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To cite this version:
Amandine ROCHER, Lindsay PEYRIGA, Annabelle Fernandez, Pascal Vandekerckove, Floriant Bellvert. Metabolic profiles of complex fermentation matrices from cream and bakery industry. Analytics2022, Sep 2022, Nantes, France. hal-03884883

HAL Id: hal-03884883
https://hal.science/hal-03884883
Submitted on 5 Dec 2022

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Metabolic profiles of complex fermentation matrices from cream and bakery industry

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Introduction

Microbial ecosystems are key factors in food production by fermentation. The metabolic potential of ecosystems is very important and varies depending on the ecosystem composition and the metabolic capacity of the different partners. The construction of the metabolic map of an ecosystem is an important tool to understand, develop and use these metabolic capacities. In this context the MetaPath Bpi France project aims to develop an integrated solution allowing this modeling. In this context, the MetaToul platform aims to develop methods adapted to different food matrices for study of the metabolism, the most accurate and global possible of these different cellular ecosystems. Our main action is first of all to develop, on these complex fermented cream and sourdoughs, the extraction and global analysis of the central and energetic metabolism.

Material and methods

Quenching

Sampling

MetaPath solution

Data Acquisition

EXTRACTION

EXTRACTION OPTIMIZATION

Fermented cream

Fresh material

Dry material

Cellular lysis

Polar metabolites extraction

Polar + apolar metabolites extraction

Polar + apolar metabolites extraction

Polar + apolar metabolites extraction

SPE Oasis Prime HLB

No Lysis

No SPE

No Lysis

No Lysis

Dilution for IC-MS analysis compatibility

Fermented cream

Fresh material

Dry material

Cellular lysis

Polar metabolites extraction

Polar + apolar metabolites extraction

Polar + apolar metabolites extraction

Polar + apolar metabolites extraction

SPE Oasis Prime HLB

No Lysis

No SPE

No Lysis

No Lysis

Dilution for IC-MS analysis compatibility

PATHWAYS COVERAGE

118 metabolites screened (ID level 1)
90 metabolites identified in fermented matrices
76% Metatoul database detected and identified

METAFFIC PROFILES PRE-SCREENING

Time

Test

TT

Lesaffre

House Database

71%

56%

64%

Validation with IDMS

Untargeted MS Workflow

Identification of discriminating features

Results and discussion

Conclusions

Different sampling and sample extraction systems have been tested and remain to be validated. They allow the detection of central and energetic metabolism but also a wider detection. We currently cover the main pathways of the studied microorganisms and they will be used for the reconstruction of metabolic maps of the studied ecosystems. These systems will be used on different conditions of culture and ecosystems.

Acknowledgments

MetaboHub (MetaboHub-ANR-11-INES-0013)

This collaboration project, META PATH, is supported by the «Programme d’Investissements d’Avenir» operated by Bpifrance