

Application of metabolomics on selecting for litter size in American mink

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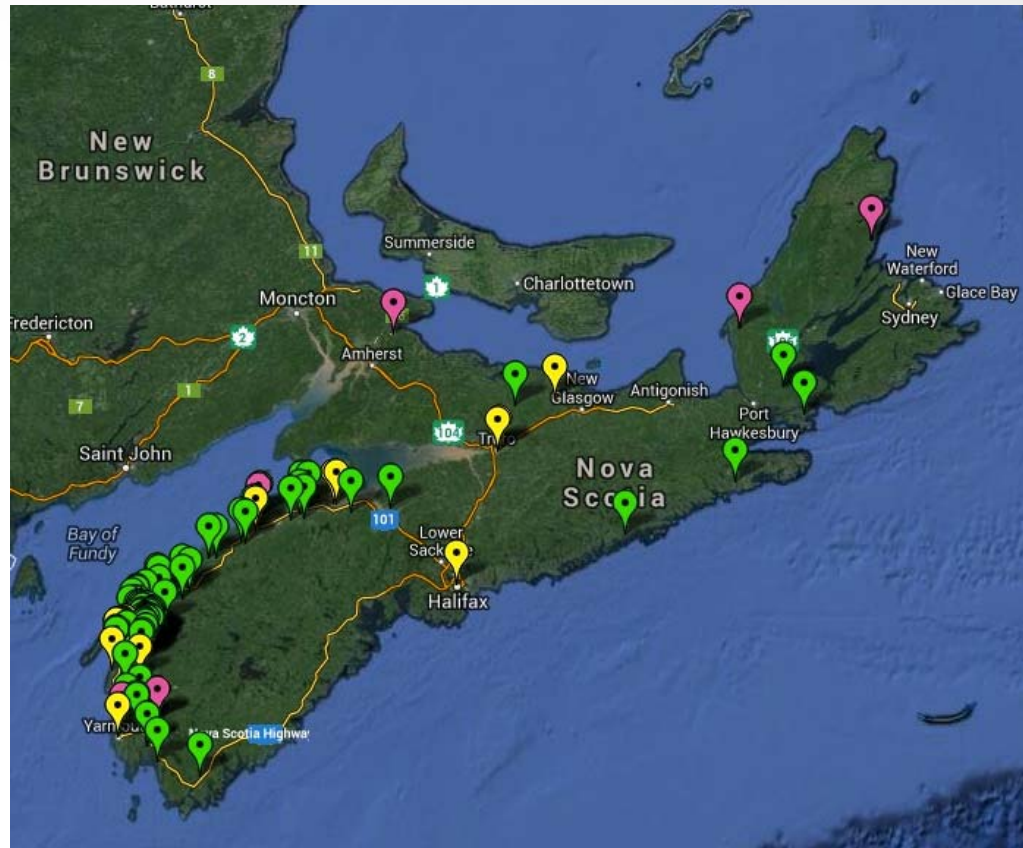
Outline



Application of metabolomics on selecting for litter size in American mink

- Mink Genomics Research Program
- Background
- Mink metabolomics
- Results

Mink Genomics Research Program



Background

- Over 99% of ranch-raised pelts sold in Canada are American mink pelts
- Nova Scotia produces 61.4% of pelts in Canada
- Increasing litter size will produce a higher financial gain than improving any other trait in mink
- This study is one of the first metabolomic studies on mink

Objectives

- To determine metabolites and their association with litter size in mink
- To assess the potential of metabolomics in selecting for economically important traits in mink



Mink Breeding

- Induced ovulators - seasonal breeder
- Gestation ranges from 40-75 days
- Litter size ranges from 0-17 kits
- Litter size heritability of 0.07 ± 0.03

Factors Affecting Litter Size

- Length of gestation
- Nutrition
- Ovulation rate

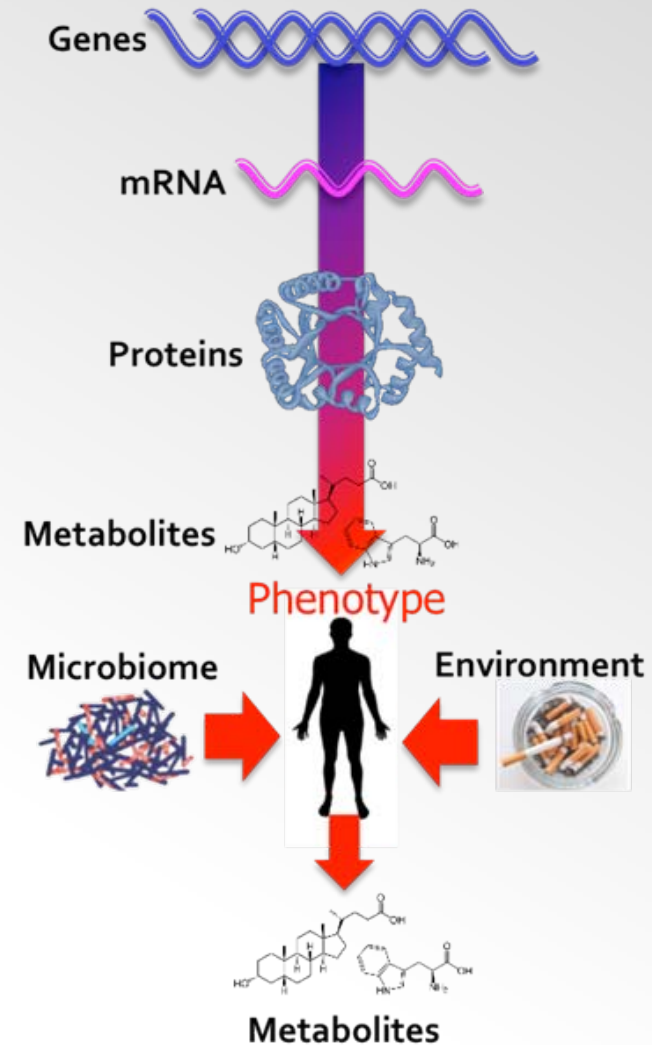


Metabolomics

- The study of metabolites present within an organism, cell or tissue
- Metabolites are substances formed in or necessary for metabolism
- Ability to study the phenotype while taking environmental stresses into account

Previous Research

- Predict desired phenotypes
 - Body mass
 - Growth rates
 - Meat quality
 - Feed intake
- Discover biomarkers for diagnosing diseases
 - Diabetes



Animals

- 21 dams from the Canadian Centre for Fur Animal Research (CCFAR) – Dalhousie AC
 - Age ranges from 2-4 years
- Selected based on the reproductive performance (2016)
 - 11 selected for high litter size (Avg. 9)
 - 10 selected for low litter size (Avg. 0)



Sample Collection

Cut toenail past quick



Collect blood into 5 capillary tubes (~350 μ L)



Centrifuge for 7 minutes



Collect plasma into labelled cryovials (~50 μ L)



Disinfect and freeze in liquid nitrogen



Store at -80 °C until further analyzed at NRC



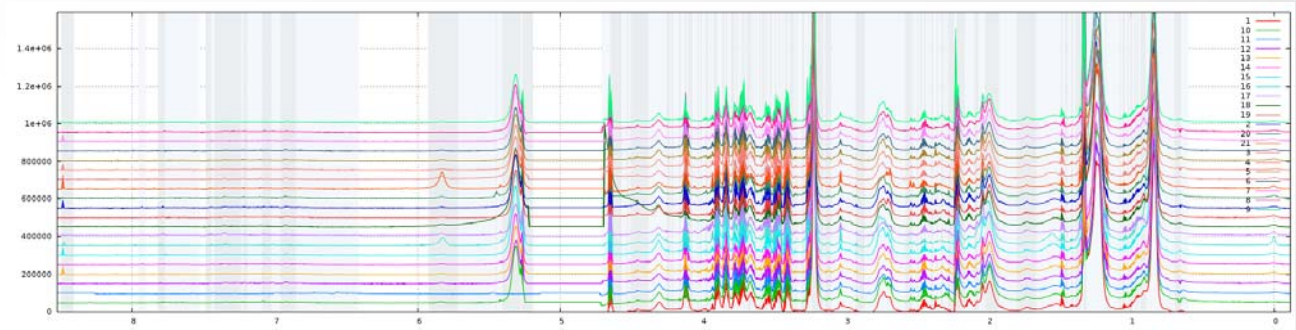
Metabolite Assay Using NMR

- Samples prepared at NRC
 - Dilute samples with D₂O to 10-20%
 - Transfer into 1.7mm NMR tubes



Data Analysis

- NMR spectra imported into NMRProcFlow 1.2
 - Alignment
 - Removal of water signal
 - Intelligent binning

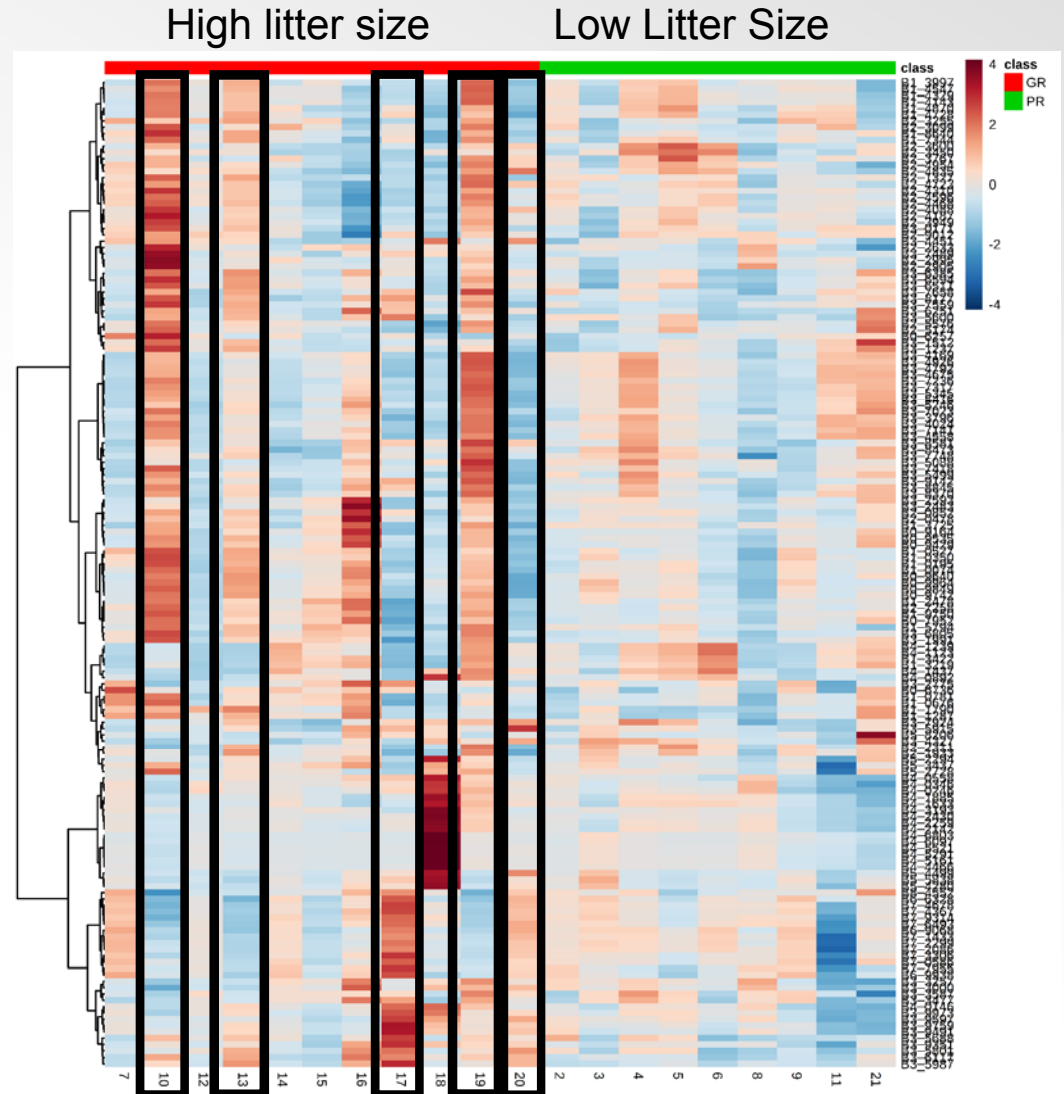


- Binned NMR spectral data then analyzed in MetaboAnalyst 3.0¹
- Principle Component Analysis (PCA) was used to visualize the impact of reproductive performance on plasma metabolic fingerprints

1. Xia, J. and Wishart, D.S. (2016) Current Protocols in Bioinformatics, 55:14.10.1-14

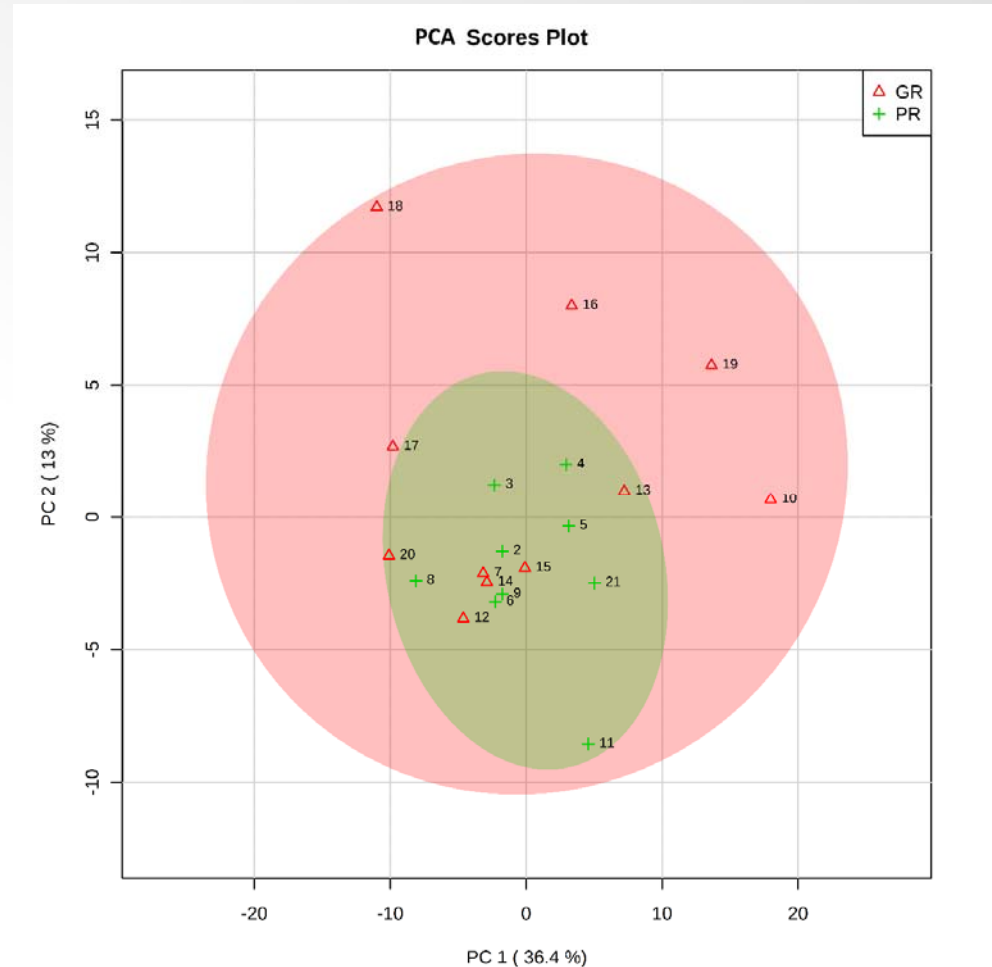
Heatmap

- No obvious separation between groups
- Remarkable variation between individuals
- Individual patterns present
 - Mink 10, 13, 19
 - Mink 17, 20



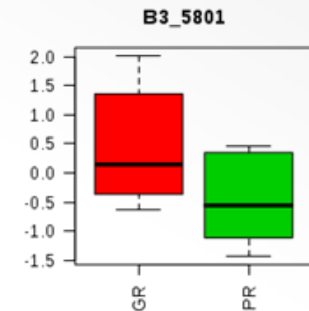
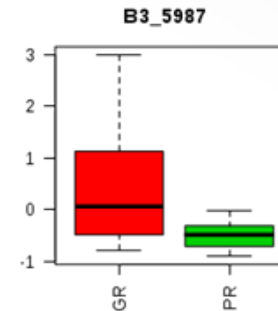
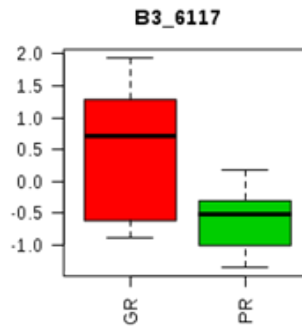
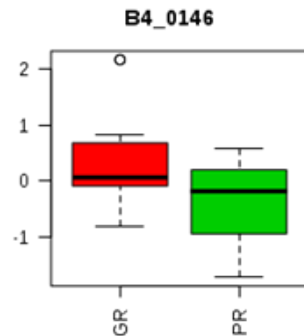
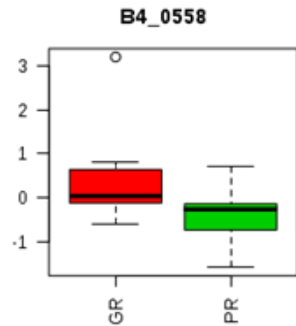
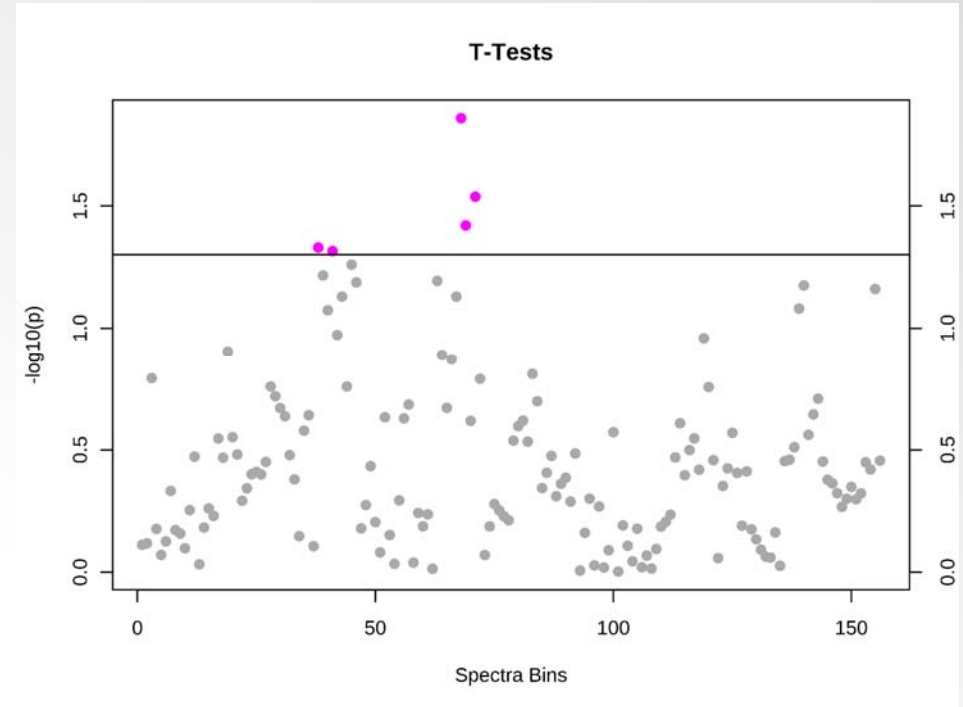
PCA Score Plot

- PC1 and PC2 accounted to 49.4% of the total variation
- Little variation seen within low litter size group
- Plenty of variation within high litter size group



T-test

- Significance level: $P < 0.05$
- Majority of spectral bins not significantly different
- Significant difference seen between 5 bins
 - Greater concentration of metabolite in high litter size group in all 5 spectral bins



Conclusion

- Lack of difference may be due to small sample size
- Next step is to determine the association between the metabolites and litter size
- Cao et al. (2015) found progesterone level to be higher in mink dams with reproductive success
- Results from this study show the good potential for future metabolomic studies in mink
 - Feed conversion
 - Aleutian disease

Acknowledgments



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**DALHOUSIE
UNIVERSITY**

FACULTY OF AGRICULTURE



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Graduate Student Positions – Mink Genomics

