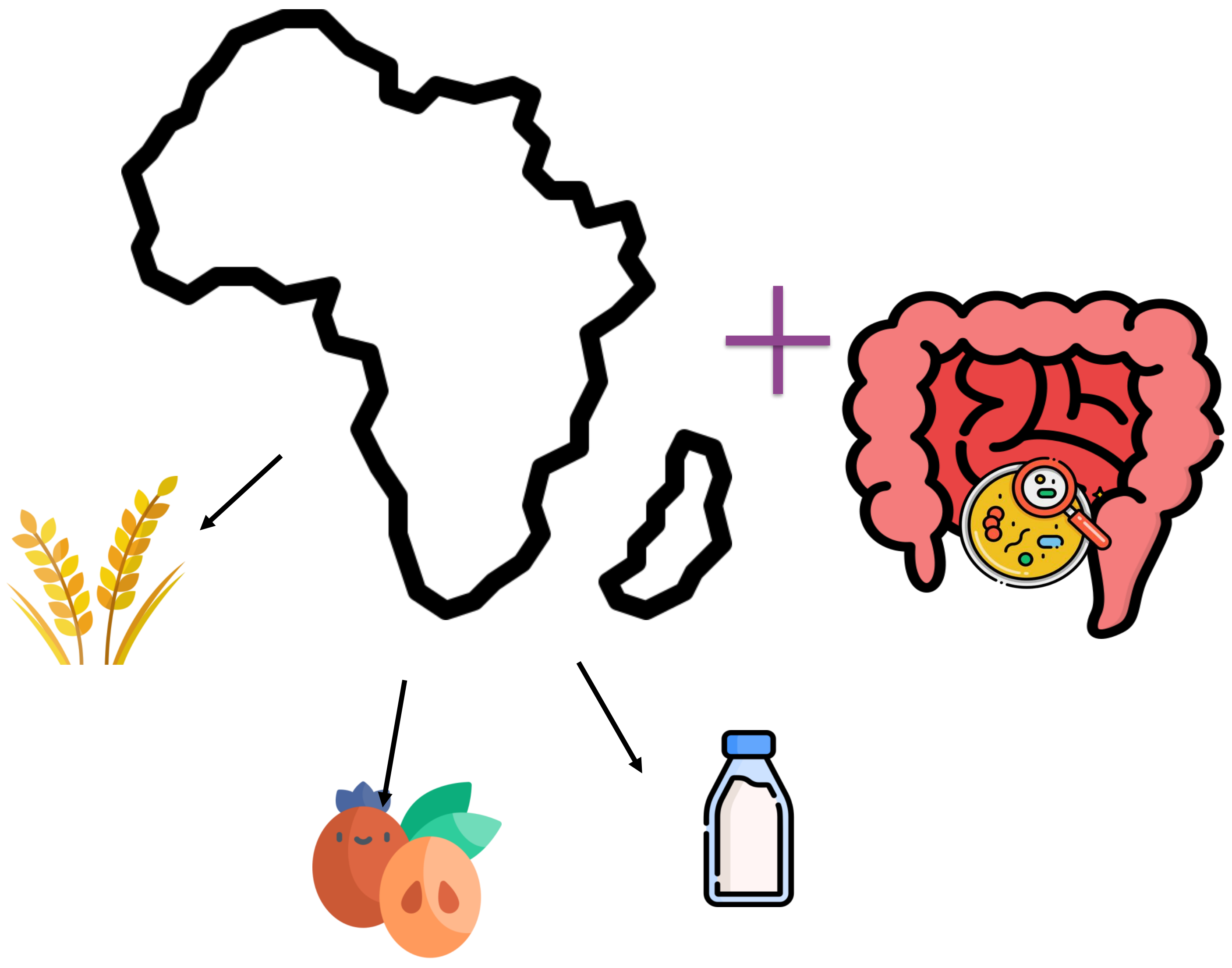
The Food-Gut Microbiome Axis: Exploring the Potential of Fermented Foods to Restore Gut Microbiome Diversity

Nadiya Dunayevska[1*], Thi Thanh Thanh Vu[1] , Vincenzo Valentino[1], Chiara M. Calvanese[1], Francesca De Filippis[1,2]
[1]Department of Agricultural Sciences, University of Naples Federico II, Piazza Carlo di Borbone 1, Portici (NA), Italy
[2]Task force on Microbiome Studies, University of Naples Federico II, Naples, Italy
*nadiya.dunayevska@unina.it

Background

Over recent decades, the progressive Westernization of lifestyle, together with the decrease in overall microbial exposure linked to hygiene practices typical of industrialized societies, has profoundly reshaped the human gut microbiome. A consistent body of evidence indicates a marked loss of microbial diversity in industrialized populations compared to rural or traditional communities, associated with the global rise of diet-associated chronic diseases such as obesity, type 2 diabetes, and inflammatory disorders. Fermented foods (FFs) represent one of the most relevant and complex sources of live microorganisms in the diet.



Objectives

The DOGMA project aims to elucidate the role of foodborne microorganisms from different non-Westernized countries (Africa, Sud America, Asia) in modulating the gut microbiome structure and functionality, exploring whether the consumption of FFs with high microbial diversity can restore gut microbial diversity and improve host health status.

OBJECTIVE 1

Isolating microorganisms from highly biodiverse fermented foods consumed by non-Westernized populations.

OBJECTIVE 2

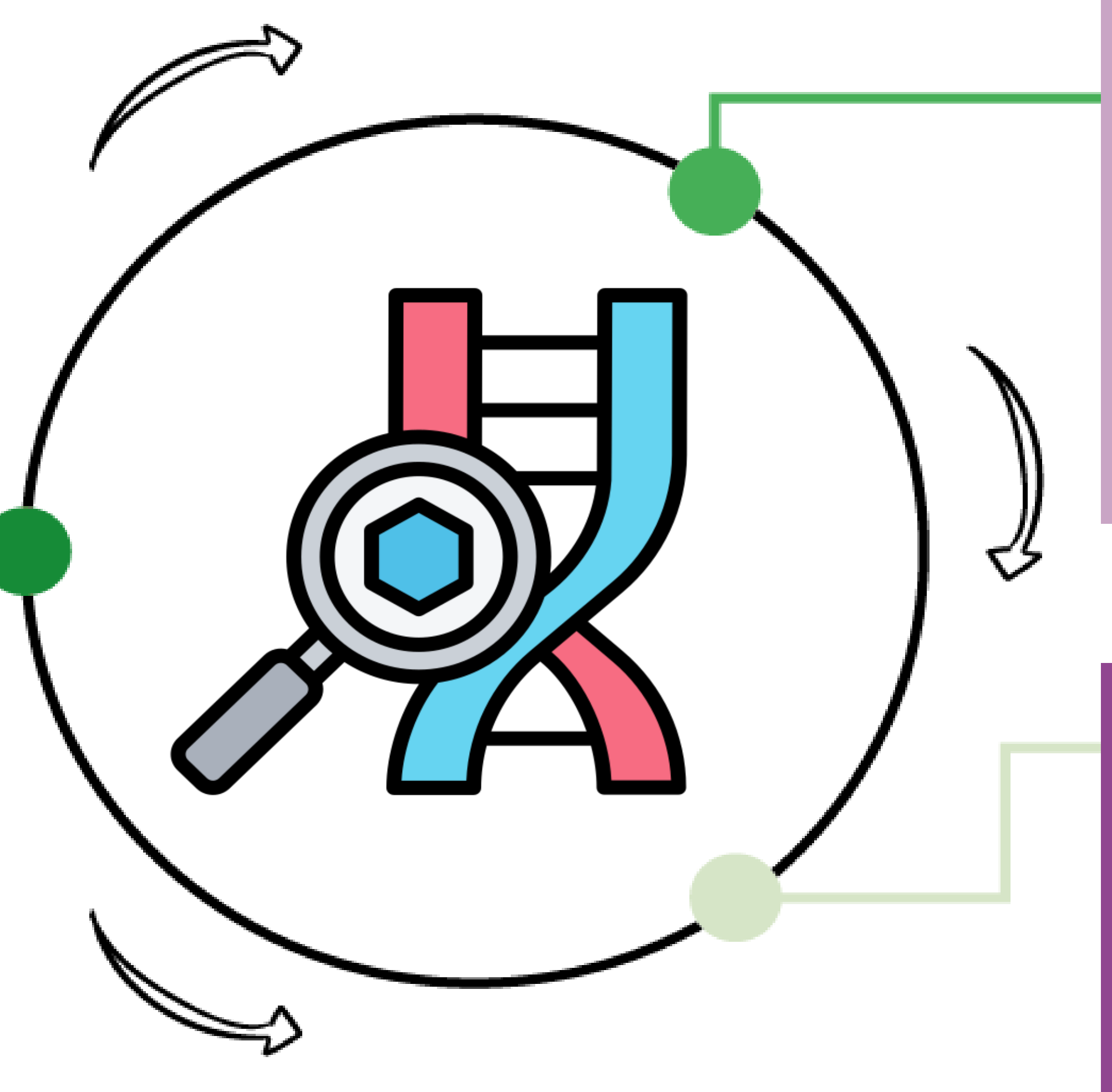
Leveraging shotgun metagenomics and MAG-derived sequence data, synthetic communities will be engineered.

OBJECTIVE 3

Understanding the impact of FF microbes on human gut microbiome and metabolome.

OBJECTIVE 4

The most promising communities will be used to develop new functionalized fermented foods.



Human gut and fermented food metagenomics

- ❖**Collection and sequencing of fermented food samples and the human gut microbiome to map microbial diversity and identify strains present in both matrices.**
- ❖**Analysis of co-occurrence patterns between FFs microorganisms and the human gut to understand potential functional interactions and dietary benefits.**

In vitro testing in mSHIME gastrointestinal simulator

- ❖**Development of synthetic communities from selected FFs, optimized to produce SCFAs, vitamins, and neuroactive molecules.**
- ❖**Gastrointestinal simulation in mSHIME to evaluate modulation of dysbiotic microbiomes and metabolic functions.**

In vivo fermented food testing

- ❖**Human trial with selected FFs, monitoring microbiome and metabolome before and after consumption.**
- ❖**Identification of functionalized FFs able to enhance microbial diversity and improve metabolic and intestinal health.**

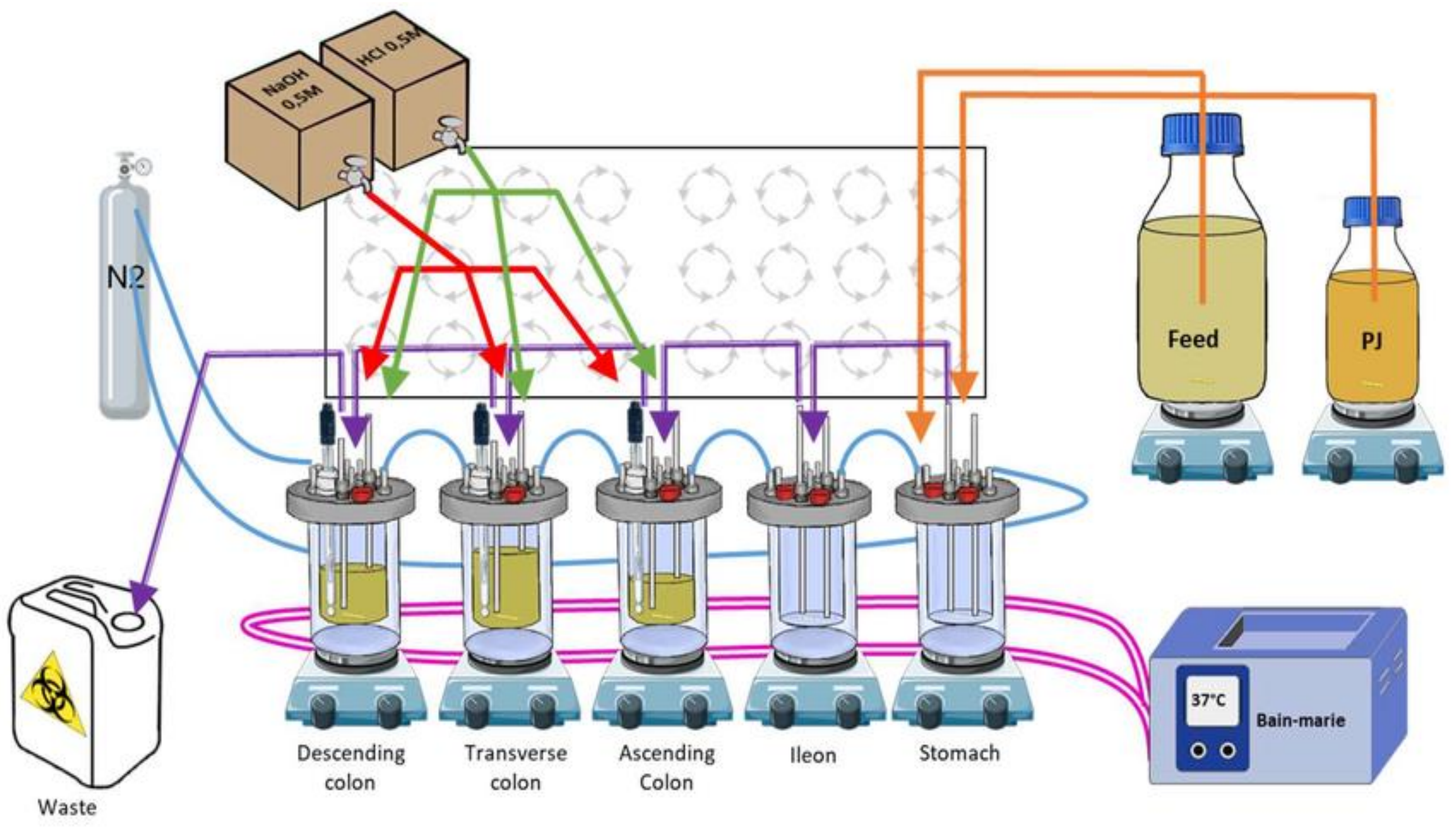


Figure 1. Example of SHIME model

Expected outcomes

DOGMA will clarify the extent to which dietary microbes contribute to the resilience and functional recovery of the gut microbiome and will provide a mechanistic framework to design evidence-based nutritional strategies aimed at counteracting the loss of gut microbial diversity

References:

1. Laforêt, F.; Antoine, C.; Lebrun, S.; Gonza, I.; Goya-Jorge, E.; Douny, C.; Duprez, J.-N.; Scippo, M.-L.; Taminiau, B.; Daube, G.; et al. Impact Assessment of vB_KpnP_K1-ULIP33 Bacteriophage on the Human Gut Microbiota Using a Dynamic In Vitro Mode
2. Quince, C., Walker, A., Simpson, J. *et al.* Shotgun metagenomics, from sampling to analysis

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