

Evaluating the digestive profile and microbiota-driven health effects of locally produced fruits in the Greater Region

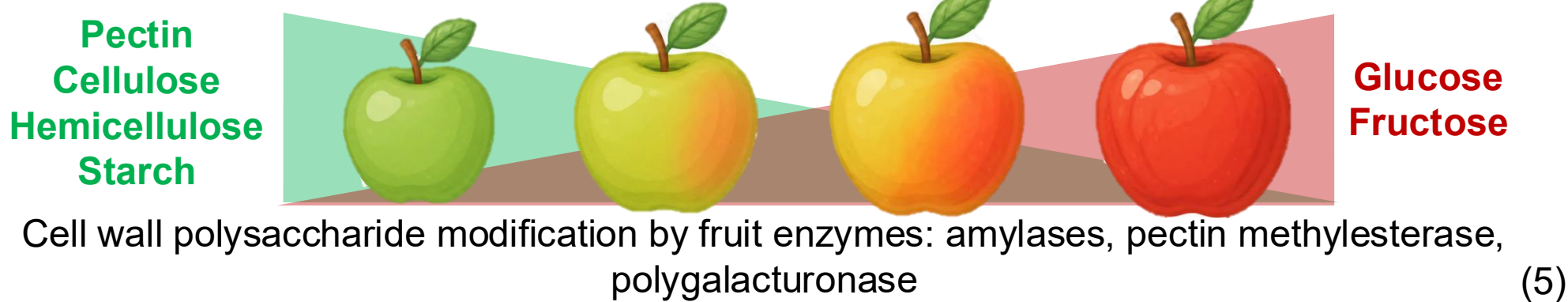
Aguilar Trujillo, N¹., Gresse, M.¹, Gonza-Quito¹, I., Katsandegwaza, B.¹, Delcenserie, V¹.

¹Department of Food Sciences, FARAH - Veterinary Public Health, University of Liège, B43b, 4000 Liège, Belgium

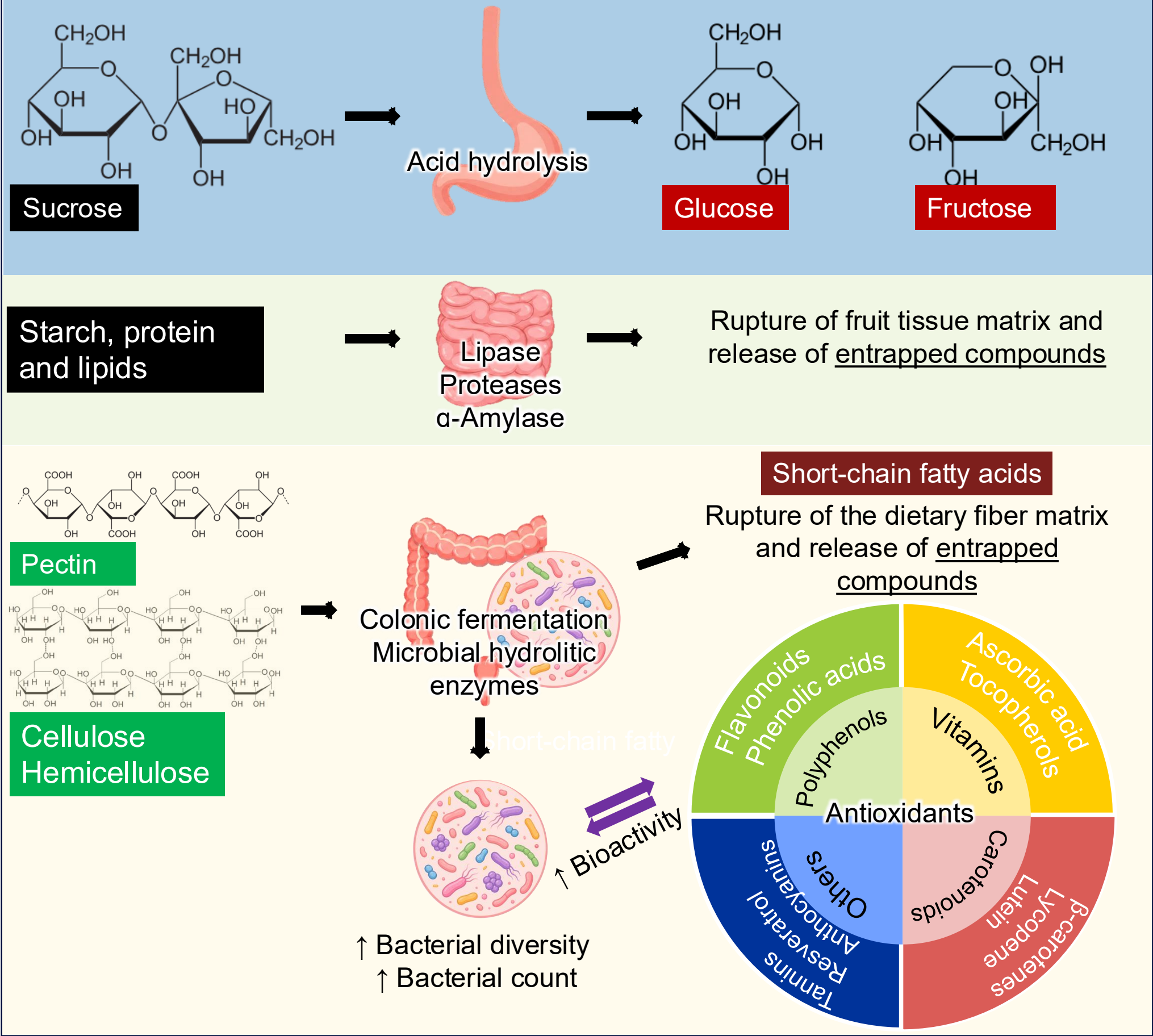
Introduction

Despite the proven beneficial health effects of fruit consumption, around 30% of food waste in the Greater Region (France, Belgium, Germany and Luxembourg) corresponds to fruits, while fruit intake remains below dietary guidelines recommendations (1,2). Locally produced fruits (apples, pears, grapes, mirabelle plums, and strawberries) are important sources of micronutrients and bioactive compounds (3). However, their nutrient composition is not static. During ripening, fruits undergo changes in their chemical composition, remarkably affecting their carbohydrate profile and the availability of bioactive compounds (4–6). Furthermore, whole fruits provide substrates that reach the colon, where the gut microbiota transforms them into bioactive compounds that may benefit the host, such as short-chain fatty acids produced from dietary fiber fermentation and polyphenol metabolites (7–9). However, studying whole fruits' effects on microbiota-driven responses presents methodological challenges, as compounds normally absorbed in the small intestine must be removed to accurately simulate colonic exposure. This study aims to assess how locally produced fruits influence microbiota-driven health outcomes, and the effect of fruit ripening on nutrient availability. For this, *in vitro* digestion models will be used to determine the digestive profile of local fruits and the transformation of fruit components by the gut microbiota.

Changes during fruit ripening



Fruit digestion



Expected results

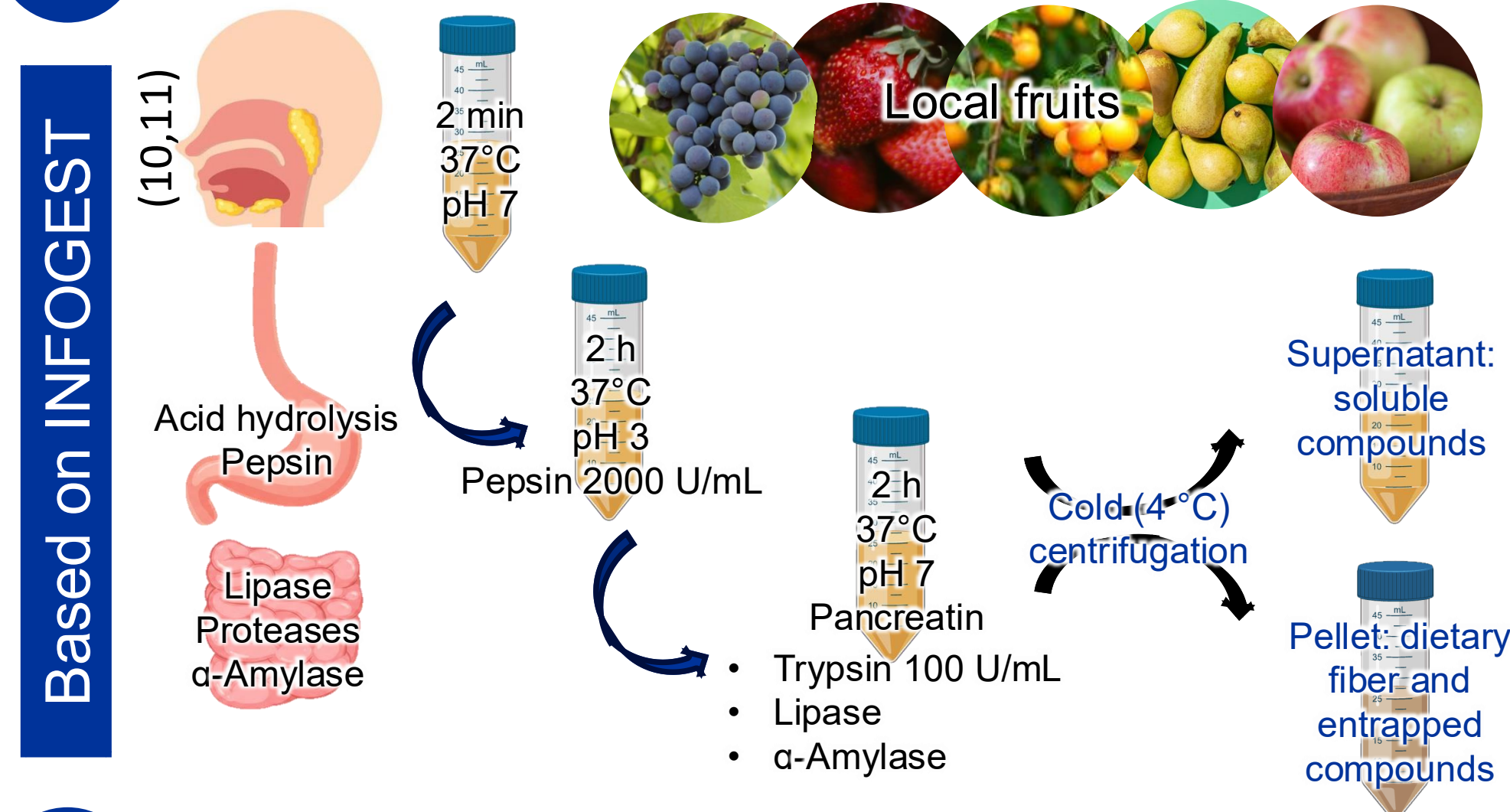
Using an integrated approach combining *in vitro* digestion, *in vitro* colonic fermentation, and cellular models, we aim to characterize fruit transformations across the gastrointestinal tract. We expect ripening-dependent differences in carbohydrate availability and bioactive compound profiles following *in vitro* digestion, as well as the production of microbial metabolites relevant to gut health, including short-chain fatty acids and polyphenol-derived compounds, after colonic fermentation. Overall, this work will improve understanding of how whole fruits interact with the gut microbiota and provide evidence to support strategies promoting fruit consumption and valorization within regional food systems.

Methods

1 Fruit characterization at different ripeness stages



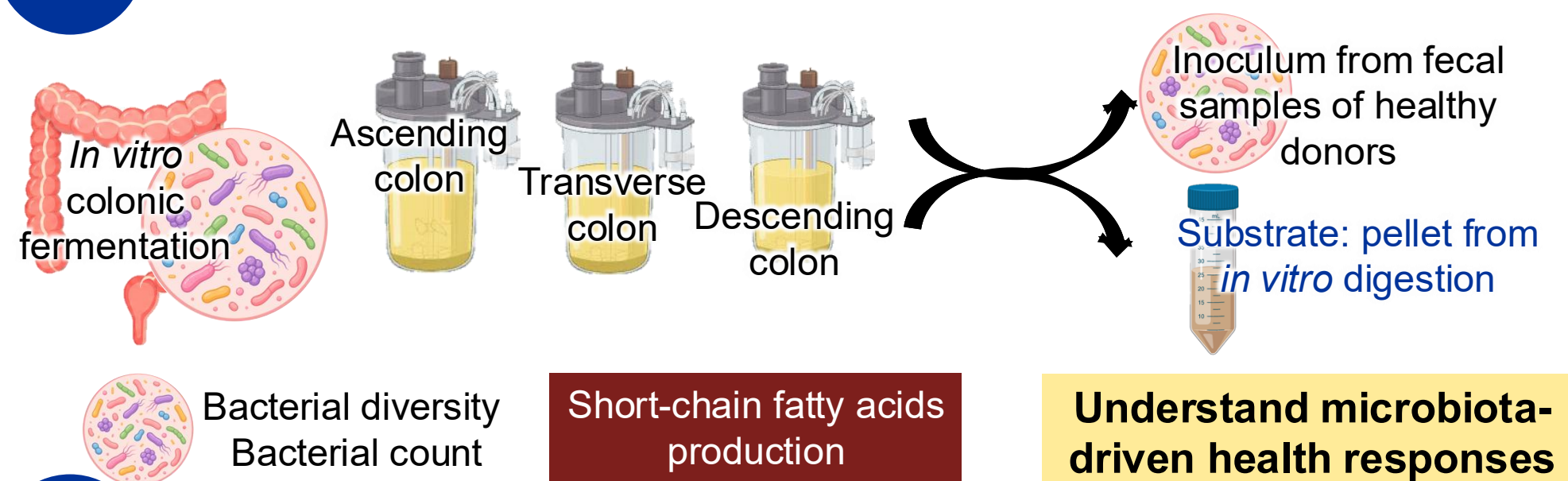
2 In vitro digestion



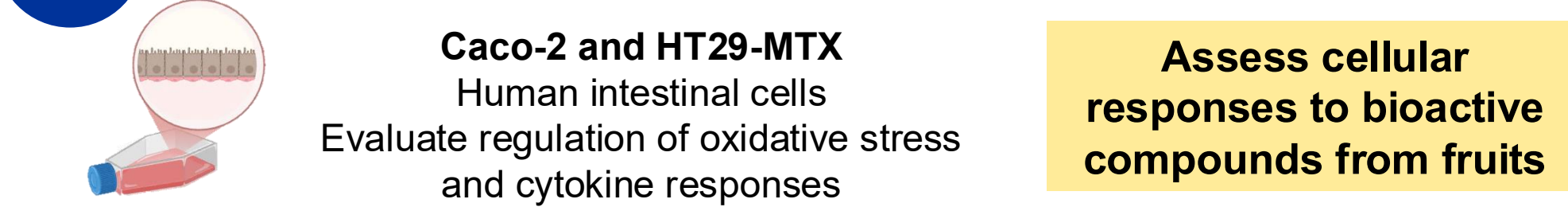
3 Fruit digesta analysis



4 In vitro colonic fermentation



5 In vitro cell assays



References

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Contact



Ninive Aguilar
nmaguilar@uliege.be