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# Probiotics for early microbiota development PEACE project

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## Introduction

The microbial colonization of the newborn (primocolonisation) plays a fundamental role in human health as it allows the proper development of the newborn and is a key factor in the establishment of its digestive, metabolic and immune systems [1, 2, 3]. When this developmental process is disrupted, there can be an impairment of the function of the intestinal barrier, and a predisposition to develop chronic diseases [4, 5]. Several factors, strongly linked to the modern western lifestyle, can alter this transmission [6]. Furthermore, changes in the microbiota accumulated during a mother's lifetime can be passed on to her offspring, which can have a cumulative effect over generations [7].

## Objectives and work plan

The aim of this study is to isolate and characterize beneficial bacteria (potential probiotics) aimed at counteracting the microbiota disturbances associated with altered primocolonisation.

The project is divided in three work packages (WP) :

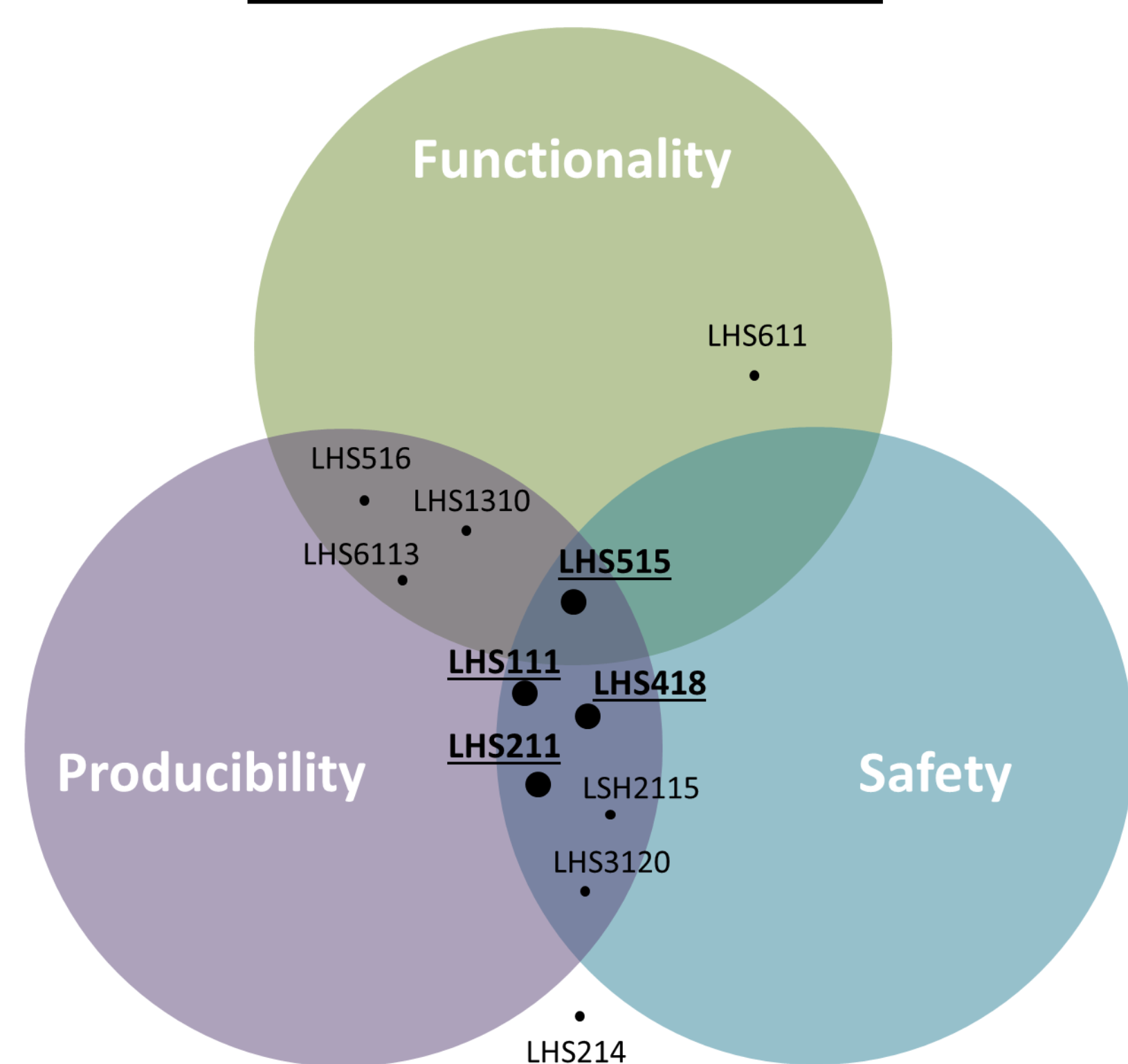
**WP1** – Bacteria isolation from healthy newborn

**WP2** – *In vitro* phenotype characterisation of isolated bacteria

**WP3** – Test bacteria isolated in mouse models of altered transmission of the microbiota

## WP2 – *In vitro* characterisation of isolated bacteria

Visual representation of the strains depending on the presence or absence of different characteristics



A first general microbiology characterization was carried out on the 11 strains of interest with a focus on the producibility and safety properties. To assess the potential probiotic capabilities of the isolated strains, functionality properties were also carried out. Based on these results, 4 strains were selected to be further characterized.

## WP1 – Bacteria isolation

6 healthy babies included in the study  
A B C D E F

↓

28 fecal samples collected  
(1 sample per month for 6 months)

↓

984 bacteria isolated from 14 fecal samples  
(samples from odd months only)

↓

280 bacteria identified from MRSc, MRS and BEA media

↓

Restriction to the genera *Bifidobacterium* and family *Lactobacillaceae*

↓

Selection of one strain per species and per sample  
(To avoid selecting the same strain twice)

↓

11 bacteria of interest found

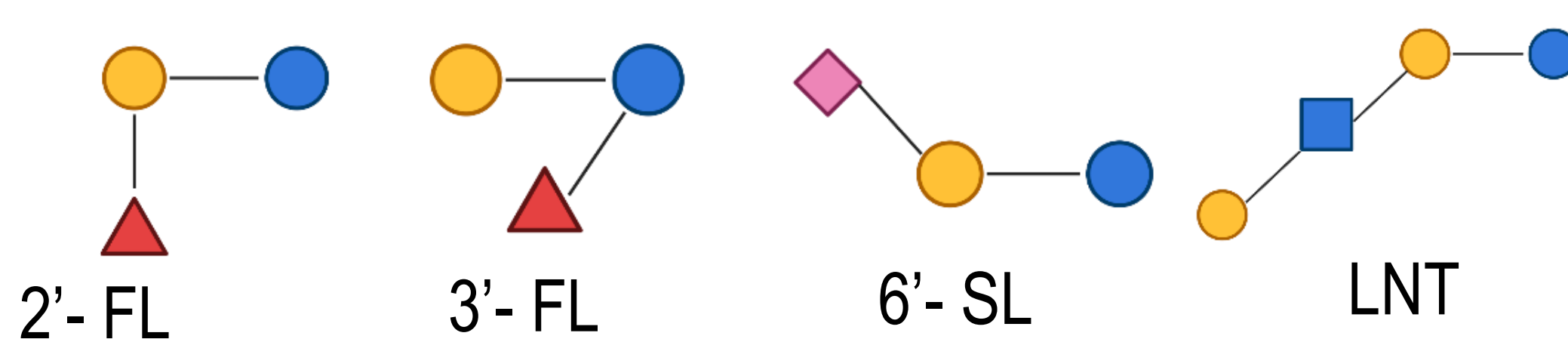
✓ LSH111	✓ LSH2115	✓ LSH515	✓ LSH6113
✓ LSH211	✓ LSH3120	✓ LSH516	✓ LSH1310
✓ LSH214	✓ LSH418	✓ LSH611	

The 6 babies were included in the study based on several inclusion criteria. The samples were collected once a month during 6 months. For the identification of the 11 bacteria a target approach was carried out focused on lactic acid bacteria and *Bifidobacterium*.

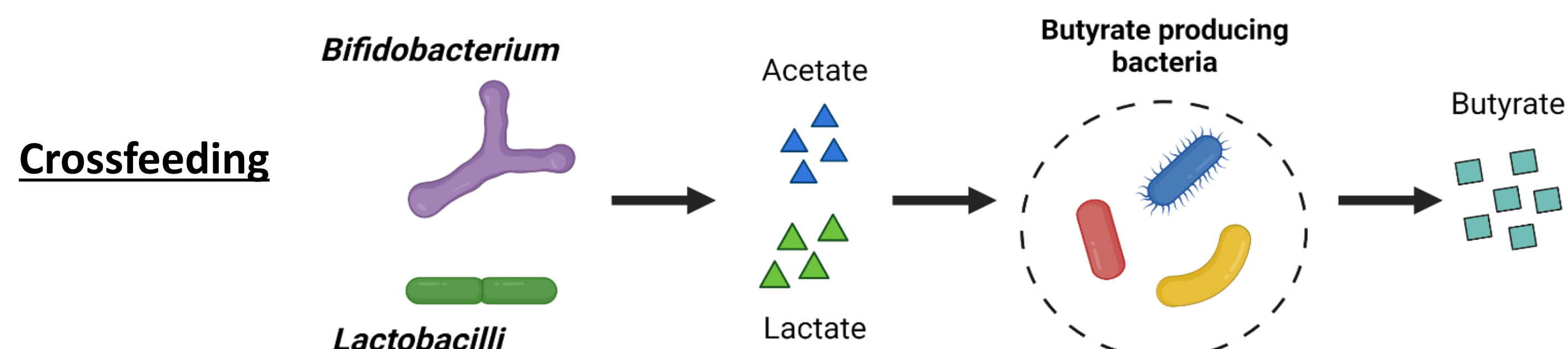
## WP2 – (Work in progress) Metabolic properties

The ability to degrade HMOs is currently assessed by growth monitoring in minimal media in the presence of a single carbon source.

Human milk oligosaccharides (HMOs)



Crossfeeding mechanisms will be studied by growth assessment, metabolic activity characterisation and Short Chain Fatty Acids (SCFA) quantification in co-cultures.



## WP3 – *In vivo* model

At the end of the WP2, 1 or 2 strains will be selected to be tested in different *in vivo* models of altered transmission of the microbiota [7,8].

Early weaning



Antibiotic use



Transgenerational model of low fibre diet



## References

- [1] Macpherson & Harris, 2004  
[2] Round & Mazmanian, 2009  
[3] Hooper et al., 2012  
[4] Marsland & Salami, 2015

- [5] Shen & Wong, 2016  
[6] Linehan K *and al.*, 2016  
[7] Sonnerburg and al., 2016  
[8] Aversa, Zaira et al. 2021

