Genetic and phenotypic parameters for body weights, harvest length, and growth curve parameters in American mink

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Abstract

Understanding the genetics underlying growth curve is important for selection of animals with better growth potential, but little is known about the genetics of growth curve parameters in mink. This study estimated the genetic parameters for body weights (BW), harvest length (HL), and growth parameters derived from the Richards model. For this purpose, individual BW of 1,088 mink measured seven times in 3-wk intervals (weeks 13 to 31 of life) were used for growth curve modeling using the Richards model. The BW traits included BW at week 13 (BW13), 16 (BW16), 19 (BW19), 22 (BW22), 25 (BW25), 28 (BW28), and 31 (BW31). Univariate analyses indicated that sex and birth-year had significant effects ($P < 0.05$) on BW, HL, asymptotic weight ($\alpha$), growth rate at mature ($k$), shape parameter ($m$), weight at the inflection point (WIP), and age at the inflection point (AIP). In contrast, the color type had only significant effect ($P < 0.05$) on BW31 and HL. Estimated heritabilities (±SE) were ranged from 0.36 ± 0.13 (BW13) to 0.46 ± 0.10 (BW22) for BW and were 0.51 ± 0.09, 0.29 ± 0.09, 0.30 ± 0.09, 0.33 ± 0.10, and 0.47 ± 0.10 for HL, $\alpha$, $k$, $m$, WIP, and AIP, respectively. The parameter $\alpha$ had non-significant ($P > 0.05$) genetic correlations (±SE) with $k$ (−0.21 ± 0.23) and $m$ (−0.10 ± 0.22), suggesting that changing shape parameters ($k$ and $m$) will not influence asymptotic weight ($\alpha$). Strong significant ($P < 0.05$) phenotypic (from 0.46 ± 0.03 to 0.60 ± 0.03) and genetic (0.70±0.13 to 0.88±0.09) correlations were observed between HL and different BW measures. The $\alpha$, AIP, and WIP parameters had significant ($P < 0.05$) genetic correlations with HL indicated that selection for higher $\alpha$, AIP, and WIP values would increase HL. Parameters $k$ and $m$ had nonsignificant ($P > 0.05$) genetic correlations with HL, indicating the change of the curve shape could not influence HL. Overall, the results suggest that growth curve parameters are heritable and can respond to genetic or genomic selection for optimizing the performance in mink.

Key words: genetic parameters, growth curve, mink, nonlinear models, Richards

Introduction

Growth is an economically important trait for farm animals, and better knowledge of animal growth is necessary for optimized management and feeding practices, and genetic improvement of farm animals. Among different approaches to understand animal growth, mathematically modeling that allows to characterize the growth patterns and to visualize the shape of growth over time is a particularly useful approach. The growth parameters derived from these models can be used to reshape the growth curve and predict the harvest weight and
length of animals. Importantly, previous research showed that these parameters are heritable and responsive to the selection programs in cattle, chicken, and sheep (DeNise and Brinks, 1985; Barbato, 1991; Lupi et al., 2016).

In many species, the observed growth curve is a sigmoidal (S-shape) structure (Akbas and Oguz, 1998; Strathe et al., 2010; Liu et al., 2011; Hossein-Zadeh, 2015; Lupi et al., 2016; Kaplan and Gürcan, 2018; Do and Miar, 2020). Among growth curve models, nonlinear models are the most applied models (Schnute, 1981). The nonlinear models allow the interpretation and understanding of growth patterns and metabolism underlying growth periods. Several nonlinear models such as Gompertz (Gompertz, 1825), Brody (Brody and Lardy, 1946), Logistic (Pearl, 1977), Bridges (Bridges et al., 1992), Jannoscheck (Wellock et al., 2004), and Richards (Richards and Kavanagh, 1945) are widely used to describe the growth curve (Kaplan and Gürcan, 2018). The significant characteristics of growth models are the number of parameters used to describe the growth curve. Several 3-parameter models such as Gompertz, Von Bertalanffy, and Logistic are less complex and require less computing demand but they often have the fixed model inflection point. The weight at the inflection point (WIP) is identified as 37% of the asymptotic weight in the Gompertz and Von Bertalanffy models but they often have the fixed model inflection point. The parameters derived from Richards model was used to compute the age at the inflection point (AIP) and WIP as follows:

\[ BW_t = \frac{a}{1 - \beta \times e^{-kt}} \]

where \( BW_t \) is the BW in kg at the time \( t \), \( a \) is the mature BW in kg, \( t \) is the age in weeks, \( \beta, k, \) and \( m \) are the parameters specific for the function, \( \beta \) characterizes the first part of growth before the inflection point, \( k \) describes the second part in which growth rate decreases until the animal reaches the asymptotic or mature weight (\( a \)), and \( m \) is the shape parameter determining the position of the inflection point.

The parameters derived from Richards model was used to compute the age at the inflection point (AIP) and WIP as follows:

\[ AIP = \frac{a}{(m + 1)^{1/m}} \]

\[ WIP = \frac{-\ln(m/\beta)}{k} \]

### Estimation of genetic and phenotypic parameters

Prior to genetic and phenotypic parameter estimation, univariate models were used to test the significance (\( P < 0.05 \)) of fixed effects, including sex (male and female), year (2018 and 2019), color type (dark, demi, mahogany, pastel, and stardust), and age of dam (1, 2, and 3) on growth curve parameters, BW and HL. The significance of random maternal effect or each trait was determined by comparing the full and reduced models using the following statistic:

\[ -2 \log L_{\text{reduced model}} - \log L_{\text{full model}} \sim \chi^2_{df} (\text{full model}) - df(\text{reduced model}) \]
where \( \log L \) and \( df \) are log-likelihood and degrees of freedom in each model, respectively.

The variance components were estimated for each trait using the following univariate model:

\[
y = Xb + Za + Wm + e,
\]

where \( y \) is the vector of phenotypic observations, \( b \) is the vector of fixed effects, \( a \) is the vector of random additive genetic effects, \( m \) is the vector of random maternal effects, and \( e \) is the vector of residual effects; and \( X, Z, \) and \( W \) are the incidence matrices relating the phenotypic observations to fixed, random additive genetic, and random maternal effects, respectively. It was assumed that random effects were independent and normally distributed:

\[
a \sim (0, \sigma^a_1^2), m \sim N(0, \sigma^m_0^2), \text{and } e \sim N(0, \sigma^e_1^2),
\]

where \( A \) is the numerator relationship matrix; \( I \) is an identity matrix; \( \sigma^a_1^2, \sigma^m_0^2, \) and \( \sigma^e_1^2 \) are the variances of random additive genetic, maternal, and residual effects. The pedigree was traced back to 16 generations, including 1,058 dams and 633 sires. All analyses were performed using Asreml-R version 4 (Butler et al., 2018).

Generally, the following bivariate model was used to analyze traits:

\[
y_1 = X_1 b + Z_{a1} a_1 + Z_{m1} m_1 + e_1,
y_2 = X_2 b + Z_{a2} a_2 + Z_{m2} m_2 + e_2,
\]

where \( y_1 \) and \( y_2 \) are the vectors of observations for the first and second trait; \( b, a, a_1, a_2, m, m_1, m_2, e, \) and \( e_1, e_2 \) are the vectors of fixed, additive genetic, maternal, and residual effects for traits 1 and 2, respectively; and \( X_1, X_2, Z_{a1}, Z_{a2}, Z_{m1}, Z_{m2}, \) and \( Z_{m} \) are the incidence matrices relating observations to fixed, random additive genetic, and random maternal effects for traits 1 and 2, respectively. It was assumed that random effects were normally distributed:

\[
a_1 \sim N (0, A \otimes \begin{bmatrix} \sigma^a_1^2 & \sigma^a_1^2 \\ \sigma^a_1^2 & \sigma^a_2^2 \end{bmatrix}),
\]

\[
m \sim N (0, I \otimes \begin{bmatrix} \sigma^m_0^2 & \sigma^m_1^2 \\ \sigma^m_1^2 & \sigma^m_2^2 \end{bmatrix}), \text{and}
\]

where \( A \) is the numerator relationship matrix; \( I \) is an identity matrix; \( \sigma^a_1^2, \sigma^a_2^2, \sigma^m_0^2, \sigma^m_1^2, \sigma^m_2^2, \) and \( \sigma^e_2^2 \) are variances of random additive genetic, maternal, and residual effects for traits 1 and 2, respectively; \( \sigma^a_{12}, \sigma^m_{12}, \) and \( \sigma^e_{12} \) are covariances of additive genetic, maternal, and residual effects between traits 1 and 2, respectively.

The final reported heritability for each trait was obtained by averaging the estimates of multiple corresponding pairwise bivariate analyses. Phenotypic and genetic correlations among traits were calculated based on the (co)variance components from bivariate models. The genetic correlations were calculated as

\[
r_g = \frac{\sigma^a_{12}}{\sqrt{\sigma^a_1^2 \times \sigma^a_2^2}},
\]

and

\[
r_m = \frac{\sigma^m_{12}}{\sqrt{\sigma^m_1^2 \times \sigma^m_2^2}},
\]

The phenotypic correlations were calculated as

\[
r_p = \frac{\sigma_{12}}{\sqrt{\sigma_1^2 \times \sigma_2^2}},
\]

The heritability of each trait was calculated as

\[
b_h = \frac{\sigma^a_1^2}{\sigma_1^2}.
\]

Results

Descriptive statistics and growth parameters estimation

Descriptive statistics for BW, HL, and growth parameters of mink was shown in Table 1. In general, the males had higher BW than females. The BW increased by the week of measurements and reached the maximum BW at week 28 in both males and females. Since 334 mink were selected for breeding in the next breeding seasons, we did not collect their harvest BW and length records at the week 31. Consequently, fewer numbers of records were available for BW31 and HL (Table 1). The coefficient of variation ranged from 9.93% to 13.57% and from 11.22% to 14.86% for BW of males and females, respectively. The values of the coefficient of variation linearly increased by the week of BW measurement. HL had a lower value of the coefficient of variation compared to BW.

| Traits | Names | Unit | Male | Female |
|--------|-------|------|------|--------|
|        |       |      | Mean (SE) | CV (%) | Mean (SE) | CV (%) |
| BW13   | BW at week 13 | kg | 510 | 1.51 ± 0.01 | 9.93 | 519 | 0.98 ± 0.01 | 11.22 |
| BW16   | BW at week 16 | kg | 510 | 1.91 ± 0.01 | 10.47 | 519 | 1.18 ± 0.01 | 12.71 |
| BW19   | BW at week 19 | kg | 510 | 2.25 ± 0.01 | 11.11 | 519 | 1.29 ± 0.01 | 13.18 |
| BW22   | BW at week 22 | kg | 510 | 2.54 ± 0.01 | 11.81 | 519 | 1.44 ± 0.01 | 13.19 |
| BW25   | BW at week 25 | kg | 509 | 2.65 ± 0.01 | 12.08 | 519 | 1.5 ± 0.01 | 14.00 |
| BW28   | BW at week 28 | kg | 509 | 2.71 ± 0.02 | 12.92 | 519 | 1.52 ± 0.01 | 14.47 |
| BW31   | BW at harvest (week 31) | kg | 389 | 2.58 ± 0.02 | 13.57 | 307 | 1.48 ± 0.01 | 14.86 |
| HL     | Body length at harvest (week 31) | kg | 389 | 48.52 ± 0.11 | 4.41 | 307 | 40.32 ± 0.13 | 5.73 |
| α1     | mature BW | kg | 507 | 2.81 ± 0.02 | 13.17 | 514 | 1.56 ± 0.01 | 15.38 |
| k      | k | | 507 | 0.24 ± 0.01 | 41.67 | 514 | 0.23 ± 0.01 | 43.48 |
| m      | m | | 507 | 0.66 ± 0.04 | 124.24 | 514 | 0.61 ± 0.04 | 140.98 |
| AIP    | Age at inflection point | week | 507 | 11.69 ± 0.06 | 12.32 | 514 | 10.11 ± 0.08 | 18.30 |
| WIP    | Weight at inflection point | kg | 507 | 1.25 ± 0.01 | 19.20 | 514 | 0.70 ± 0.01 | 25.71 |

1: mature body weight in kg; k: second part of the growth curve, in which growth rate decreases until the animal reaches the asymptotic or mature weight (α); m: shape parameter determining the position of curve inflection point, N: number of mink, CV: coefficient of variation, SE: standard errors of mean.
Estimated growth parameters varied between gender with higher mean values of \( \alpha \), \( k \), \( m \), AIP, and WIP for males. The coefficients of variation for parameters related to the shape of the growth curve (\( k \) and \( m \)) were also higher than the values for other growth parameters (\( \alpha \), AIP, and WIP).

**Variance components and estimated heritability for BWs, HL, and growth parameters**

The fixed and random effects used for estimation of genetic and phenotypic parameters were shown in Table 2. Sex had a significant effect (\( P < 0.05 \)) on all traits, except for parameters \( k \) and \( m \). Color type had only significant effect (\( P < 0.05 \)) on harvest weight and length. Age of dam had only significant effect (\( P < 0.05 \)) on BW13. Birth-year also significantly (\( P < 0.05 \)) affected most of the studied traits except for BW22, \( \alpha \), and WIP (\( P > 0.05 \)). The random maternal effect was significant (\( P < 0.05 \)) for the majority of traits except for harvest weight and length. Estimated variance components and heritabilities obtained from univariate models were shown in Table 3. Additive genetic variances varied among the traits but always higher than maternal variances. Maternal variances explained from 8% to 17% of the phenotypic variances of growth parameters (from \( \pm 0.04 \) for \( k \) to \( \pm 0.04 \) for WIP); however, it explained a considerable variance (from 9% to 26%) for BW (from \( \pm 0.04 \) in BW25 and BW28 to \( \pm 0.06 \) in BW13).

**Genetic and phenotypic correlations estimated for BWs, HL, and growth parameters**

Estimated heritabilities, phenotypic (\( r_p \)), and genetic correlations (\( r_g \)) among BW, HL, and growth parameters were shown in Table 4. Estimated heritabilities (\( \pm \)SE) for BW ranged from 0.36 ± 0.13 (BW13) to 0.46 ± 0.10 (BW22). Heritability estimates (\( \pm \)SE) for HL, \( \alpha \), \( k \), \( m \), WIP, and AIP were 0.51 ± 0.09, 0.29 ± 0.09, 0.30 ± 0.09, 0.33 ± 0.10, 0.44 ± 0.10, and 0.47 ± 0.10, respectively. Strong and significant (\( P < 0.05 \)) phenotypic and genetic correlations were found among the BW traits. Both phenotypic (\( r_p = 0.95 \pm 0.01 \)) and genetic correlations (\( r_g = 0.98 \pm 0.01 \)) between BW22 and BW25 were very strong. Moderate-to-high phenotypic (from 0.46 ± 0.03 to 0.60 ± 0.03) and genetic (from 0.70 ± 0.13 to 0.88 ± 0.09) correlations were observed between HL and BW. The parameters \( \alpha \) and WIP had moderate-to-high significant genetic correlations with all BW and HL traits (\( P < 0.05 \)). The parameters related to the shape of the growth curve (\( k \) and \( m \)) had very weak or nonsignificant genetic correlations (\( P > 0.05 \)) with BW and HL traits. Between the growth curve parameters, strong and significant genetic correlations (\( P < 0.05 \)) were observed between \( \alpha \) and AIP (0.60 ± 0.26), \( \alpha \) and WIP (0.69 ± 0.14), WIP and AIP (0.96 ± 0.03) as well as between \( k \) and \( m \) (0.89 ± 0.03). Weak and nonsignificant genetic correlations (\( P > 0.05 \)) were also observed between \( \alpha \) and \( m \) (−0.21 ± 0.23), \( \alpha \), and \( m \) (−0.10 ± 0.22).

**Discussion**

Growth curves have been proven useful to analyze and understand longitudinal data such as BW and population growth. However, they are known to be varied among species, among populations/breeds within species, as well as among individuals within each population or breed. Unlike many major species, mink are raised purely for fur production. In mink, BW and HL are important traits for the pelt size that is one of the factors determining the fur price. In this study, BW traits were increased with age until reaching the maximum values, which were generally in agreement with the results from previous studies in mink (Sørensen et al., 2003; Liu et al., 2011; Shirali et al., 2015; Do and Miar, 2020). Moreover, BW were also varied by gender, which were also consistent with previous reports (Sørensen et al., 2003; Liu et al., 2011; Do and Miar, 2020). Notably, the average harvest BW (BW31) for males (2.58 kg) and females (1.48 kg) mink (Table 1) were lower than the average values of 3.10 kg for males and 1.69 kg for females in a commercial farm in Canada (Do and Miar, 2020). This might be due to the differences in the feed sources and management systems in the two farms. Similar to the previous studies (Sørensen et al., 2003; Liu et al., 2011; Do and Miar, 2020), we also observed that males had higher HL than females (Tables 1 and 2).

The estimated growth parameters varied among sexes, which were also reported in previous studies (Sørensen et al., 2003; Liu et al., 2011; Do and Miar, 2020). As expected, the growth patterns were different between males and females, with slower growth and late mature observed in females (Sørensen et al., 2003; Liu et al., 2011; Do and Miar, 2020). The univariate results reported that color type did not significantly (\( P > 0.05 \)) affect growth parameters in the current mink population, which was due to the different management systems in the two farms. Similar to the previous studies (Sørensen et al., 2003; Liu et al., 2011; Shirali et al., 2015; Do and Miar, 2020), we also observed that males had higher HL than females (Tables 1 and 2).

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**Table 2.** Significance of fixed and random effects used to estimate the genetic and phenotypic parameters for BWs, HL, and growth parameters in mink

| Traits                  | Names                      | Unit  | Sex | Color type | Birth year | Age of dam | Animal | Maternal |
|-------------------------|----------------------------|-------|-----|------------|------------|------------|--------|----------|
| BW13                    | BW at week 13              | kg    | *   | NS         | *          | *          | NT     | *        |
| BW16                    | BW at week 16              | kg    | *   | NS         | *          | NS         | NT     | *        |
| BW19                    | BW at week 19              | kg    | *   | NS         | *          | NS         | NT     | *        |
| BW22                    | BW at week 22              | kg    | *   | NS         | NS         | NS         | NT     | *        |
| BW25                    | BW at week 25              | kg    | *   | NS         | *          | NS         | NT     | *        |
| BW28                    | BW at week 28              | kg    | *   | NS         | *          | NS         | NT     | *        |
| BW31                    | BW at harvest (week 31)    | kg    | *   | *          | *          | NS         | NT     | NS       |
| HL                      | Body length at harvest     | kg    | *   | *          | *          | NS         | NT     | NS       |
| H1                      | mature BW                  | kg    | *   | NS         | NS         | NS         | NT     | *        |
| k                       | k                          | NS    | *   | NS         | *          | NT         | *      | *        |
| m                       | m                          | NS    | *   | NS         | NS         | NT         | *      | *        |
| AIP                     | Age at inflection point    | week  | *   | NS         | NS         | NT         | *      | *        |
| WIP                     | Weight at inflection point | kg    | *   | NS         | *          | NT         | *      | *        |

1: mature BW in kg; \( k \): second part of the growth curve, in which growth rate decreases until the animal reaches the asymptotic or mature weight (\( \alpha \)), \( m \): shape parameter determining the position of curve inflection point; NS: nonsignificant; NT: not tested; *Significance at \( P < 0.05 \).
Moreover, we also observed higher heritability for BW in the late part of the growth curve, in which growth rate decreases until the animal reaches the asymptotic or mature weight ($\alpha$; shape parameter determining the position of curve inflection point, AIP: age at inflection point, WIP: weight at inflection point, $\sigma_m^2$, $\sigma_e^2$: additive, maternal and residual variances; $c_{im}^2$: proportion of variance explained by maternal effects, NE: not estimated.

Table 3. Variance components and heritabilities from univariate models estimated for BWs, HL, and growth parameters in mink

| Traits       | $\sigma_a^2$ | $\sigma_m^2$ | $\sigma_e^2$ | Heritability | $c_{im}^2$ |
|--------------|--------------|--------------|--------------|--------------|------------|
| BW13$^1$     | 6.03E-03 ± 2.49E-03 | 4.45E-03 ± 1.06E-03 | 6.08E-03 ± 1.31E-03 | 0.35 ± 0.13 | 0.26 ± 0.06 |
| BW16         | 1.07E-02 ± 3.97E-03 | 5.28E-03 ± 1.54E-03 | 1.48E-02 ± 2.18E-03 | 0.35 ± 0.12 | 0.17 ± 0.05 |
| BW19         | 2.09E-02 ± 6.10E-03 | 2.07E-02 ± 3.32E-03 | 5.67E-03 ± 2.08E-03 | 0.44 ± 0.11 | 0.12 ± 0.04 |
| BW22         | 3.00E-02 ± 8.05E-03 | 6.75E-03 ± 2.68E-03 | 2.82E-02 ± 4.41E-03 | 0.46 ± 0.11 | 0.10 ± 0.04 |
| BW25         | 3.15E-02 ± 8.71E-03 | 6.42E-03 ± 2.91E-03 | 3.30E-02 ± 4.81E-03 | 0.44 ± 0.11 | 0.09 ± 0.04 |
| BW28         | 3.04E-02 ± 1.01E-02 | 8.08E-03 ± 3.66E-03 | 4.82E-02 ± 5.79E-03 | 0.35 ± 0.11 | 0.09 ± 0.04 |
| BW31         | 3.15E-02 ± 8.69E-03 | 5.21E-02 ± 6.33E-03 | 0.38 ± 0.09 | 0.38 ± 0.09 | NE |
| HL           | 2.45 ± 0.52 | 2.39 ± 0.36 | 0.51 ± 0.17 | 0.51 ± 0.17 | NE |
| $\alpha$     | 2.49E-02 ± 8.44E-03 | 1.01E-02 ± 3.86E-03 | 6.17E-02 ± 5.42E-03 | 0.26 ± 0.08 | 0.10 ± 0.04 |
| $k$          | 3.28E-03 ± 1.18E-03 | 8.23E-04 ± 4.39E-04 | 6.85E-03 ± 7.20E-04 | 0.30 ± 0.10 | 0.08 ± 0.04 |
| $m$          | 2.38E-07 ± 8.20E-08 | 8.40E-08 ± 3.23E-08 | 4.18E-07 ± 4.84E-08 | 0.32 ± 0.10 | 0.11 ± 0.04 |
| AIP          | 1.39E+00 ± 3.50E-01 | 3.93E-01 ± 1.25E-01 | 1.04E+00 ± 1.88E-01 | 0.49 ± 0.14 | 0.14 ± 0.04 |
| WIP          | 2.14E-02 ± 5.87E-03 | 8.19E-03 ± 2.21E-03 | 1.75E-02 ± 3.15E-03 | 0.45 ± 0.11 | 0.17 ± 0.05 |

$^1$BW (13 to 31): BW at corresponding measurement week (13 to 31), HL: body length at harvest (week 31), $\alpha$: mature BW in kg; $k$: the second part of the growth curve, in which growth rate decreases until the animal reaches the asymptotic or mature weight ($\alpha$), $m$: shape parameter determining the position of curve inflection point, AIP: age at inflection point, WIP: weight at inflection point, $\sigma_m^2$, $\sigma_e^2$: additive, maternal and residual variances; $c_{im}^2$: proportion of variance explained by maternal effects, NE: not estimated.

in contrast with Liu et al. (2011), that reported color type affected the shapes of the curve and growth parameters in Chinese mink breeds. This difference might be due to the differences in genetics, sample size, number of color types, nutrition, and management factors between the two farms, but it also might be due to the different models used to test the significance of the color type. Liu et al. (2011) used a linear model without including additive genetic effects that were different from our animal model (containing both fixed and random additive and maternal effects). The color type had only significant ($P < 0.05$) effects on traits measured postmortem (BW31 and HL). Previous studies indicated that the color types are important for reproductive performance in mink (Ślaska et al., 2009; Felaska-Blaszczzyk et al., 2010). It is not clear how the color types influence the harvest BW and weight. One of the possible reasons is the difference in using of energy during the furring period as some mink require more energy for priming their fur (Kenttämies and Vilva, 1988).

A previous study showed that there was a correlated response to selection for BW and fur quality in mink (Lagerkvist et al., 1994). It was also observed that the colors of mink were controlled by a large number of mutations in the genomes (Song et al., 2017; Manakho et al., 2019). Therefore, it could be interesting to investigate if these genes have pleotropic effects in controlling colors and BW in mink. Moreover, the coefficients of variation of shape parameters ($k$ and $m$) were higher than other studied traits (Table 1), which implies that there are more opportunities to change the shape of the growth curve by altering $k$ and $m$ compared with other traits.

The random maternal effects are important for the majority of the studied traits. Previous studies reported the importance of maternal effects for different traits in mink, such as reproduction traits in the current population (Karimi et al., 2018) and fur quality traits (Thirstrup et al., 2017). As expected, the variance explained by maternal effects was reduced with the growth of animals indicated that environmental factors contribute more to the phenotypic variances at the later stage of life. The importance of maternal effects for growth was also reported in other species such as sheep (Safari et al., 2007) and cattle (Meyer, 1992; Elter et al., 1995). Heritabilities for BW ranged from 0.36 (BW13) to 0.46 (BW22) in the current study that overlapped with the range of heritabilities estimated for BW in previous studies (Lagerkvist et al., 1993; Shirali et al., 2015; Thirstrup et al., 2017). Moreover, we also observed higher heritability for BW in the late furring period (Table 4) which was in an agreement with the estimated heritabilities from 0.73 to 0.84 for males and 0.69 to 0.85 for females in furring periods obtained by Shirali et al. (2015).

Up to our best knowledge, there is no study to devote for the estimation of heritabilities for growth curve parameters in mink so far. However, moderate heritabilities for growth parameters were also observed in other species such as goat (Ghiasi et al., 2018) and chicken (Grossman and Bohren, 1985). The estimated heritability for HL was 0.51 in the current study, which was higher than estimated heritabilities of 0.43 and 0.21 for mink length in August and November, respectively (Kenttämies and Vilva, 1988) but similar to the value of 0.51 reported for Chinese mink (Liu et al., 2017).

Strong positive genetic correlations of $\alpha$ with WIP (0.69 ± 0.14) and AIP (0.60 ± 0.26) suggested that maximum growth could be achieved by increasing AIP or WIP. A notable strong positive genetic correlation between AIP and $k$ (0.61 ± 0.14) indicated that increasing AIP could increase the growth rate after maturation. Increasing $k$ will shift the Richards growth curve to the right and consequently leading to earlier mature growth. The genetic correlations among growth curve parameters varied among studies largely depending on the sources and amounts of data used. For instance, a strong negative genetic correlation between $\alpha$ and $k$ ($r_\alpha = -0.76$) was reported in goats (Ghiasi et al., 2018), while a nonsignificant correlation among these traits was reported in chickens (Grossman and Bohren, 1985). The strong genetic correlation ($r_\alpha = 0.96 ± 0.03$) between AIP and WIP found in this study was also reported ($r_\alpha = 0.99$) in goats (Ghiasi et al., 2018). Importantly, strong positive genetic correlations between $\alpha$ with BW (from 0.57 to 0.90) and HL ($0.44 ± 0.03$) were found, indicating that $\alpha$ could be used for indirect selection of BW or HL in mink. The strong genetic correlation between $\alpha$ and BW in our study (from 0.57 to 0.90) agreed with previous studies in other species (Akbascedilli and Yaylak, 2000; Aslam et al., 2011). The highest genetic correlations in this study were observed among BW at the furring periods (BW22 to 28) that could be explained by little changes in BW during this period as animals have almost reached their maximum growth. The high genetic correlations among BW the growing and furring periods in the current study were also observed in Danish mink (e.g., 0.69 to 0.99 for growth period and 0.90 to 0.99 for furring period in males; Shirali et al., 2015). These high genetic correlations suggested that it is possible to select mink at the end of the growth period or the
Table 4. Estimated heritabilities (diagonal), genetic correlations (below diagonal), and phenotypic correlations (above diagonal) for BWs, HL, and growth parameters in mink

| BW  | α   | m   | k   | WIP | AIP |
|-----|-----|-----|-----|-----|-----|
| 13  | 0.36 ± 0.04* | 0.29 ± 0.04* | 0.19 ± 0.06* | 0.48 ± 0.37* | 0.61 ± 0.05* |
| 16  | 0.48 ± 0.03* | 0.46 ± 0.03* | 0.56 ± 0.02* | 0.95 ± 0.01* | 0.81 ± 0.01* |
| 19  | 0.61 ± 0.03* | 0.66 ± 0.02* | 0.72 ± 0.02* | 0.70 ± 0.02* | 0.52 ± 0.03* |
| 22  | 0.72 ± 0.02* | 0.85 ± 0.06* | 0.98 ± 0.01* | 0.46 ± 0.10* | 0.95 ± 0.01* |
| 25  | 0.74 ± 0.03* | 0.88 ± 0.07* | 0.94 ± 0.03* | 0.98 ± 0.01* | 0.37 ± 0.10* |
| 31  | 0.74 ± 0.13* | 0.76 ± 0.15* | 0.86 ± 0.10* | 0.91 ± 0.07* | 0.94 ± 0.05* |
| HL  | 0.88 ± 0.09* | 0.70 ± 0.13* | 0.74 ± 0.11* | 0.74 ± 0.11* | 0.80 ± 0.10* |

**Notes:**
- *P < 0.05.

1 BW (13 to 31): BW at corresponding measurement week (13 to 31), HL: body length at harvest (week 31), α: the second part of the growth curve, in which growth rate decreases, k: shape parameter determining the position of curve inflection point, WIP: weight at inflection point, AIP: age at inflection point.

**Conclusions**

This is the first genetic study of growth curve parameters in mink. Heritabilities for growth parameters obtained here suggest that the selection program to optimize the slope of the growth curve in mink may be feasible. The results of genetic correlations between growth parameters indicate that it is possible to change the shape of the growth curve without impacting the harvest weight and length of animals. Further studies are required to determine the effectiveness of reshaping the growth curve in mink via a breeding program.

**Conflict of Interest Statement**

The authors declare no real or perceived conflicts of interest. The funders had no role in the design of the study, data collection, data analyses, interpretation, writing of the manuscript, and decision to publish the results.

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Butler, D., B. Cullis, A. Gilmour, B. Gogel, and R. Thompson. 2018. ASReml-R Reference Manual Version 4. Brisbane, QLD. The beginning of the furring period for optimal BW. HL had strong genetic correlations with BW (from 0.70 to 0.88) indicated that indirect selection of pelt length could be reached by selection for higher BW. However, it is important to note that BW might have unfavorable genetic correlations with fertility, fitness, and fur quality traits (Lagerkvist et al., 1994). A selection program in mink should consider these unfavorable genetic correlations to balance between weight and length with the fitness traits.

**Conclusions**

This is the first genetic study of growth curve parameters in mink. Heritabilities for growth parameters obtained here suggest that the selection program to optimize the slope of the growth curve in mink may be feasible. The results of genetic correlations between growth parameters indicate that it is possible to change the shape of the growth curve without impacting the harvest weight and length of animals. Further studies are required to determine the effectiveness of reshaping the growth curve in mink via a breeding program.

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