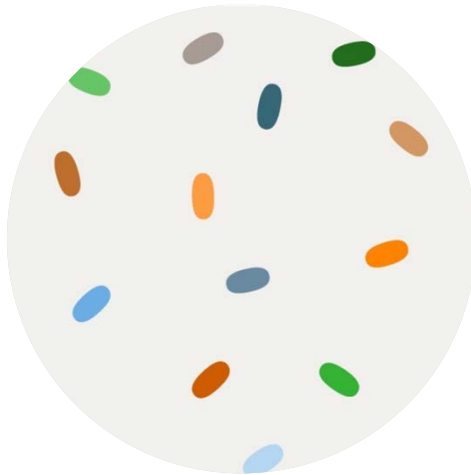


# The use of omics in exposure assessment

Heidy den Besten, Jeanne-Marie Membré

Alejandro Amézquita, Sara Bover-Cid, Stéphane Dagnas,  
Mariem Ellouze, Sandrine Guillou, George Nychas, Cian  
O'Mahony, Fernando Pérez-Rodriguez



# QMRA

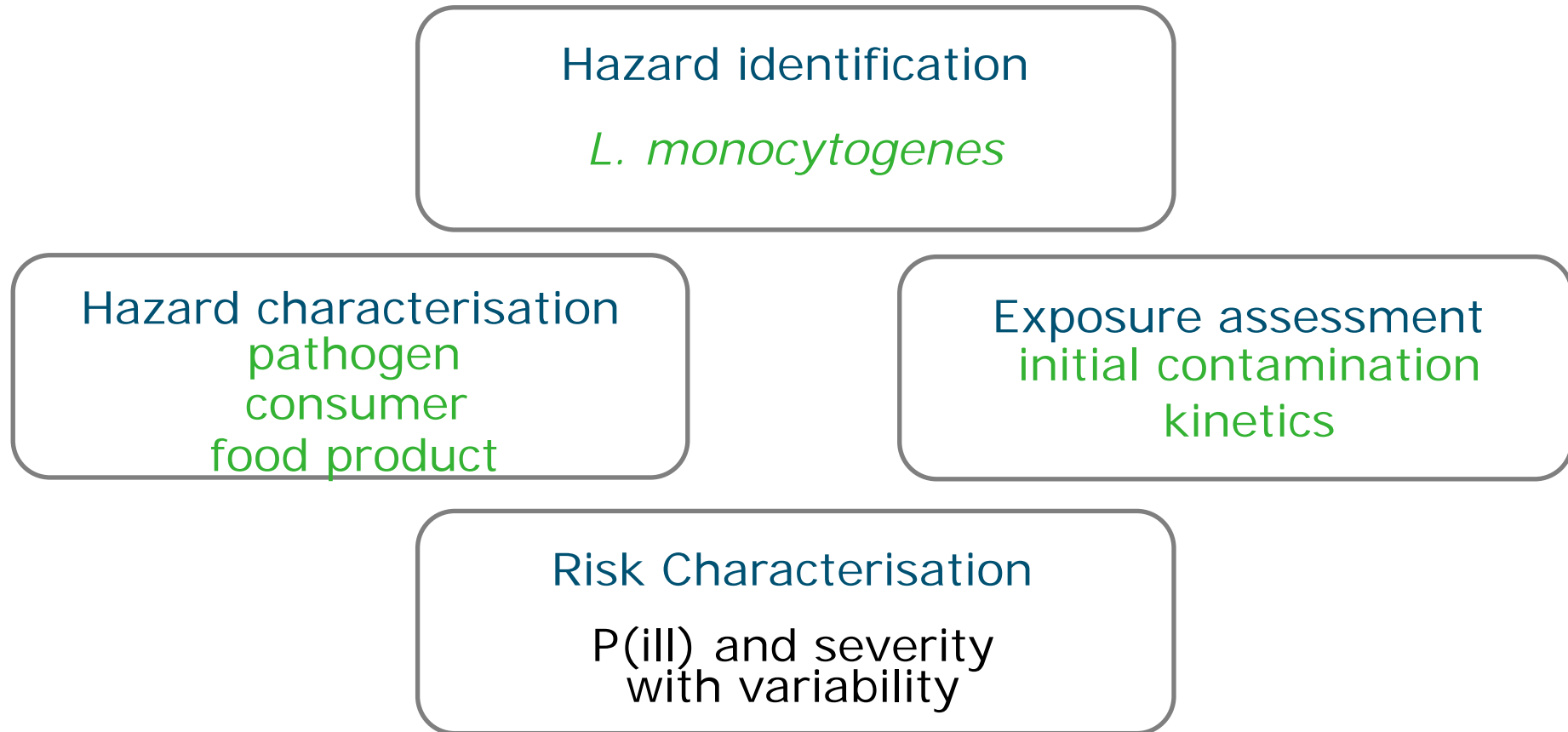
Hazard identification  
potential adverse health effect

Hazard characterisation  
P(ill) and severity  
as function of dose

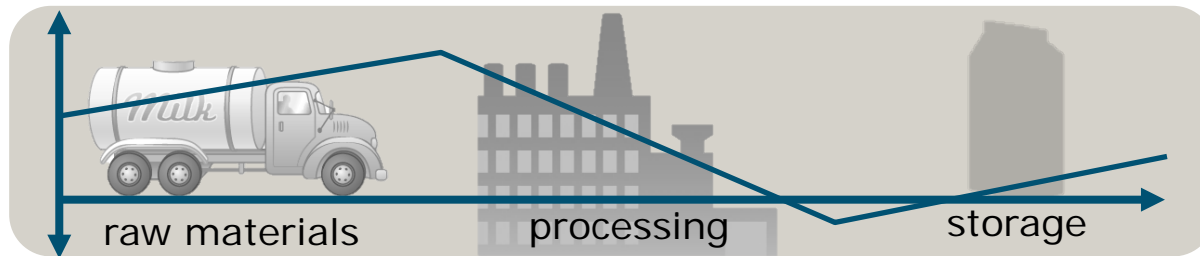
Exposure assessment  
dose at consumption

Risk Characterisation  
P(ill) and severity  
with variability

# QMRA



# How will my troublemaker(s) behave?

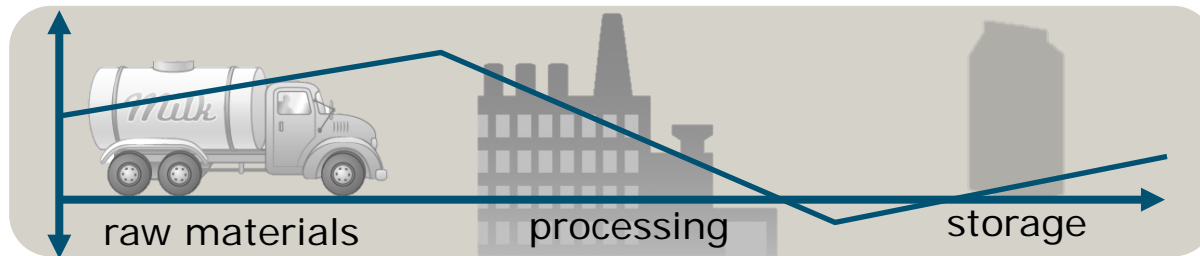


## Exposure assessment

Levels and kinetics

Quantification of growth, inactivation, survival, contamination

# How will my troublemaker(s) behave?



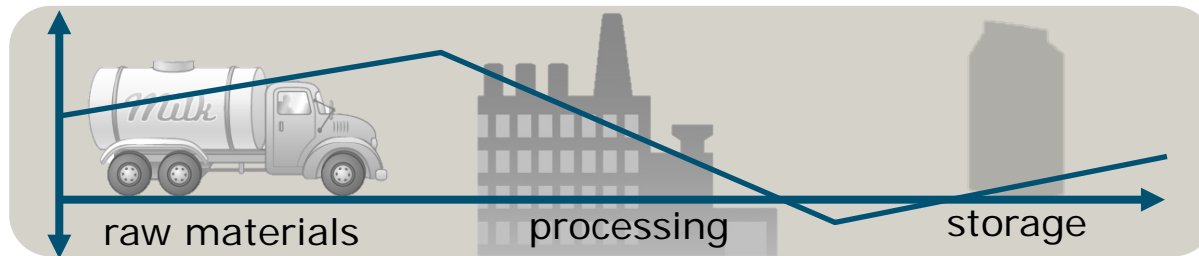
## Exposure assessment

phenotypic experiments  
quantitative microbiology

Output: characteristic numbers

**Rank effects and prioritize**

# How will my troublemaker(s) behave?



## Exposure assessment

Balance of each stage

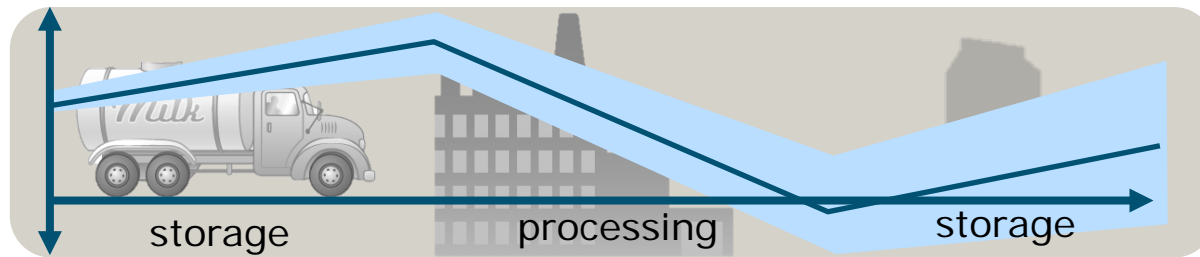
out=(in + cont.)\* inactivation or growth

$$N_{\text{out}} = (N_{\text{in}} + r_c)e^{kt}$$

or

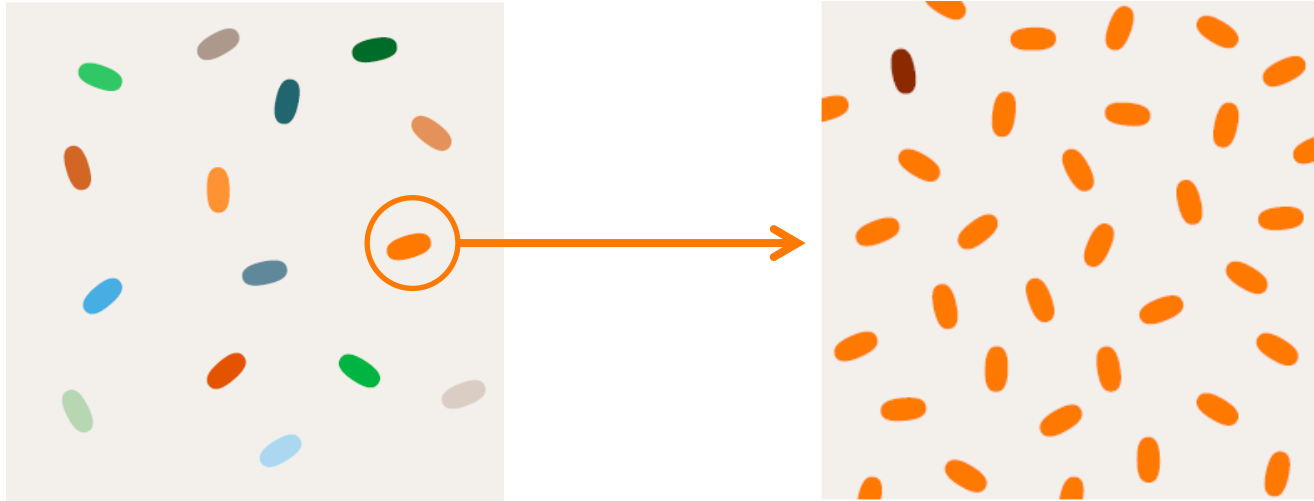
$$N_{\text{out}} = (N_{\text{in}} + r_c)e^{\mu t}$$

# How could omics makes a difference?



- Predicting pathogen behaviour variability
- Understanding dynamics in complex food eco-systems

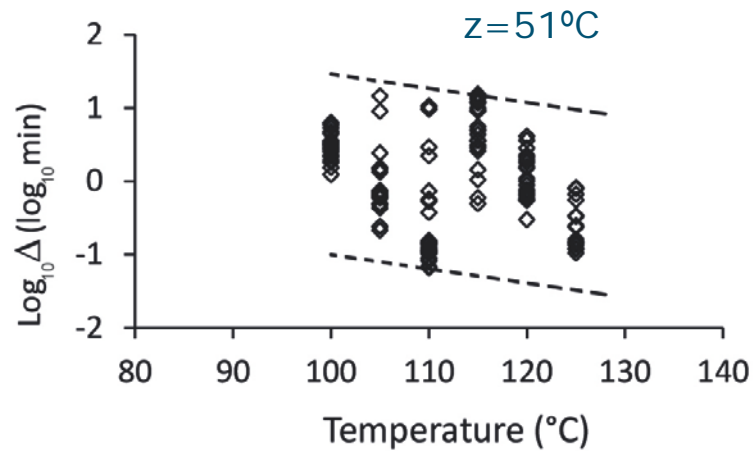
# Microbiological variability



- Strain variability
- Population heterogeneity

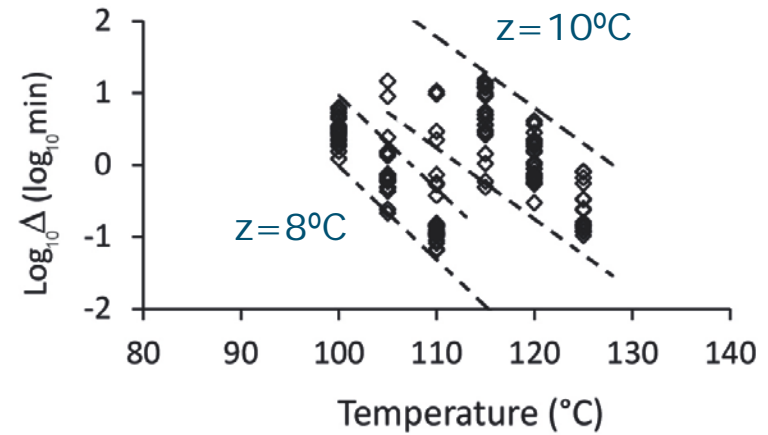
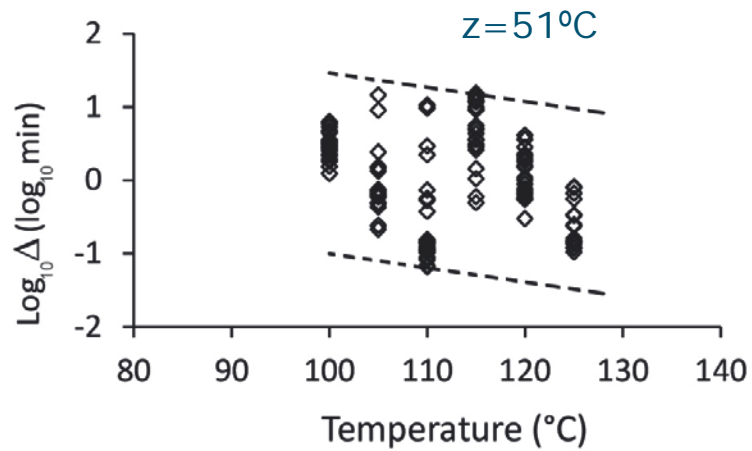


# Strain variability



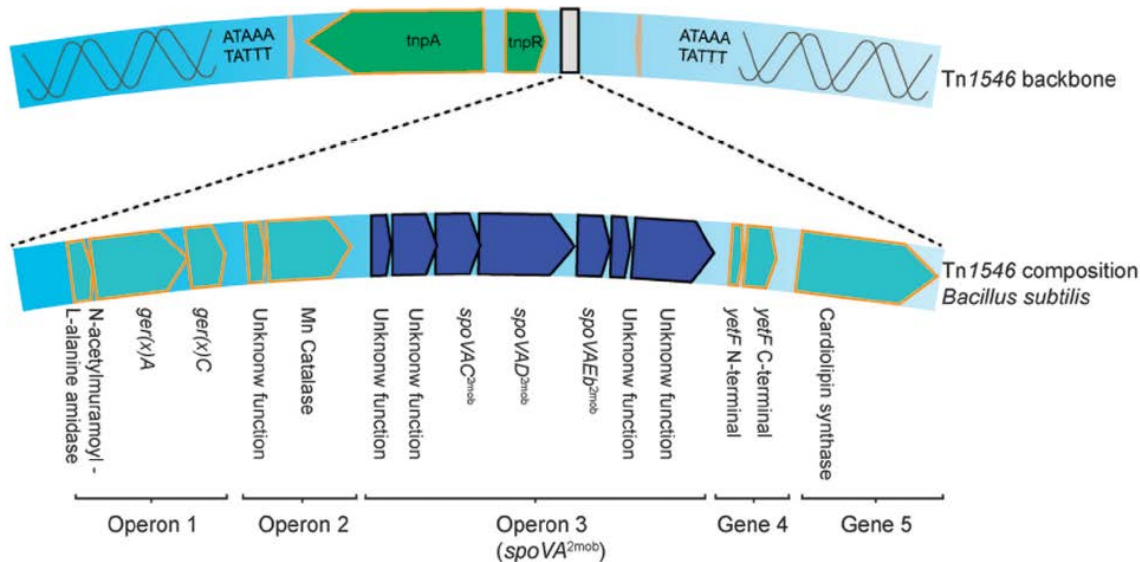
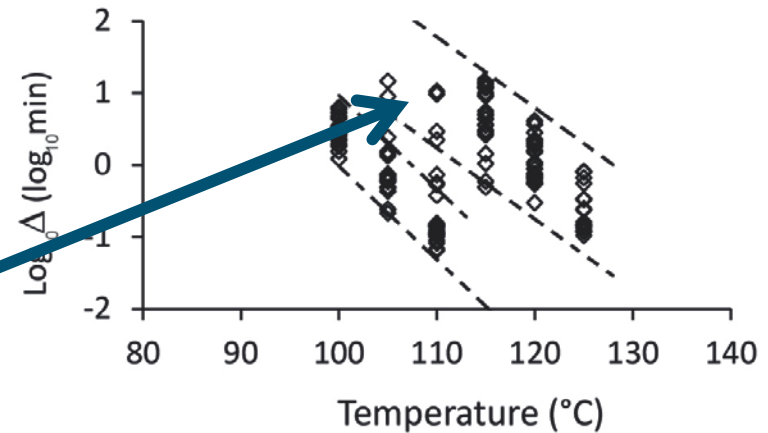
*B. subtilis*  
spores  
20 strains

# Strain variability



# Strain variability and biomarker

- Genetic element only present in heat resistant group
- Genetic biomarker for robustness



Berendsen et al., 2016  
Den Besten et al., submitted  
NIZO Food Research, TIFN

# Mechanistic insight to fine-tune EA

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- Biomarkers for robustness can be used to make subgroups
- Fine tune EA taking into account phenotypes of the subgroups

# Mechanistic insight to fine-tune EA

- *B. cereus* group: seven major phylogenetic groups
- Differences in Temp growth ranges between groups

Group	% strains with growth at:												
	4°C	5°C	7°C	8°C	10°C	15°C	20°C	37°C	40°C	43°C	45°C	50°C	55°C
VII	0	0	0	0	0	0	100	100	100	100	100	100	0
III	0	0	0	0	0	100	100	100	100	100	85	0	0
IV	0	0	0	0	100	100	100	100	100	83	58	0	0
I	0	0	0	0	75	100	100	100	100	25	0	0	0
V	0	0	0	14	100	100	100	100	100	0	0	0	0
II	0	0	73	87	100	100	100	100	100	0	0	0	0
VI	0	40	100	100	100	100	100	86	0	0	0	0	0

# Mechanistic insight to fine-tune EA

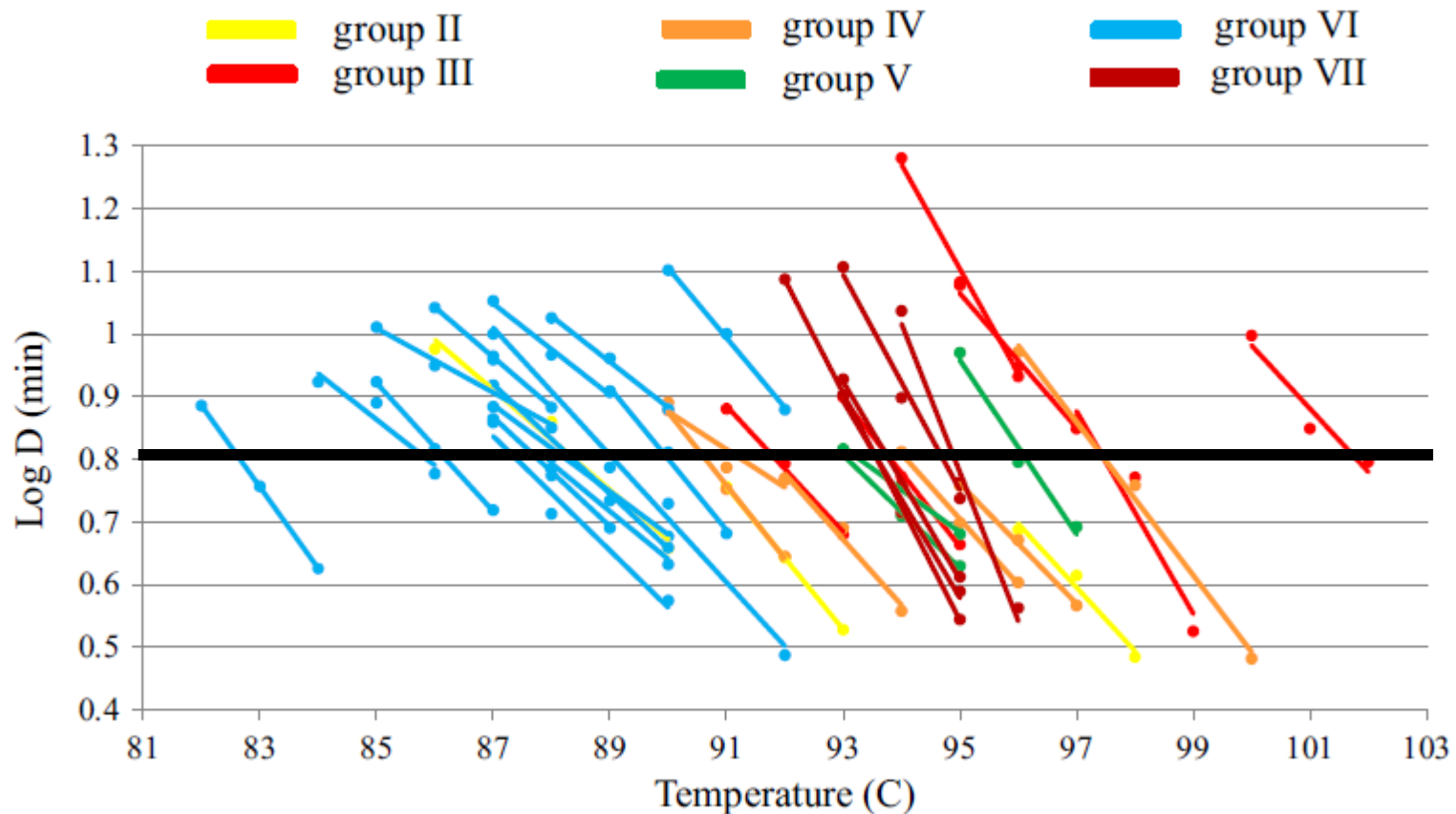
- *B. cereus* group: seven major phylogenetic groups
- Differences in Temp growth ranges between groups, pH limits and [NaCl] limits

Group	% strains with growth at a pH of				
	7.4	5	4.8	4.6	4.3
II	100	100	100	100	17
VII	100	100	100	100	25
III	100	100	100	88	25
I	100	100	100	83	0
IV	100	100	100	67	0
V	100	100	100	40	0
VI	100	100	67	17	0

Group	% strains with growth at a [NaCl] of				
	0.5%	5%	6%	8%	10%
II	100	100	100	100	100
VII	100	100	100	100	75
III	100	100	100	100	33
I	100	100	100	67	0
IV	100	100	100	40	0
V	100	100	83	0	0
VI	100	67	0	0	0

# Mechanistic insight to fine-tune EA

- Also clear difference in heat robustness



# Mechanistic insight to fine-tune EA

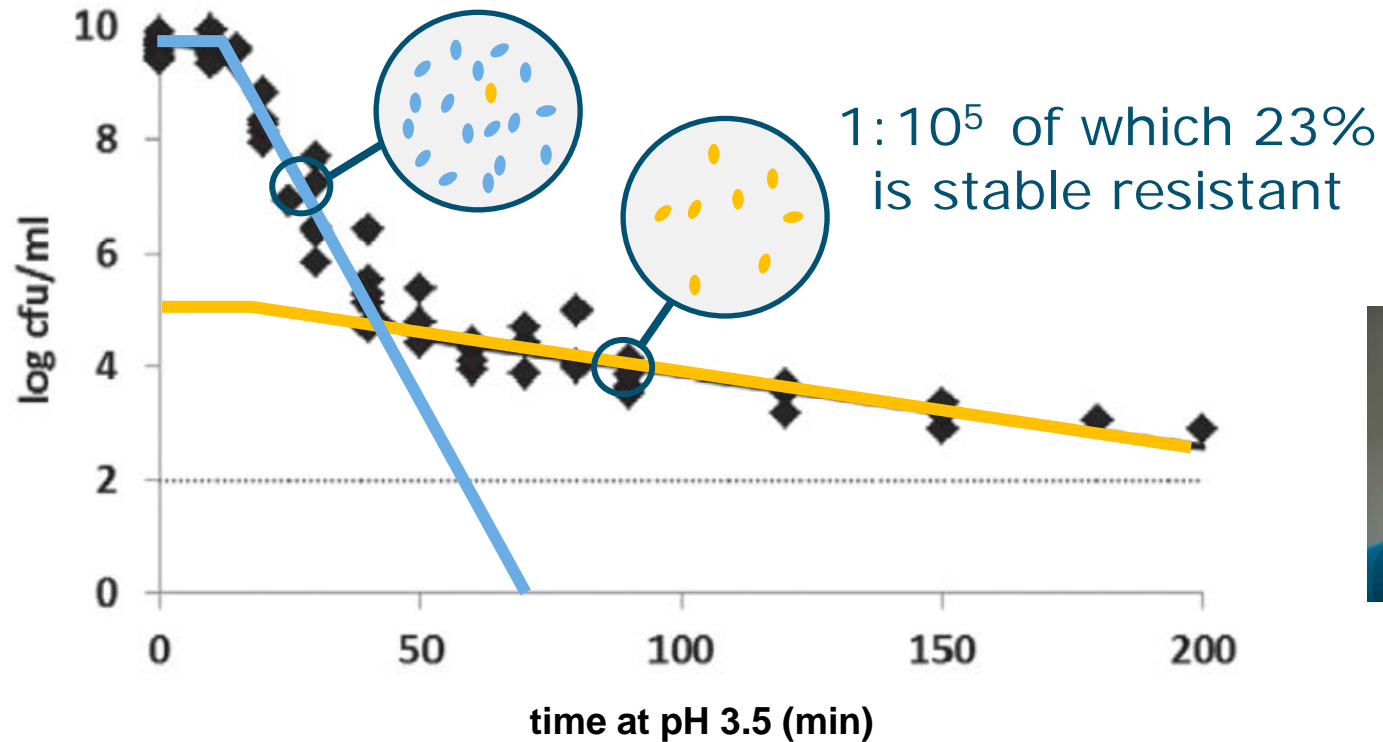
- Also clear difference in heat robustness

Group	$T_{\log D=0.8}$ (°C) $\pm$ SD	z-value (°C) $\pm$ SD
III	96.6 $\pm$ 3.5	8.4 $\pm$ 1.9
VII	94.3 $\pm$ 0.9	5.7 $\pm$ 0.9
V	94.1 $\pm$ 1.4	11.0 $\pm$ 3.8
IV	93.3 $\pm$ 2.6	10.5 $\pm$ 3.1
II	91.4 $\pm$ 2.7	10.2 $\pm$ 2.2
VI	88.5 $\pm$ 2.4	12.0 $\pm$ 2.9

- Subgrouping based on mechanistic insight provides more precision in EA than when taking the group as a whole



# Impact of population heterogeneity



Contents lists available at ScienceDirect

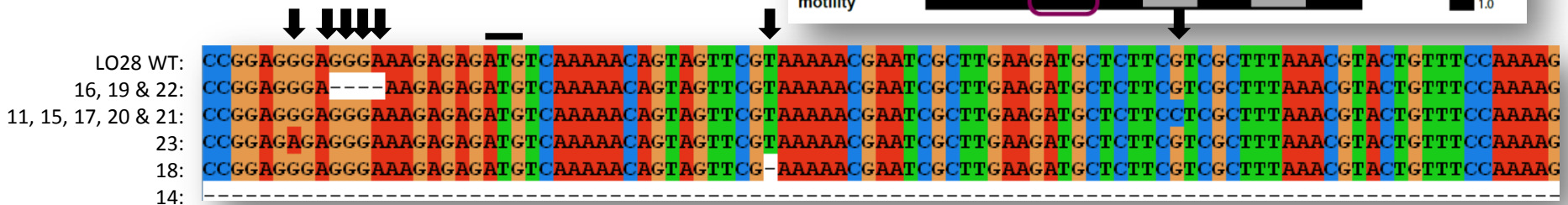
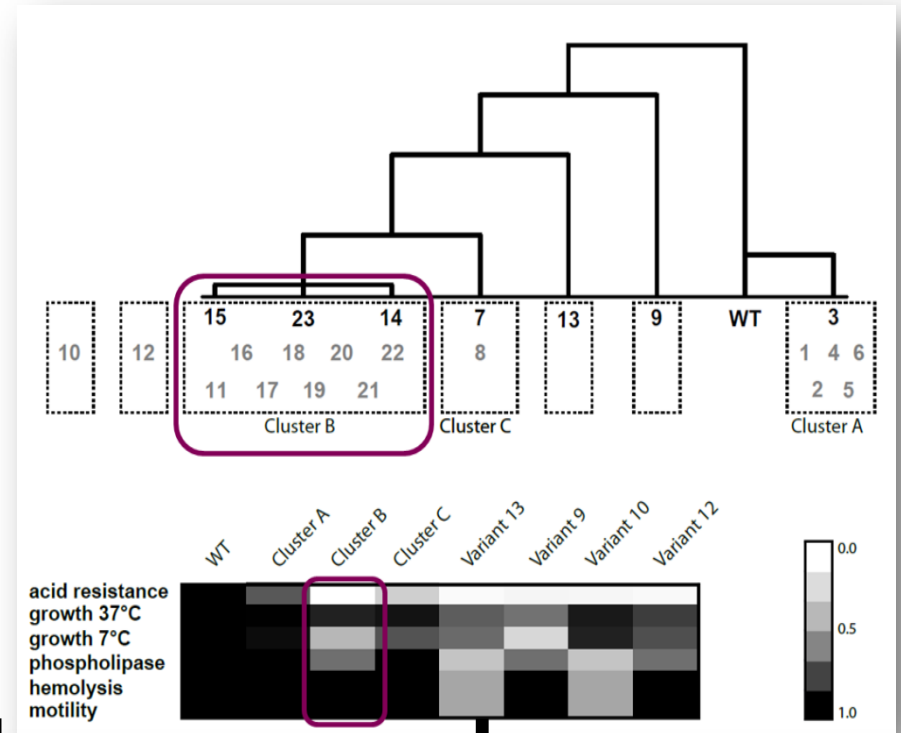
International Journal of Food Microbiology

journal homepage: [www.elsevier.com/locate/ijfoodmicro](http://www.elsevier.com/locate/ijfoodmicro)

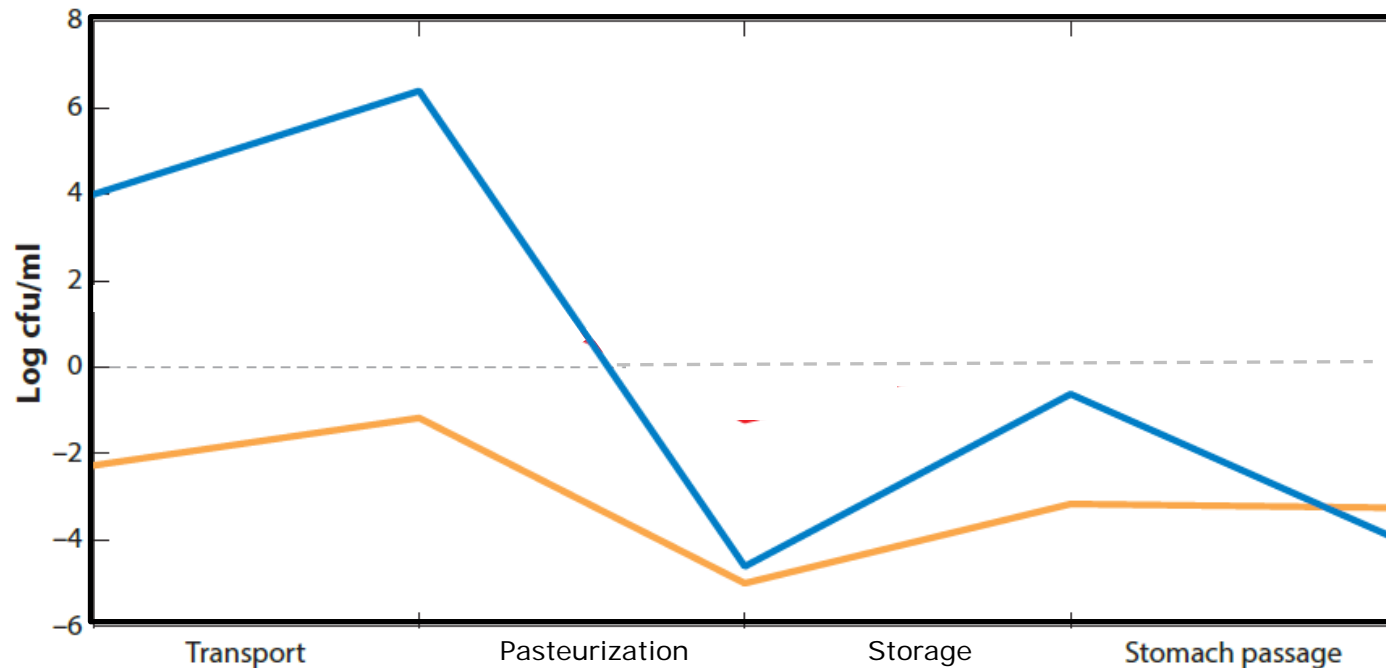
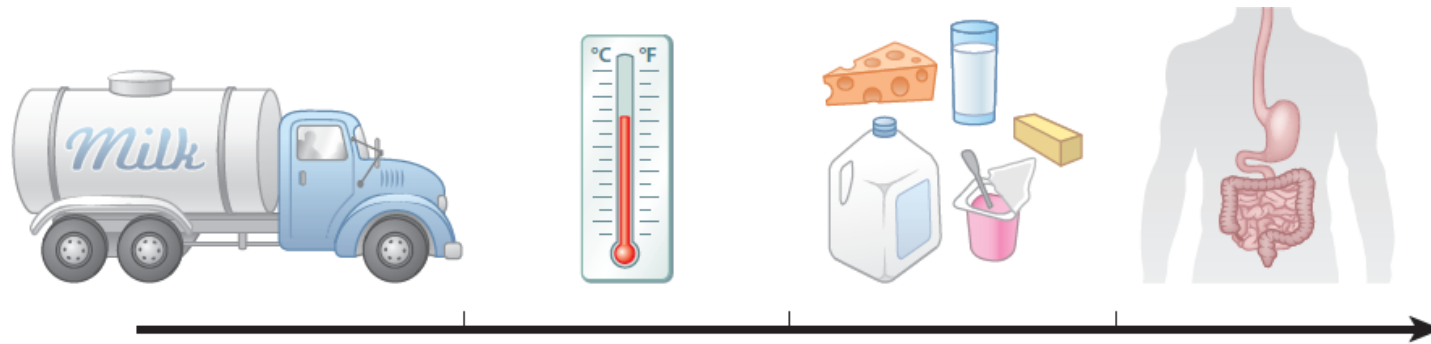


# Mechanism for increased resistance

## ■ Mutations in *rpsU* gene

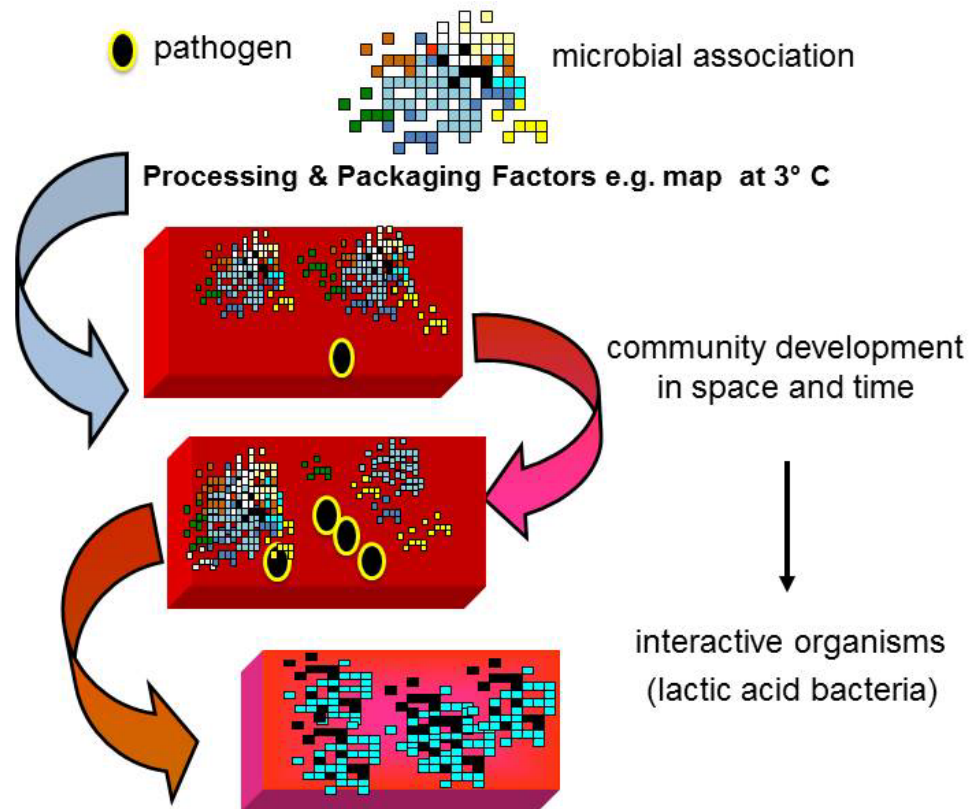


# Modelling population heterogeneity



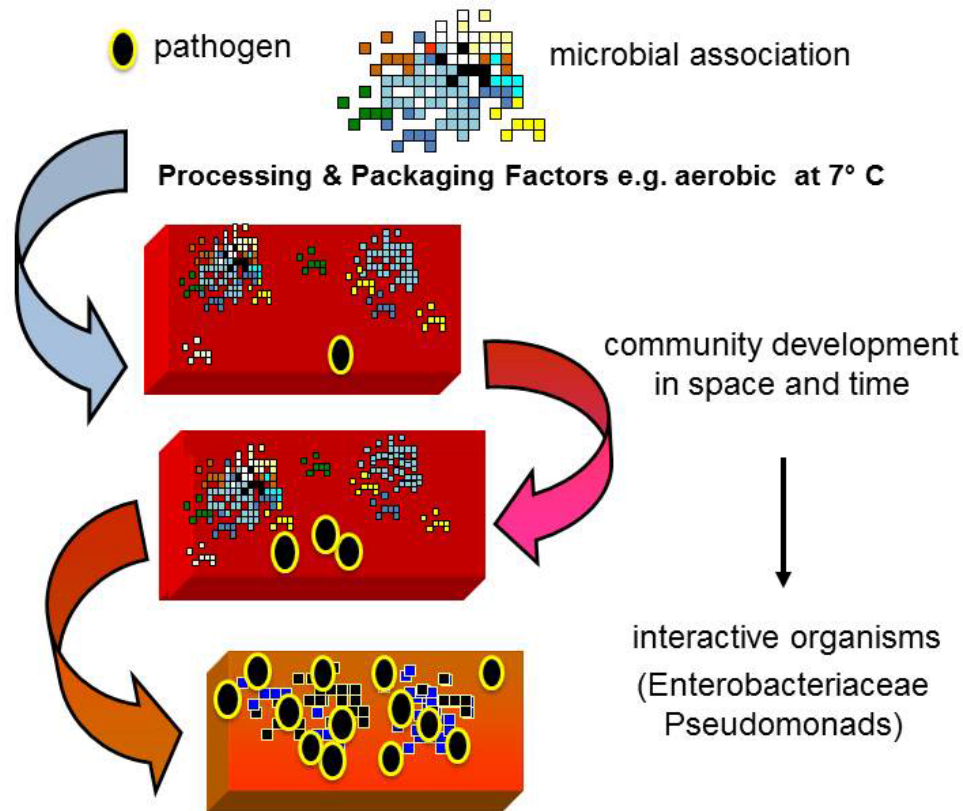
# Food ecosystem dynamics

- Microbial communities affect dynamics of pathogens



# Food ecosystem dynamics

- Microbial communities affect dynamics of pathogens

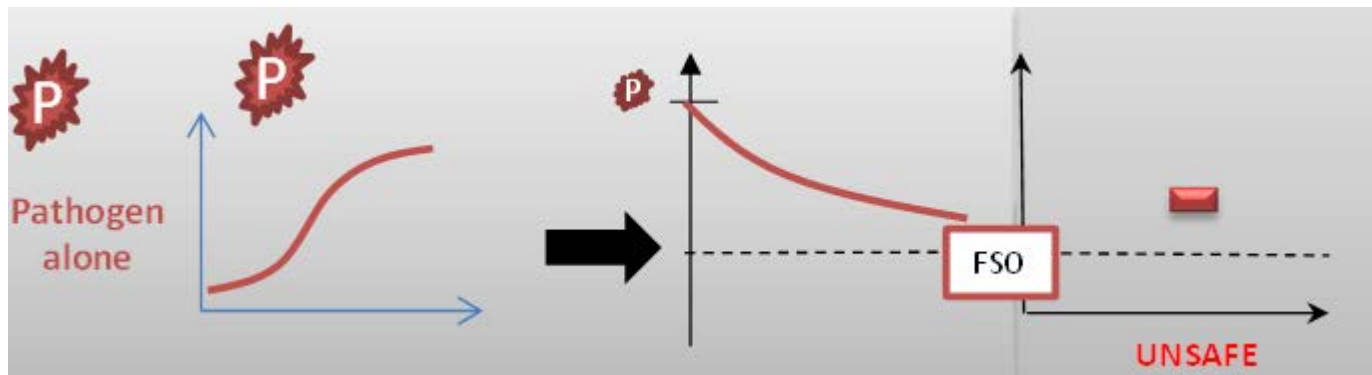


# Food ecosystem dynamics

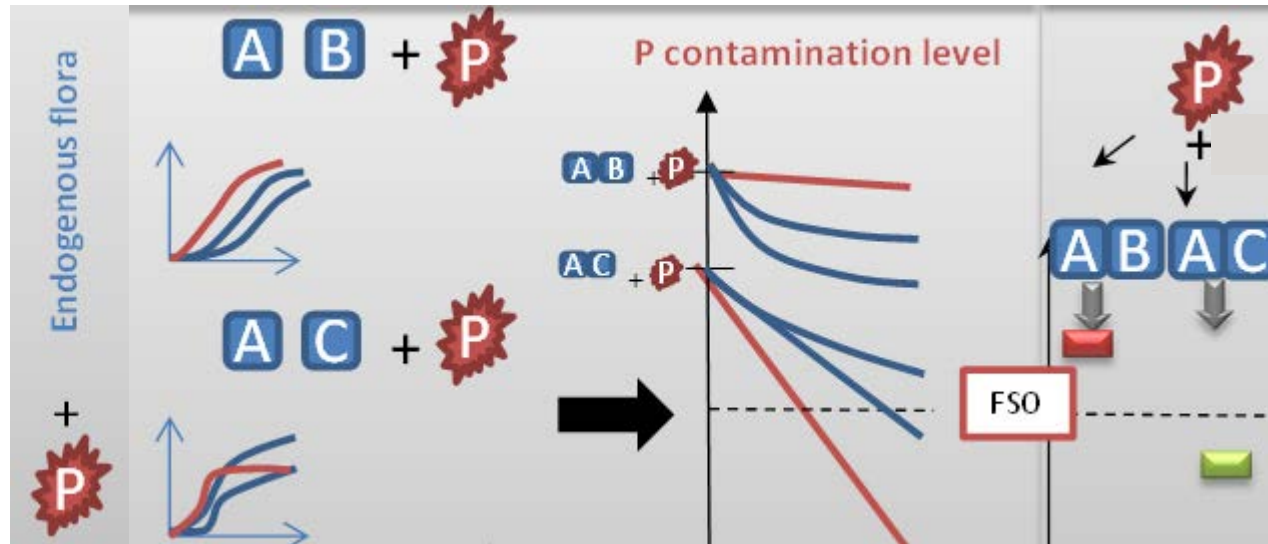
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- Microbial communities affect dynamics of pathogens
- Metagenomics to understand ecosystem dynamics
  - Characterise communities
  - Elucidate transmission routes

# Towards ecosystem modelling



# Towards ecosystem modelling

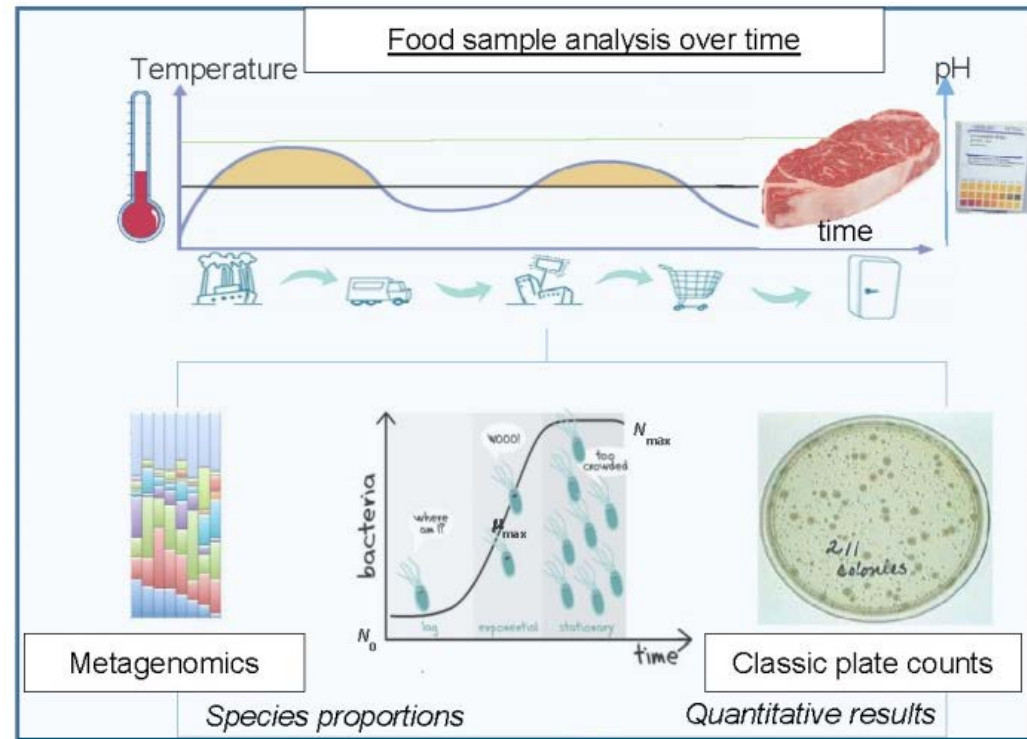


- Challenges: low prevalence of pathogens, multi species environments



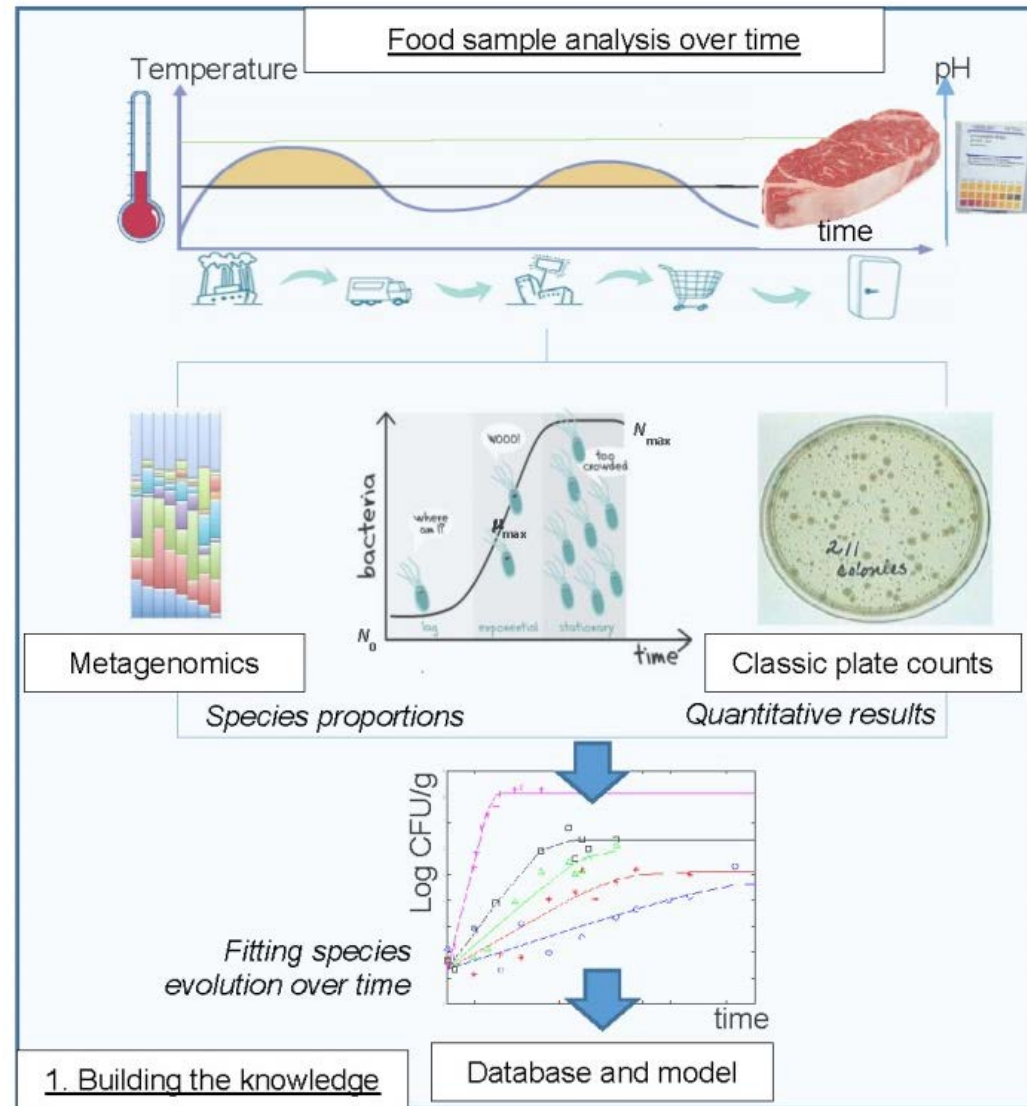
# Food ecosystem dynamics: spoilage

- Meta data collection
  - Food (pH, aw)
  - Chain (Temp)
  - Metagenomics
  - Enumeration



# Food ecosystem dynamics: spoilage

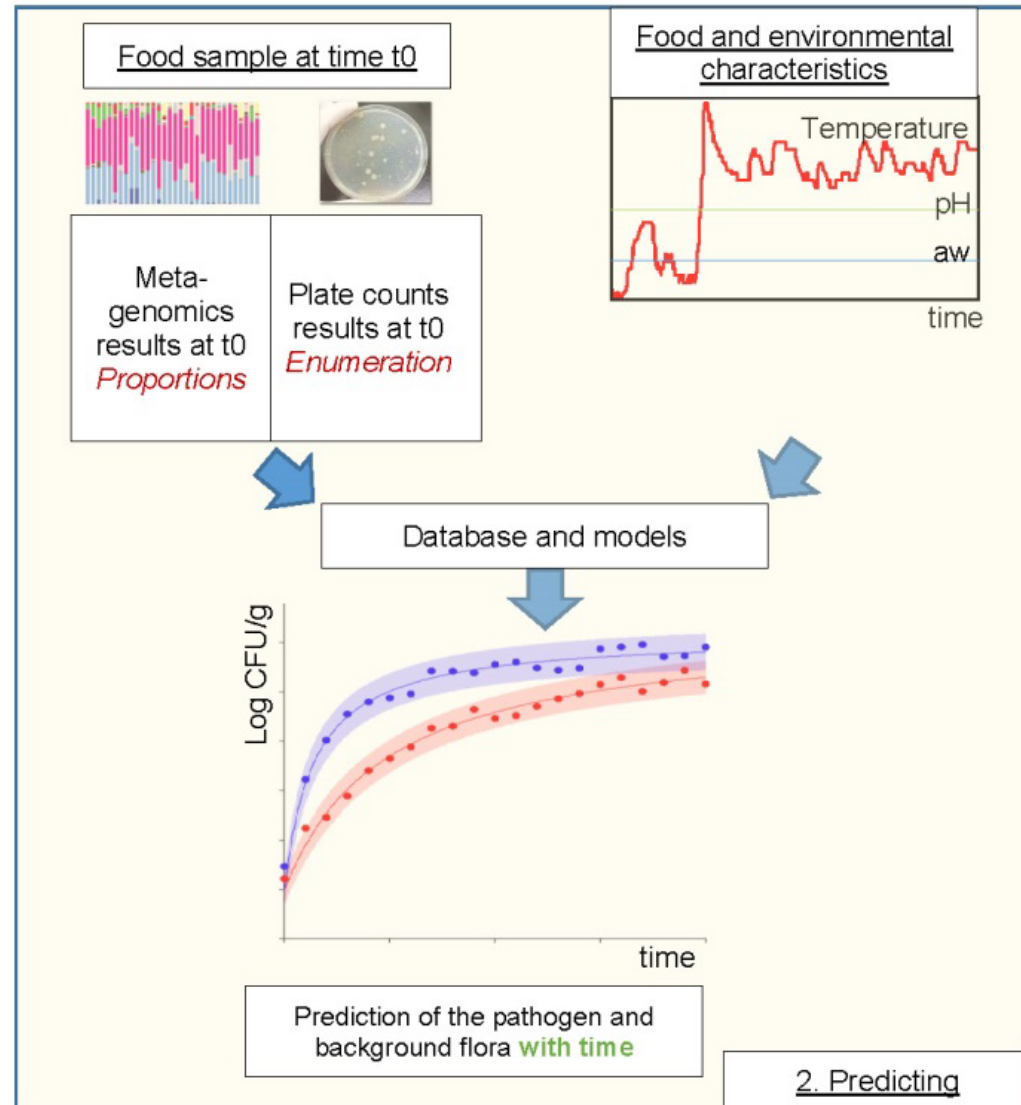
- Meta data collection
  - Food (pH, aw)
  - Chain (Temp)
  - Metagenomics
  - Enumeration
- Database of kinetics of relevant species



# Food ecosystem dynamics: spoilage

## ■ Prediction

- Based on database and models



# Challenges of omic data in EA

- Low prevalence of pathogens; needle in the haystack

# Potential of omic data in EA

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- Better understanding of biology: behaviour of pathogens, food ecosystems and its dynamics
- Biomarkers help to quantify strain variability
- Help to fine tune EA
- Reducing uncertainty in EA

# Joined efforts

## NEXT GENERATION OF MICROBIOLOGICAL RISK ASSESSMENT:

### Potential of Omics data for exposure assessment

Heidy M.W. den Besten<sup>1</sup>, Alejandro Amézquita<sup>2</sup>, Sara Bover-Cid<sup>3</sup>, Stéphane Dagnas<sup>4</sup>, Mariem Ellouze<sup>5</sup>, Sandrine Guillou<sup>6</sup>, George Nychas<sup>7</sup>, Cian O'Mahony<sup>8</sup>, Fernando Pérez-Rodríguez<sup>9</sup>, Jeanne-Marie Membré<sup>6\*</sup>

