

# METAFUN

*Functional metagenomic*

MetaFun is a functional metagenomic platform which aims at exploring the expression diversity of the human intestinal microbiota **to better understand the interactions between gut bacteria and human cells.**

This innovative approach is based **on a set of high throughput screening technologies** enabling the analysis of the entire genome of all microorganisms belonging to an ecological niche, including those which are not cultivable.

## Method

**Construction of large insert genomic and metagenomic libraries**

**Functional screening of large clone libraries with large genomic or metagenomic DNA fragments**

- ▶ Identification of bacteria –cell cross-talk

**Implementation of cell-based bioassays using a high-throughput strategy.**

- ▶ Identification of functional bacterial genes and metabolic pathways involved in the dialogue with the host.



## Applications

**Identification of useful microbial features:** anti-inflammatory, anti-proliferative effects, satogenic properties...

- ▶ Probiotics (strains selection, mechanisms of action)
- ▶ Molecules with potential therapeutic applications

**Validation of nutritional intervention strategies : nutritional supplements and food providing targeted benefits**

- ▶ dietary recommendations

## The strengths of the platform

### Expertise

- ▶ Identification of dozens of interesting bioactive clones towards the identification of the involved molecules
- ▶ **18** publications since 2010
- ▶ **3** patent applications

### Experience

- ▶ **3** European projects including MetaCardis
- ▶ **4** ANR projects including one coordination
- ▶ **3** industrial projects

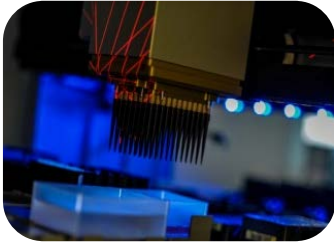
### Performance

- ▶ A screening capacity of 500 000 bioactive clones per year
- ▶ Automated process ensuring high quality standards

### Main technologies

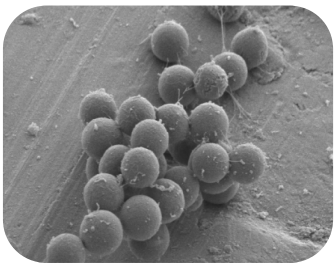
- ▶ Building of metagenomic library
- ▶ Replication of libraries
- ▶ Automatic culture of bacterial clones, followed by lysis and filtration
- ▶ Development of new screening tools (cell based assay using the reporter gene technology)
- ▶ High-throughput screening on human epithelial cells, including measurement of reporter gene activities (luminescence (HTS), fluorescence (HCS), absorbance)
- ▶ Flow cytometry analysis and cell sorting

## PARTNERSHIPS



**METAFUN is ready to collaborate with the scientific and industrial communities, by applying its skills and know-how for:**

- ➔ The design of functional metagenomic projects:
  - Expert advice to design the study
  - Construction of large insert genomic and metagenomic libraries
  - Functional screening and analysis
  
- ➔ High throughput screening from existing libraries:
  - From the construction of the project to the analysis of the results



### Some significant publications

De Wouters et al. *PLoS One* in press 2014 - Optimization of all stages of the screening process – development of SOPs

Cotillard A et al. *Nature* 2013 – Dietary intervention impact on gut microbial gene richness

Blottière HM et al. *Curr Opin Microbiol.* 2013 – Human intestinal metagenomics: state of the art and future

Nepelska M et al. *PLoS One* 2012 – Butyrate Produced by commensal bacteria potentiates phorbol esters induced AP-1 response in human intestinal epithelial cells

Lakhdari O et al. *PLoS One* 2010 – Identification of NF- $\kappa$ B modulation capabilities within human intestinal commensal bacteria



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