

A multi-omics' approach to characterise the metabolic response to the ingestion of fermented dairy products in healthy men.

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The biological mechanisms underpinning the health benefits associated with fermented dairy consumption are not fully understood. By associating metabolomics and transcriptomic analyses, the present project aimed at characterising the metabolic response of healthy men to the ingestion of a fermented dairy product. A randomized crossover study was conducted in 14 healthy men. Serum samples were taken 6h postprandially after the ingestion of 800g of either milk or yoghurt. Metabolomes of the test products and serum samples were assessed by LC-MS–based untargeted metabolomics; regulated compounds were selected using multivariate statistical analysis. Whole blood transcriptome was assessed by RNA sequencing (Illumina HiSeq); differential changes in gene expression were evaluated by Limma followed by ORA and GSEA pathway analyses. The integration of metabolomics and transcriptomic datasets was performed using the SNF and DIABLO tools.

The intake of the fermented milk resulted in specific serum metabolomics profiles and was characterised by the modulation of metabolites of exogenous or endogenous origin, such as bile acids, amino acids, or amino acids derivatives. Changes in the expression of genes representing six metabolic genesets were observed. Notably, a significant, similar modulation of inflammatory and glycolytic genes after both yoghurt and milk intake, although distinct kinetics differentiated the dairy products. Finally, the integration of the two datasets resulted in a better differentiation of serum samples and allowed the selection of correlated genes and metabolites.

The use of omics' tools and their integration allowed the identification of metabolic pathways regulated by the ingestion of the fermented dairy test food.