Enhancing Production and Aleutian Disease Resilience in Mink Through Advanced Genomics

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MOTIVATION

The fur industry has used American mink (*Neovison vison*) as the major source of fur for decades. **Feed efficiency**, **reproduction**, **growth** rates, **fur quality**, and skin **size** are the most important traits in most mink breeding programs according to the mink industry priorities. Additionally, **Aleutian disease (AD)** caused by the Aleutian mink disease virus, is the most economically significant disease impacting mink production in Canada and worldwide (1). Although this disease has no vaccine or treatment, genetic variation in AD resilience exists in mink due to the variability in their immune response to infection. **Genomics** technology provides tremendous opportunities to elucidate the biology of these key traits but the potential of this technology has not yet been investigated in mink.

Figure 1. American mink. Courtesy of *DAVE ELLIS.*

PURPOSE

The goals of this project are to use **genomics** and **bioinformatics** approaches paired with analysis of immunity to advance our understanding of the genetic mechanisms underlying economic traits in mink. This project will seek to:
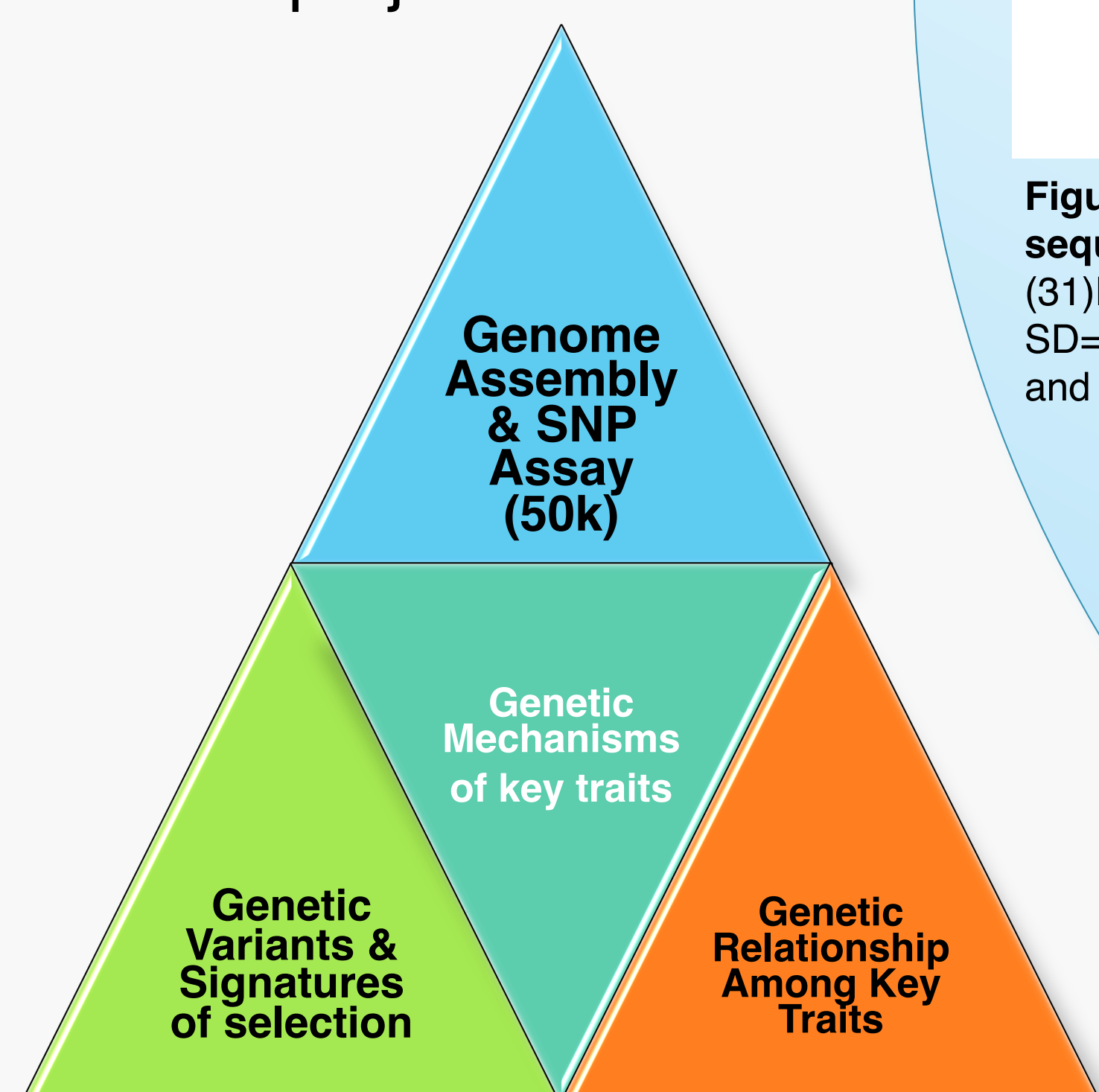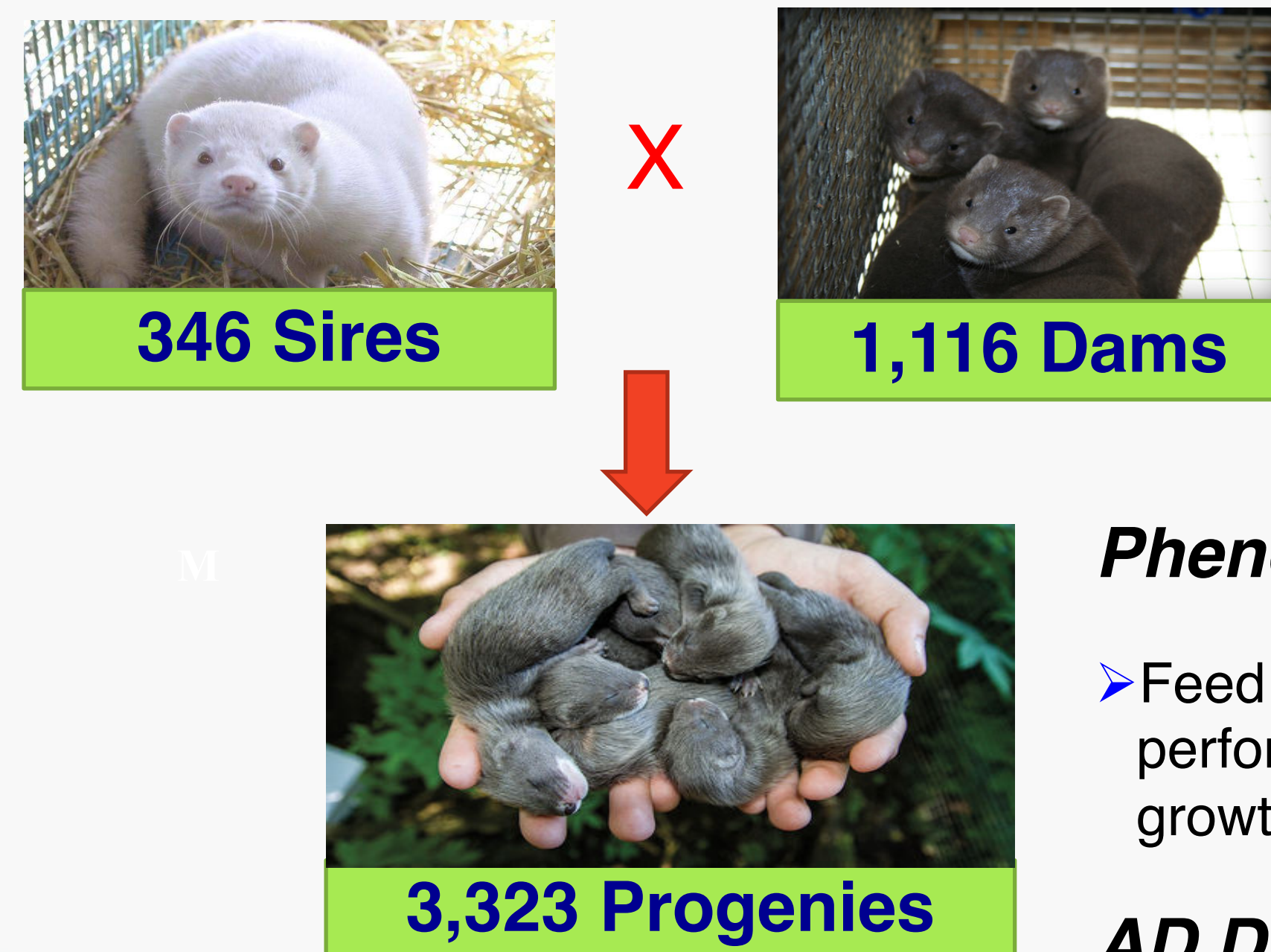

Figure 2. Objectives of this project to understand the genetic mechanisms underlying key traits in mink.

METHODS

Research Design

346 Sires X **1,116 Dams**

3,323 Progenies

Phenotyping

➤ Feed efficiency, reproductive performance, fur quality traits, growth rate and pelt size.

AD Diagnostic Tests

➤ Counter-immunoelectrophoresis (CIEP) and Quantitative enzyme-linked immunosorbent assay (qELISA).

Genomics

➤ De novo assembly of most homozygous individual using PacBio Sequel II, Hi-C, and 10x genomics technologies.

Figure 3. PacBio Sequel II technology for genome assembly.

➤ Development of SNP panel (50k) using NGS data (>30x) of 100 mink from 5 colour-types (50 AD+ and 50 AD-).

➤ Genotyping using 50K panel.

RESULTS & DISCUSSIONS

Table 1. Descriptive statistics of economically important traits in mink.

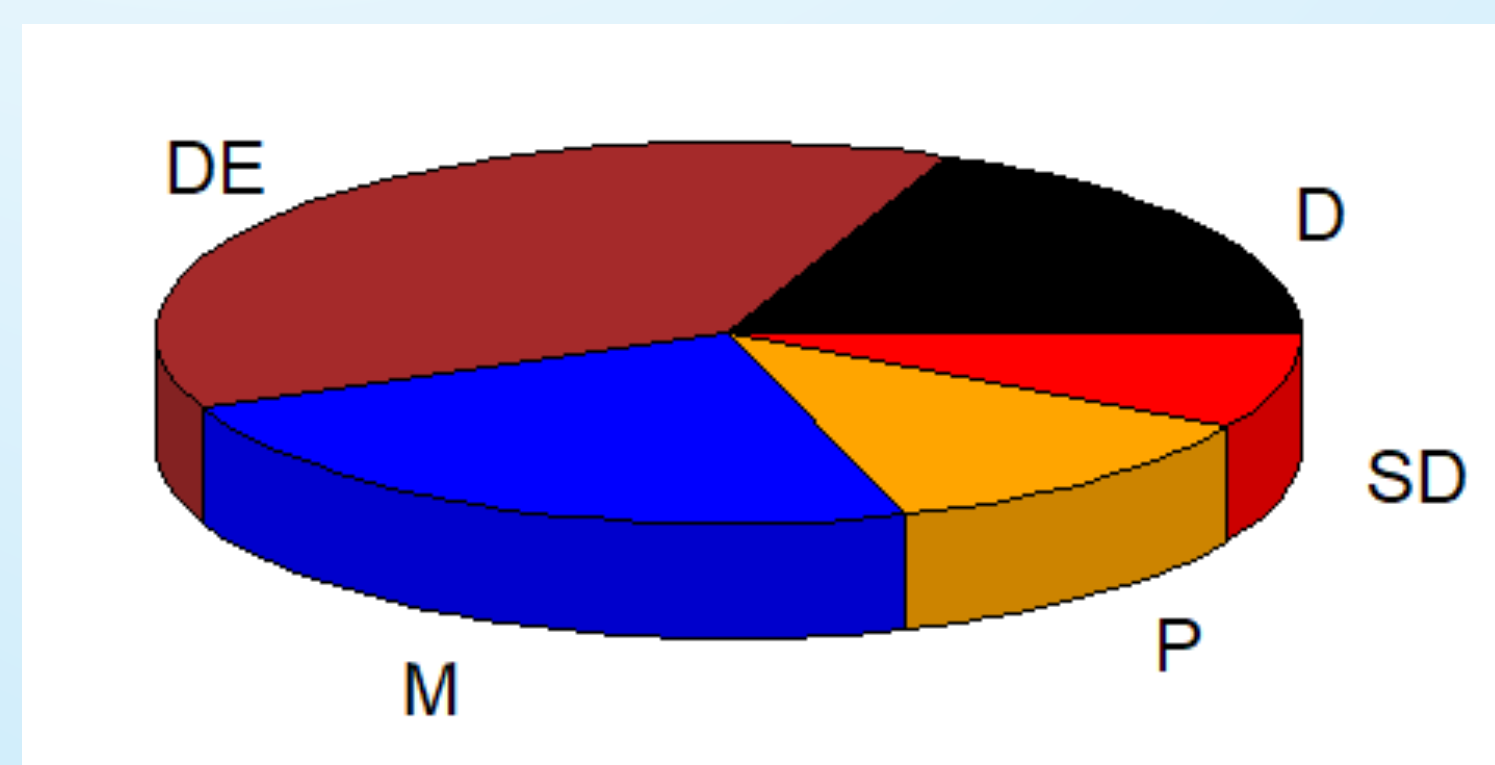| Traits	N	Mean(±SE)	Range
CIEP	1944	0.47±0.01	+(924)/-(1020)
qELISA	2359	0.72±0.01	0-3.74
Harvest body length, cm	2350	45.35±0.10	33-59
Harvest body weight, kg	2352	2.24±0.02	0.9-4.1
Gestation length, d	4190	46.41±0.07	32-75
Total born kits	5326	6.64±0.04	1-17
Number of kits alive after 24h	5326	5.77±0.04	0-14
Number of kits alive after 3 weeks	2731	4.33±0.04	0-10

Figure 4. Selection of 100 mink for whole-genome sequencing (>30x). Five Colour-types of D=Dark (31)DE=Demi (32), M=Mahogany (20), P=Pastel (10), and SD=Stardust (7) were sequenced and 50 of them were AD+ and 50 of them were AD-.
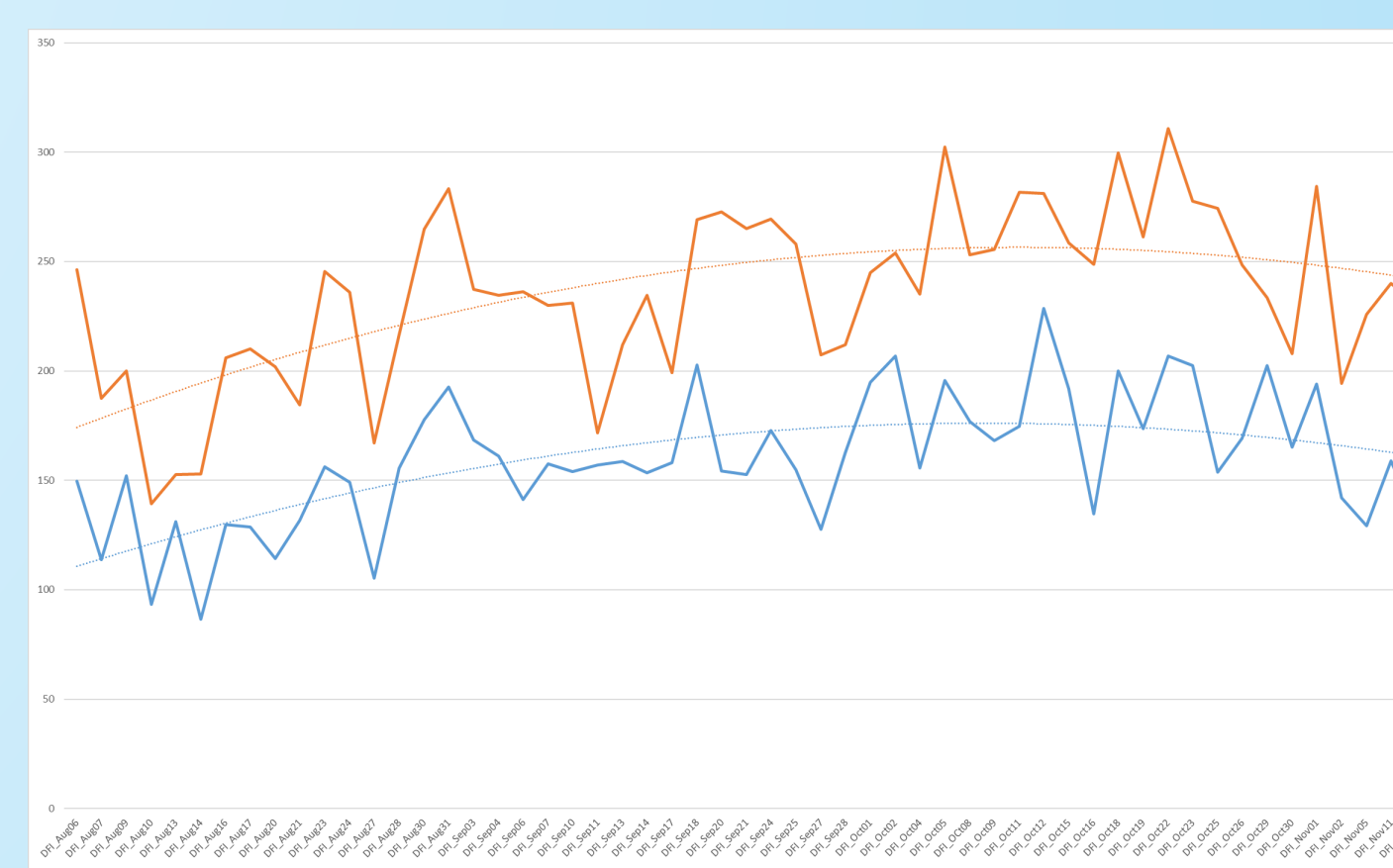

Figure 5. Daily feed intake (g/Day) in mink. Red line shows the feed intake of males and blue lane shows the feed intake of females.

Figure 6. The growth curve of mink based on the best (Richards), and the worst (Brody) model. Red line shows the growth curve of females and blue lane shows the growth curve of males (2).

ANTICIPATED RESULTS

➤ It is anticipated that information gained in this project will contribute novel insights into genetic architecture of economic traits in mink and how this may impact mink health and productivity.

➤ This work will help reduce the costs of AD and increase the production efficiency in the mink industry.
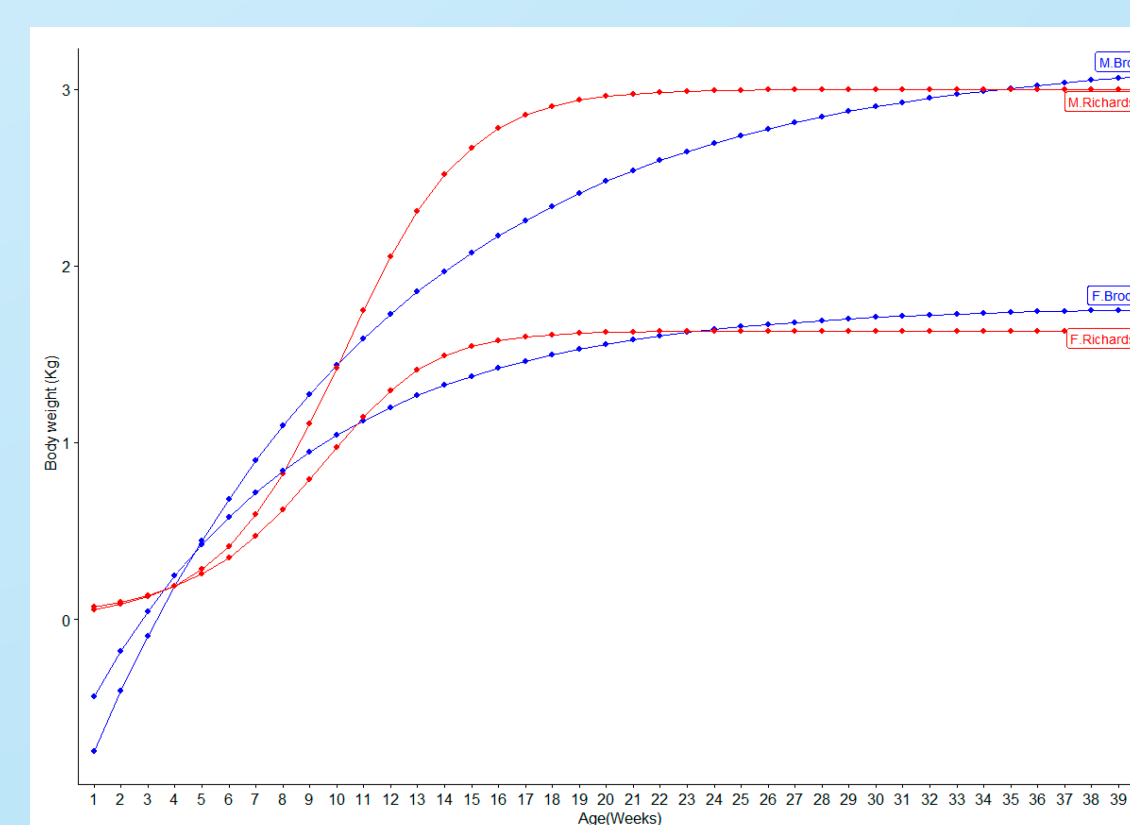
CONCLUSIONS

➤ Sufficient variation is present in all of traits to detect genetic variants related to these traits.

➤ Phenotyping is completed except for dried pelt quality measurements, which will be completed soon. Genotyping using our developed SNP assay will begin soon.

➤ The future genomics analyses will identify QTL regions and genes within these regions associated with key traits in mink. It is hoped that this will lead to tools that will be able to make improvement in mink production and health.

ACKNOWLEDGEMENTS

REFERENCE

1. Bloom, M.E. et al. 1994. Infect. Agents Dis. 3:279-301.
2. Do, D.N & Miar Y. 2020. Animals. 10:22.