Genetic and phenotypic parameters for litter size, survival rate, gestation length, and litter weight traits in American mink¹

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ABSTRACT: The economic efficiency of mink production is greatly influenced by reproductive performance. Therefore, the objective of this study was to estimate phenotypic and genetic parameters for reproduction traits including total number of kits born (TB), number of live kits at birth (LB), number of live kits at weaning (LW), survival rate at birth (SB), survival rate at weaning (SW), gestation length (GL), average kit weight per litter at birth (AWB), average kit weight per litter at week 3 (AW3), and average kit weight per litter at weaning (AWW) in American mink. Data included records of 3,046 litters collected by the Canadian Centre for Fur Animal Research at Dalhousie Faculty of Agriculture between 2002 and 2016. Significance ($P < 0.05$) of fixed effects (year, number of matings, color type, age of dam, origin of dam, sex ratio, and number of live kits) and random effects of permanent environment were determined using univariate repeatability models. A significant effect of permanent environment was only found for survival rate traits ($P < 0.05$). Subsequently, genetic and phenotypic parameters for all traits were estimated by fitting a set of bivariate models using ASREML

4.0. Heritabilities ($\pm$ SE) were estimated to be 0.07 ± 0.03 for TB, 0.07 ± 0.02 for LB, 0.09 ± 0.04 for LW, 0.13 ± 0.03 for SB, 0.10 ± 0.02 for SW, 0.29 ± 0.03 for GL, 0.28 ± 0.05 for AWB, 0.19 ± 0.04 for AW3, and 0.10 ± 0.04 for AWW. Moderate positive genetic correlation was observed between AWB with SB (0.66 ± 0.10) and SW (0.61 ± 0.13). Furthermore, genetic correlations of LB with SW and AWB were 0.55 ± 0.16 and 0.53 ± 0.18 , respectively. On the other hand, negative and moderate genetic correlations were observed between GL and survival rates at birth (-0.43 ± 0.14) and at weaning (-0.37 ± 0.15). These results indicated that selection for higher litter weights at birth can effectively improve survival rate and number of live kits in mink farms. It was suggested to incorporate litter weight traits as a selection criterion to increase maternal ability in mink breeding programs. Unfavorable genetic trends were observed for the studied traits indicating that phenotypic selection with low selection intensity had not been an efficient method to improve them over the last 10 yr. It was recommended to use genetic or genomic evaluation methods for mink selection.

Key words: American mink, genetic correlation, heritability, litter traits, repeatability

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INTRODUCTION

American mink (*Neovison vison*) has been known as one of the most favorite animals in the world's fur industry. The main breeding objectives in mink production have been largely focused on litter size, pelt size, and fur quality traits. Mink is known as a multiparous species and can give birth to a large number of kits in each litter. Litter size at birth and survival rates from birth to weaning are 2 major components of numerical productivity in mink. A higher number of pelted kits per breeding female can effectively improve the total economic output in fur production systems (Lagerkvist, 1997; Gautason, 2017). The newborn kits are blind, very small, furless, and physiologically immature. Hence, maternal abilities such as milk production and feed intake play important roles in survival and early growth rates of kits (Hansen and Berg, 1997). As a composite trait, litter weight at preweaning ages can reflect maternal ability in terms of fertility, early growth, and survival rate of young kits (Milligan et al., 2002; Snowden and Fogarty, 2009). Therefore, selection on these traits could improve profitability by increasing the weight and number of kits pelted per dam in each year. Genetic parameters of litter weights have been extensively studied in other species such as pig (Varona et al., 2007; Pardo et al., 2013), mice (Gutiérrez et al., 2006), sheep (Lôbo et al., 2009), and rabbit (Sorhue et al., 2014). However, there is no information for genetic parameters of litter weight traits in American mink. Estimation of genetic variation and interaction of litter weights with other reproductive performance traits are of significant interest for mink breeders. Therefore, the objectives of this study were 1) to estimate variance components of litter weight, litter size, gestation length (GL), and survival rate traits in American mink and 2) to investigate the phenotypic and genetic correlations among these traits to facilitate multitrait selection in American mink.

MATERIALS AND METHODS

The mink used in this study were cared for according to the Code of Practice for the Care and Handling of Farmed Mink (NFACC, 2013) guidelines.

Data and Management

Data were collected by the Canadian Centre for Fur Animal Research (CCFAR) at Dalhousie Faculty of Agriculture (Truro, Nova Scotia,

Canada) during the period 2002 to 2016. Data included a total of 3,046 litters from 2,314 dams and 632 sires. Number of records per dam was between 1 and 4 with an average of 1.5 repeated records per female. The pedigree file included 18,477 animals (755 founder and 17,722 nonfounder individuals) and was traced through 15 generations. The population size was ranged between 1,039 and 2,454 during the period 2002 to 2016.

Mink were housed under standard farming conditions, and diets were adjusted according to animal requirements in each production period. Each annual cycle of mink reproduction was started by mating between males and females on the beginning of March. Females were moved into the male pens for breeding. If females were mated more than once (up to 3 times), the same males were used for further matings. The second mating was carried out at 9 d after the first one. The whelping season lasted from late April to middle of May. Number of dead kits was recorded at 24 h after birth. Live kits were counted and weighed at 24 h and 3 wk after birth. In addition, kits were counted at week 6 after whelping when they were separated from their dams. Mink were phenotypically selected for pelting or breeding depending on their fur grades, disease history, weight, and litter sizes in November or early December. Animals that were weak and infertile were culled from the herd, and those that had higher BW were selected for breeding. However, a persistent breeding program was not applied for selecting animals during these years (2002 to 2016). For example, selection is mostly based on resistant to Aleutian disease during recent years.

Traits

Total number of kits born (TB), number of live kits at birth (LB), and number of live kits at weaning (LW) were included as litter size traits. Survival rate at birth (SB) was calculated by dividing the number of kits alive at birth by the total number of kits born. The proportion of the number of kits alive at weaning to the number of kits alive at birth was defined as survival rate at weaning (SW). Average kit weight per litter at birth (AWB), week 3 (AW3), and weaning (AWW) were defined as litter weight traits. These values were calculated by dividing the total weight of kits by the number of live kits in each litter at the corresponding ages. Gestation length was defined as the number of days between the last mating and whelping (Hansen et al., 2010b).

Statistical Analyses

Variance components of random additive genetic and permanent environmental effects were primarily estimated using the following univariate repeatability animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wpe} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of phenotypic observations; $\mathbf{b}$ is the vector of fixed effects; $\mathbf{a}$ is the vector of random additive genetic effects of dams; $\mathbf{pe}$ is the vector of random permanent environmental effects; $\mathbf{e}$ is the vector of residual effects; and $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are incidence matrices relating the phenotypic observations to fixed, random additive genetic, and permanent environmental effects, respectively. It was assumed that random effects are independent and normally distributed:

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

where $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{I}$ is the identity matrix, σ_a^2 is the direct additive genetic variance, σ_{pe}^2 is the random permanent environmental variance, and σ_e^2 is the residual variance. Fixed effects were year (2002 to 2016), number of matings (1, 2, and 3 mating per breeding season), color type (11 color types), origin of dam (farms: CCFAR, combo, and donated), age of dam (1, 2, 3, and 4 yr), and sex ratio (the ratio of male to female kits in each litter). In addition, numbers of live kits at birth, week 3, and weaning were included as fixed effects for analyzing the AWB, AW3, and AWW, respectively. Fixed effects were statistically tested using REML procedure in ASREML 4.0 (Gilmour

et al., 2015), and only significant effects ($P < 0.1$) were kept in the subsequent mixed model analyses of each trait (Table 1). Significance of the random permanent environmental effect in each trait was tested by comparing the full model and the reduced model (excluding permanent environmental effect) using the following statistic:

$$\begin{aligned} & -2(\log L_{\text{reduced model}} - \log L_{\text{full model}}) \\ & \sim \chi_{\text{df}(\text{full model}) - \text{df}(\text{reduced model})}^2, \end{aligned}$$

where $\log L$ and df are log likelihood and degrees of freedom in each model, respectively. Permanent environmental effect was only found to be significant ($P < 0.05$) for SB and SW traits.

A set of bivariate models was implemented using ASREML 4.0 (Gilmour et al., 2015) to estimate genetic and phenotypic correlations between traits. Relevant significant fixed effects were included in bivariate analyses for each trait (Table 1). Generally, the following bivariate model was used to analyze traits:

$$\begin{aligned} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} &= \begin{bmatrix} \mathbf{X}_1 & 0 \\ 0 & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{a1} & 0 \\ 0 & \mathbf{Z}_{a2} \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} \\ &+ \begin{bmatrix} \mathbf{Z}_{pe1} & 0 \\ 0 & \mathbf{Z}_{pe2} \end{bmatrix} \begin{bmatrix} \mathbf{pe}_1 \\ \mathbf{pe}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix}, \end{aligned}$$

where $\mathbf{y}_1$ and $\mathbf{y}_2$ are the vectors of observations for the first and second traits; $\mathbf{b}_1$, $\mathbf{b}_2$, $\mathbf{a}_1$, $\mathbf{a}_2$, $\mathbf{pe}_1$, $\mathbf{pe}_2$, $\mathbf{e}_1$, and $\mathbf{e}_2$ are the vectors of fixed, additive genetic, permanent environmental, and residual effects for trait 1 and trait 2, respectively; and $\mathbf{X}_1$, $\mathbf{X}_2$, $\mathbf{Z}_{a1}$, $\mathbf{Z}_{a2}$, $\mathbf{Z}_{pe1}$, and

Table 1. Significance of fixed effects used to estimate genetic parameters for litter size, survival rate, gestation length, and litter weight traits

Traits ¹	Fixed effects						
	Year	Number of matings	Age of dam	Origin of dam	Color type	Number of live kits	Sex ratio
TB	**	*	NS ²	**	*	NT ³	NS
LB	**	NS	**	**	NS	NT	NS
LW	**	**	NS	**	**	NT	NS
SB	**	NS	**	NS	**	NT	NS
SW	**	NS	**	NS	NS	NT	NS
AWB	**	NS	**	NS	*	**	**
AW3	**	NS	**	NS	**	**	**
AWW	**	NS	**	**	**	**	**
GL	**	**	**	NS	**	NT	NS

¹TB = total number of kits born; LB = number of kits alive at birth; LW = number of kits alive at weaning; SB = survival rate at birth; SW = survival rate at weaning; AWB = average kit weight per litter at birth; AW3 = average kit weight per litter at week 3; AWW = average kit weight per litter at weaning; GL = gestation length.

²NS = nonsignificant.

³NT = not tested.

* $P < 0.1$; ** $P < 0.05$.

Z_{pe2} are the incidence matrices relating observations to fixed, random additive genetic, and permanent environmental effects for traits 1 and 2, respectively. The random effect of permanent environment was only included for SB and SW traits. It was assumed that the random effects were normally distributed:

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

$$\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} \sim N \left(0, I \otimes \begin{bmatrix} \sigma_{pe1}^2 & \sigma_{pe1 pe2} \\ \sigma_{pe1 pe2} & \sigma_{pe2}^2 \end{bmatrix} \right), \text{ and}$$

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

where A is the numerator relationship matrix; I is an identity matrix; σ_{a1}^2 , σ_{a2}^2 , σ_{pe1}^2 , σ_{pe2}^2 , σ_{e1}^2 and σ_{e2}^2 , are variances of random additive genetic, permanent environmental, and residual effects for traits 1 and 2, respectively; $\sigma_{a1 a2}$, $\sigma_{pe1 pe2}$, and $\sigma_{e1 e2}$ are covariances of additive genetic, permanent environmental, and residual effects between traits 1 and 2, respectively.

Phenotypic variance was calculated as $\sigma_P^2 = \sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2$ for SB and SW traits and as $\sigma_P^2 = \sigma_a^2 + \sigma_e^2$ for other traits. Heritability (h^2) and repeatability (r^2) were defined as follows:

$$h^2 = \frac{\sigma_a^2}{\sigma_P^2} \quad \text{and}$$

$$r^2 = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_P^2}.$$

Phenotypic and genetic correlations among traits were calculated using (co)variance components estimated by bivariate models.

In addition, genetic trends were evaluated by regressing the mean of standardized breeding values on birth year for all traits. Breeding values were estimated using the REML procedure in ASREML 4.0 (Gilmour et al., 2015). Estimated breeding values were standardized such that the mean and SD of EBVs for individuals born in 2011 were equal to 100 and 10, respectively (Koivula et al., 2010).

RESULTS AND DISCUSSION

Descriptive Statistics

Genetic and phenotypic parameters for litter size, survival rate, litter weight, and GL traits in American mink were analyzed in this study. Number of records, mean, SD, range, and CV for each trait are presented in Table 2. The highest CV were observed for litter size traits (39.91% to 48.82%). These results implied that there is high potential to improve litter size traits in mink using genetic selection. These CV were similar to the ranges of 36% to 39% reported by Koivula et al. (2010) for litter sizes at week 2 and 39% to 53% reported by Hansen et al. (2010b) for litter sizes from birth to 6 mo.

Compared with other traits, the lowest CV (10.3%) was found for GL. The average number of kits alive at birth (5.77) and survival rate at birth (87.94%) decreased to 5.12 and 78.40% at weaning age, respectively. The average kit weight per litter at birth (12.09 g) increased to 130.2 and 371.53 g at week 3 and weaning, respectively.

Permanent Environmental Effects

The univariate estimates of variance components, heritability, proportion of permanent environmental effect (c_{pe}^2), and repeatability for each

Table 2. Descriptive statistics for litter size, survival rate, litter weight, and gestation length traits in American mink

Traits ¹	Number of records	Mean	SD	Range	CV (%)
TB	3,041	6.69	2.67	1 to 17	39.91
LB	3,046	5.77	2.49	0 to 14	43.15
LW	2,722	5.12	2.50	0 to 14	48.82
SB (%)	2,804	87.94	19.71	0 to 100	22.41
SW (%)	2,481	78.40	24.90	0 to 100	31.76
AWB (g)	2,447	12.09	2.29	5 to 23	18.94
AW3 (g)	2,442	130.20	19.85	56 to 197	15.24
AWW (g)	2,437	371.53	65.61	118 to 586	17.65
GL (d)	2,144	46.60	4.80	39 to 75	10.30

¹TB = total number of kits born; LB = number of kits alive at birth; LW = number of kits alive at weaning; SB = survival rate at birth; SW = survival rate at weaning; AWB = average kit weight per litter at birth; AW3 = average kit weight per litter at week 3; AWW = average kit weight per litter at weaning; GL = gestation length.

trait are presented in Table 3. The proportion of variance of permanent environmental effects was not significant ($P > 0.05$) for LB (0.00 ± 0.01) and LW (0.00 ± 0.01) in this study. Koivula et al. (2009) did not observe any significant effect of permanent environment on litter size traits in mink, which were in agreement with our results. On the contrary, higher proportions of permanent environmental effects (0.06 to 0.12) were reported by Gautason (2013) for litter size traits in American mink. This discrepancy might be due to the variability of feed quality in Icelandic mink farms that was not considered in their statistical model. Only for SW trait, variance component of permanent environment (50.18) was found to be larger than the additive genetic component (49.07). The highest proportions of permanent environmental variation ($\pm$ SE) were estimated for SB (0.10 ± 0.05) and SW (0.09 ± 0.04) traits. Log-likelihood ratio test confirmed that fitting models for survival rate traits were significantly ($P < 0.05$) improved by including permanent environmental effect in the models. However, significant effect ($P < 0.05$) of permanent environment was not observed for the other studied traits (Table 3). In contrast to our results, Hansen et al. (2010b) did not observe significant effect ($P < 0.05$) of permanent environment on survival rate traits in American mink. This disagreement can be somewhat attributed to different random and fixed effects used in their study compared with our study. However, similar significant ($P < 0.05$) proportions of permanent environmental effect were observed by Su et al. (2007) for piglet survival traits (0.07 to 0.08) in Landrace and Yorkshire breeds. Hatcher et al.

(2010) also reported similar permanent environmental effects (0.06 to 0.09) for lamb survival rates from birth to weaning in Australian Merino sheep.

For litter weight traits, c_{pe}^2 ranged from 0.02 to 0.04 and were not significantly different from zero ($P > 0.05$). Similarly, Hansen and Berg (1997) showed that permanent environmental component had a small effect on BW (0.00 to 0.10) and weight gain (0.00 to 0.06) during the suckling period of mink. Our findings revealed that permanent environmental effect is an important determinant of repeatability for survival rate traits. The repeatability rate is a measure to predict probable response to selection in the current generation. The estimated repeatabilities ($\pm$ SE) for SB and SW were 0.23 ± 0.04 and 0.17 ± 0.04 , respectively, indicating that survival rates of current generation can be improved by culling dams with low maternal ability from the breeding stock.

Heritability Estimations

Bivariate estimations of heritability ($\pm$ SE) for all analyzed traits are presented in Table 4 (diagonal elements). These values were similar to those obtained by univariate analyses. Minor differences between these estimates can be due to the missing records for some traits and the absence of permanent environmental component in bivariate analyses for most of the traits. Low heritabilities ($\pm$ SE) were estimated for TB (0.07 ± 0.03), LB (0.07 ± 0.02), LW (0.09 ± 0.04), SB (0.13 ± 0.03), SW (0.10 ± 0.02), AW3 (0.19 ± 0.04), and AWW (0.10 ± 0.04) traits. Moderate heritability estimates

Table 3. Variance components and genetic parameter estimates for litter traits in American mink

Traits ¹	Variance components ²			Genetic parameters ³		
	$\sigma_a^2 \pm$ SE	$\sigma_{pe}^2 \pm$ SE	$\sigma_e^2 \pm$ SE	$h^2 \pm$ SE	$c_{pe}^2 \pm$ SE	$r^2 \pm$ SE
TB	0.40 ± 0.16	0.22 ± 0.28	5.73 ± 0.29	$0.06 \pm 0.02^*$	0.03 ± 0.04	$0.09 \pm 0.04^*$
LB	0.35 ± 0.18	0.00 ± 0.01	4.10 ± 0.23	$0.08 \pm 0.04^*$	0.00 ± 0.01	$0.08 \pm 0.04^*$
LW	0.41 ± 0.13	0.00 ± 0.01	4.41 ± 0.16	$0.08 \pm 0.02^*$	0.00 ± 0.01	$0.08 \pm 0.02^*$
SB	45.16 ± 12.72	36.25 ± 17.94	278.12 ± 16.05	$0.13 \pm 0.03^*$	$0.10 \pm 0.05^*$	$0.23 \pm 0.04^*$
SW	49.07 ± 18.94	50.18 ± 20.79	491.85 ± 29.03	$0.08 \pm 0.03^*$	$0.09 \pm 0.04^*$	$0.17 \pm 0.04^*$
AWB	0.95 ± 0.24	0.14 ± 0.27	2.39 ± 0.22	$0.27 \pm 0.06^*$	0.04 ± 0.07	$0.31 \pm 0.06^*$
AW3	50.99 ± 16.45	9.50 ± 22.10	232.61 ± 19.86	$0.17 \pm 0.05^*$	0.03 ± 0.07	$0.20 \pm 0.06^*$
AWW	377.74 ± 179.02	58.69 ± 266.80	2937 ± 251	$0.11 \pm 0.05^*$	0.02 ± 0.08	0.13 ± 0.07
GL	4.82 ± 0.92	0.29 ± 1.01	11.93 ± 0.82	$0.28 \pm 0.04^*$	0.02 ± 0.05	$0.30 \pm 0.04^*$

¹TB = total number of kits born; LB = number of kits alive at birth; LW = number of kits alive at weaning; SB = survival rate at birth; SW = survival rate at weaning; AWW = average kit weight per litter at weaning; AW3 = average kit weight per litter at week 3; AWW = average kit weight per litter at weaning; GL = gestation length.

² σ_a^2 = additive genetic variance; σ_{pe}^2 = permanent environmental variance; σ_e^2 = residual variance.

³ h^2 = heritability; c_{pe}^2 = proportion of permanent environmental effect; r^2 = repeatability.

* $P < 0.05$.

Table 4. Estimates of heritabilities (diagonal), phenotypic correlations (below diagonal), genetic correlations (above diagonal), and their SE among litter size, survival rate, gestation length, and litter weight traits

Traits ¹	TB	LB	LW	SB	SW	AWB	AW3	AWW	GL
TB	0.07 ± 0.03*	0.78 ± 0.08*	0.57 ± 0.15*	-0.13 ± 0.18	-0.29 ± 0.23	-0.08 ± 0.24	0.08 ± 0.23	0.02 ± 0.31	-0.10 ± 0.16
LB	0.84 ± 0.01*	0.07 ± 0.02*	0.92 ± 0.04*	0.27 ± 0.06*	0.55 ± 0.16*	0.53 ± 0.18*	0.03 ± 0.22	-0.01 ± 0.29	-0.29 ± 0.16
LW	0.71 ± 0.01*	0.89 ± 0.01*	0.09 ± 0.04*	0.39 ± 0.17*	0.44 ± 0.19*	0.58 ± 0.15*	0.17 ± 0.21	-0.18 ± 0.09*	-0.26 ± 0.14
SB	-0.12 ± 0.01*	0.34 ± 0.02*	0.34 ± 0.01*	0.13 ± 0.03*	0.94 ± 0.04*	0.66 ± 0.10*	0.43 ± 0.15*	-0.02 ± 0.22	-0.43 ± 0.14*
SW	-0.13 ± 0.02*	0.25 ± 0.02*	0.52 ± 0.01*	0.73 ± 0.09*	0.10 ± 0.02*	0.61 ± 0.13*	0.12 ± 0.09	-0.26 ± 0.26	-0.37 ± 0.15*
AWB	-0.43 ± 0.02*	0.12 ± 0.03*	0.15 ± 0.03*	0.34 ± 0.02*	0.29 ± 0.02*	0.28 ± 0.05*	0.78 ± 0.10*	0.73 ± 0.17*	0.33 ± 0.14*
AW3	-0.19 ± 0.11	-0.19 ± 0.03*	-0.04 ± 0.03	0.20 ± 0.03*	0.13 ± 0.09	0.44 ± 0.02*	0.19 ± 0.04*	0.61 ± 0.16*	0.15 ± 0.13
AWW	-0.12 ± 0.08	-0.11 ± 0.03*	-0.02 ± 0.03	0.09 ± 0.03*	0.01 ± 0.03	0.33 ± 0.03*	0.64 ± 0.02*	0.10 ± 0.04*	0.07 ± 0.18
GL	-0.23 ± 0.02*	-0.22 ± 0.02*	-0.19 ± 0.02*	-0.30 ± 0.02*	-0.15 ± 0.02*	0.21 ± 0.03*	0.14 ± 0.03*	0.09 ± 0.03*	0.29 ± 0.03*

¹TB = total number of kits born; LB = number of kits alive at birth; LW = number of kits alive at weaning; SB = survival rate at birth; SW = survival rate at weaning; AWB = average kit weight per litter at birth; AW3 = average kit weight per litter at week 3; AWW = average kit weight per litter at weaning; GL = gestation length.

* $P < 0.05$.

(± SE) were only obtained for GL (0.29 ± 0.03) and AWB (0.28 ± 0.05) among studied traits.

The heritabilities previously reported for the number of kits born alive were in the range of 0.06 to 0.15 (Hansen et al., 2010a,b; Thirstrup et al., 2014), which corresponded with the results of current study (0.07 to 0.09). Low heritability estimates for litter size traits in the present study (0.07 to 0.09) were also in agreement with previous reports for litter size at weaning (0.03 to 0.06) by Hansen et al. (2010b), litter size at week 2 after whelping (0.11 to 0.15) by Koivula et al. (2009, 2010, 2011), and litter size at week 3 after whelping (0.03 to 0.06) by Gautason (2013) in American mink. The estimated heritability for TB in this study (0.07 ± 0.03) was higher than the estimates of 0.02 and 0.01 reported by Hansen et al. (2010b) and Kołodziejczyk and Socha (2011), respectively. This inconsistency may be due to differences in model components, sample sizes, and environmental effects. However, similar heritability (0.09 ± 0.05) was estimated for total number of kits born by Lagerkvist et al. (1994) in a study of correlated response to selection for litter size traits in mink. Although litter sizes at different ages have been known as lowly heritable traits in American mink, there are some evidences for improving these traits through genetic selection (Lagerkvist et al., 1994; Koivula et al., 2011; Kołodziejczyk and Socha, 2011). However, due to the negative genetic correlations between reproductive traits and other economically important traits such as BW (Hansen et al., 2010b) and animal size (Koivula et al., 2010), genetic correlations among traits must be incorporated into future multitrait selection indices to increase the response to selection.

In the current study, heritability estimates (± SE) for SB and SW traits were equal to 0.13 ± 0.03

and 0.10 ± 0.02 , respectively. Hansen et al. (2010b) reported similar estimates for SB (0.14 to 0.18) and SW (0.07 to 0.1) in American mink. However, a wide range of heritability estimates were observed for survival rates in other species such as the heritability estimates of 0.01 to 0.24 by Su et al. (2007) and Roehe et al. (2009, 2010) in pig, 0.01 to 0.09 by Hatcher et al. (2010) and Vatankhah (2013) in sheep, 0.06 to 0.15 by Goyache et al. (2003) in cattle, and 0.03 to 0.07 by Gagliardi et al. (2010) in rhesus macaques.

The heritability estimates (± SE) for AWB, AW3, and AWW were 0.28 ± 0.05 , 0.19 ± 0.04 , and 0.10 ± 0.04 , respectively. To our knowledge, no heritability estimates for litter weight traits in American mink were previously reported, and this would be worth further investigation. However, the estimated heritability of AWB (0.28 ± 0.05) in the present study was in the range of estimates (0.19 to 0.39) reported by David et al. (2017) in the study of the relationship between birth weight and litter size in rabbits and pigs. Our result was also in accordance with the report (0.29 ± 0.07) by Ajayi and Akinokun (2013) for Nigerian indigenous pigs. In addition, Putz et al. (2015) estimated similar heritabilities in Large White (0.24 ± 0.02) and Landrace (0.26 ± 0.02) breeds for average weight of piglets at birth. On the other hand, lower heritabilities were reported for AWB by Ferraz and Eler (2000) in rabbit (0.06 to 0.12), by Gutiérrez et al. (2006) in mice (0.11 to 0.13), by Costa et al. (2016) in pig (0.09), and by Lôbo et al. (2009) in sheep (0.15). These discrepancies may result from differences in the genetic backgrounds, sample sizes, and statistical models. In addition, the estimated heritability for AW3 in the present study (0.19 ± 0.04) was in agreement with the reports of 0.22 ± 0.05 by Lundgren et al. (2014) for Landrace sows and 0.16 ± 0.02 by Fernández et al.

(2008) for Iberian pigs. On the other hand, the estimated heritability obtained for AW3 in the current study (0.19 ± 0.04) was higher than the estimates of 0.07 to 0.09 and 0.05 observed by Chen et al. (2003) and Costa et al. (2016) in pigs, respectively. This discordance may result from difference in genetic backgrounds, breeding designs, and statistical methods. The estimation of heritability for AWW in this study (0.10 ± 0.04) corresponded to estimates of 0.11 and 0.13 obtained by Lôbo et al. (2009) and Vatankhah et al. (2008) in sheep, respectively.

The estimated heritability of GL in the present study was 0.29 ± 0.03 . Hansen et al. (2010b) obtained a slightly higher heritability (0.37) for this trait in American mink, which might be due to the difference in environmental conditions, selection schemes, and adjustment of fixed effects. On the other hand, lower heritability (0.17) was obtained by Kołodziejczyk and Socha (2011) for this trait in American mink. Inconsistency of heritability estimations among various studies can be attributed to several factors affecting the genetic parameter estimations including statistical models, breeding structure, pedigree completeness, sample size, trait definition, and purity of breeds (Miar et al., 2014a,b).

Genetic Correlations between Survival Rate and Litter Size Traits

The phenotypic and genetic correlations between survival rate and litter size traits are presented in Table 4. A strong positive genetic correlation was observed between LB and TB (0.78 ± 0.08). Hansen et al. (2010b) observed high positive genetic correlation between number of kits alive at birth and total number of kits born in American mink ($r_g = 0.56$), which was in agreement with our estimate. Our findings indicated a high positive genetic correlation between LW and TB (0.57 ± 0.15), which was in agreement with the study (0.68) conducted by Kołodziejczyk and Socha (2011). Moreover, a high positive genetic correlation (0.92 ± 0.04) was observed between LB and LW. This was in accordance with those obtained in mink (0.91) by Kołodziejczyk and Socha (2011) and in Arctic fox (0.95) by Wierzbicki and Jagusiak (2006).

Total number of kits born had low phenotypic correlations with SB (-0.12 ± 0.01) and SW (-0.13 ± 0.02). However, the genetic correlations of TB with SB (-0.13 ± 0.18) and SW (-0.29 ± 0.23) were not significant ($P > 0.05$). These results revealed that higher number of kits born increases the risk of mortality for kits in the first 24 h after whelping, which can be mainly due to environmental effects. Higher competition among kits and increased risk of

being crushed by dam are caused by higher number of born kits and can subsequently reduce survival rate in mink kits (Martino and Villar, 1990). Lagerkvist et al. (1994) estimated a low genetic correlation (0.14) between total number of kits born and kit mortality at week 3 in mink. However, this low estimate can be due to adjusting the mortality rate for number of live born kits in their study. Moreover, Schou and Malmkvist (2017) indicated that total number of kits born was positively correlated with higher risks of kit death and reduced growth rate in farmed mink ($P < 0.001$). In addition, studies on commercial pig breeds indicated that despite the considerable genetic improvement obtained for litter size at birth during the past decades, preweaning piglet mortality has been relatively high (Su et al., 2007; Hellbrügge et al., 2008). These results strongly suggest that number of kits alive at weaning can be considered as a more applicable criterion to improve litter size traits in farmed mink. It should be pointed out that total number of kits born includes both number of dead kits and number of live kits at the first 24 h after whelping. Therefore, genetic correlations of TB with other traits could be influenced by this element.

Number of kits alive at birth was positively genetically correlated with SB (0.27 ± 0.06) and SW (0.55 ± 0.16). As expected, high genetic correlation was observed between SB and SW (0.94 ± 0.04). These results revealed that selecting for higher survival rate at weaning can greatly improve the litter sizes in mink farming. Hansen et al. (2010b) observed no significant ($P > 0.05$) genetic correlation between survival rate at weaning and number of live born kits (-0.04 ± 0.24) using a model including additive genetic effects of dams and sires. However, they reported positive significant genetic correlations between number of live born kits with survival rate at day 7 (0.42) and between number of weaned kits with survival rate at 6 mo (0.65). Schou and Malmkvist (2017) indicated that total number of living kits was significantly ($P < 0.001$) negatively associated with kits mortality rates (slope = -0.25), whereas the total number of born kits had a significant ($P < 0.001$) positive influence on kit mortality rates (slope = 0.24) in farmed mink. Furthermore, Lagerkvist et al. (1994) observed that selection for litter size at week 3 resulted in a reduced genetic trend for kit mortality in mink, which was in agreement with our results.

Genetic Correlations of Litter Weight Traits with Survival Rate and Litter Size

Significant positive genetic correlation ($P < 0.05$) was observed between LB and AWB (0.53 ± 0.18). Interestingly, there were strong positive genetic

correlations between AWB with SB (0.66 ± 0.10) and SW (0.61 ± 0.13). These results indicated that higher birth weight of mink kits is correlated with higher preweaning survival rates. In addition, a positive genetic correlation (0.43 ± 0.15) was observed between SB and AW3. [Schneider and Hunter \(1993\)](#) investigated the major causes of preweaning mortality in mink kits. The mortality rate from birth to weaning was equal to 20% in their study, and 91% of losses occurred within the first 3 d after birth. They confirmed that the average birth weight of healthy kits (10.7 g) was significantly ($P < 0.05$) higher than the average weight of dead kits (7.9 g) at 24 h after whelping. The main cause of neonatal mortality in mink kits was due to physiological and physical underdevelopment. Moreover, BW can also influence the thermoregulatory capacity of kits within 25 to 35 d after birth. Hypothermia is more likely in kits having lower BW ([Harjunpää and Rouvinen-Watt, 2004](#)). Similarly, birth weight has been known as an important factor influencing preweaning survival rates in pigs ([Arango et al., 2006](#)). Higher litter weight at birth was positively correlated with higher piglet survival rates until weaning ([Fix et al., 2010](#); [Ferrari et al., 2014](#)). To our knowledge, genetic correlations between litter weight traits and other economically important traits were not previously investigated in American mink and would be worth further investigation. However, similar genetic correlations of 0.67 and 0.64 were observed between litter weight at birth and number of kits born alive in rabbit ([Odubute and Somade, 1992](#)) and pigs ([Dube et al., 2012](#)), respectively. Average kit weight per litter at weaning had a low negative genetic correlation with LW (-0.18 ± 0.09). No significant genetic correlation ($P > 0.05$) was observed between AWW with SB (-0.02 ± 0.22) and SW (-0.26 ± 0.26) in the present study. These results confirmed the decreasing effect of BW on survival rate from week 3 to weaning.

In spite of nonsignificant ($P > 0.05$) genetic correlation between TB and AWB (-0.08 ± 0.24), their phenotypic correlation was significant ($P < 0.05$) in the present study (-0.43 ± 0.02) indicating that environmental effects play an important role in the interaction between litter size and prenatal weight of kits. For example, intrauterine competition for nutrients has been known as the major reason for lower birth weight in mink kits ([Schneider and Hunter, 1993](#)). Antagonistic relationship between average birth weight and increasing litter sizes has also been demonstrated in other multiparous species such as rabbits ([Castellini et al., 2010](#)), pigs ([Pardo et al., 2013](#)), and mice ([Reading, 1966](#); [van Engelen et al., 1995](#)). In addition, dystocia, suffocation, and

crushing by the dam reduce total number of kits born alive in mink. However, underdeveloped kits are more susceptible to these environmental factors ([Schneider and Hunter, 1993](#)). The negative phenotypic correlation obtained between SB and TB (-0.12 ± 0.01) in the present study can be partly explained by these findings.

Genetic Correlations between GL and Other Traits

The genetic correlations of GL with LB (-0.29 ± 0.16) and LW (-0.26 ± 0.14) were not significant ($P > 0.05$) in the present study. [Hansen et al. \(2010b\)](#) reported no significant genetic correlation ($P > 0.05$) between litter sizes and GL in American mink, which is in agreement with our results. Similar genetic correlation (-0.17 to -0.27) was estimated between GL and litter size traits in Arctic fox ([Wierzbicki and Jagusiak, 2006](#)). Gestation length had moderate negative genetic correlations with SB (-0.43 ± 0.14) and SW (-0.37 ± 0.15) in the present study. These results indicated that prolonged GL had unfavorable effects on survival rates in American mink. Variability of GL has been known as one of the most remarkable characteristics in mink reproduction. This variability is mainly the consequence of delayed implantation during the mating season ([Dukelow, 1966](#)). [Murphy et al. \(1983\)](#) demonstrated that longer delayed implantation periods can increase embryonic losses in farmed mink. Our results indicated that genetic selection for reduced GL could improve genetic progress of survival rate traits in farmed mink. In addition, management techniques such as a more limited period of mating, for example moving the mating date to the end of March, can be applied to shorten the GL in mink ([Bowness, 1968](#)). [Hansen et al. \(2010b\)](#) did not find any significant ($P > 0.05$) genetic correlation between survival rates and GL in American mink. This inconsistency can be due to differences in their sample size, breeding structure, and statistical models compared with our study.

Genetic Trends

Genetic trends for the studied traits from 2006 to 2016 are presented in [Fig. 1](#). Similar genetic trends were observed for survival rates at birth and at weaning ([Fig. 1a](#)). Although the mean of breeding values tended to increase in the first 4 yr (until 2009), there was no considerable improvement in survival rate traits after 2009. A negative genetic trend was observed for these traits in 2014. This decline can be due to prevalence of Aleutian disease in the studied population. Genetic trends of litter weight

Figure 1. Genetic trends for studied traits in American mink: (a) survival rates including survival rate at birth (SB) and survival rate at weaning (SW); (b) litter weights including average kit weight per litter at birth (AWB), average kit weight per litter at week 3 (AW3) and average kit weight per litter at weaning (AWW); (c) gestation length (GL); and (d) litter sizes including total number of kits born (TB), number of kits alive at birth (LB), and number of kits alive at weaning (LW).

traits were similar to survival traits but with lower fluctuations during this timeframe (Fig. 1b). No genetic progress was observed for these traits in this timeframe. However, there were minor fluctuations in the genetic trends of GL (Fig. 1c). Litter sizes at birth and at weaning had similar genetic trends (Fig. 1d) probably due to high positive genetic correlation (0.92 ± 0.04) between these 2 traits. These results might be due to low selection intensity for reproductive traits (on average 0.96 on females) during this timeframe. In addition, the proportion of mink kept as breeders was not stable over the different years (23% to 55% for females and 7% to 18% for males). Lack of systematic breeding program led to changing selection criteria in different years. For example, resistance to Aleutian disease has been the main breeding objective during recent years. On the other hand, phenotypic selection in this mink farm did not effectively improve genetic gains for reproductive traits during the studied period. Phenotypic selection is relatively ineffective for reproductive traits due to their low heritabilities (Koivula et al., 2011). Kołodziejczyk and Socha (2011) observed a decreasing genetic trend for number of reared kits in American mink. This

unfavorable trend was attributed to ineffectiveness of phenotypic selection for lowly heritable traits of reproduction. Although there are several emerging breeding programs based on genetic evaluations in some countries such as Denmark and Finland, lack of systematic breeding programs is one of the most important challenges in the mink production system and most farmers select animals based on their phenotypic characteristics (Lagerkvist et al., 1994; Kołodziejczyk and Socha, 2011; Gautason, 2017). Additive genetic values must be considered as the main criterion in mink breeding programs to improve the genetic gain of economically important traits. Therefore, collection of phenotypic data on economic traits and considering the appropriate breeding designs are 2 major steps to evaluate the genetic merit of animals in mink farms.

Effectiveness of mink production is greatly influenced by reproductive performance. The low-to-moderate estimated heritability for reproductive performances in this study indicated that improvement of these traits will be possible through genetic and genomic breeding programs. Our results revealed that selection for higher total number of kits born can result in an increased rate of kit mortality after

birth. Accordingly, it is recommended that number of kits weaned be used as a better criterion for selecting dams to increase the reproductive performance of mink breeding programs. Furthermore, the selection objectives in mink breeding programs should include traits related to the maternal ability of dams. It was concluded that permanent environmental effects should be considered to improve survival rate traits in farmed mink. In addition, litter weight can be included in mink breeding programs to increase the maternal ability. These results imply that selection for higher litter weights at birth can effectively improve survival rates and number of live kits in mink farms. Estimation of genetic and phenotypic parameters for litter weight traits in the current study provides a new contribution to the knowledge of mink breeders. The estimated genetic correlations in the present study can be incorporated into multitrait selection indices providing opportunities to improve reproductive performance in mink breeding programs.

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