



HAL
open science

Metabolomics to decode microbial interactions in kombucha beverage

Thierry Tran, Chloé Roullier-Gall, Francois Verdier, Antoine Martin, Philippe Schmitt-Kopplin, Hervé Alexandre, Cosette Grandvalet, Raphaëlle Tourdot-Maréchal

► To cite this version:

Thierry Tran, Chloé Roullier-Gall, Francois Verdier, Antoine Martin, Philippe Schmitt-Kopplin, et al.. Metabolomics to decode microbial interactions in kombucha beverage. 10th FEMS Congress of European Microbiologists, Jul 2023, Hambourg, Germany. , 2023. hal-04209781

HAL Id: hal-04209781

<https://institut-agro-dijon.hal.science/hal-04209781>

Submitted on 19 Sep 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Metabolomics to decode microbial interactions in kombucha beverage

Thierry Tran¹, Chloé Roullier-Gall¹, François Verdier², Antoine Martin², Philippe Schmitt-Kopplin^{3,4},
Hervé Alexandre¹, Cosette Grandvalet¹, Raphaëlle Tourdot-Maréchal¹

¹Univ. Bourgogne Franche-Comté, Institut Agro Dijon, PAM UMR A 02.102, F-21000 Dijon, France Dijon. Equipe Vin Aliments Micro-organismes Stress (VAIMIS) Institut Universitaire de la Vigne et du Vin Jules Guyot, rue Claude Ladrey, BP 27877, 21000 Dijon, France.

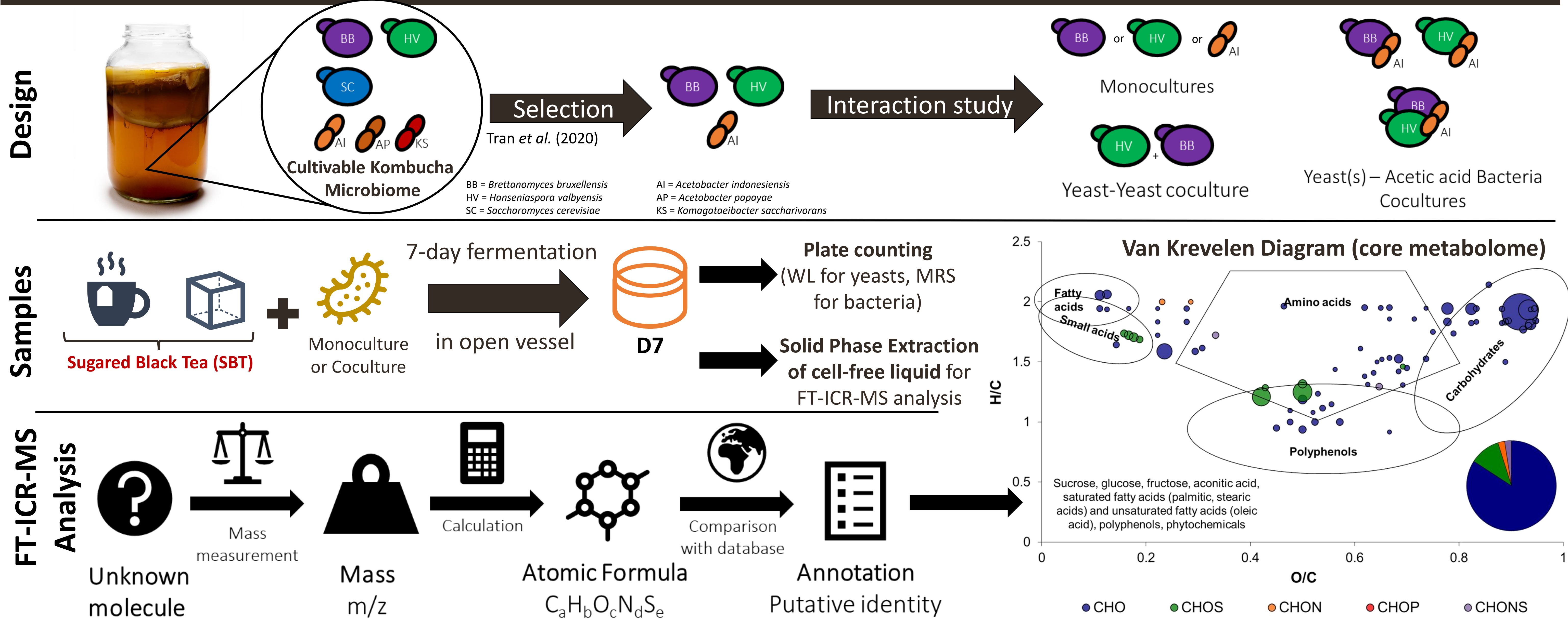
²Biomère, 14 rue Audubon, 75120 Paris, France.

³Comprehensive Foodomics Platform, Technische Universität München, 85354 Freising, Germany.

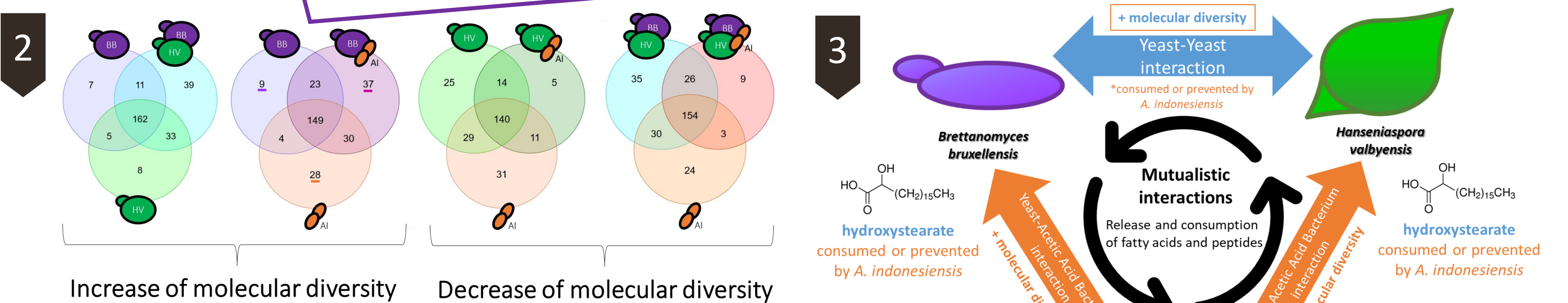
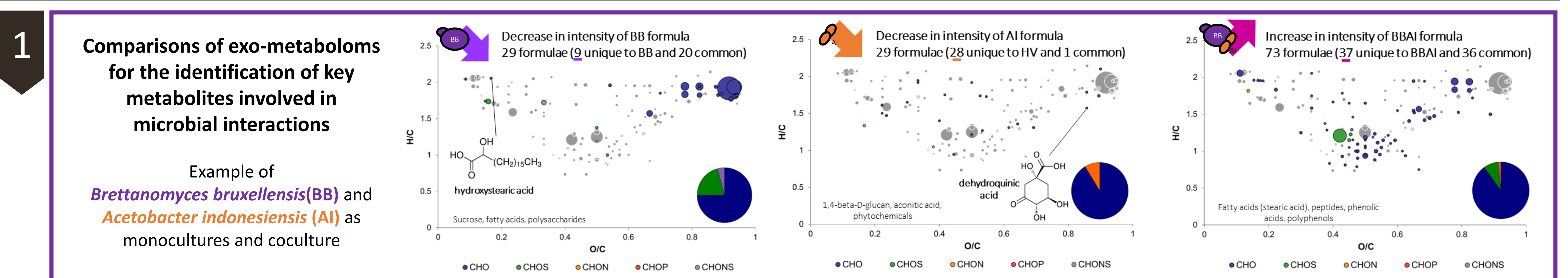
⁴Research Unit Analytical BioGeoChemistry, Department of Environmental Sciences, Helmholtz Zentrum München, 85764 Neuherberg, Germany

Kombucha is a fermented beverage produced from sugared tea through the activity of a yeasts and bacteria consortium, which exists in multiple microbiological diversities. Interactions taking place among yeasts and bacteria raise questions regarding the control of fermentations. Metabolic interplays involved in the production of organic acid from sugars have already been described, at the expense of other metabolites. Interactome between kombucha microorganisms was investigated by reducing an original consortium to three selected microorganisms: two yeasts (*Brettanomyces bruxellensis* and *Hanseniaspora valbyensis*) and one acetic acid bacteria (*Acetobacter indonesiensis*). Population levels were determined by plate counting and metabolomics was performed by Fourier Transform-Ion cyclotron-Mass Spectrometry on products, including a data treatment of 506 putative metabolites.

Material and methods



Results



Conclusions

1. Metabolites impacted (consumed or produced) by interactions included various chemical families (including carbohydrates, fatty acids, organic acids, peptides, phenolic acids and phytochemicals).
2. Molecular diversity was impacted differently depending on the yeast species. Simultaneous presence of *H. valbyensis* and *A. indonesiensis* induced a loss of molecular diversity.
3. Metabolomics analysis highlights metabolites exchanges as peptides and fatty acids, involved in the yeast-yeast interaction.
4. The presence of *H. valbyensis* affected positively the growth of *B. bruxellensis* and also *A. indonesiensis*. With the presence of *A. indonesiensis* in the trio coculture, yeast metabolites previously mentioned were either consumed or not produced, echoing the disappearance of growth benefits brought by *H. valbyensis*.

Key metabolites involved in the mutualistic interactions occurring between kombucha microorganisms have been uncovered, calling for further targeted investigations.

