

Genetic, phenotypic and environmental trends of conformation traits in arctic fox *Alopex lagopus* (L.)

Heliodor WIERZBICKI¹, Andrzej FILISTOWICZ¹, Piotr PRZYSIECKI²

¹Department of Genetics and Animal Breeding, Agricultural University of Wrocław, Poland
²Śniaty Fox Farm, Poland

Abstract. Data on 3782 arctic foxes, bred on a Śniaty fox farm (Poland) in 1985-1998 were used to estimate the genetic, phenotypic and environmental trends of conformation 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 BLUP with a single-trait animal model was used to estimate the genetic trends. The estimates of genetic and phenotypic trends were positive for BS, CT, CP, HL, GA, TS and ranged from 0.0006 to 0.0995 point/year and from 0.0100 to 0.1302 point/year, respectively, but were negative for CD (– 0.0374 point/year and – 0.0262 point/year, respectively). The environmental trends ranged from – 0.0024 point/year for CT to 0.0304 point/year for TS.

Key words: arctic fox, conformation traits, environmental trend, genetic trend, phenotypic trend.

Introduction

Changes in genetic and phenotypic values of a population in the course of time are temporary. In animal breeding the magnitude and direction of these trends are mostly affected by selection and changes in farm environment. Hence, the genetic trend is a measure of breeding work efficiency, whereas phenotypic trend reflects both the genetic improvement of a population and environmental changes.

The mixed model methodology for prediction of breeding values and genetic trends of traits under improvement have been widely used in livestock (BARILLET et al. 1992, CANTET et al. 1993, ŻUK et al. 1994, SONESSON et al. 1998). The genetic gain has been assessed in pigs and sheep with respect to body weight and lit-

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Correspondence: H. WIERZBICKI, Department of Genetics and Animal Breeding, Agricultural University, ul. Koźuchowska 7, 51-631 Wrocław, Poland.

ter size (BHUIYAN, CURRAN 1993, HOFER et al. 1992), in cattle and sheep in relation to weight and milk yield (CUNNINGHAM, KLEI 1995, SERRANO et al. 1996, SULLIVAN et al. 1999) and in poultry with regard to weight gain in broilers and egg number in layers (PRIBYLOVA, PRIBYL 1991). The rates, expressed as percentages of the means, are found within the range from 1% to 2% per year (FALCONER, MACKAY 1996).

In fox farming the new methods of breeding value estimation have not been widely used in practice. In Finland, however, the on-farm programme based on BLUP with an animal model was introduced in the early 1990s (SMEDS 1992). On Polish farms the conformation evaluation or simplified selection index are the criteria for animal selection. Hence, the accuracy of selection is not high and, consequently, the genetic progress is slower. To our knowledge, in Poland only SOCHA (1996) has estimated the genetic trends for conformation traits in an arctic fox population. However, the author used regression analyses (SMITH 1962) instead of the mixed model methodology.

This paper presents the estimates of genetic and phenotypic trends for conformation traits in an arctic fox population in 1985-1998. Environmental trends in the population were estimated as well.

Material and methods

The fox population consisted of 3782 individuals bred on a Śniaty fox farm (Poland) in 1985-1998. The analyses comprised white (329 individuals) and blue (3453 individuals) arctic foxes from three types of mating: white \times white, white \times blue and blue \times blue. Only the animals with known parents and full performance information were taken into account in statistical analyses. The data were extracted from Farm Book (1985-1988) and from a LISY computer database (1988-1998) (CHUDOBA et al. 1988). The data in the Farm Book were considered reliable enough, therefore they were not verified. The performance records collected in the database were automatically verified by the computer programme, i.e. sire was excluded if dam had been mated with at least two males during the heat. More details concerning population structure in consecutive years are shown in Table 1.

Assessment of conformation traits was done by a skilled judge according to the rules accepted by the Central Animal Breeding Office (FRINDT et al. 1984). 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). The data were not adjusted for age because all animals within birth-year group were born in the same whelping season. No transformation of data was applied. Table 2 shows the score scales and statistical description of the traits.

Table 1. Population structure in the consecutive years of study

Year	Number of sires	Number of dams	Number of kits
1985	42	44	341
1986	64	66	429
1987	65	68	497
1988	43	53	351
1989	40	41	230
1990	27	27	118
1991	28	30	151
1992	51	56	251
1993	49	52	137
1994	67	68	244
1995	76	77	285
1996	78	80	264
1997	87	89	290
1998	64	64	194
Total	781	815	3782

Table 2. Scales of conformation scores, means and standard deviations (SD) of studied traits

Trait	Scale of conformation scores	Mean	SD
Body size	0-3	2.74	0.51
Colour type	0-6	5.64	0.84
Colour purity	0-6	4.75	1.06
Coat density	0-6	5.28	0.64
Hair length	0-6	5.51	0.62
General appearance	0-3	2.92	0.27
Total score	0-30	26.82	1.99

The genetic evaluations were performed using the BLUP with the following single-trait 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.

Table 3. Additive genetic ($\hat{\sigma}_a^2$) and error ($\hat{\sigma}_e^2$) variance components estimates for studied traits

Trait	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$
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

The estimates of the variance components used in calculations (Table 3) were obtained using the Restricted Maximum Likelihood (REML) method. The computations were performed using the PEST computer package (GROENEVELD et al. 1999).

The average annual genetic and phenotypic trends were estimated as a regression of breeding and phenotypic values on time, respectively. The environmental effects, defined as a part of trait phenotypic value determined by environmental changes, were calculated as a difference between trait phenotypic values and genetic effect predicts. The environmental trends were estimated as a regression of environmental effects on time. The results are expressed in absolute terms (points).

Results and discussion

The results of the study are shown in Tables 4, 5 and 6. The estimated genetic trends were positive for six out of seven traits analysed (Table 4). The highest average annual progress was achieved for TS (0.0995), followed by CT (0.0604), BS (0.0449), CP (0.0177), GA (0.0174) and the lowest positive genetic trend was estimated for HL (0.0006). A negative trend was noted for CD (−0.0374).

SOCHA (1996) carried out studies on the population of blue fox and found the highest annual genetic trends for TS (0.0734), followed by CT and CP (0.0582 and 0.0260, respectively). The remaining genetic trend estimates ranged from 0.00001 to 0.0318 with the exception of the trend for BS, which was negative (−0.0051). According to the author, the unsatisfactory genetic progress indicates a low efficiency of selection resulting from: (1) small variability of traits, (2) inconsistent selection over a longer period of time and (3) negative correlations between improved traits.

However, the results reported by SOCHA (1996) cannot be compared to those presented in this paper. The author estimated the genetic trends for a fox popula-

Table 4. Mean additive genetic effects across years of birth and the average annual genetic trends of analysed traits

Year	BS	CT	CP	CD	HL	GA	TS
1985	0.027	-0.842	-0.129	0.082	-0.027	-0.032	-0.900
1986	-0.070	-0.339	-0.184	0.161	0.270	0.027	-0.121
1987	-0.356	-0.368	0.537	0.229	0.110	-0.120	-0.016
1988	-0.305	0.099	-0.075	0.428	-0.143	-0.130	-0.118
1989	-0.489	0.099	0.609	-0.218	-0.195	-0.150	-0.369
1990	-0.092	0.203	-0.577	0.057	-0.481	0.055	-0.844
1991	0.219	0.360	-0.476	-0.274	-0.231	0.098	-0.308
1992	0.267	0.361	-0.738	-0.159	-0.002	0.081	-0.191
1993	0.188	0.361	-0.433	-0.175	0.192	0.039	0.174
1994	0.257	0.379	-0.458	0.009	-0.005	0.063	0.245
1995	0.255	0.368	-0.451	-0.051	0.143	0.072	0.344
1996	0.245	0.295	0.602	-0.148	-0.172	0.076	0.886
1997	0.245	0.139	0.299	-0.332	0.001	0.074	0.425
1998	0.261	0.120	0.636	-0.335	0.016	0.076	0.767
b	0.0449	0.0604	0.0177	-0.0374	0.0006	0.0174	0.099

BS = body size, CT = colour type, CP = colour purity, CD = coat density, HL = hair length, GA = general appearance, TS = total score;

b = linear regression coefficient of trait phenotypic values on years of birth

Table 5. Mean phenotypic values across years of birth and the average annual phenotypic trends of analysed traits

Year	BS	CT	CP	CD	HL	GA	TS
1985	2.68	4.56	4.29	5.18	5.39	2.88	25.01
1986	2.65	5.21	4.41	5.34	5.70	2.93	26.27
1987	2.43	5.44	5.25	5.51	5.47	2.80	26.90
1988	2.52	5.82	4.71	5.73	5.37	2.81	26.98
1989	2.23	5.89	5.72	5.12	5.47	2.75	26.98
1990	2.71	5.95	4.42	5.41	5.08	2.99	26.57
1991	2.96	6.00	4.26	5.00	5.38	3.00	26.60
1992	2.94	6.00	4.07	5.06	5.61	3.00	26.70
1993	2.93	5.90	4.30	5.05	5.68	2.96	26.92
1994	2.98	5.97	4.22	5.27	5.54	2.98	26.99
1995	2.98	5.96	4.36	5.31	5.70	3.00	27.24
1996	2.98	5.89	5.49	5.21	5.37	2.99	27.96
1997	2.98	5.76	5.02	5.02	5.57	3.00	27.37
1998	3.00	5.70	5.42	4.99	5.56	3.00	27.67
b	0.0450	0.0580	0.0287	-0.0262	0.0100	0.0141	0.1302

BS = body size, CT = colour type, CP = colour purity, CD = coat density, HL = hair length, GA = general appearance, TS = total score;

b = linear regression coefficient of trait phenotypic values on years of birth

Table 6. Environmental effects across years and the average annual environmental trends of analysed traits

Year	BS	CT	CP	CD	HL	GA	TS
1985	-0.09	-0.21	-0.28	-0.16	-0.07	-0.01	-0.80
1986	-0.02	-0.06	-0.11	-0.08	-0.06	0.04	-0.32
1987	0.05	0.20	0.01	0.02	-0.13	0.00	0.21
1988	0.07	0.11	0.09	0.04	0.02	0.02	0.39
1989	-0.02	0.18	0.41	0.08	0.18	-0.02	0.64
1990	0.06	0.14	0.30	0.09	0.07	0.02	0.70
1991	0.00	0.03	0.04	0.01	0.12	-0.02	0.20
1992	-0.06	0.03	0.11	-0.04	0.12	0.00	0.18
1993	0.00	0.01	0.03	-0.03	0.00	0.00	0.03
1994	-0.01	-0.02	-0.02	0.00	0.06	0.00	0.03
1995	-0.01	-0.02	0.11	0.10	0.07	0.01	0.18
1996	0.00	-0.01	0.19	0.10	0.05	0.00	0.37
1997	0.00	0.01	0.03	0.09	0.08	0.01	0.23
1998	0.00	-0.03	0.08	0.07	0.05	0.01	0.19
b	0.0004	-0.0024	0.0111	0.0114	0.0094	-0.0002	0.0304

BS = body size, CT = colour type, CP = colour purity, CD = coat density, HL = hair length, GA general appearance, TS = total score;

b = linear regression coefficient of environmental effects on years of birth

tion from a farm located in a different region of Poland, in 1984-1990. Moreover, the estimates of the genetic trend were obtained using the method described by SMITH (1962), with regression analyses to estimate the breeding values. Therefore, the estimates obtained using Smith's method are less accurate as compared to those estimated using the mixed model.

The curves showing the genetic trends are plotted in Figure 1. It can be noticed that an almost steady increase in the breeding value was obtained for CT, GA and TS. Although the genetic trends for BS, CP and HL were also positive, the breeding value of the traits varied considerably between years. The average breeding values of CP and HL fluctuated widely throughout the observation period, whereas the genetic merit of BS had sharp declining and increasing phases only in 1985-1992. A decreasing tendency is clearly seen in the breeding value of CD. The trait was improved markedly in the late 1980s (reaching the maximum in 1988), but the later rapid decrease led to its lowest breeding value in 1998, and as a consequence, a negative genetic trend was obtained for the entire study period.

The low genetic merit noted for almost all traits (except CT) in 1989 and 1990 (Figure 1) was probably caused by a reduced reproduction performance (diagnosed as a dysfunction resulting from improperly balanced feed ration). As a result of culling, the number of animals from the breeding stock decreased considerably (Table 1), leading to a lower breeding value of parents and their progeny.

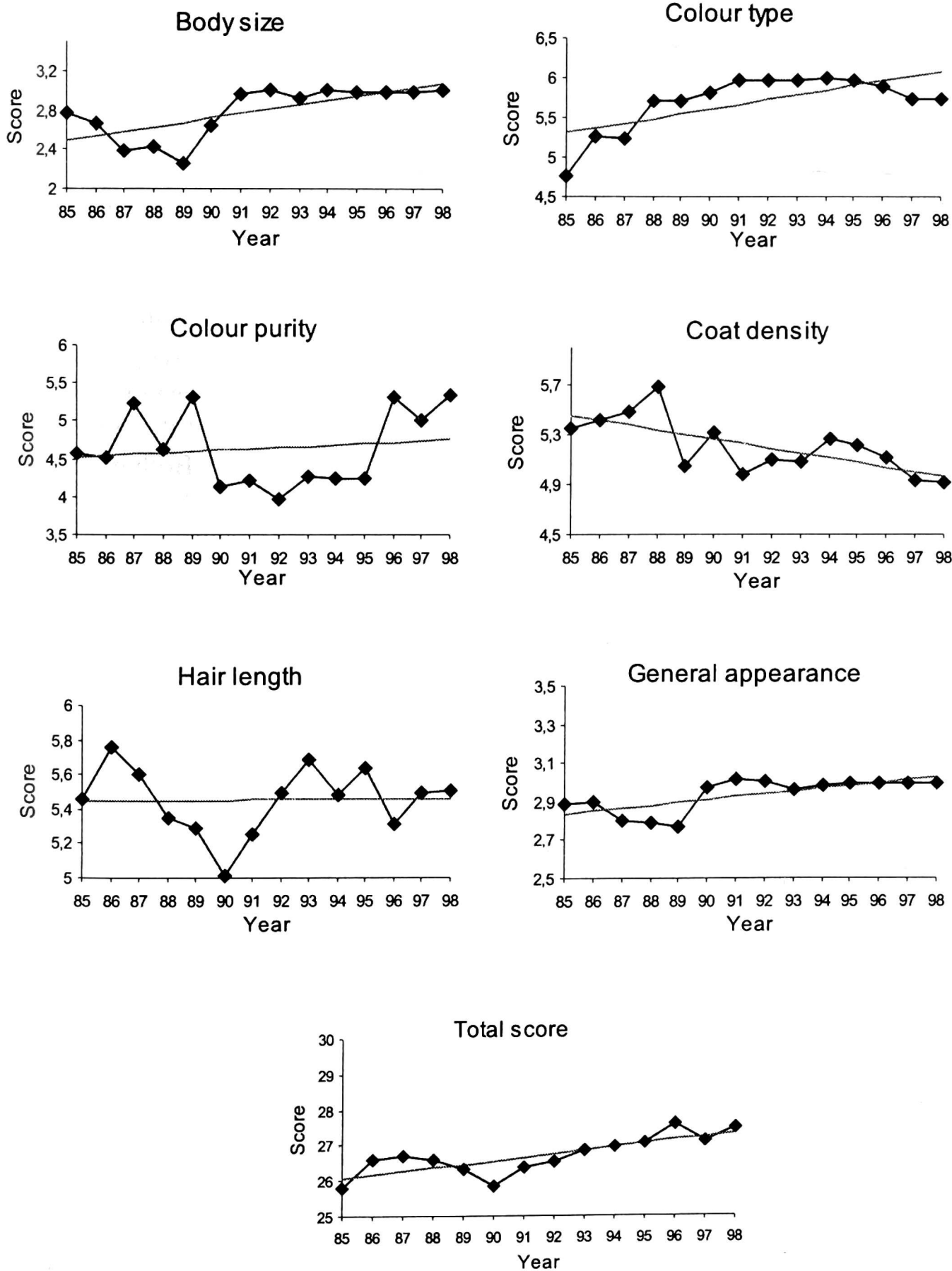


Figure 1. Estimated genetic trends (overall mean + additive genetic effect) for conformation traits

— regression line, ◆—◆ mean additive genetic effects over years

Estimates of phenotypic trends are shown in Table 5. The highest values were estimated for TS (0.1302), CT (0.0580) and BS (0.0450), and they corresponded to the genetic trends of these traits (Table 4). A slower phenotypic progress was noted for GA (0.0141) and HL (0.0100), while CD exhibited a negative phenotypic trend (−0.0262).

The environmental trends (Table 6) indicate that farm environment was improving at a slower rate than the breeding value of the majority of the analysed traits. The average annual environmental effects were positive for BS, CP, CD, HL and TS and ranged from 0.0004 to 0.0304. Negative trends were estimated for CT and GA (−0.0024 and −0.0002, respectively).

The breeding strategy for the fox population selected for the study can be considered effective, since six out of seven genetic trends were positive, as expected by the breeders. Although the trend magnitude for some traits was not fully satisfying, e.g. for hair length (Table 4), the genetic improvement of these traits was clearly seen. However, an alarming tendency was noted for CD. Both genetic and phenotypic trends estimated for the trait were negative. According to SŁAWOŃ (1994, 1995) the fox skin offered by Polish breeders is much smaller and of lower quality than that available in Finland and Norway. The international skin market is open only to high quality skins, therefore, appropriate steps must be undertaken in order to foster the genetic progress in the Polish population of arctic foxes.

The small variability of traits and inconsistent selection, suggested by SOCHA (1996) as the main reasons for the low efficiency of breeding work, probably did not affect the genetic trends in the population under study. Gene flow into the population (import of animals from Norway, Finland and domestic farms) and avoidance of inbreeding should result in a large genetic and phenotypic variation of traits. Furthermore, the breeding work on the farm is assisted by a LISY computer system (CHUDOBA et al. 1988), which guarantees consistent selection.

In the fox population, the animals are selected on the basis of TS. The individuals with at least one trait assessed negatively (score = 0) are discarded. The magnitude of genetic trend for conformation traits results from selection intensity (the main selection criterion is TS) and from selection pressure (in fox populations each trait has its own weight contributing to TS, see Table 2). Table 4 and Figure 1 show that the traits with a wider range of weights have been improved slower (CP, HL) or reached negative trends (CD), as compared to those within the narrow range of weights (GA and especially BS).

When evaluating fox conformation the judge can give 0,2,4,6 points for CT and CP or 0,1,2,3,4,5,6 points for CD and HL. In practice, however, the judges mainly score the highest points or zero, and this disadvantage of subjective evaluation is likely to hinder the genetic progress.

A similar conclusion was drawn by JEŻEWSKA and MACIEJOWSKI (1983), who found that unsatisfactory genetic gain could be brought about by subjective evaluation of animals' conformation. The assessment of conformation based on

the point scale cannot be considered unbiased, therefore it does not reflect the genetic and phenotypic variation of traits.

Apart from the method of conformation evaluation, the second drawback of the selection scheme is evaluation of the genetic merit. The breeding value of foxes kept on Polish farms is not evaluated with the use of new methods based on mixed model methods, hence considerably biased.

In recent years an action has been taken to change this situation. The old evaluation pattern (6 scores of 0-30 points for TS) was replaced by a new one, considered more objective (4 scores with maximum 20 points for TS) (CSHZ 1997, 1998). Furthermore, the change in the selection criteria for fur quality traits, i.e. replacing *in vivo* evaluation by skin evaluation or placing skin evaluation beside *in vivo* evaluation in breeding programmes as well as introduction of "real" economic weights have been suggested by FILISTOWICZ et al. (1999).

Conclusions

The estimates of genetic, phenotypic and environmental trends were positive for the majority of traits under investigation. However, the magnitudes of the average annual genetic trend were not satisfactory, which proves that the breeding programme requires improvement.

Although an action has recently been taken to improve reliability of fox evaluation, it is still unsatisfactory. It is desirable to replace the current methods for conformation and breeding value evaluation by more accurate ones in order to make the selection decisions more robust and the genetic progress faster.

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