Milk metabolites and their genetic variability

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Motivation

- Decomposition of milk into its metabolic components
  - assess energy status of cow
  - explore metabolic (production) diseases (e.g. ketosis, milk fever etc.)
  - study heritability and mode of inheritance of novel milk traits

Experimental Data

- milk sample of 1295 Holstein cows
- first lactation between 21\textsuperscript{st}–120\textsuperscript{th} day
- half sibs (192 sires) on 18 farms
- genotypes at 37 180 SNPs
- pedigree with 23 819 animals
- 190 metabolites measured via GC-MS

Conclusions

- GBLUP is suitable to study genetics of metabolic components
  - small to intermediate level of inheritance, mainly due to additive
  genetic sources of variation
  - Some milk traits are well predicted from metabolite profiles
  - identify locus-specific effects on selected metabolites (see Melzer et al., Session 12)

Theory

Linear mixed model (GBLUP)\textsuperscript{2} on log\textsubscript{2}-transformed metabolite measurements with genomic (realised) and pedigree (expected) relationship was extended to include the correlation of dominance deviations.

Likelihood ratio tests\textsuperscript{3} and FDR-corrected \( P \)-values

\[
H_0: \sigma_p^2 = 0 \text{ vs. } H_A: \sigma_p^2 > 0 \quad \text{(polygenic)}
\]

\[
H_0: \sigma_a^2 = 0 \text{ vs. } H_A: \sigma_a^2 > 0 \quad \text{(dominance)}
\]

\[
RLRT \sim 1 \chi_0^2 + 1 \chi_1^2
\]

\[
H_0: \sigma_a^2 = 0 \land \sigma_p^2 = 0 \text{ vs. } H_A: \sigma_a^2 > 0 \lor \sigma_p^2 > 0 \quad \text{(additive)}
\]

\[
RLRT \sim 1 \chi_0^2 + 1 \chi_1^2 + 1 \chi_2^2
\]

References


Cooperation partners

- LKV Güstrow
- Max Planck Institute for Molecular Plant Physiology, Potsdam-Golm
- vit Verden
- Helmholtz Zentrum München

Results

- broad-sense heritability \( 0 \leq H^2 \leq 0.70 \)
- narrow-sense heritability \( 0 \leq h^2 \leq 0.57 \)
- 55 metabolites with significant additive genetic variation, mainly in sugars (6), amino (10) and carboxylic (6) acids
- no metabolite with significant dominance variation at 5% level
- \( \geq 80\% \) of phenotypic variation explained by GBLUP model (via leave-one-out cross-validation)