Development of mathematical models of the formation of flavour compounds by lactic acid bacteria

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Fermentation of dairy products by lactic acid bacteria (LAB) leads to tasty and healthy foods. In order to extend the knowledge of flavour formation by LAB, development of mathematical models will be instrumental to integrate the complex biological mechanisms involved. Our approach is threefold. First, GC-MS analysis of the flavour compounds produced under several environmental conditions will improve the understanding of factors that control the flavour profiles of *Lactococcus lactis* and *Lactobacillus plantarum.* Second, fermentation experiments under regimes of different amino acid availability, in combination with bioinformatics approaches, will result in the definition of the metabolic pathways in charge of the formation of the flavour compounds. Third, microarray experiments will be used to identify the regulatory mechanisms involved in amino acid conversion. By coupling analytical and statistical techniques, the metabolic map of LAB will be extended by flavour forming pathways and their regulation. Thus, by integrative modelling we will be able to represent the formation of flavour compounds linked to the environmental condition and to the genetic characteristics of these two LAB species.