

Milk metabolite composition and its relation to nutritional and technological quality

Sundekilde UK¹, Poulsen NA¹, Buitenhuis AJ², Gustavsson F³, Paulsson M³, L. B. Larsen¹,

¹Department of Food Science, Aarhus University, Denmark. ²Department of Molecular Biology and Genetics, Aarhus University, Denmark. ³Department of Food Technology, Engineering and Nutrition, Lund University, Sweden

Ulrikk.Sundekilde@agrsci.dk
Tel. +4587154882

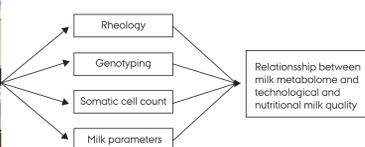
Introduction

Milk quality is closely correlated to the specific milk composition: including lipids, proteins, and metabolites. Milk coagulation, a substantial technological quality trait, is reflected in the milk metabolome (Sundekilde et al., 2011). Milk metabolite profiles are essential prerequisites for evaluation of genetic analyses in order to enhance technological or nutritional quality by implementing metabolite traits in breeding goals

Aim

The aim is to identify genetically contingent differences in the metabolite profile of milk and investigate its impact on bovine milk parameters: including coagulation properties, essential nutrients, and somatic cell counts (SCC).

Method



Milk and blood/tissue samples were collected from 1200 Danish Holstein Friesian, Danish Jersey and Swedish Red cows. NMR spectroscopy was performed using a Bruker Avance III 600 MHz NMR spectrometer. Coagulation properties were assessed using free oscillation. Genotyping was performed using the BovineHD bead-chip capable of assaying 777,962 SNPs. SCC was analysed by flow cytometry. Data was analysed using principal component analysis (PCA), partial least squares regression (PLS), orthogonal PLS discriminant analysis (O-PLS-DA), and by univariate statistics.



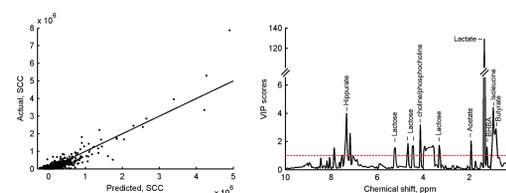
Results

Based on the milk metabolomes, the samples were classified according to their ability to coagulate. Choline was found to be positively associated with well-coagulating samples, whereas an elevated level of carnitine was associated with non-coagulating milk samples. The association of milk metabolomes to elevated SCC (commonly associated with mastitis) were also investigated, and several metabolites were found to be correlated with elevated SCC. Lactic acid, acetate, and β -hydroxybutyrate were increased, whilst butyrate, fumarate, hippurate, and isoleucine were decreased in milk samples with elevated SCC. The genetic analyses revealed that several metabolites have a high heritability; including orotic acid, β -hydroxybutyrate, carnitine, and choline, indicating that the content of these can be altered through breeding strategies.

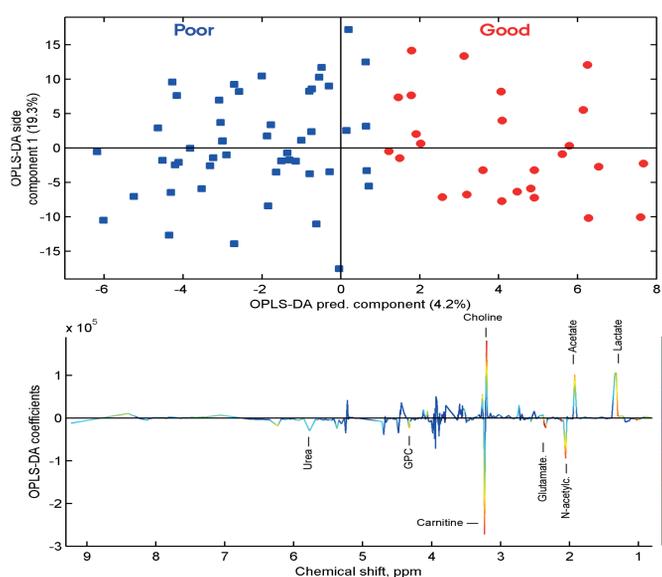
time, and choline, indicating that the content of these can be altered through breeding strategies.

Conclusion

In conclusion, variability in milk metabolomes can be associated with coagulation properties, SCC, and nutritional quality. The MVDA and rheological analyses indicate novel metabolites correlated with coagulation properties, and accordingly cheese yield and quality, whereas the genetic analyses can elucidate metabolites that are regulated by a genetic component.



Actual versus predicted plot of SCC obtained from a nine-component PLS regression model established on 876 samples ($R^2 = 0.89$, $Q^2 = 0.76$). Corresponding VIP scores plot.



OPLS-DA scores plot of a model of SR metabolite profiles of non-coagulating ($n = 50$) and well-coagulating ($n=26$) milk samples. OPLS-DA coefficients plot.

Metabolite	Heritability
Galactose-1-phosphate	0.43
Creatinine	0.45
Choline	0.48
Glycerophosphocholine	0.48
cis-Aconitate	0.48
Malonate	0.48
Glucose-1-phosphate	0.49
N-acetyl-carbohydrates	0.50
Glutamate	0.52
Hippuric acid	0.53
Citric acid	0.54
Glucose	0.55
Carnitine	0.63
Orotic acid	0.86

Estimates of heritability.

References

Sundekilde UK, Frederiksen PD, Clausen MR, Larsen LB, & Bertram HC. 2011. J. Agric. Food Chem. 59:7360-7367.