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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 (α), 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 (\pm 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 ± 0.1 , 0.44 ± 0.10 , and 0.47 ± 0.10 for HL, α , k , m , WIP, and AIP, respectively. The parameter α had non-significant ($P > 0.05$) genetic correlations (\pm 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 (α). 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 α , AIP, and WIP parameters had significant ($P < 0.05$) genetic correlations with HL indicated that selection for higher α , 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

Abbreviations

AIP	age at the inflection point
HL	harvest length
α	asymptotic weight
k	growth rate at mature
m	shape parameter
WIP	weight at the inflection point

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 Gürçan, 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 Gürçan, 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 and 50% of the Logistic growth function (Kaplan and Gürçan, 2018). The 4-parameter models such as Bridges, Jannoscheck and Richards are more complex than 3-parameter models, and they have the flexible inflection point; therefore, they often yield better goodness of fit (Perotto et al., 1992; Tjørve and Tjørve, 2010; Wang et al., 2012).

Mink is a major animal used in the fur industry. The price of the pelt is the most economically important factor for mink farmers, and it is known to have strong correlations with body weight (BW) and length at pelting (Thirstrup et al., 2017). Currently, the Canadian mink farmers select their breeding animals based on the phenotypic performance of reproduction, growth traits, and fur quality, and therefore, understanding the biology of growth traits are important and useful for successful breeding programs. Growth curves of mink were successfully modeled previously (Sørensen et al., 2003; Liu et al., 2011; Do and Miar, 2020), and Richards was shown to be the most appropriate model for modeling the growth in Canadian mink (Do and Miar, 2020). However, there is no reported study on genetic and phenotypic parameters for the derived parameters from the growth curve. Therefore, this study aimed to estimate the genetic and phenotypic parameters for growth curve parameters derived from Richards growth model and estimate the correlations of the growth curve parameters with BWs and harvest length (HL) in American mink.

Materials and Methods**Animal resources and data collection**

The proposed work was approved by the Dalhousie University Animal Care and Use Committee (certification# 2018-009), and

mink used in this study were cared for according to the Code of Practice for the Care and Handling of Farmed Mink (https://www.nfacc.ca/pdfs/codes/mink_code_of_practice.pdf) guidelines.

Mink were all raised individually in each cage under standard farming conditions at the Canadian Centre for Fur Animal Research at Dalhousie University, Faculty of Agriculture (Truro, Nova Scotia, and Canada). Mink diets were adjusted according to the animal requirements in each production period, which was based on the by-products of human food production. Mink kits were produced by randomly selected parents for breeding in November or early December in 2017 and 2018. Initially, 1,088 mink born in 2018 and 2019 by mating 67 sires and 216 dams were selected for data collection. These animals were born from the end of April to early May and were weaned around the end of June (~7 wk of age). Mink were weighed every 3 wk from week 13 after birth (01, August) to the harvest day (10, December). The BW included BW at week 13 (BW13), 16 (BW16), 19 (BW19), 22 (BW22), 25 (BW25), 28 (BW28), and 31 (BW31). After removing the individuals with missing data, the final data of 1,030 mink (511 males and 519 females) was used for testing the growth model performance. Among them, 475 mink were born in 2018 by mating 78 dams and 27 sires, and 555 mink were born in 2019 by mating 135 dams and 40 sires.

Growth modeling and evaluations

The following Richards model was used to fit BW records for each mink separately using nlsLM functions in stats and minpack.lm packages (Elzhov et al., 2016) in R software (R Development Core Team, 2011):

$$BW_t = \frac{\alpha}{(1 - \beta \times e^{-kt})^{1/m}},$$

where BW_t is the BW in kg at the time t , α is the mature BW in kg, t is the age in weeks, β , k , and m are the parameters specific for the function, β 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 (α), 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:

$$AIP = \frac{\alpha}{(m+1)^{1/m}}$$

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

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:

$$a \sim (0, A\sigma_a^2), m \sim N(0, I\sigma_m^2), \text{ and } e \sim N(0, I\sigma_e^2),$$

where A is the numerator relationship matrix; I is an identity matrix; σ_a^2 , σ_m^2 , and σ_e^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:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where y_1 and y_2 are the vectors of observations for the first and second trait; b_1 , b_2 , a_1 , a_2 , m_1 , m_2 , e_1 , and 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} , and Z_{m2} 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:

$$\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} \sim N\left(0, A \otimes \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1a2} \\ \sigma_{a1a2} & \sigma_{a2}^2 \end{bmatrix}\right),$$

$$\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} \sim N\left(0, I \otimes \begin{bmatrix} \sigma_{m1}^2 & \sigma_{m1m2} \\ \sigma_{m1m2} & \sigma_{m2}^2 \end{bmatrix}\right), \text{ and}$$

$$\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \sim N\left(0, I \otimes \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e1e2} \\ \sigma_{e1e2} & \sigma_{e2}^2 \end{bmatrix}\right),$$

where A is the numerator relationship matrix; I is an identity matrix; σ_{a1}^2 , σ_{a2}^2 , σ_{m1}^2 , σ_{m2}^2 , σ_{e1}^2 , and σ_{e2}^2 are variances of random additive genetic, maternal, and residual effects for traits 1 and 2, respectively; σ_{a1a2} , σ_{m1m2} , and σ_{e1e2} 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 $r_g = \sigma_{a1a2} / \sigma_{a1} \times \sigma_{a2}$. The phenotypic correlations were calculated as $r_p = \frac{(\sigma_{a1a2} + \sigma_{m1m2} + \sigma_{e1e2})}{[(\sigma_{a1}^2 + \sigma_{m1}^2 + \sigma_{e1}^2) \times (\sigma_{a2}^2 + \sigma_{m2}^2 + \sigma_{e2}^2)]^{1/2}}$ for the traits having the maternal effect and as $r_p = \frac{(\sigma_{a1a2} + \sigma_{e1e2})}{[(\sigma_{a1}^2 + \sigma_{e1}^2) \times (\sigma_{a2}^2 + \sigma_{e2}^2)]^{1/2}}$ for the traits that did not have the random maternal effects in their models. The significance of these estimates was tested using a Z-test with the null hypothesis that the estimates are equal to zero ($\alpha = 0.05$).

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.

Table 1. Descriptive statistics for BWs, HL, and growth parameters in mink

Traits	Names	Unit	Male			Female		
			N	Mean (SE)	CV (%)	N	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
α^1	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 α : 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 α , 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 (α , 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, α , 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 0.08 ± 0.04 for k to 0.17 ± 0.04 for WIP); however, it explained a considerable variance (from 9% to 26%) for BW (from 0.09 ± 0.04 in BW25 and BW28 to 0.26 ± 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, α , 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 α 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 α and AIP (0.60 ± 0.26), α 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 α and k (-0.21 ± 0.23), α , 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 BL 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

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	Fixed effects				Random effects	
			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 (week 31)	kg	*	*	*	NS	NT	NS
α^1	mature BW	kg	*	NS	NS	NS	NT	*
k	k		NS	NS	*	NS	NT	*
m	m		NS	NS	*	NS	NT	*
AIP	Age at inflection point	week	*	NS	NS	NS	NT	*
WIP	Weight at inflection point	kg	*	NS	*	NS	NT	*

¹ α : 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 (α), m : shape parameter determining the position of curve inflection point; NS: nonsignificant; NT: not tested; *Significance at $P < 0.05$.

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

Traits	σ_a^2	σ_m^2	σ_e^2	Heritability	c_m^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 ± 6.53E-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
α	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

¹BW (13 to 31): BW at corresponding measurement week (13 to 31), HL: body length at harvest (week 31), α : 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 (α), m: shape parameter determining the position of curve inflection point, AIP: age at inflection point, WIP: weight at inflection point, σ_a^2 , σ_m^2 , σ_e^2 : additive, maternal and residual variances; c_m^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; Felska-Błaszczuk et al., 2010). It is not clear how the color types influence the harvest BW and length. 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; Manakhov et al., 2019). Therefore, it could be interesting to investigate if these genes have pleiotropic 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; Eler 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 α 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 α and k ($r_g = -0.76$) 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 ($r_g = 0.96 \pm 0.03$) between AIP and WIP found in this study was also reported ($r_g = 0.99$) in goats (Ghiasi et al., 2018). Importantly, strong positive genetic correlations between α with BW (from 0.57 to 0.90) and HL (0.44 ± 0.03) were found, indicating that α could be used for indirect selection of BW or HL in mink. The strong genetic correlation between α and BW in our study (from 0.57 to 0.90) agreed with previous studies in other species (Akbascedillā 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

	BW13	BW16	BW19	BW22	BW25	BW28	BW31	HL	α	k	m	WIP	AIP
BW13 ¹	0.36 ± 0.13												
BW16	0.88 ± 0.06*	0.36 ± 0.12											
BW19	0.80 ± 0.09*	0.94 ± 0.03*	0.43 ± 0.12										
BW22	0.72 ± 0.12*	0.85 ± 0.06*	0.98 ± 0.01*	0.46 ± 0.10									
BW25	0.74 ± 0.12*	0.88 ± 0.07*	0.94 ± 0.03*	0.98 ± 0.01*	0.45 ± 0.10								
BW28	0.79 ± 0.12*	0.84 ± 0.08*	0.90 ± 0.05*	0.96 ± 0.03*	0.98 ± 0.01*	0.37 ± 0.10							
BW31	0.74 ± 0.13*	0.76 ± 0.15*	0.86 ± 0.10*	0.91 ± 0.07*	0.94 ± 0.05*	0.94 ± 0.05*	0.37 ± 0.09						
HL	0.88 ± 0.09*	0.70 ± 0.13*	0.74 ± 0.11*	0.74 ± 0.11*	0.77 ± 0.12*	0.80 ± 0.10*	0.78 ± 0.08*	0.51 ± 0.09					
α	0.60 ± 0.18*	0.57 ± 0.03*	0.68 ± 0.02*	0.84 ± 0.01*	0.86 ± 0.01*	0.90 ± 0.01*	0.73 ± 0.02*	0.44 ± 0.03*	0.29 ± 0.09				
k	-0.20 ± 0.24	0.19 ± 0.04*	0.22 ± 0.04*	0.12 ± 0.04*	-0.02 ± 0.04	-0.17 ± 0.04*	-0.14 ± 0.04*	-0.01 ± 0.05	-0.21 ± 0.22	0.30 ± 0.09			
m	-0.29 ± 0.22	0.14 ± 0.04*	0.25 ± 0.04*	0.20 ± 0.04*	0.08 ± 0.04*	-0.04 ± 0.04	0.03 ± 0.04	0.07 ± 0.05	-0.10 ± 0.22	0.89 ± 0.03*	0.33 ± 0.10		
WIP	0.24 ± 0.22	0.52 ± 0.03*	0.71 ± 0.02*	0.73 ± 0.02*	0.67 ± 0.02*	0.58 ± 0.03*	0.54 ± 0.03*	0.35 ± 0.04*	0.69 ± 0.14*	0.96 ± 0.01*	0.78 ± 0.08*	0.44 ± 0.10	
AIP	0.22 ± 0.18	0.19 ± 0.04*	0.41 ± 0.03*	0.46 ± 0.03*	0.42 ± 0.03*	0.32 ± 0.04*	0.35 ± 0.04*	0.15 ± 0.05*	0.60 ± 0.26*	0.61 ± 0.14*	0.87 ± 0.06*	0.96 ± 0.03*	0.47 ± 0.10

¹BW (13 to 31): BW at corresponding measurement week (13 to 31), HL: body length at harvest (week 31), α : 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 (α), m: shape parameter determining the position of curve inflection point, WIP: weight at inflection point, AIP: age at inflection point, * : $P < 0.05$.

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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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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