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How metabolomics is used to support the MetaPath solution through metabolic profiling of cheese fermentation industry ecosystem models ?

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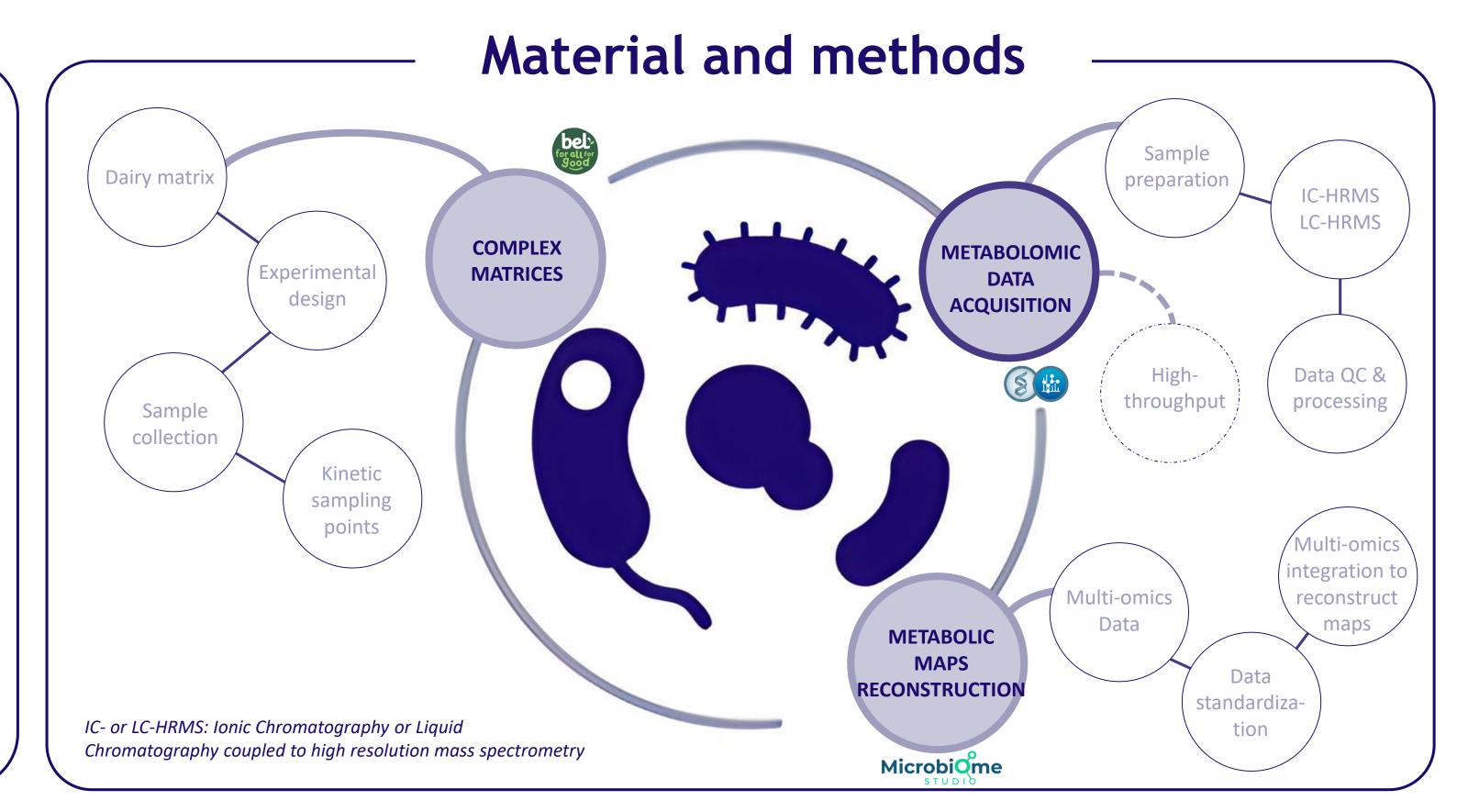
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Introduction

Consumer expectations and societal evolutions are at the heart of the concerns of fermentation professionals. The organoleptic properties of their products are closely correlated to its manufacturing process but also to its composition specifically the **microbial ecosystems** introduced to produce this fermentation.

In this context, the Bpifrance MetaPath project aims to reconstruct the metabolic maps of these microbial ecosystems in order to guide the industrialist in the selection of microbial strains at the time of product design. This will enable them to better control and understand the organoleptic properties of finished products in a natural way, in line with consumer expectations. As a partner in the MetaPath project, the MetaToul platform aims to perform metabolic profiling of ecosystems in the cheese model of industrial partner Bel.



Results and discussion I-COMPLEX MATRICES 3- METABOLIC MAPS RECONSTRUCTION Т°С Time Metabolomic Metabolomic data data Microbial ecosystem Dairy matrix Stirring Ecosystem Standardization of for all for good -0-0results files Kinetic FERMENTATION sampling Volatilomic points data Integration of multi-omics Detected layers in MetaPath Not detected solution Controlled industrial production conditions for all for good Microbione for all for good Transcriptomi Curd G Genomic data data *Heatmaps – C12/C13 ratios* 2- METABOLOMIC DATA ACQUISITION Color Key

