



# Monitoring and modelling of microbial ecosystem in Belgian white pudding: a new example for combining metagenetics and predictive microbiology



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## INTRODUCTION

In order to control food losses and waste, studies highlight the importance of monitoring the microbial diversity of food products.

Classical culture-based methods may not be relevant to understand the modifications of the microbial ecology in food products.

Metagenetic analysis targeted on 16S ribosomal DNA can elucidate microbial community structures at a much higher resolution than was previously possible.



This work proposed to study the bacterial microbiota of white- pudding, a typical Belgian pork meat product, using culture-dependent and independent methods in combination with predictive microbiology.

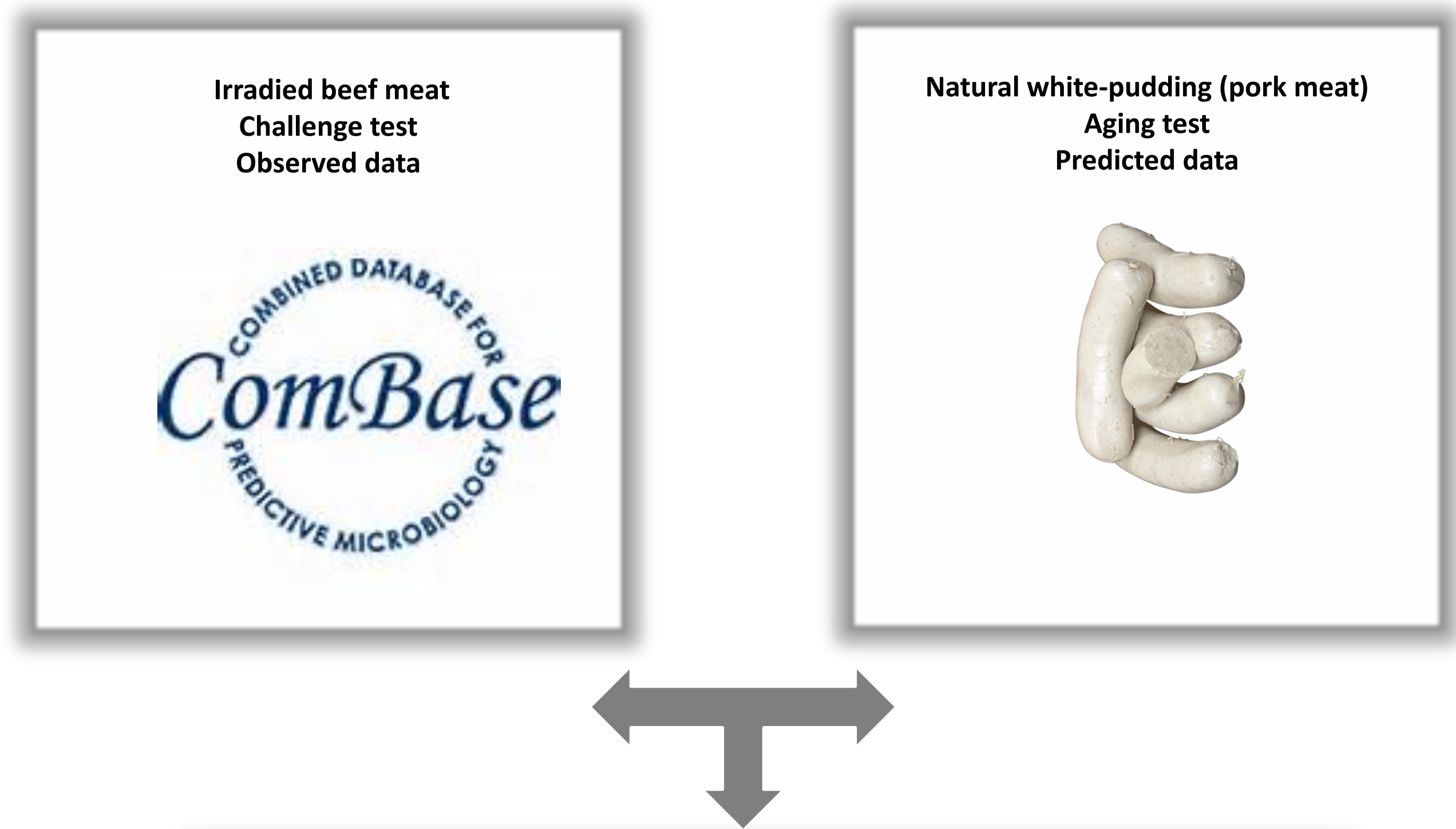
## RESULTS AND DISCUSSION

### Secondary model

Bacterial species	Tmin	μref		
		MAP	FW	VP
Brochothrix thermosphacta	-3,36 (Leroi et al., 2012)	0,39	0,60	0,64
Pseudomonas sp.	-5,00 (Rashid et al., 2001)	0,16	0,30	1,60

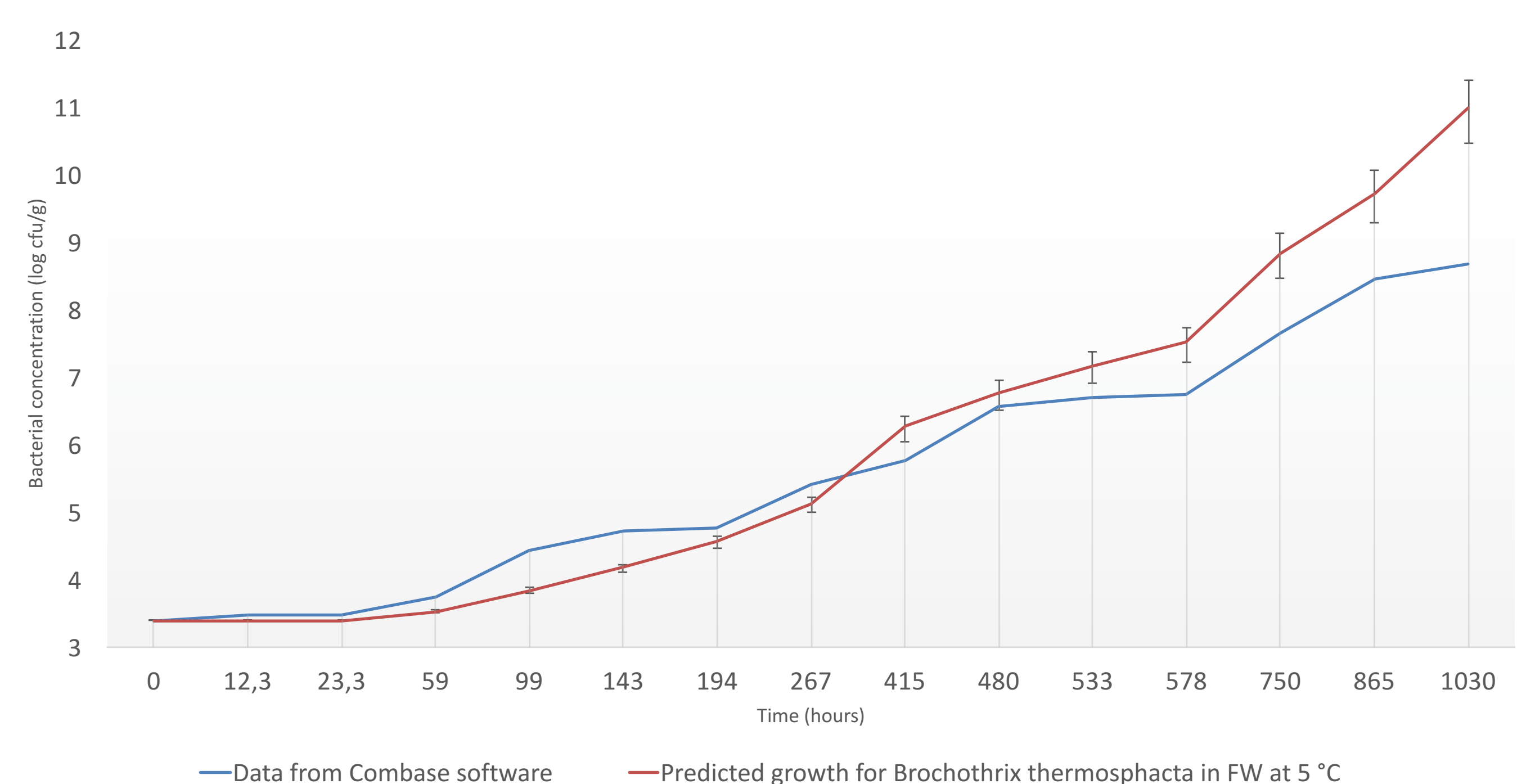
Tmin (minimal temperature for growth, °C), μref (bacterial growth rate of reference, h<sup>-1</sup>)

### Tertiary model: model validation by Combase software

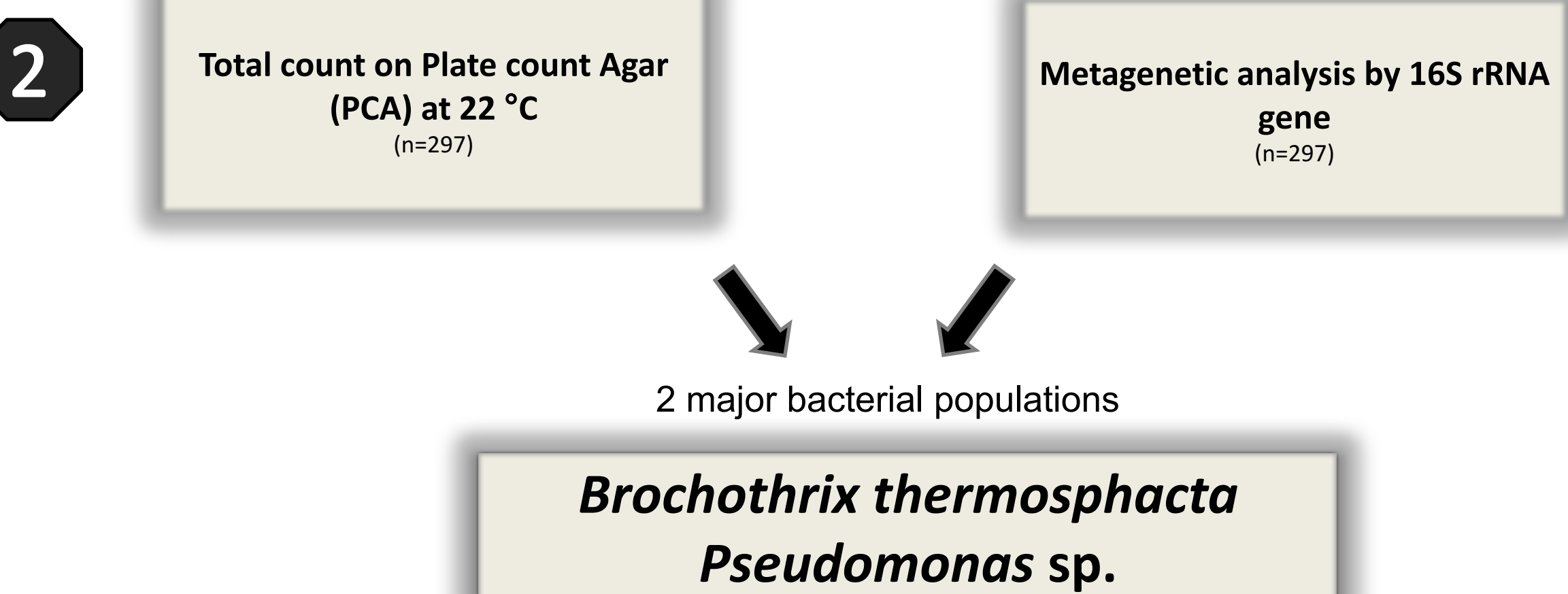
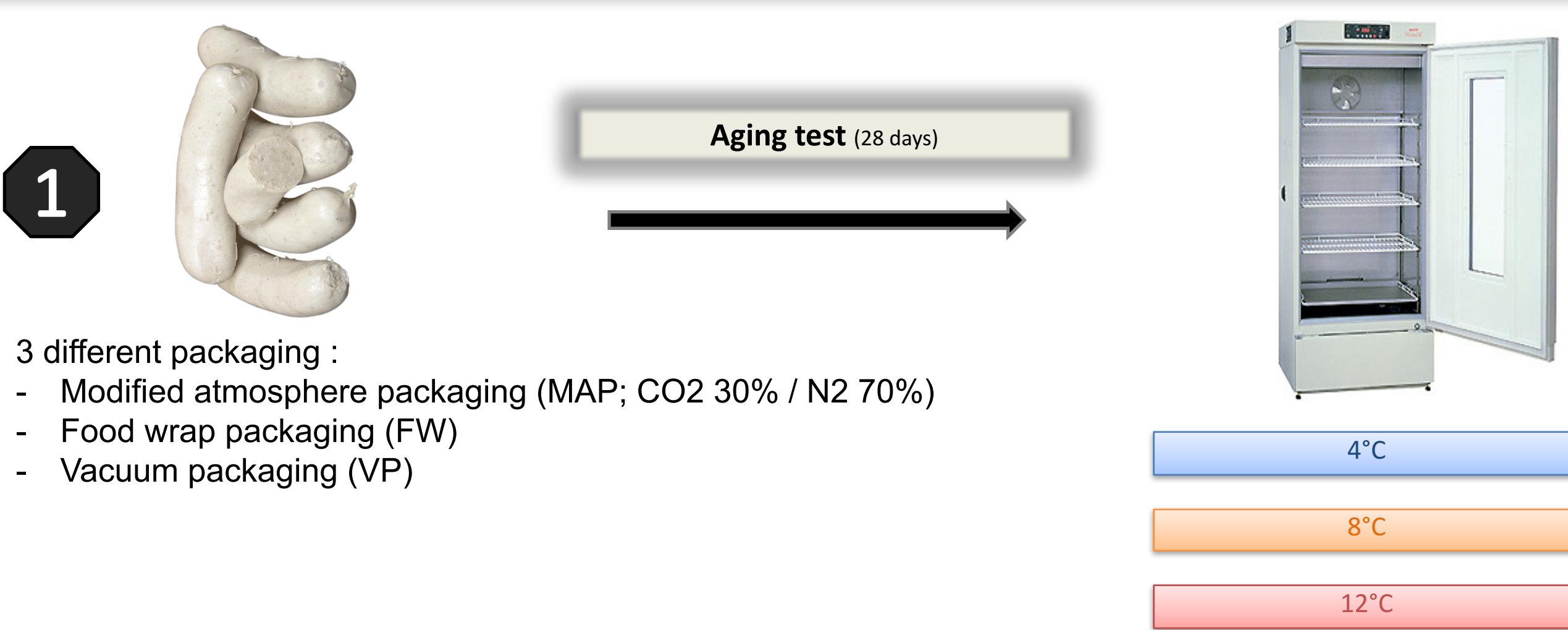


The results of the simulation show a good compliance between predicted and observed data from Combase.

Example for growth of *Brochothrix thermosphacta* in FW at 5 °C



## MATERIALS AND METHODS



3 Primary model : Baranyi equation  
Secondary model : Square Root Model  
Tertiary model : Buchanan with lag-time



## RESULTS AND DISCUSSION

### Primary model adjustment

<i>Brochothrix thermosphacta</i>				<i>Pseudomonas sp.</i>				
Conditions	Temp	μmax	Lag	Conditions	Temp	μmax	Lag	
MAP	4	0,06	83,52	MAP	4	0,02	85,96	
	8	0,09	52,08		MAP	8	0,04	73,84
	12	0,15	26,5			MAP	12	0,08
FW	4	0,07	72,56	FW			4	0,04
	8	0,16	36,37		FW		8	0,10
	12	0,23	23,68			FW	12	0,12
VP	4	0,09	159,7	VP			4	0,02
	8	0,16	67,36		VP		8	0,05
	12	0,23	36,85			VP	12	1,84

Higher growth parameters in VP and FW conditions for both bacterial strains.

Temp (temperature, °C); μmax (maximal bacterial growth rate, h<sup>-1</sup>); lag (lag-time, hours)

## CONCLUSIONS

This study investigate the combining of culture-dependent and independent methods with predictive microbiological models, as a new approach to take into account bacterial populations dynamics in perishable foods under different environmental conditions.

Compared to culture based methods on selective media and previous independent culture techniques, metagenetic analysis combined with predictive microbiology gives more valuable information.

And could be considered as a technological breakthrough to follow intrinsically the evolution of each strains on the bacterial ecosystem.