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ANALYSIS OF EFFECTIVENESS OF BREEDING WORK AND ESTIMATION OF GENETIC AND PHENOTYPIC TRENDS OF CONFORMATION TRAITS IN SELECTED VARIETIES OF COLOURED AMERICAN MINK

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ABSTRACT

The objective of the study was to analyse the effectiveness of breeding for conformation traits in American mink as well as estimate genetic and phenotypic trends in the traits. Minks of the standard, pastel and palomino varieties were examined. They were raised at two breeding farms situated in north-western Poland. The analysis included a 10-year period of breeding and was performed on 3583 animals. Assessment was made of mink body weight, size, colour purity and fur quality as well as total point score.

Using the statistical package SAS, genetic parameters were determined for each trait in addition to phenotypic and genetic trends. Average values of the traits calculated for individual years were used to determine phenotypic trends whereas genetic trends were determined based on breeding values estimated by the BLUP method.

Of the traits analysed, fur colour purity tended to be the most prone to selection. The heritability of this trait was 0.33. The strongest genotypic associations were between mink body weight and body size (0.74), the phenotypic correlation of the traits being much lower than the genotypic one (0.21). The difference may indicate that there was a substantial influence of genetic factors on the traits analysed.

Genetic trend lines for conformation traits reflected an increasing tendency, which may indicate that selection for the traits was effective. Unlike genetic trends, phenotypic trends were relatively stable, their lines displaying a downward tendency, however. This, in turn, indicates a need to change the selection system and methods of breeding work on farms.

KEY WORDS: American Mink, Conformation Traits, Heritability, Genotypic and Phenotypic Correlations, Phenotypic Trends, Genetic Trends

INTRODUCTION

Breeding of fur animals enjoys a long tradition. However, at the beginning it was mainly an amateur activity. Only after World War II did it become economically important. In the 1950s mink breeding was particularly rapid. As its main aim was to produce animals and not fur, the production was quite unprofitable [13]. The turning point was the 1960s when breeding standards started to be regularly applied, which resulted in higher numbers of fur animals, including minks, of better quality.

Interest in mink breeding in Poland is on the increase all the time. Demand for mink pelts is higher and higher due to the fact that, compared with skins of other fur animals, the pelts have more applications.

The standard mink is the basic variety in breeding [2]; however, there is more and more interest in other coloured varieties which are a result of breeding work. The varieties are not found among wild animals and their auction price is higher compared with the standard variety.

An auction price is the best measure of skin quality of fur animals [20]. Thus, attempts at improving the animals, including mink, also include selection for usable traits. The selection is for animal size and fur properties.

The objective of the study was to analyse the effectiveness of breeding work and estimation of genetic and phenotypic trends of mink conformation traits of the standard, pastel and palomino variety.

MATERIAL AND METHODS

The minks examined were raised on two breeding farms located in north-western Poland. The farms breed foxes and minks. The animals kept on the farms constitute a valuable breeding material, which is reflected by their ranks at skin shows and Polish exhibitions of fur animals [4, 5, 6, 14].

The studies were conducted over the period of 10 years. The analysis included a total of 3583 females from the foundation stock including: 2609 standard, 799 pastel and 175 palomino. The following traits of mink conformation were analysed: body weight (in grams), animal size, fur colour purity, fur quality and the total score.

The average values of each trait in individual years included in the analysis were used to determine phenotypic trends. The SAS package [22] was applied to perform calculations.

The components of covariance were estimated with REML using multiple-trait individual animal model. Calculations were done by the DMU computing package [17].

Variance and covariance components, estimated based on models including factors presented in Table 1, were used to determine the breeding value of the animals. Breeding values estimated by means of the BLUP method were the basis of determining genetic trends of body conformation [17]. The traits examined were characterized by discrete variation, so the probit transformation of the parameters obtained was used, according to the methodology presented by Żuk [28].

Table 1. Factors taken into consideration while estimating genetic parameters for conformation traits

Trait	Type ^a	Body weight	Body size	Fur colour purity	Fur quality	Total score
Year of birth	F	x	x	x	x	x
Sex	F	x	x		x	x
FarmxOrigins	F	x	x	x	x	x
Colour variety	F			x		
Number of litter (at birth)	C	x	x			
Additive effect of an individual	A	x	x	x	x	x

x – occurrence of a factor in the model for the trait analyzed

Factor type^a: A – random, linked to the matrix of relationship; F – fixed; C – covariance variable

RESULTS AND DISCUSSION

Table 2 presents heritability coefficients of conformation traits in mink. The highest value, $h^2=0.33$, of the parameter was obtained for fur colour purity. As this trait is very prone to selection, fur colour purity usually assumes high values of heritability coefficient. According to Wierzbicki and Filistowicz [27], it is usually around 0.6. Studies on fur colour heritability had been previously conducted by Cholewa [7], Børsting and Clausen [3] as well as Pingel et al. [19]. The authors found that the heritability varies considerably but, as a rule, assumes high values. A relatively high heritability for fur colour purity indicates that it is possible to improve the trait by means of selection.

Table 2. Heritability coefficients (h^2) of American mink conformation traits

Trait	h^2
Body weight	0.11
Animal size	0.23
Colour purity	0.33
Fur quality	0.13
Total score (points)	0.19

The heritability of mink body size estimated in the present work was 0.23 (Table 2). The result is comparable with the values reported by Socha and Olechno [26] as well as Puera et al. [18]. In the existing literature on genetic parameters of body size there are reported various values of heritability coefficients (0.15-0.55) according to the method of calculation chosen (selected component). Body weight heritability estimated on the basis of the maternal component assumes values of around 0.5 whereas for the paternal component it is much lower and equals 0.15. By contrast, a heritability coefficient of 0.33 was obtained when applying both the components, that is maternal and paternal one [23]. Higher values of heritability coefficient estimated based on the maternal component may result from an increased genetic effect due to a consistent influence of environmental factors which are shared by the litter [10]. The maternal effect was also clearly noticeable for mink body weight and fur quality in the study by Berg [1]. The maternal effects constituted from 10 to 40% of overall variation in the body weight of mink. Different results have been reported by Jeżewska and Maciejowski [12] who obtained the heritability coefficient of 0.44 based on the paternal component and a lower value (which was half as low as the aforementioned coefficient) when estimated in the same way but based on the maternal component.

Body weight heritability obtained in the present work was 0.11 (Table 2) and remained within the range for this parameter reported by Filistowicz and Żuk [11]. In turn, Jeżewska and Maciejowski [12] demonstrated that the body weight heritability coefficient ranged between 0.2 and 0.98, which is associated with the way the parameter was estimated, as previously mentioned.

A relatively low value of heritability coefficient was also found for fur quality. The character had the heritability coefficient of 0.13 (Table 2). Similar values were reported by Rozempolska-Rucińska [21], whereas studies by Socha and Kołodziejczyk [25] showed that heritability of fur quality was higher and amounted to 0.24. Values of this parameter reported in literature differ according to the method of its estimation as well as the effect various factors may have on this parameter. According to Einarsson [9], the heritability coefficient of fur quality estimated based on the paternal component ranges from 0.15-0.31 and 0.1-0.38 when estimated depending on sex and colour type [3].

The total score, calculated from points obtained during assessments made based on animal size, fur colour purity and fur quality, was similar to the previous trait as it had a similar heritability coefficient. The value of this parameter obtained in the present work for the total point score was 0.19 (Table 2). A substantially higher heritability of the trait was reported by Socha [24]. In the work of this author heritability of the total score was 0.499.

Table 3 presents genetic and phenotypic correlations of mink conformation traits. Relatively high positive correlations were found between the total point score and the remaining traits. There was one exception, that is the phenotypic correlation of body weight and total score, which was low and equalled 0.18. In the case of the remaining traits, that is animal size, colour purity and fur quality, the correlations were, respectively: 0.51; 0.54 and 0.70 (Table 3). The genetic correlations between the traits discussed were at a similar level and their respective values were: 0.55; 0.60 and 0.49. By contrast, the genetic association between body weight and the total score tended to be much higher than the phenotypic association for these traits (0.51) (Table 3).

Table 3. Genetic and phenotypic correlations [respectively, below and above the diagonal] of American mink conformation traits

Trait	Body weight	Animal size	Colour purity	Fur quality	Total score
Body weight		0.21	0.03	0.08	0.18
Animal size	0.74		-0.03	-0.01	0.51
Colour purity	-0.11	-0.01		0.10	0.54
Fur quality	0.25	-0.06	-0.07		0.70
Total score	0.51	0.55	0.60	0.49	

Negative and low correlations (genetic and phenotypic) were found between animal size and fur quality. Also, negative genetic correlations were determined between fur colour purity and fur quality, as well as fur colour purity and mink body size and weight (Table 3).

Low and negative correlations obtained in the present work between animal size and fur quality indicate that selection for increased body weight, and thus animal size, decreases fur quality. Similar opinions have been expressed by Lohi and Hansen [16] as well as Lagerkvist [15]. Also studies by Rozempolska-Rucińska [21] have indicated an unfavourable influence on fur quality of selection for increased body size.

It is worth noting that, although phenotypic and genetic associations between fur quality and animal body size are negative, the same associations are positive for body weight (in grams) and fur quality (respectively, 0.08 and 0.25). It may follow from the fact that more restrictive standards are set for the trait when assessed in points than in grams.

Of the correlations estimated in the present work, the highest was the genetic correlation of body weight and body size (0,74). The result seems to make sense as an increased body weight increases its size. In turn, the phenotypic correlation of body weight and size was much lower than the genetic correlation (0,21) (Table 3). A relatively large discrepancy between the genetic and phenotypic correlations indicates that genetic factors very much influenced the traits examined.

Correlation analysis should be performed bearing in mind that genetic and environmental associations between traits estimated in the present work are in fact correlations between scores and not absolute values of these characters.

While performing estimation of genetic parameters of mink conformation traits, it was also important to estimate phenotypic and genetic trends of the traits analysed. The trends are presented in figures: 1 (genetic trends) and 2 (phenotypic trends).

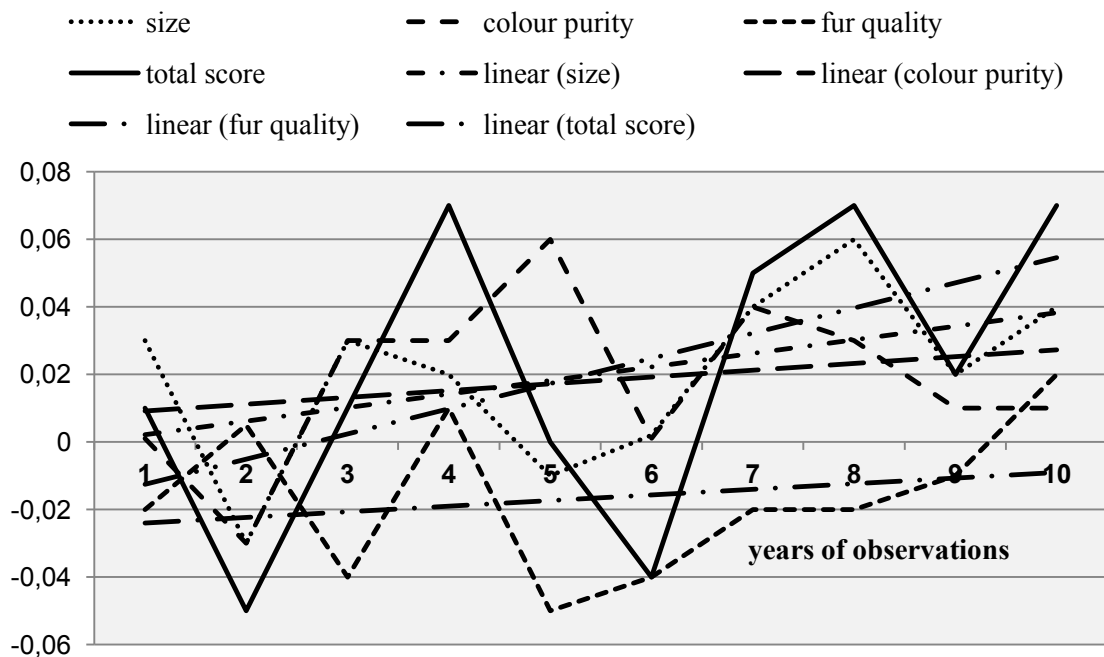


Fig. 1. Genetic trends of American mink conformation traits in successive years of observations

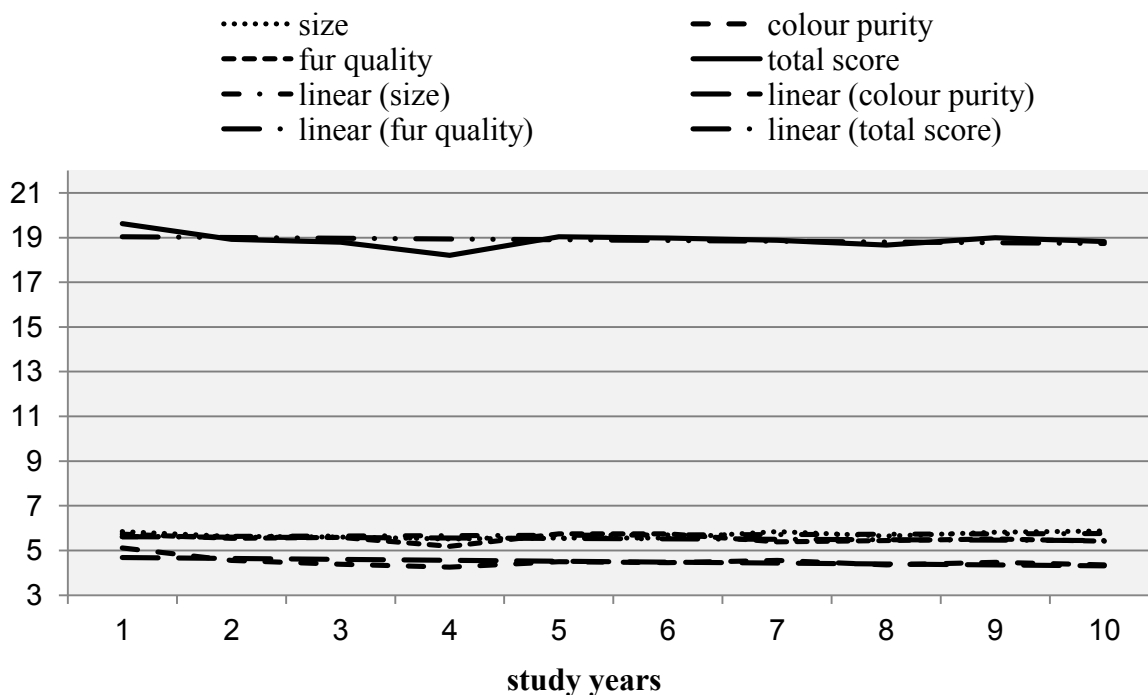


Fig. 2. Phenotypic trends of conformation traits in successive study years

Genetic trends of the mink conformation traits analyzed were characterized by substantial diversity over the examined 10-year period. In spite of substantial fluctuations in the breeding value of conformation traits, lines of genetic trends in these traits went upwards (Fig. 1). The most beneficial changes pertained to the total point score, which indicates that the quality of breeding material was good in terms of conformation. An increase in breeding value was noticed for each trait of mink assessment. So it can be assumed that selection for increased animal body weight and improved colour purity and fur quality was successful.

However, the breeding value of animals is not tantamount to their usable value. Lines of phenotypic trends of conformation traits estimated in the present work went downwards although their course was relatively smooth (Fig. 2), which may indicate that it is necessary to change the selection system on the farms. According to Clausen et al. [8], selection of fur animals is different in terms of methodology of animal assessment and criteria of their selection. The difference follows, among others, from the specificity of the country in which selection is performed. Thus, it would be advisable to make criteria and methods of breeding work uniform on fur animal farms both in Poland and abroad.

SUMMARY

To sum up, purity of fur colour was the trait which was most prone to selection. The lines of genetic trends of conformation traits in mink tended to increase, which may be indicative of successful selection for the trait. The estimated phenotypic trends, unlike the genetic trends, tended to decrease. Reduced values of conformation traits in mink indicate that levels of these traits need to be improved and the methods of animal breeding and usable value estimation should be modified.

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