

Changes in milk proteome and metabolome associated with cow health

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During the last decades, technological and methodological developments in the -omics field have generated large amounts of data in different fields of biology. Systems biology attempts to characterize and predict the dynamics of networks, and looking individually at each -omic field hinders this objective. In our research, we therefore aim at analysing the effect of cow health in a broader -omics perspective, with the final aim to better understand the underlying physiology. One specific cow health issue of interest is negative energy balance, which will be used as an example of this multi-omics-approach. The early lactation period of dairy cows, which produce high quantities of milk, is normally characterized by an insufficient energy intake to cover milk production and maintenance requirements. Therefore, mobilization of body reserves occurs to compensate this negative energy balance (NEB) and probably as a consequence there is a higher susceptibility to diseases and metabolic disorders. To better understand the physiological mechanism of NEB, milk of cows with different energy balance status, subjected to different dry periods was analysed by untargeted metabolomics (lipid and serum fraction) and proteomics techniques. The aims were 1) to identify and quantify low abundant proteins and metabolites in milk from cows during early lactation that may be indicators for NEB, and 2) to test whether combining different -omics datasets improve our understanding of cow physiology. Milk of cows in severe NEB showed higher concentrations of acute phase response proteins, unsaturated fatty acids and galactose-1-phosphate, indicating an upregulated immune system and leakage of intracellular components. Improved energy balance (EB) resulted in higher concentration of N-acetylated sugars, cholesterol, cholesterol synthesis related proteins and stomatin, which we related to a higher content of glycosylation, especially around lipid rafts of the cell membrane. Our results therefore suggest that the mammary epithelial cells of cows in different EB work and are organized differently. These findings support the idea that combining information of different omics tools aid in a better understanding of the physiology of lactating cows. Further, some components found warrant more in-depth research to assess their applicability as robust indicators of health issues in dairy cows.

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