrhu u vlastností kožešiny a reprodukce

V práci jsou předloženy odhady dědivosti vlastností kožešiny a reprodukce u lišky polární a lišky stříbrné chovaných na polských farmách. Odhady komponent rozptylu byly provedeny pomocí metody DFREML a animal modelů pro jednu vlastnost. Kvůli diskrétnímu charakteru vlastností kožešiny jsme provedli dvojí analýzu: (1) bez normalizace

rozložení jejich bodového hodnocení, (2) po transformaci jejich bodového hodnocení na normální stupnici pravděpodobnosti. Lineární modely zahrnovaly náhodné aditivní genetické efekty a efekty společného prostředí vrhu, a dále pevné efekty farma x ročník x období narození u lišky stříbrné nebo efekt ročník x období narození u lišky polární, jakož i pevný efekt věku matky při analýze reprodukčních vlastností. Kromě toho k odhadu komponent rozptylu pro vlastnosti kožešiny byl použit lineární model s koeficienty inbrídinku zařazeným jako lineární souproměnná (Model 2) a lineární model bez těchto koeficientů (Model 1). U lišky polární zařazení inbrídinku a transformace dat nijak výrazně neovlivnily odhady dědivosti ani podíl proměnlivosti vrhu, které jsme stanovili pro vlastnosti kožešiny. Efekt inbrídinku byl zanedbatelný (s výjimkou velikosti trupu – BS) pravděpodobně v důsledku nízké úrovně inbrídinku v populaci lišky polární. Porovnání odhadů získaných za použití dvou rozdílných lineárních modelů a dvou souborů dat u lišky stříbrné naznačilo více rozdílů než u lišky polární. Zařazení inbrídinku obvykle vedlo k nižším odhadům dědivosti, zejména když jsme dědivosti určovali z dat transformovaných na normální stupnici pravděpodobnosti. Většina odhadů dědivosti reprodukčních vlastností se nacházela v rozsahu hodnot uváděných ostatními autory. Avšak o něco vyšší dědivosti jsme zjistili pro velikost vrhu při narození – LSB (0,205) a pro velikost vrhu při odstavu – LSW (0,250).

Klíčová slova: liška polární; kožešina; dědivost; transformace na normální stupnici pravděpodobnosti; reprodukce; liška stříbrná

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