Metatranscriptomics and metabolic modeling to identify bacterial metabolic interactions during the manufacture of a model pressed cheese.

Wenfan Cao, Maxime Lecomte, Solène Le Fur, Julie J. Aubert, Marie-Bernadette Maillard, Aurélie Nicolas, Stéphanie-Marie Deutsch, Sandrine Parayre, Françoise Boissel, Arlette Leduc, et al.

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Submitted on 20 Sep 2022

Metatranscriptomics and metabolic modeling to identify bacterial metabolic interactions during the manufacture of a model pressed cheese.

Hélène Falentin – URM STLO – RENNES

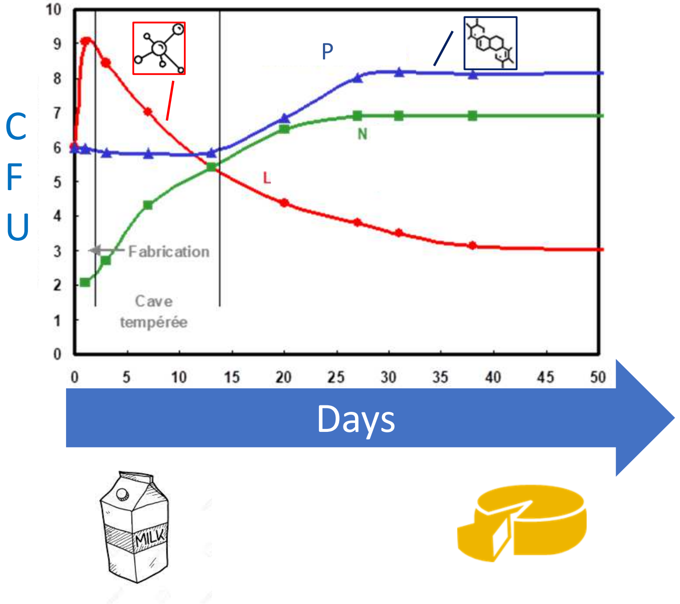
Founded by

Context et questions

Context

Activity of cheese microbiota responsible for organoleptic quality

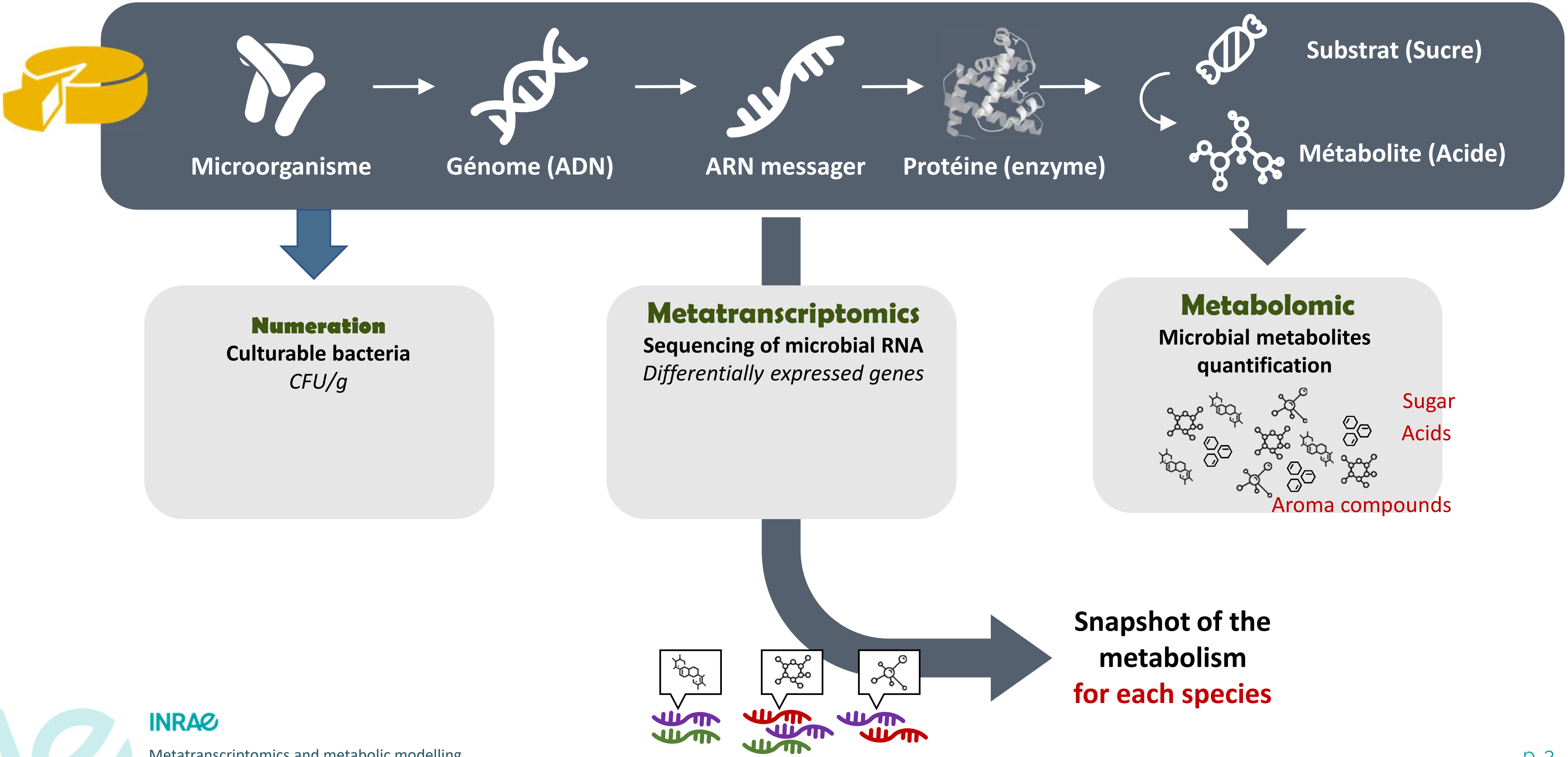
- Successive growths of microbes
- Specific and complementary microbial metabolisms
- Metabolic interactions between microbes



Scientific questions

- Which species contributes to acidification ?
- Which species contributes to aroma compound production?
- Which metabolic pathways are activated ?
- When are they activated ?
- Which bacterial metabolic interactions contributes to the functioning of microbial ecosystem ?

Strategy using multi-omics



Microorganisme → Génome (ADN) → ARN messager → Protéine (enzyme) → Substrat (Sucre) → Métabolite (Acide)

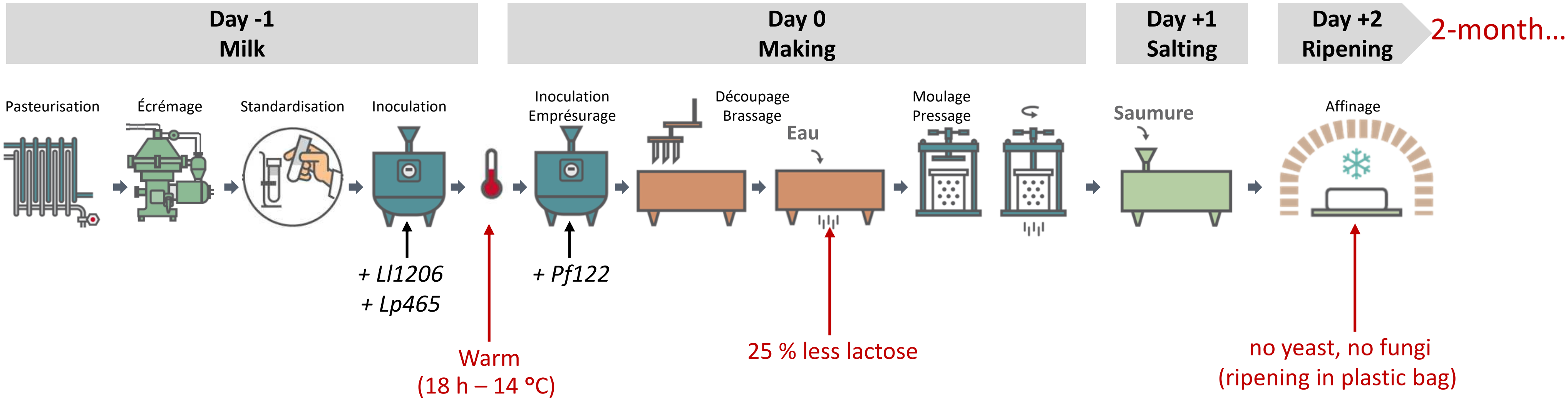
Numeration
Culturable bacteria
CFU/g

Metatranscriptomics
Sequencing of microbial RNA
Differentially expressed genes

Metabolomic
Microbial metabolites quantification

Snapshot of the metabolism
for each species

Cheese making of semi hard cheeses



Day -1
Milk

Day 0
Making

Day +1
Salting

Day +2
Ripening

2-month…

+ Ll1206
+ Lp465

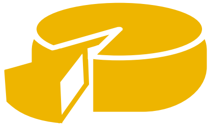
Warm
(18 h – 14 °C)

+ Pf122

25 % less lactose

no yeast, no fungi
(ripening in plastic bag)

Semi hard cheeses
(without yeast)



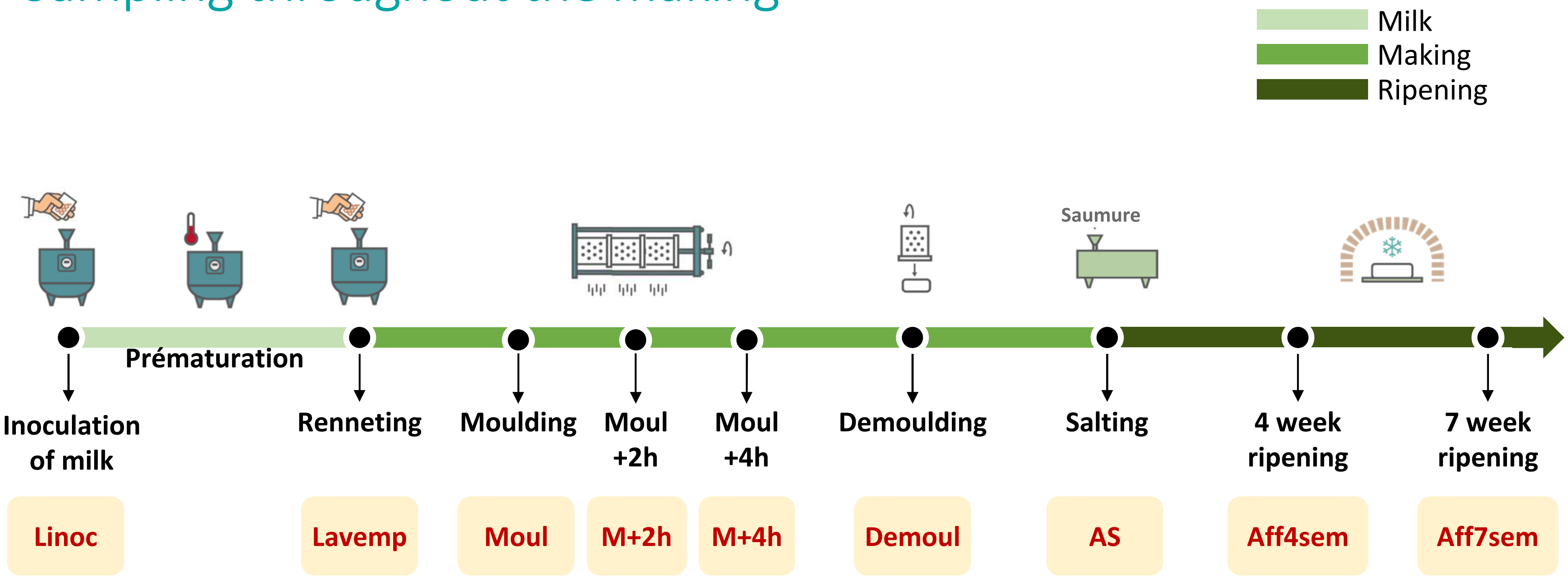
Lactococcus lactis CIRM-BIA1206

Lactiplantibacillus plantarum CIRM-BIA465

Propionibacterium freudenreichii CIRM-BIA122

Cao et al. 2021, J. Agric. Food Chem.

Sampling throughout the making



- Milk
- Making
- Ripening

Saumure

Prématuration

Inoculation of milk	Renneting	Moulding	Moul +2h	Moul +4h	Demoulding	Salting	4 week ripening	7 week ripening
Linoc	Lavemp	Moul	M+2h	M+4h	Demoul	AS	Aff4sem	Aff7sem

Microbiology

Chemistry

Biochemistry

Molecular biology

Computational science

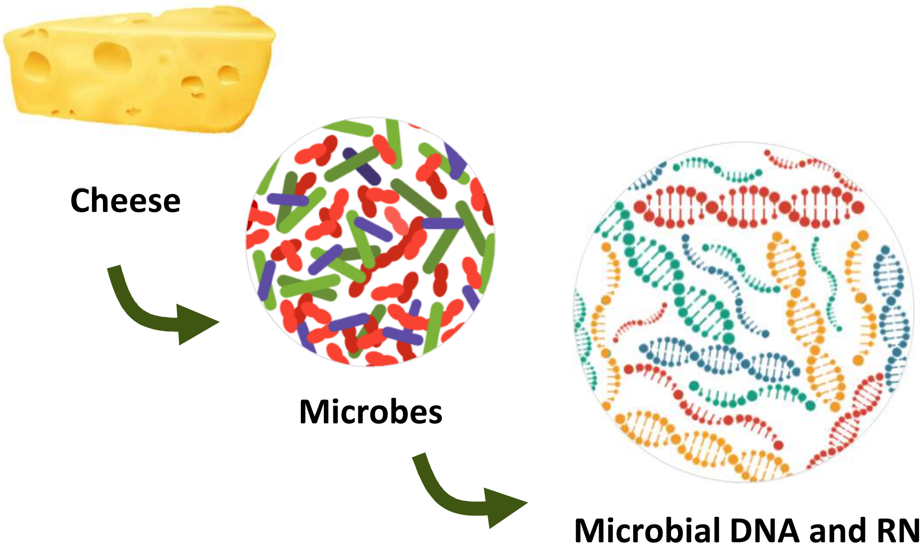
Microbiological methods

Microbiology

- ***L. lactis*** : M17 + lactose
- ***L. plantarum*** : MRS pH5.4
- ***P. freudenreichii*** : Yela

Biochemistry

- **Nitrogen**: Kjeldhal
- **Sugar and acids**: HPLC
- **Aroma compound**: head space + GCMS



Cheese

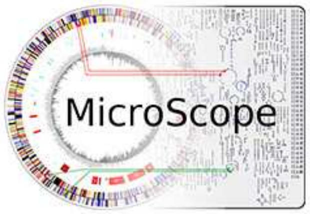
Microbes

Microbial DNA and RNA

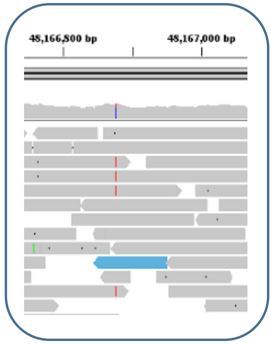
Molecular biology

- **DNA :** Dneasy Tissue kit
- **RNA :** QIAzol + Rneasy mini kit
- **Quality control :** Nanodrop, Qubit, Bioanalyzer
- **Sequencing :** Illumina pairé, PacBio

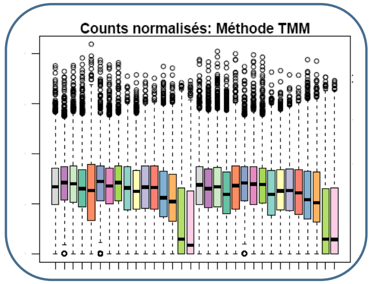
Computational methods



Automatic annotation of genomes
Reconstruction of metabolic pathways using Pathway Tools



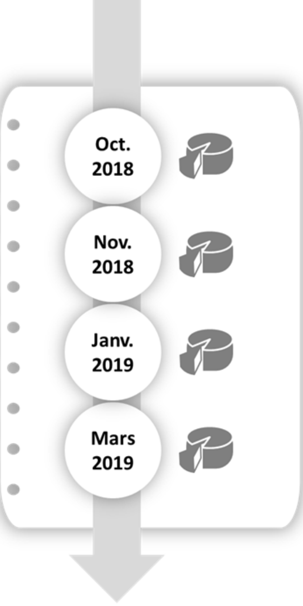
Metatranscriptomics
Reads mapping using Bowtie
Reads counting using htseq count

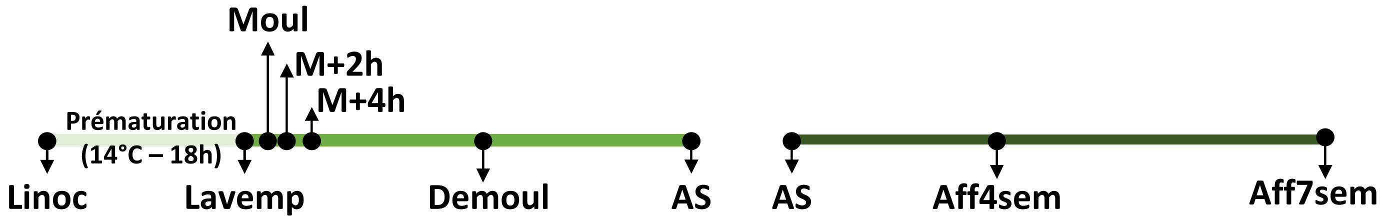


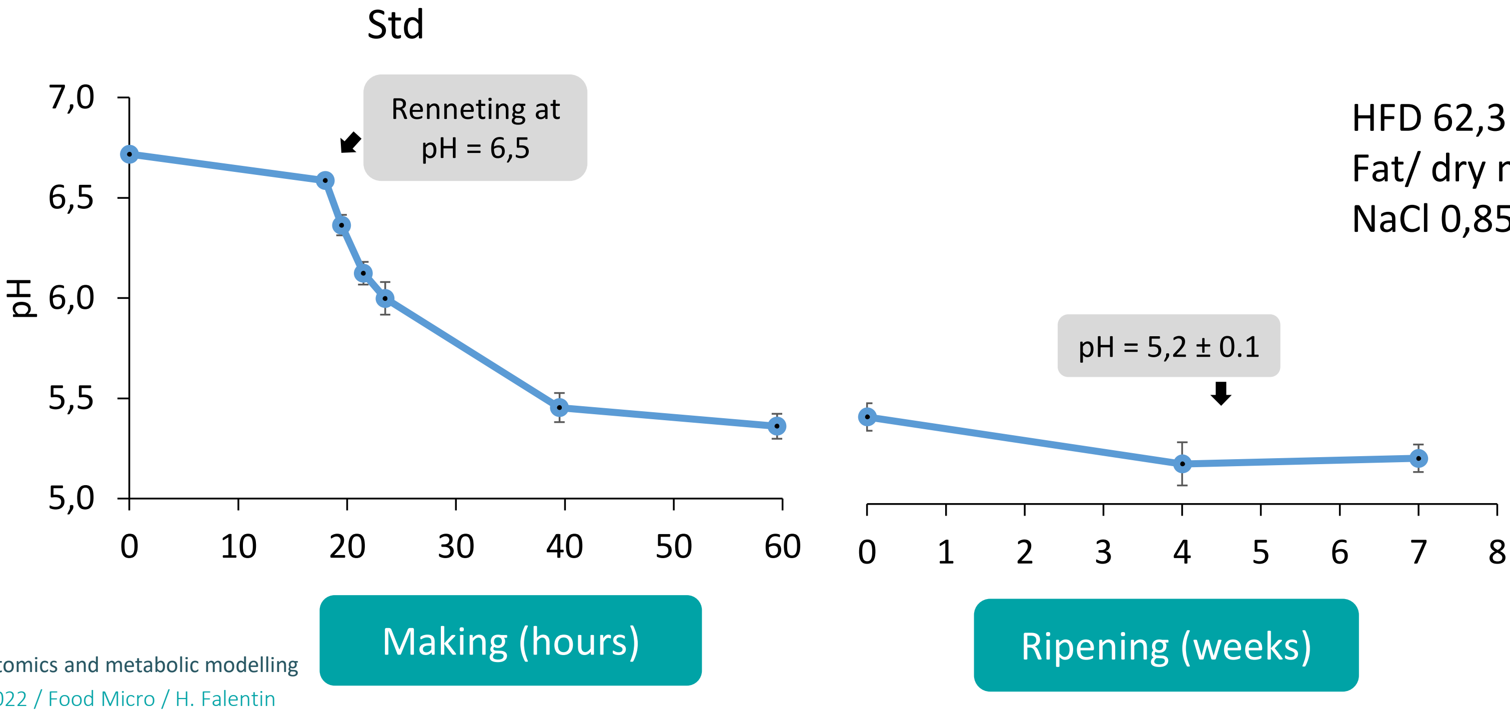
Normalisation using TMM multi species
Identification of DE genes using EdgeR
Significativity padj< 0.05

Langmead et al., 2009
Robinson et al., 2010
Karp et al., 2021

Repeatability of semi hard cheeses (X4)

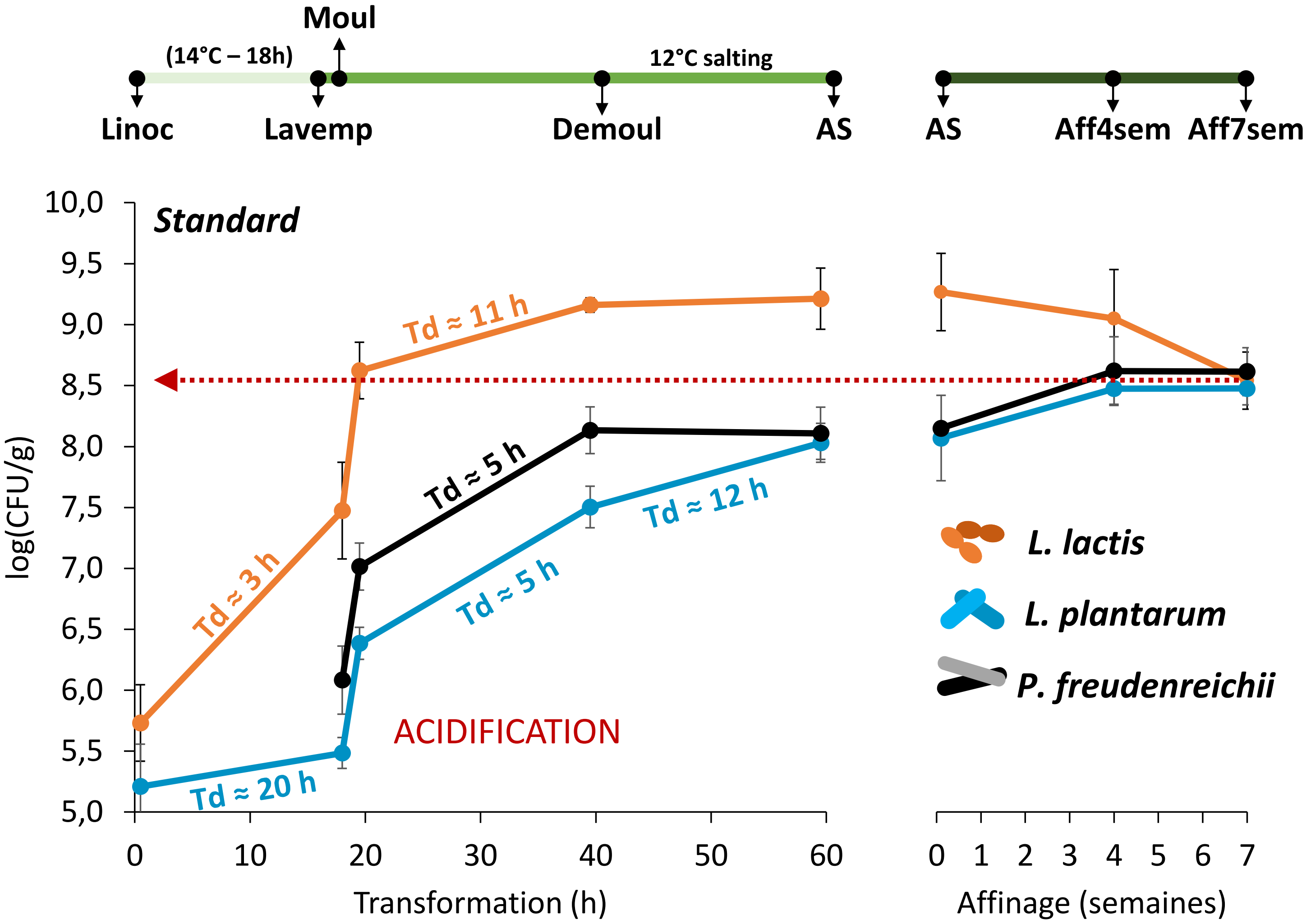






HFD 62,3 %
Fat/ dry matter 47,5 %
NaCl 0,85 g / 100 g

Lactic and propionic bacterial growth



Td : time of doubling

Cao et al. 2021, J. Agric. Food Chem.

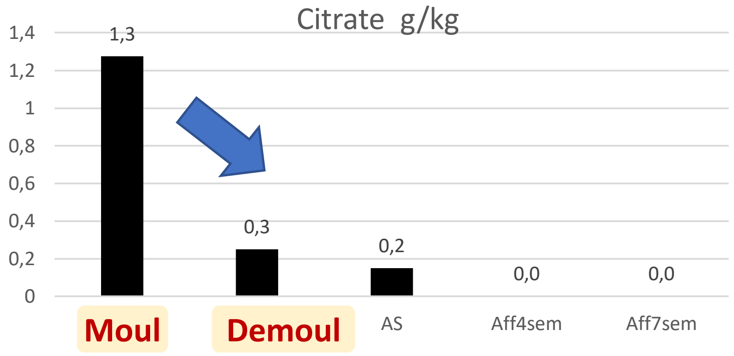
Assembly and genome annotations

	Replicon	Seq length	% GC	CDS	tRNA	rRNA
***L. lactis* 1206**	**Chromosome**	**2 365 039**	35,34	2417	62	19
	plasmid 1	59 643	34,85	67	0	0
	plasmid 2	36 823	34,41	42	0	0
	plasmid 3	8 277	34,81	12	0	0
	plasmid 4	8 243	30,60	8	0	0
	plasmid 5	4 632	36,25	5	0	0
	plasmid 6	3 597	33,28	2	0	0
	plasmid 7	2 119	34,21	3	0	0
***L. plantarum* 465**	**Chromosome**	**3 121 980**	44,72	3016	67	16
	plasmid 1	40 748	39,81	40	0	0
	plasmid 2	30 463	41,80	27	0	0
	plasmid 3	9 152	36,21	13	0	0
	plasmid 4	2 012	37,87	2	0	0
***P. freudenreichii* 122**	**Chromosome**	**2 688 484**	67,21	2589	45	6

→ Metatranscriptomics : mapping of RNA reads / genomes

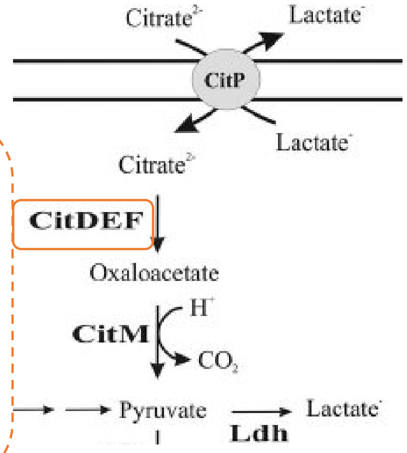
Citrate utilization by *Lc. lactis*

Moulding > Demoulding



*cit*CDEFG
LLACBIA1206_v1_1311-1316

Induction logFC X 2-3 by
L. lactis

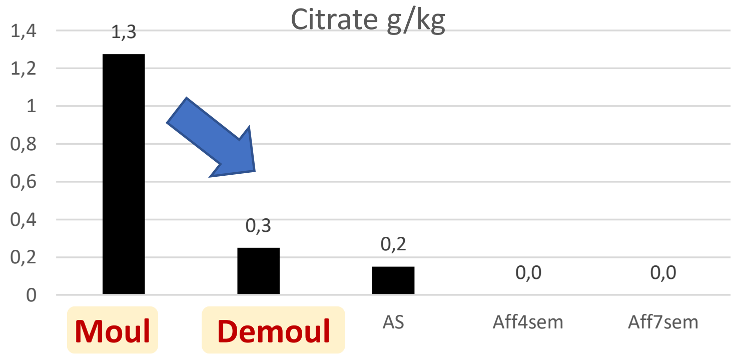


LLACBIA1206_v1_pc0002
LLACBIA1206_v1_1007

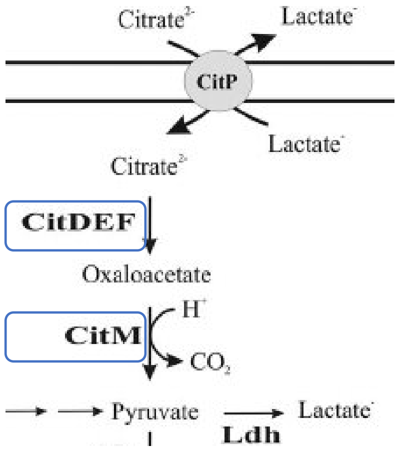
Modified from Garcia-Quintas et al. 2008, AEM

Citrate utilization by *L. plantarum*

Moulding > Demoulding



LPLABIA465_v1_0482



Induction logFC X15 chez *L. plantarum*

*cit*MCDEF
LPLABIA465_v1_0962-0966

Induction logFC X13-16 chez *L. plantarum*

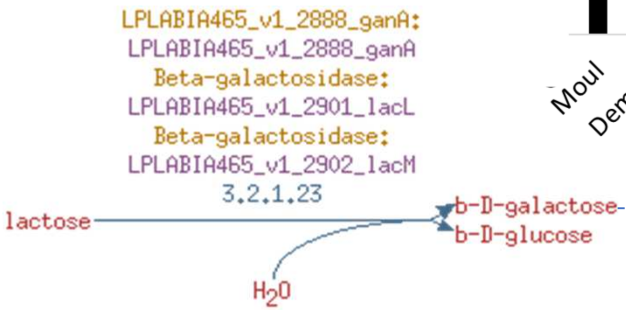
Metabolic interaction = competition for citrate

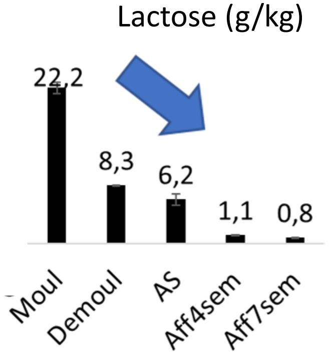
Fonctional redondancy using the same pathway induced at the same time in *L. lactis* et *L. plantarum*

Lactose utilization by *L. plantarum*

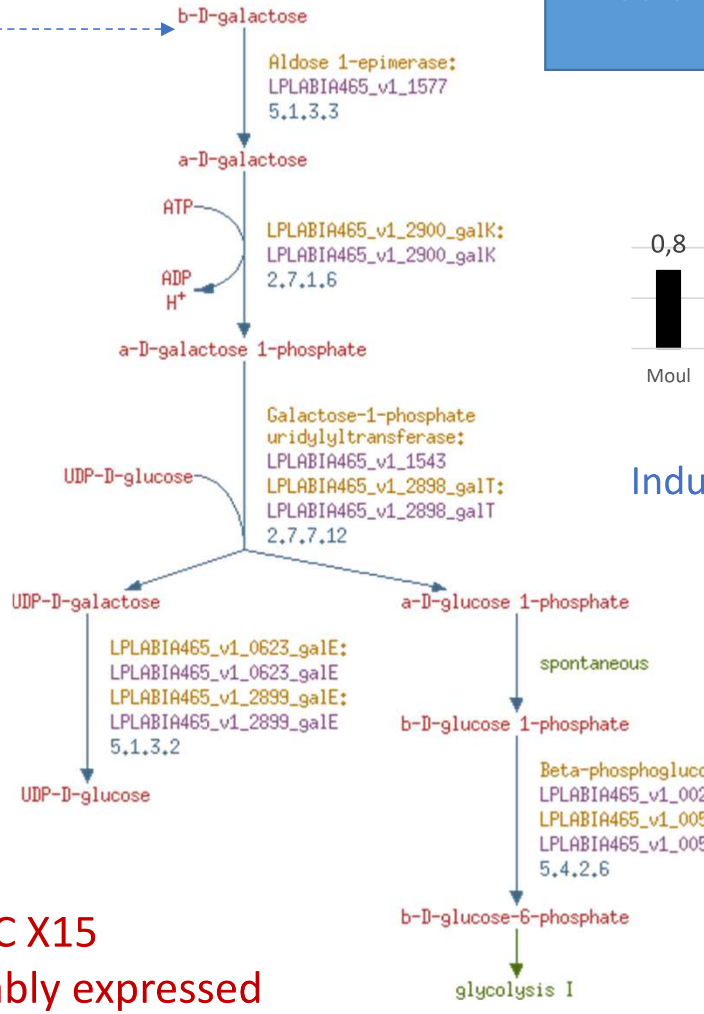
Moulding > Demoulding

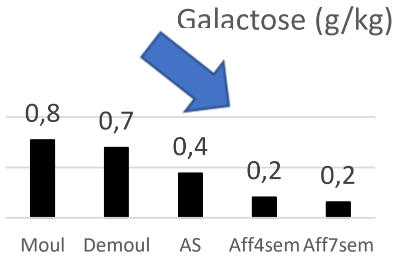
*lac*LM
Induction logFC X 6-7



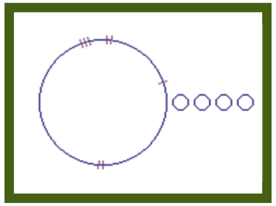


Leloir pathway





*gal*RTEK
Induction logFC X 5-6

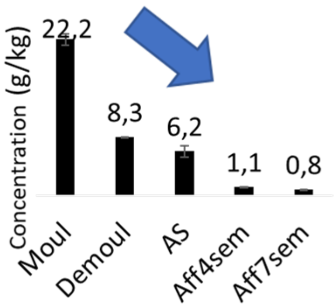


MicroScope

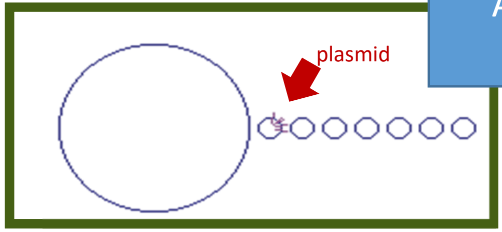
In P. freudenreichii induced logFC X15
In L. lactis same pathway but stably expressed

Lactose utilization by *Lc. lactis*

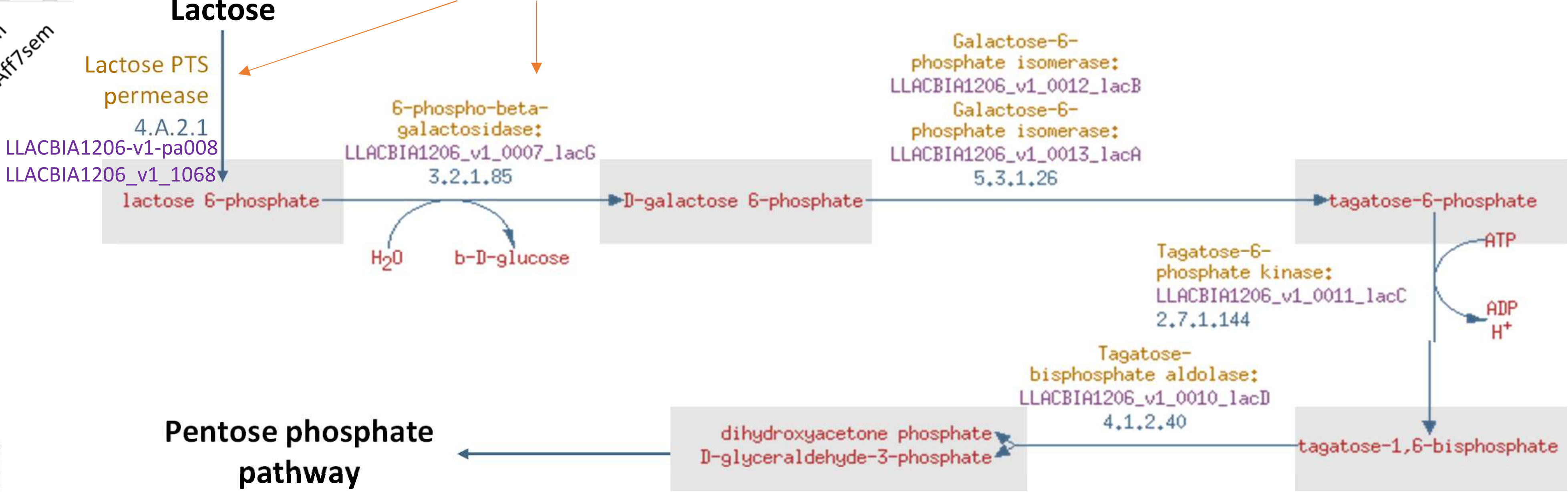
Lactose (g/kg)



AFF4sem > AFF7sem



Plasmidic induction logFC X2

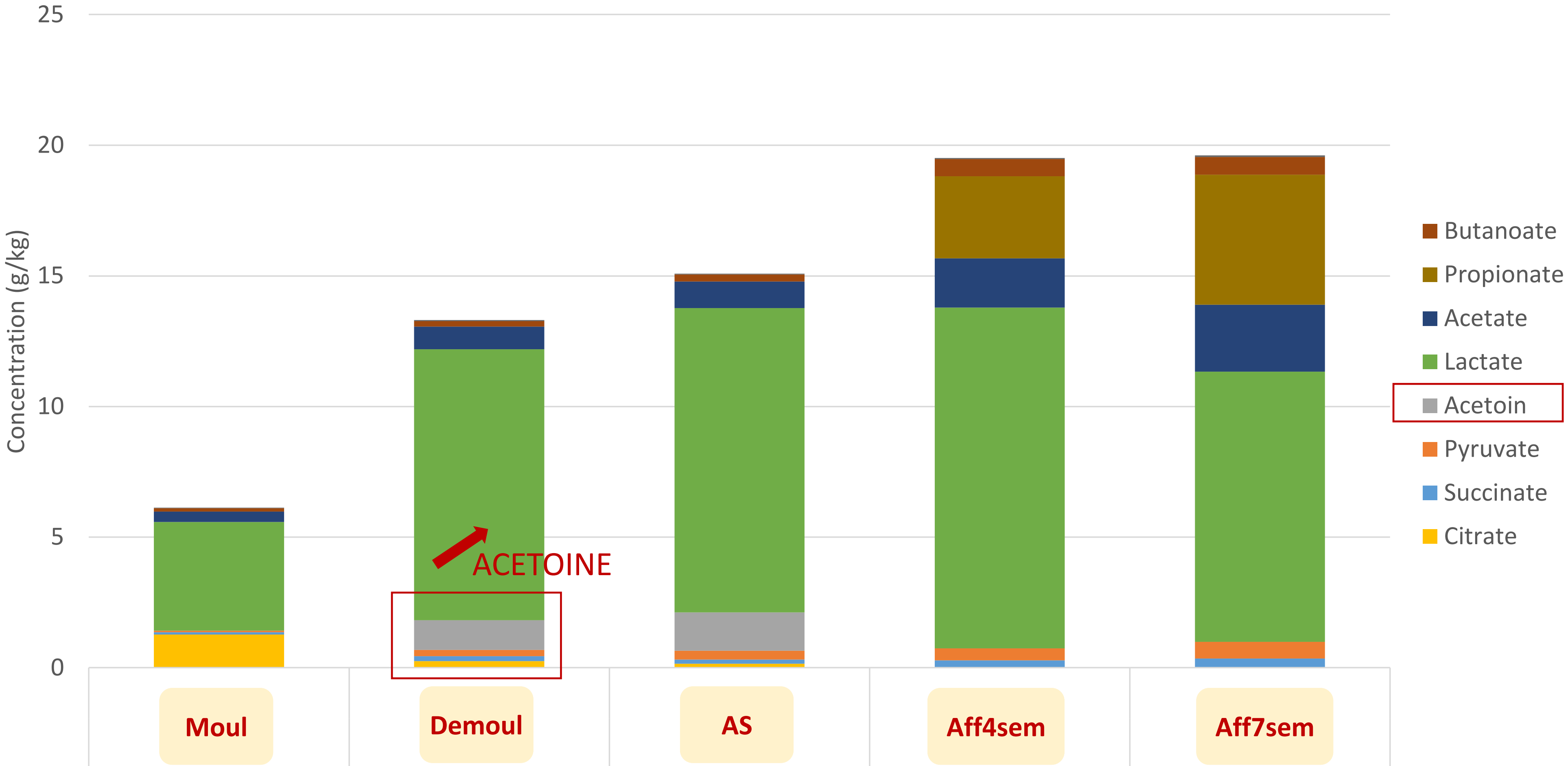


Pathway in agreement with Raynaud et al. 2005

Metabolic interaction = competition for lactose

Functional redondancy with different pathways induced at different times

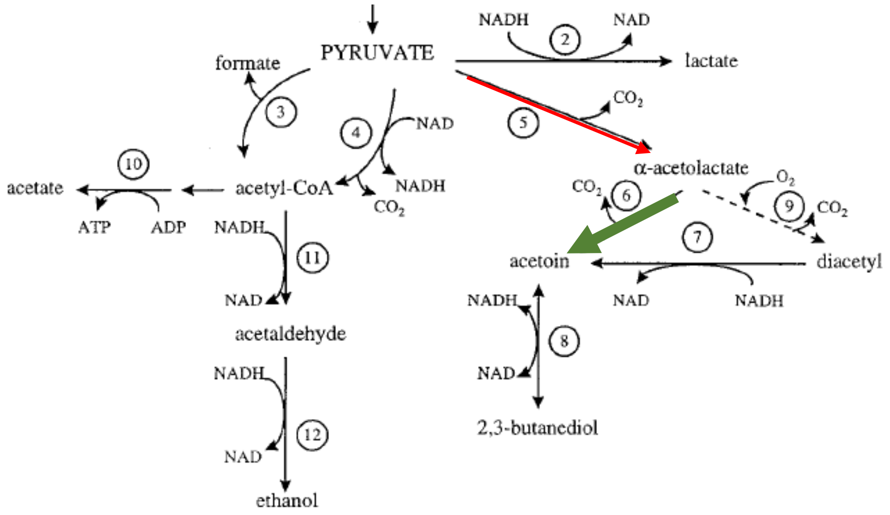
Production of acetoin (cheesy aroma coumpound)



Cao et al. 2021, J. Agric. Food Chem.

Production of acetoin

Moulage > démoulage



Acetolactate synthase 2.2.1.6 (*als*)

→ Induction x2-4 logFC in *Lc. lactis* and *L. plantarum*

Acetolactate decarboxylase 4.1.1.5 (*ald*)

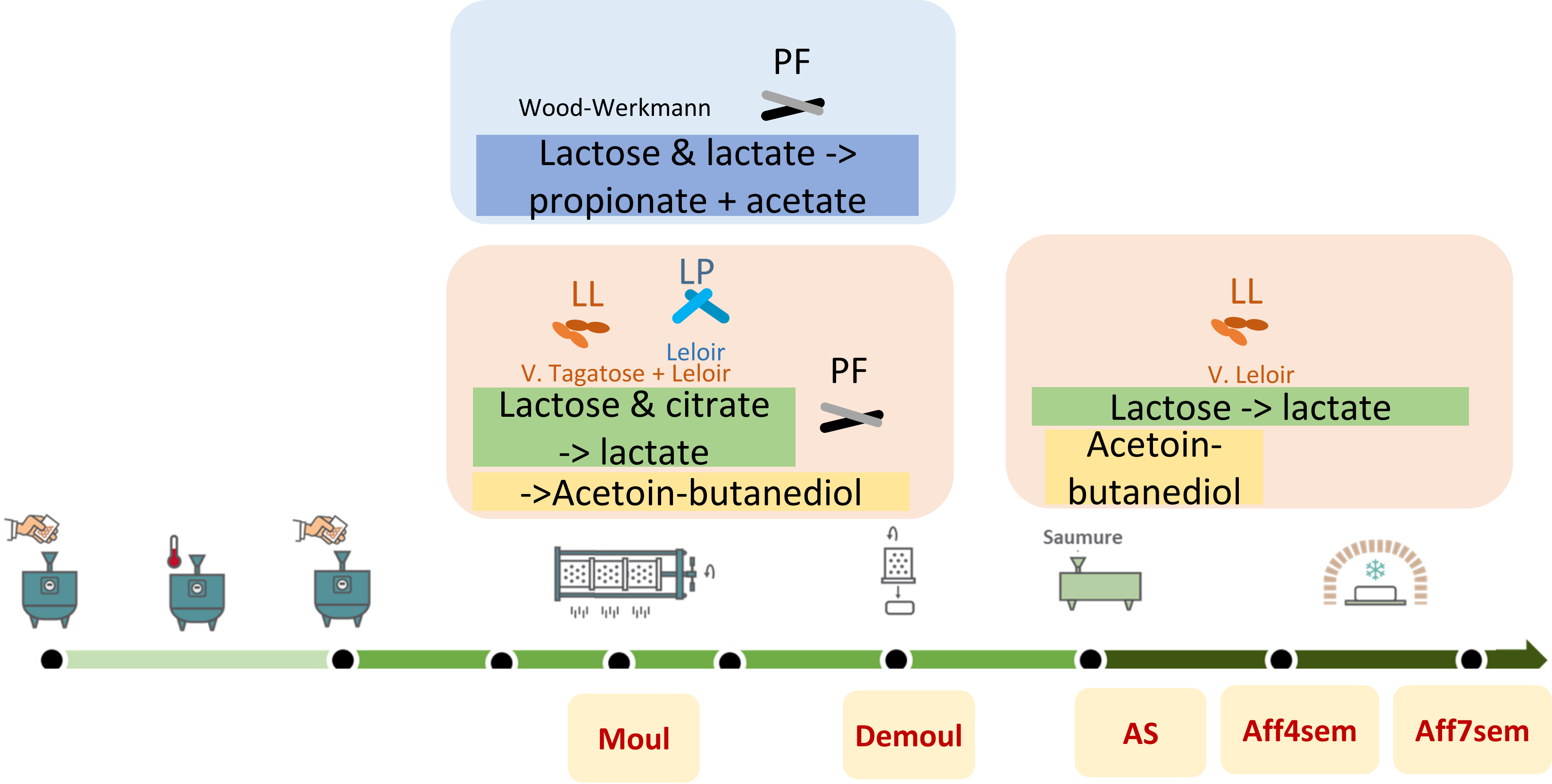
→ Induction *14 logFC in *P. freudenreichii*

Modified from Boumerdassi et al. 1997 AEM

→ Interaction: division of labor

Functional redondancy with specific inductions of genes

Successive carbon metabolisms by each species



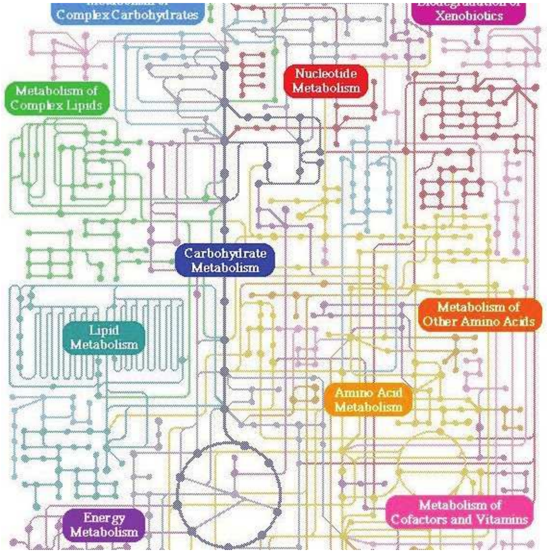
Team spirit of bacteria for degradation and production…
but do they exchange metabolites ?

Metabolic modeling to identify metabolite exchanges

INRIA-INRAE PhD student Maxime Lecomte

Annotated genome

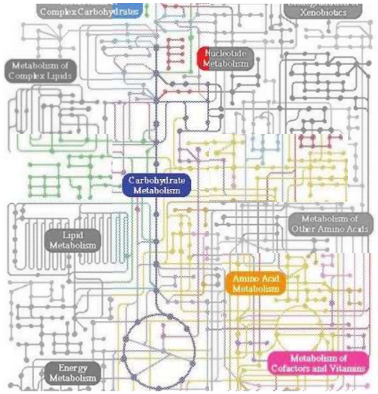
automatic
+ manual curation



Metabolic network

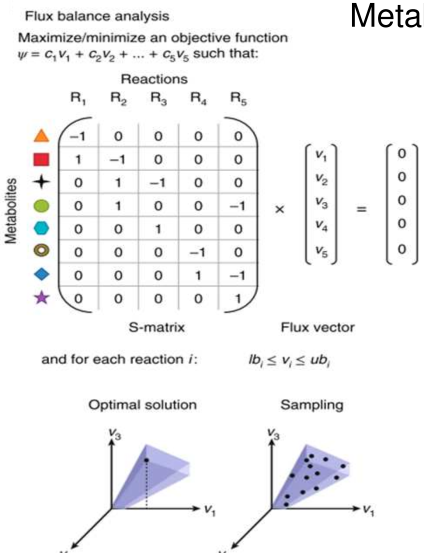
Modelisation

INPUT
Molecules present in milk



Metabolic network

OUTPUT
Microbial metabolites



$$\begin{array}{c} \\ \\ \end{array}\begin{pmatrix} -1 & 0 & 0 & 0 & 0 \\ 1 & -1 & 0 & 0 & 0 \\ 0 & 1 & -1 & 0 & 0 \\ 0 & 1 & 0 & 0 & -1 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

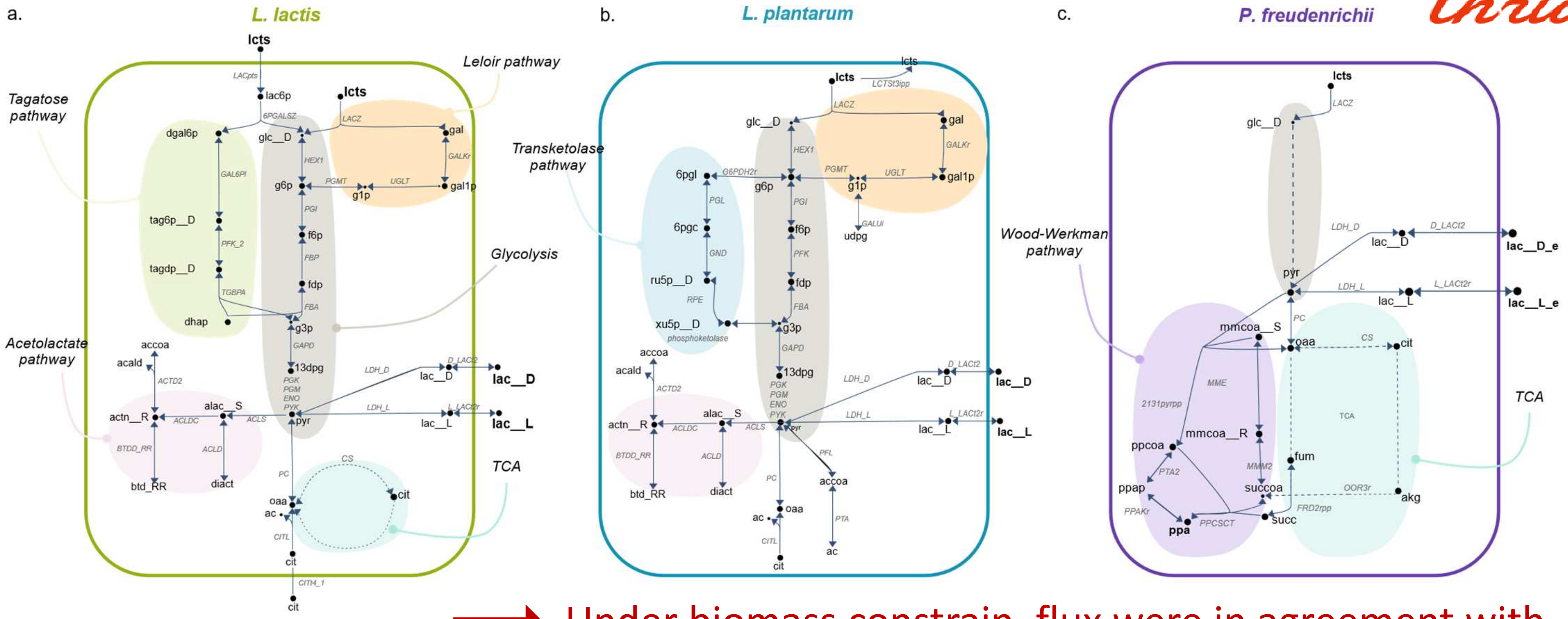
Méthodologies :

- Qualitative using CarveMe
- Quantitative modelling (FBA): parameters were adjusted using data from single strain culture grown in milk

Machado et al. 2018.
Orth et al. 2010

Overview of carbon metabolism of the 3 strains

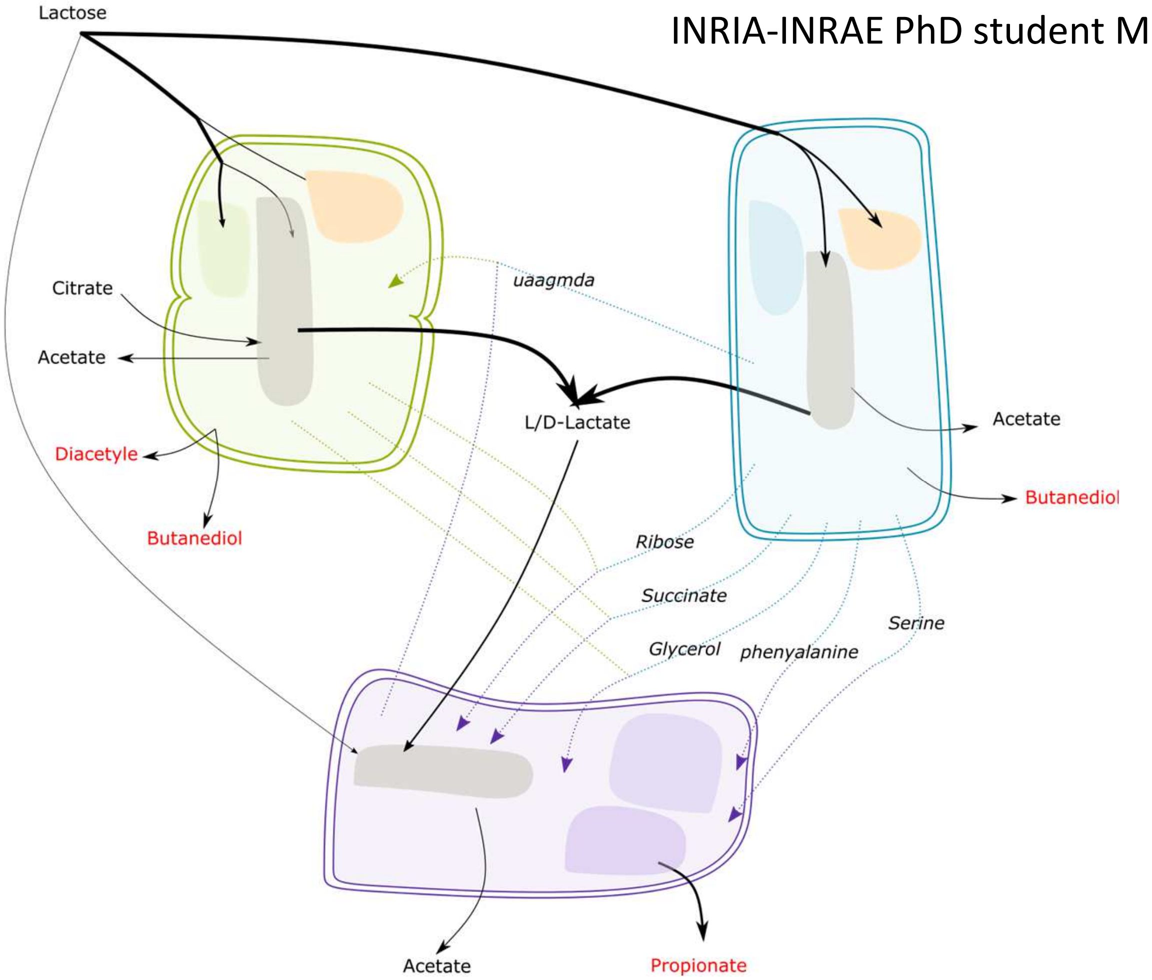
INRIA-INRAE PhD student Maxime Lecomte



Under biomass constrain, flux were in agreement with metatranscriptomics and targeted metabolomics

Modèle métabolique à l'échelle de l'écosystème : identification d'interactions

INRIA-INRAE PhD student Maxime Lecomte

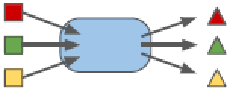


Logiciel Smetana
Zelezniak et al. 2015 PNAS

Identification of potential interaction to be validated

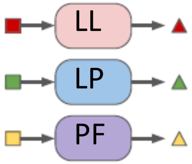
Take home messages

✓ Identification of induced pathways in each species



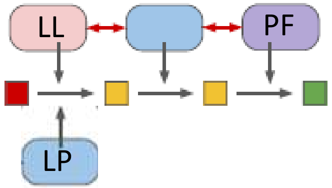
✓ Giving snapshots of successive metabolisms during cheese making

- Microbial competition for citrate and lactose utilization



Citrate
Lactose

- Division of labor for the production of acetoin



acetoin

✓ Metabolic modeling gives clues of metabolite exchanges between species

Perspectives

This strategy can be applied to any fermented food to decipher metabolisms and interactions.

Since, most identified pathways are species and strain-dependant …

This kind of knowledge opens new avenues to select and combine strains to develop new fermented food products.

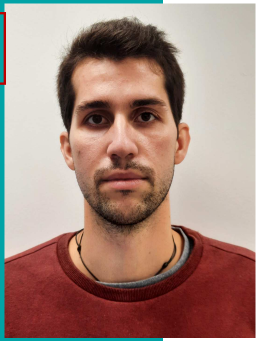
Thank you for your attention

Hélène Falentin
Stéphanie Deutsch
Sandrine Parayre
Anne Thierry
Wenfan Cao

Marie-Bernadette Maillard
Gilles Garric
Marielle Harel-Oger
Arlette Leduc

Françoise Boissel
Jean-Luc Thomas
Bénédicte Camier
Clémence Frioux

Simon Labarthe
Maxime Lecomte
Julie Aubert
Solène Le Fur
David Sherman
Clémence Frioux



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Cirm
Bactéries d'Intérêt Alimentaire

migale

MicroScope

Inria