

## **ANALYSIS OF EFFECTIVENESS OF BREEDING WORK AND ESTIMATION OF GENETIC AND PHENOTYPIC TRENDS FOR REPRODUCTIVE TRAITS IN AMERICAN MINK**

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### **Abstract**

The aim of the study was to analyse the effectiveness of breeding work for reproductive traits in American minks. Four colour types were tested: standard, pastel, palomino, and palomino with 50 and 25% of genes from standard variety. The minks came from two breeding farms in the north of Poland. The analyses were performed during the period of 10 years of breeding and productive life. The traits tested were number of kits born and reared, and length of gestation. The multiple factor analysis of variance was performed for each trait and significance of differences between traits was verified using the least squares method. The components of covariance were estimated by Restricted Maximum Likelihood (REML) methodology using a multi-trait repeatability animal model. Arithmetic means of each trait were used to estimate phenotypic trends, whereas genetic trends were evaluated using breeding values. Reproductive traits were characterized by very low coefficients of heritability (0.01 for the number of minks born; 0.02 for the number of minks reared; 0.17 for gestation length). Repeatability of traits tested was also on a very low level (0.06 for the number of minks born and reared; 0.18 for gestation length). The highest genetic correlations were found between the number of kits born and reared (0.68). The genetic trend lines estimated for reproductive traits showed an upward tendency, possibly indicating that the breeding programme is headed in the right direction. However, the results obtained were low, which shows the need for changing some criteria and methods of the breeding programme.

**Key words:** American mink, genetic parameters, reproductive traits, phenotypic trends, genetic trends

American mink breeding has been gaining more and more popularity both in Poland (Bielański et al., 2003) and all over the world. Profitable prices of mink skins are an encouragement for breeders to increase the number of animals in their farms (Socha et al., 2003; Bielański et al., 2005) and to improve the effectiveness of breeding work, which could be accomplished through selection.

Reproductive performance greatly affects the effectiveness of breeding work in minks. Therefore, reproductive ability should be taken into consideration in each production process (Maciejowski and Jeżewska, 1993). There is no doubt that reproductive traits should be analysed in selection schemes.

Reproduction is a very complex process, which depends on both environmental and genetic factors (Maciejowski and Jeżewska, 1993). However, this process is affected to a small extent by genetic variability. Very low coefficients of heritability for prolificacy (from 0.1 to 0.15) were found in different animal species (Filistowicz and Žuk, 1995). The predominant influence of environmental factors on reproductive traits makes breeding work difficult and, as a result, the responses to selection are not satisfactory (Rozempolska-Rucińska et al., 2000).

The aim of the investigation was to analyse the effectiveness of breeding work and to estimate genetic and phenotypic trends for reproductive traits in minks of the following strains: standard, pastel, palomino, and palomino with 50 and 25% of genes from standard variety in Poland.

### **Material and methods**

The experimental material came from two breeding farms in the north of Poland. The farm facilities enabled the foundation stock to be bred. The minks were fed according to their feed requirements and current standards (Barabasz et al., 1994).

The analyses comprised 10 years of mink breeding and performance recording.

The data on reproduction were collected from 1,763 females of the foundation stock in farm A and from 2,912 females of the foundation stock in farm B. Minks of standard, pastel and palomino strains as well as crossbreds 1 and 2 were used as experimental material. The crossbreds were obtained by mating palomino to standard minks. Thus, the crossbreds were minks of the palomino strain with 50% (crossbred 1) and 25% (crossbred 2) of standard mink genes. Crossbreds 2 were only bred for two years and crossbreds 1 for three years.

The main three reproductive traits analysed were the number of kits born, the number of kits reared and gestation length. Statistical analysis and multiple factor analysis were conducted for each trait tested, and the significance of some factors was verified by the least squares method. Calculations were done using the Statistical Analysis System (SAS) computer program (1996). The components of covariance were estimated with REML using a multiple-trait individual animal model. Calculations were performed using DMU computing package (Madsen and Jensen, 2000).

Breeding values of animals were estimated by Best Linear Unbiased Prediction (BLUP) procedure using the components of variance and covariance (Madsen and Jensen, 2000). The factors included in the statistical classification are listed in Table 1.

Because the tested traits were characterized by step variations, the probit transform of the parameters was applied according to the method presented by Žuk (1989). Breeding values, which were estimated by the BLUP method, were used to determine genetic trends for each trait (Madsen and Jensen, 2000).

Table 1. Factors used to estimate genetic parameters for reproductive traits

Trait	Type <sup>a</sup>	Number of minks born	Number of minks reared	Gestation length
Year of performance	F	x	x	x
Number of matings	F	x	x	
Farm × origin	F	x	x	
Colour type × female age	F	x	x	
Colour type × number of matings	F			x
Female age × number of matings	F			x
Gestation length	C	x	x	
Litter size	C		x	
Additive effect of individual	A	x	x	x
Specific habitat of an animal	R	x	x	x

x – appearance of a factor in the model for a trait analysed.

Factor type <sup>a</sup>: A – random, related to relationship matrix; R – random; F – stable; C – variable.

## Results

Genetic parameters for kits born and reared as well as for gestation length were tested in the study. Reproductive traits were characterized by extremely low coefficients of heritability and repeatability (Table 2).

Genetic and phenotypic correlations for reproductive traits are shown in Table 3. The largest phenotypic (0.91) and genetic (0.68) correlations were found between litter size and the number of kits reared. Relatively low, but positive genetic correlation coefficients (0.08) were established for the number of minks reared and gestation length (Table 3).

Table 2. Coefficients of heritability ( $h^2$ ) and repeatability ( $r^2$ ) for reproductive traits in minks

Trait	$h^2$	$r^2$
Number of minks born	0.01	0.06
Number of minks reared	0.02	0.06
Gestation length	0.17	0.18

Table 3. Genetic correlations (under diagonal) and phenotypic correlations (above diagonal) for reproductive traits in minks

Trait	Number of minks born	Number of minks reared	Gestation length
Number of minks born		0.91	-0.17
Number of minks reared	0.68		0.63
Gestation length	-0.73	0.08	

Phenotypic and genetic trends for the number of kits born and reared were also analysed. The trend values were illustrated by changes obtained during the period of one year. Phenotypic trends for the traits tested are presented in Figure 1, and genetic trends in Figure 2.

Phenotypic trend lines for reproductive traits showed considerable differences during the study period. Despite the changes, phenotypic trends for the number of kits reared tended to increase. There was, however, a slightly negative trend for the number of kits born (Figure 1).

Genetic trend lines for the traits tested also revealed some changes during the 10-year study period. Genetic changes for the number of kits born were particularly favourable. The negative breeding value for the trait in the first year of the study (-0.081) and its positive value in the last year (0.004) were stated (Figure 2). Genetic trends for the number of kits reared also tended to increase, but the differences between the breeding values in the first and last year of the study were smaller compared to those for the litter size. The breeding value for the number of kits reared was -0.03 in the first year and 0.003 in the last year (Figure 2).

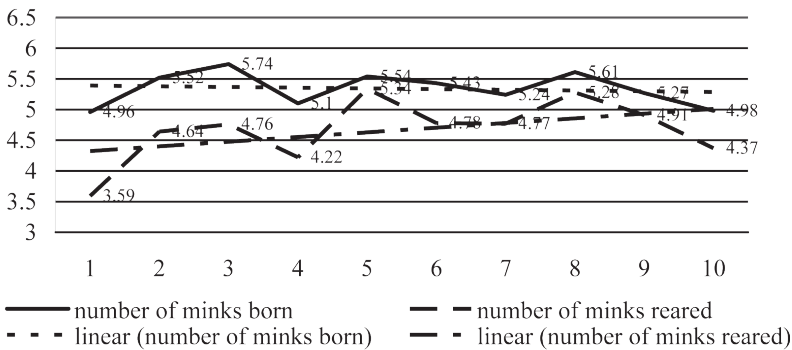


Figure 1. Phenotypic trends for reproductive traits during the study years

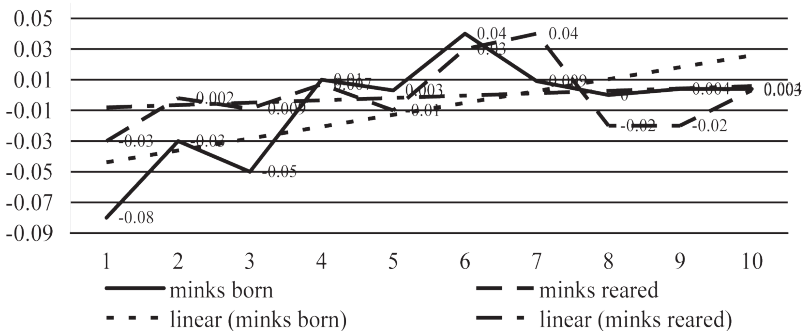


Figure 2. Genetic trends for reproduction trends in minks (total colour strains) during the study years

Genetic trends for reproductive traits in individual colour types of minks were also tested (Figures 3–7). Genetic trends for reproductive traits in minks of the standard strain are shown in Figure 3.

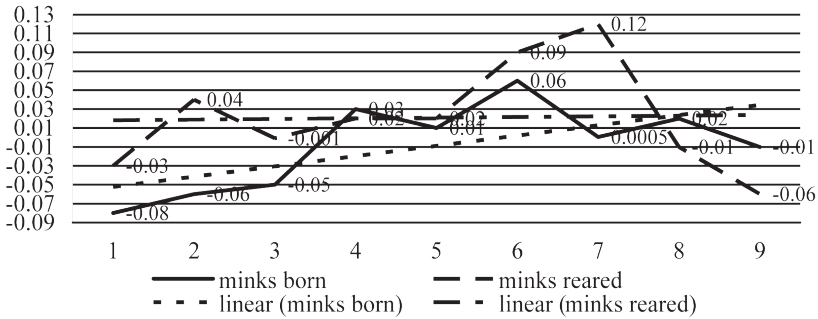


Figure 3. Genetic trends for reproductive traits in minks of standard strain

Despite the fact that the genetic trend for litter size in minks of the standard strain had different values, it was an upward trend. The genetic trend for the number of kits reared was slightly positive although there was a slightly downward trend at the end of the experimental period. Particularly unfavourable changes were observed in the 7th and 8th year of the study, when the breeding values for the trait were negative.

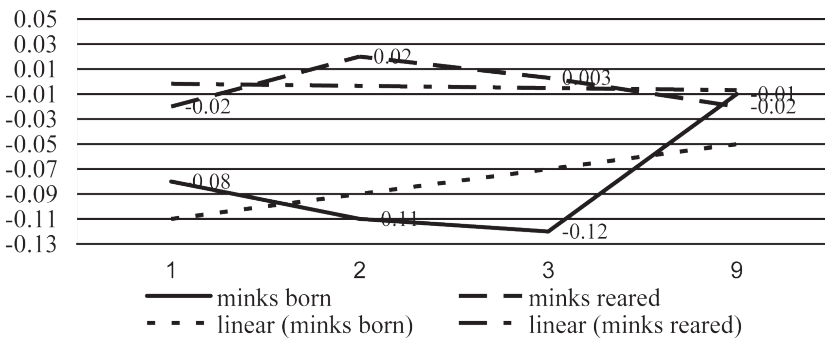


Figure 4. Genetic trends for reproductive traits in minks of palomino strain

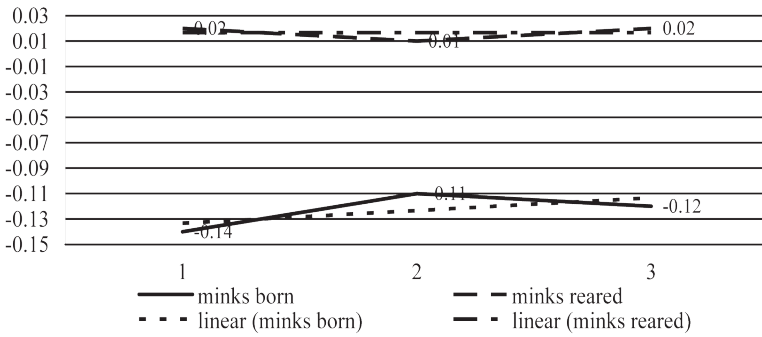


Figure 5. Genetic trends for reproductive traits in minks of palomino strain with 50% of standard strain genes (crossbred I)

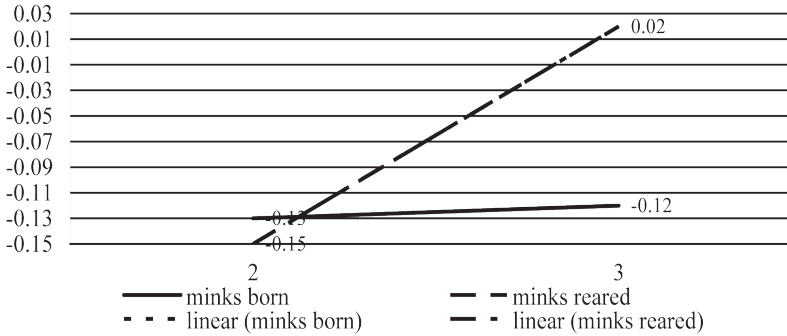


Figure 6. Genetic trends for reproductive traits in minks of palomino strain with 25% of standard strain genes (crossbred II)

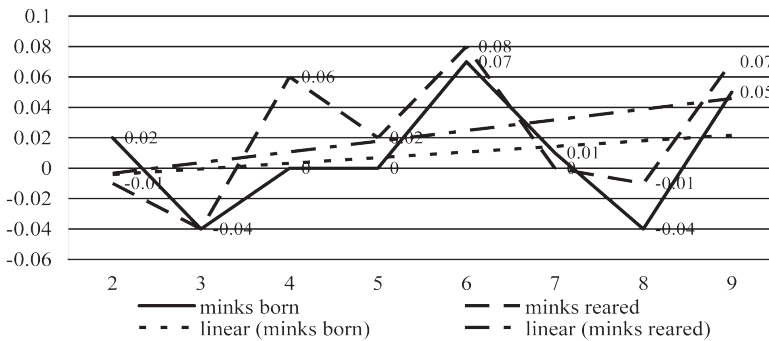


Figure 7. Genetic trends for reproductive traits in minks of pastel strain

As for the palomino strain, the genetic trends for the number of kits per litter tended to decrease considerably for the first 3 years of the study, whereas breeding values for the trait in the year before last were larger than those in the previous years. Moreover, the trends for the number of kits reared tended to increase in the beginning, but then there was a considerable downward trend in the breeding value (Figure 4).

Genetic trends for reproductive traits in minks of the palomino strain with 50% of standard genes (crossbred 1) are presented in Figure 5. The trends for the number of kits born were positive. Females in the 2nd year of the study were characterized by the highest breeding value. The values decreased in the next year, but the average breeding value was higher than that in the first year of the experiment. Furthermore, the trends for the number of kits reared also tended to increase. More attention should be given to the 2nd year of the study due to better breeding value for the litter size but a deteriorating breeding value for the number of kits reared as compared to those in the 1st and 3rd year of the analyses (Figure 5).

A considerable positive trend was found for the number of kits reared in crossbred 2 (palomino with 25% of standard genes). The trend for litter size also tended to increase; however, it was characterized by more gentle changes compared to the trend for the number of kits reared (Figure 6).

Genetic trends for the number of kits born and reared in the pastel strain are shown in Figure 7. It can be seen in the graph that there were many considerable changes in breeding value during the study period. Despite the changes, there was an upward trend for both the number of kits born and reared. The highest prolificacy in pastel minks in the 6th year of the study and slightly lower prolificacy in the 9th year were found (Figure 7). The 3rd and 8th year of the experiment were the least favourable with regard to mink prolificacy.

## Discussion

Reproduction results are the main factors that determine profitability of fur animal breeding. Reproduction is a complex process, which is studied with regard to many traits such as fertility, prolificacy, litter size and gestation length.

The present study revealed very low coefficients of heritability and repeatability for reproductive traits, which were also reported by other authors (Maciejowski and Jeżewska, 1993; Lagerkvist et al., 1993; Rozempolska-Rucińska, 2004; Peura et al., 2004). The coefficients of heritability and repeatability for the number of kits born and reared indicated a very small effect of genetic factors on the variability of the traits. The gestation length was also characterized by low heritability and repeatability coefficients of 0.17 and 0.18, respectively (Table 2).

The low coefficients of heritability and repeatability for reproductive traits in minks may be largely attributable to environmental factors. Therefore, breeders could play a great role in the improvement of the traits by appropriate feeding, caring of animals and welfare.

However, low heritability and repeatability for reproductive traits in fur animal breeding does not mean the lack of selection response for the traits. Scientific research and practice in breeding work indicate that breeding animals have accomplished better parameters than the ones tens of years ago. This shows that selection to improve prolificacy is advisable and brings desired results.

Positive correlations, both genetic and phenotypic, between the number of kits reared and all reproductive traits were found in the present study. The largest phenotypic correlation was found between the number of kits born and reared (0.91). The correlation was similar to that observed by Rozempolska-Rucińska (0.89) (2004).

The large and positive phenotypic correlation between the number of kits reared and gestation length was stated in the study. The correlation amounted to 0.63 and was similar to that reported by Ślaska (2002). On the other hand, the negative phenotypic correlation between the number of kits born and gestation length ( $-0.17$ ) and the negative genetic correlation between the traits ( $-0.73$ ) were proved. Genetic correlations between traits were of vital significance for animal breeding. The largest genetic correlations between the number of kits born and reared were noticed during the study period.

Genetic correlations between prolificacy of female minks and their gestation length were tested by many researchers (Elofson et al., 1989; Malmkvist et al., 1997; Sulik and Felska, 2000). The authors stated that gestation length influenced mink prolificacy. However, very low values of genetic correlations between prolificacy in minks and their gestation length indicated a lack of dependences between the traits.

The aim of the study was also to estimate genetic and phenotypic trends of traits such as the number of kits born and reared as well as gestation length.

Phenotypic trends for prolificacy in minks differed considerably over the years (Figure 1). Variations for the number of kits born and reared in particular years of the study were affected by undefined environmental factors. Despite the fact that prolificacy in female minks varied in years, there was an upward phenotypic trend for the number of kits reared. However, the phenotypic trend for the number of kits born was negative (Figure 1), which showed the need to improve reproductive traits in minks.

Selection among fur animals in the Polish farms is conducted based on animal's own phenotype, which makes breeding work difficult and enables fast response to selection due to different values of genetic parameters for particular traits (Lagerkvist et al., 1993). Genetic values in animals differ from their production values, and phenotypic trends noted in the present study indicated the need for changing some criteria and methods in the selection scheme.

Increasing genetic trends for the number of kits born and reared were found in the present study. Taking mink strains into consideration, it could be concluded that genetic trends for the number of kits born tended to increase in all strains studied. There was a positive genetic trend for minks reared in all strains, except for the palomino strain.

The decreasing trend for the number of minks reared in palomino strain showed a lack of efficiency in selection, which could be caused by choosing inappropriate selection methods, a lack of consequence in selection or individual characteristics in



minks of the strain. Selection based on the animal's own phenotype was not efficient also in other strains. Although genetic trend lines showed an increasing trend for the traits, breeding values differed considerably during the 10-year study. The results obtained indicated that some changes of criteria in choosing animals for the foundation stock should be the main purpose in mink breeding. It is concluded that genetic improvement of stocks, which is based only on the animal's own phenotype, is not sufficient. The selection system could be applied for traits for which the coefficients of heritability are almost 1.00; however, reproductive traits are among lowly heritable traits.

Changes of criteria and methods that are used in the breeding programme should include applying more sources of information and standardizing the evaluation of breeding animals in fur farms all over the world.

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DOROTA KOŁODZIEJCZYK, STANISŁAW SOCHA

**Analiza skuteczności pracy hodowlanej i oszacowanie trendów genetycznych i fenotypowych cech reprodukcyjnych norki amerykańskiej**

## STRESZCZENIE

Celem badań była analiza skuteczności pracy hodowlanej na cechy rozrodu norki amerykańskiej. Odmianami barwnymi poddanymi analizie były norki standard, pastel i palomino oraz palomino z 50% i 25% udziałem genów odmiany standardowej, pochodzące z dwóch ferm hodowlanych, znajdujących się w północnej Polsce. Analizą objęto okres 10 lat hodowli i użytkowania nerek. Oceniane były następujące cechy: liczba urodzonych i odchowanych młodych nerek oraz długość ciąży. Dla każdej z badanych cech przeprowadzono wieloczynnikową analizę wariancji, weryfikując istotność wybranych czynników metodą najmniejszych kwadratów. Komponenty kowariancji oszacowano metodą REML w oparciu o wielocechowy, powtarzalnościowy model osobniczy. Średnie wartości każdej badanej cechy posłużyły do oszacowania trendów fenotypowych, natomiast w oparciu o wartości hodowlane zwierząt oszacowano trendy genetyczne.

Analizowane cechy rozrodu charakteryzowały się bardzo niskimi współczynnikami odziedziczalności (liczba norcząt urodzonych – 0,01; liczba norcząt odchowanych – 0,02; długość ciąży – 0,17). Również powtarzalność analizowanych cech kształtowała się na niskim poziomie (liczba szczeniąt urodzonych i odchowanych – 0,06; długość ciąży – 0,18). Korelacje genetyczne okazały się najwyższe pomiędzy liczbą urodzonych a liczbą odchowanych młodych nerek – 0,68.

Linie oszacowanych w pracy trendów genetycznych cech rozrodu nerek wykazały tendencję wzrostową, co może świadczyć o prawidłowym kierunku pracy hodowlanej. Jednak uzyskane wyniki pozostają na niskim poziomie, co wskazuje na potrzebę zmiany kryteriów i metod prowadzonej pracy hodowlanej.