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# Standards in microbiomics - lessons from intestinal metagenome studies

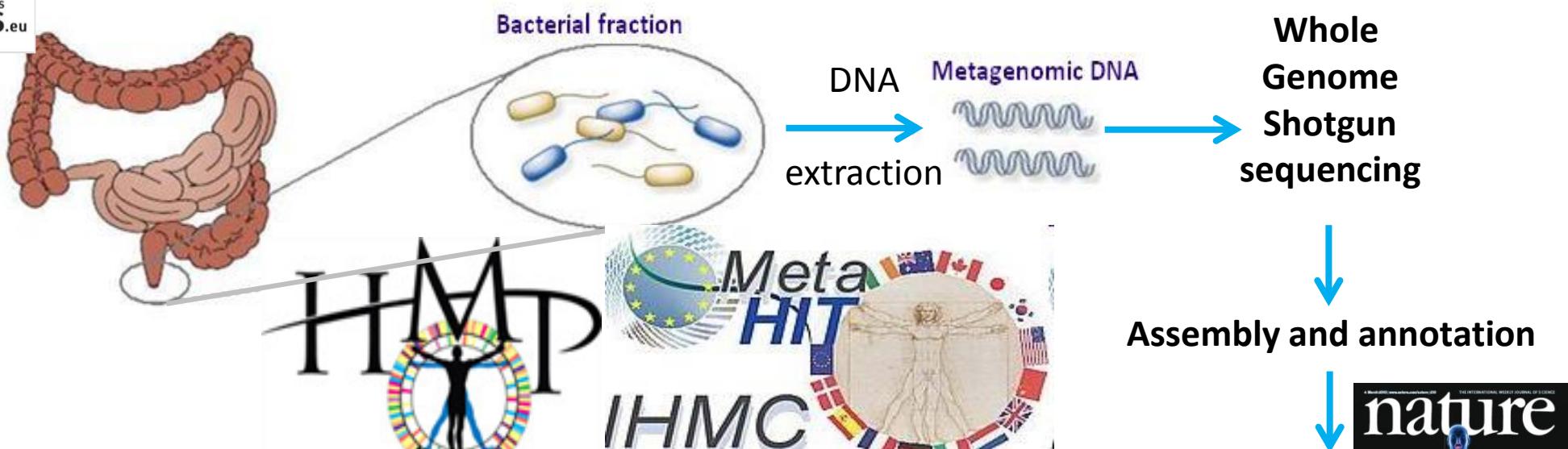
**Joël Doré & IHMS consortium**

MetaGenoPolis & Micalis, INRA, Jouy en Josas, France



# METAGENOME, GENOME OF ALL DOMINANT MICROBES

A technical revolution since the turn of the century



## Lessons from early human intestinal tract metagenomics:

Reference gene catalogs, highlighting both core metagenome & rare genes

- 3.3 million genes Qin *Nature 2010* to 10 million genes Li *Nature Biotech 2014*

Co-abundant gene clustering and metagenomic species Nielsen *Nature Biotech 2014*

Mouse gene catalog ; environment dependent Xiao *Nat Biotech 2015*

**3 enterotypes / preferred ecological arrangements Arumugam *Nature 2011***

stability at SNPs level (strains) Schloissnig *Nature 2012*

nutrition and intestinal metabolome are linked Shoae *Cell Metabol 2015*

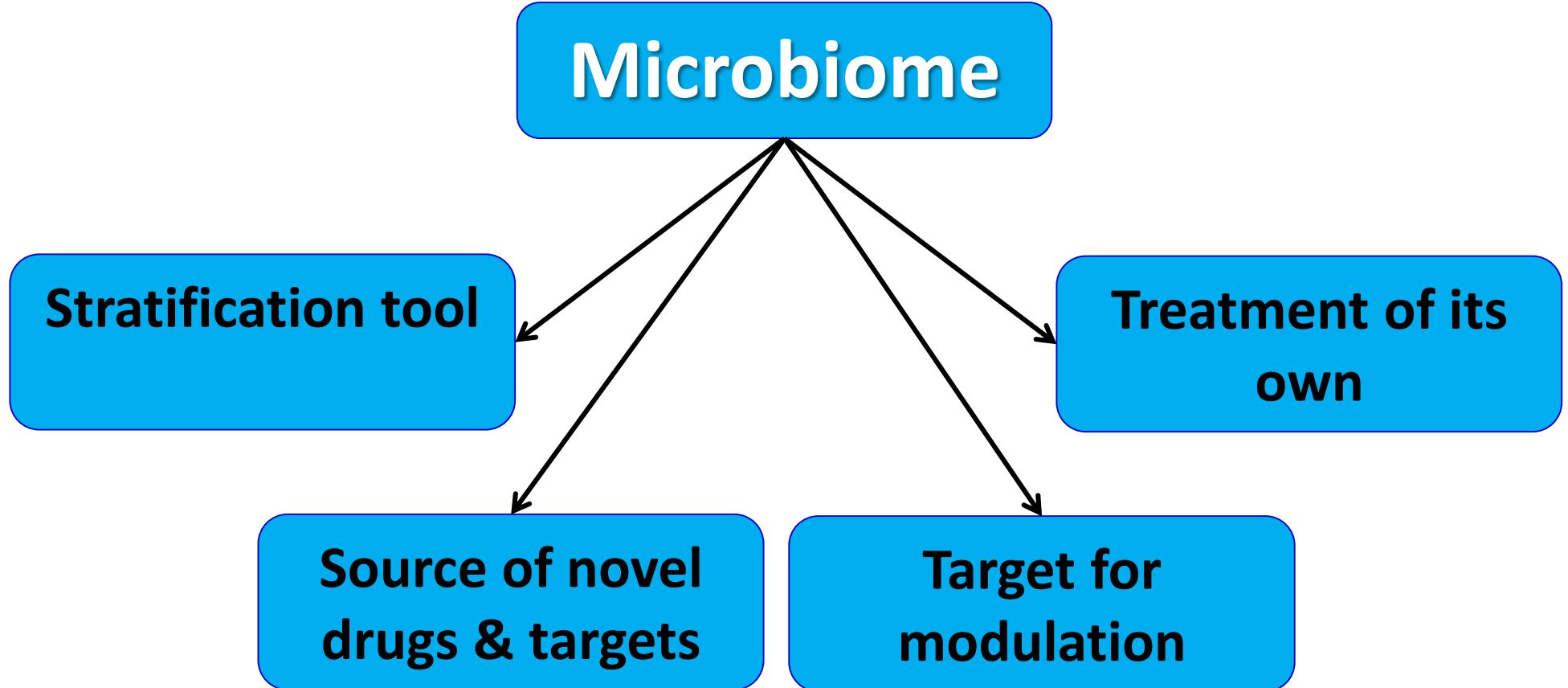
=> **metagenomic dysbiosis ; diagnostic signatures ; predictive models..**

- in T2D Qin *Nature 2012*, in Obesity Le Chatelier *Nature 2013*, in Liver cirrhosis Qin *Nature 2014*

=> **low gene count is a key stratifier Cotillard *Nature 2013***

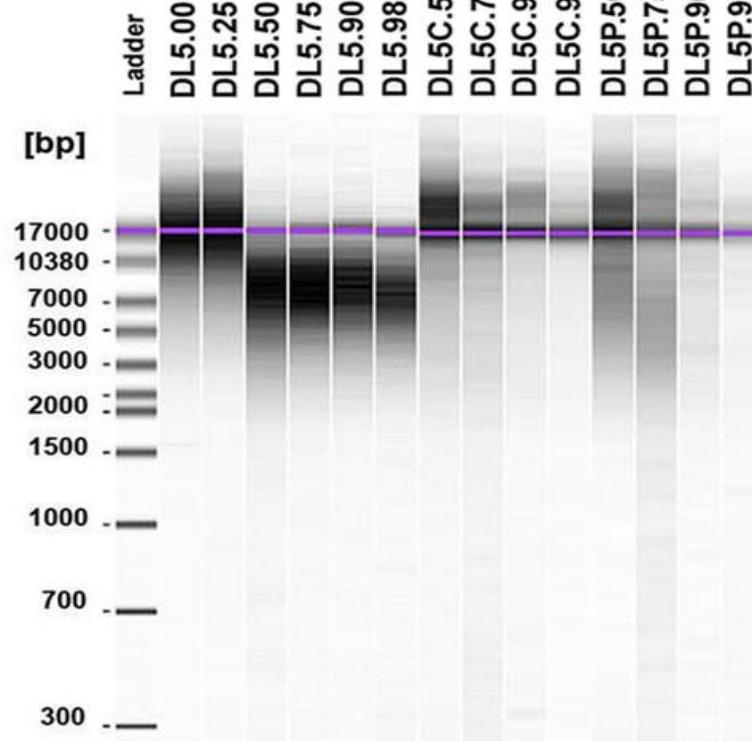


# *Microbiome – source of innovation for health*



**A**

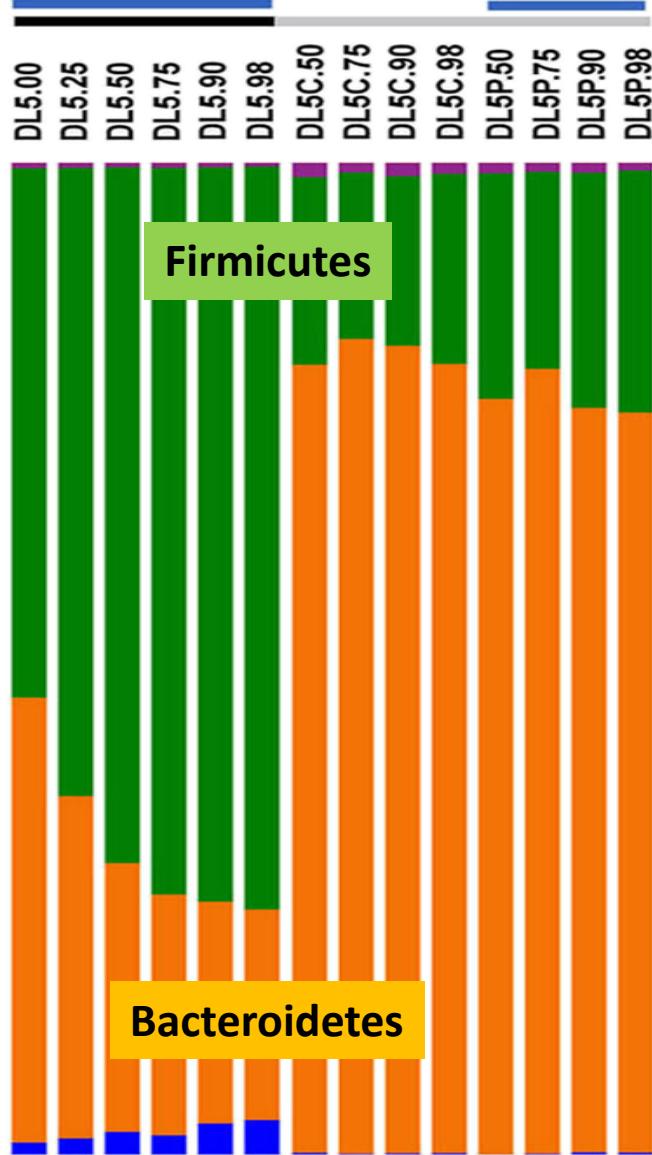
— Subjected to bead-beating



Bead-beating strongly impacts recovery of Firmicutes

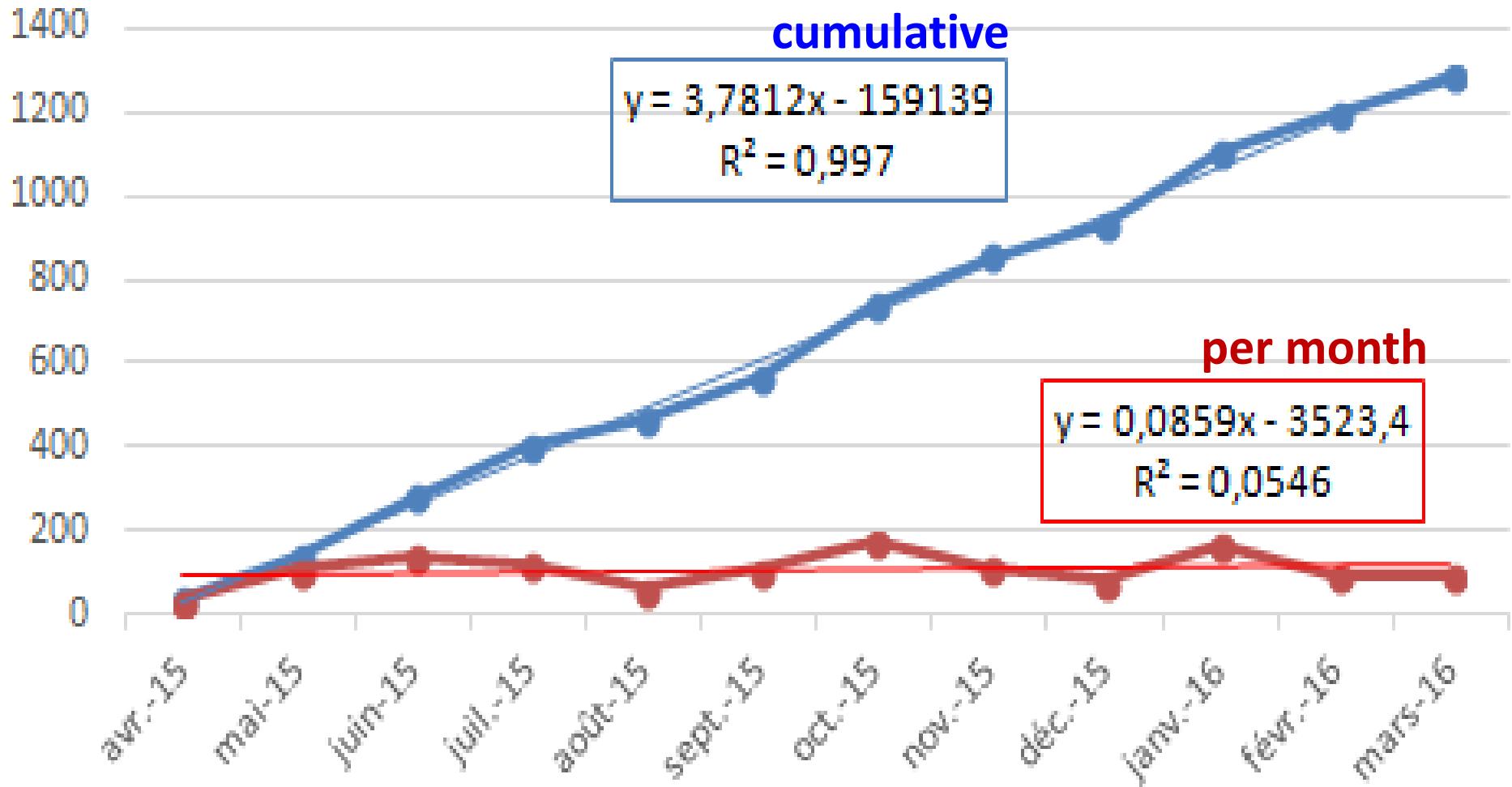
- Archaea; Euryarchaeota
- Bacteria; Actinobacteria
- Bacteria; Bacteroidetes
- Bacteria; Firmicutes
- Bacteria; Proteobacteria
- Bacteria; Tenericutes

**B**



## IDENTIFICATION, COLLECTION, PROCESSING SOPS

## International Human Microbiome Standards SOPs downloads



# Merci de votre attention

## IHMS Partners



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## IHMS Participants



a place of mind  
THE UNIVERSITY OF BRITISH COLUMBIA



**European Commission & Agence Nationale pour la Recherche**