

# Unveiling Microbial Community Dynamics in Response to Pear Brown Spot Disease and Management Strategies



S. Iacono<sup>1</sup>, M. Menghini<sup>1</sup>, D. Giovanardi<sup>2</sup>, L. Solieri<sup>2</sup>, M. Collina<sup>1</sup>, R. Baroncelli<sup>1</sup>

<sup>1</sup> Department of Agricultural and Food Sciences (DISTAL), University of Bologna, 40127 Bologna, Italy.

<sup>2</sup> Department of Life Sciences, University of Modena and Reggio Emilia, 42122 Reggio Emilia, Italy.

E-mail: marina.collina@unibo.it

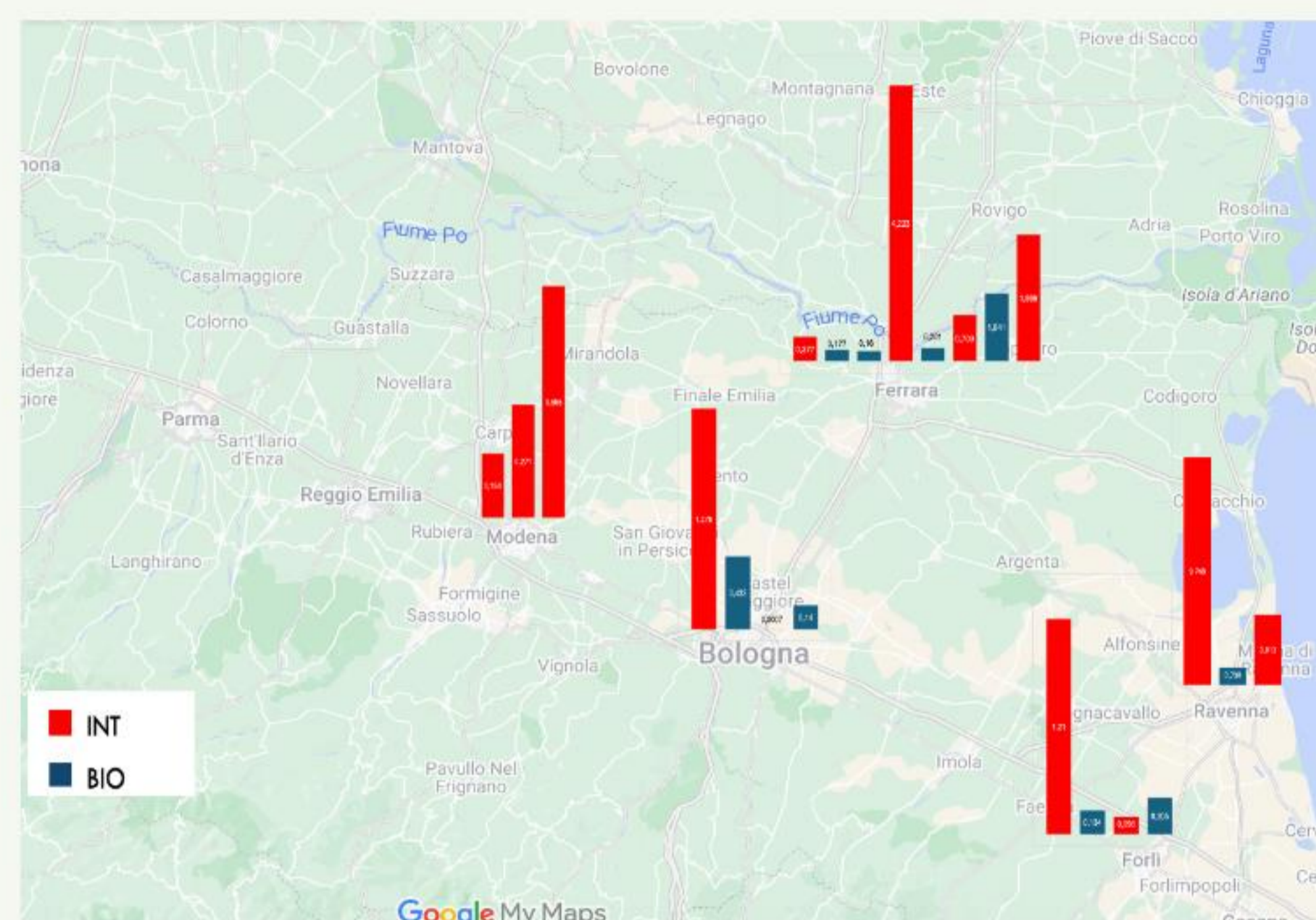


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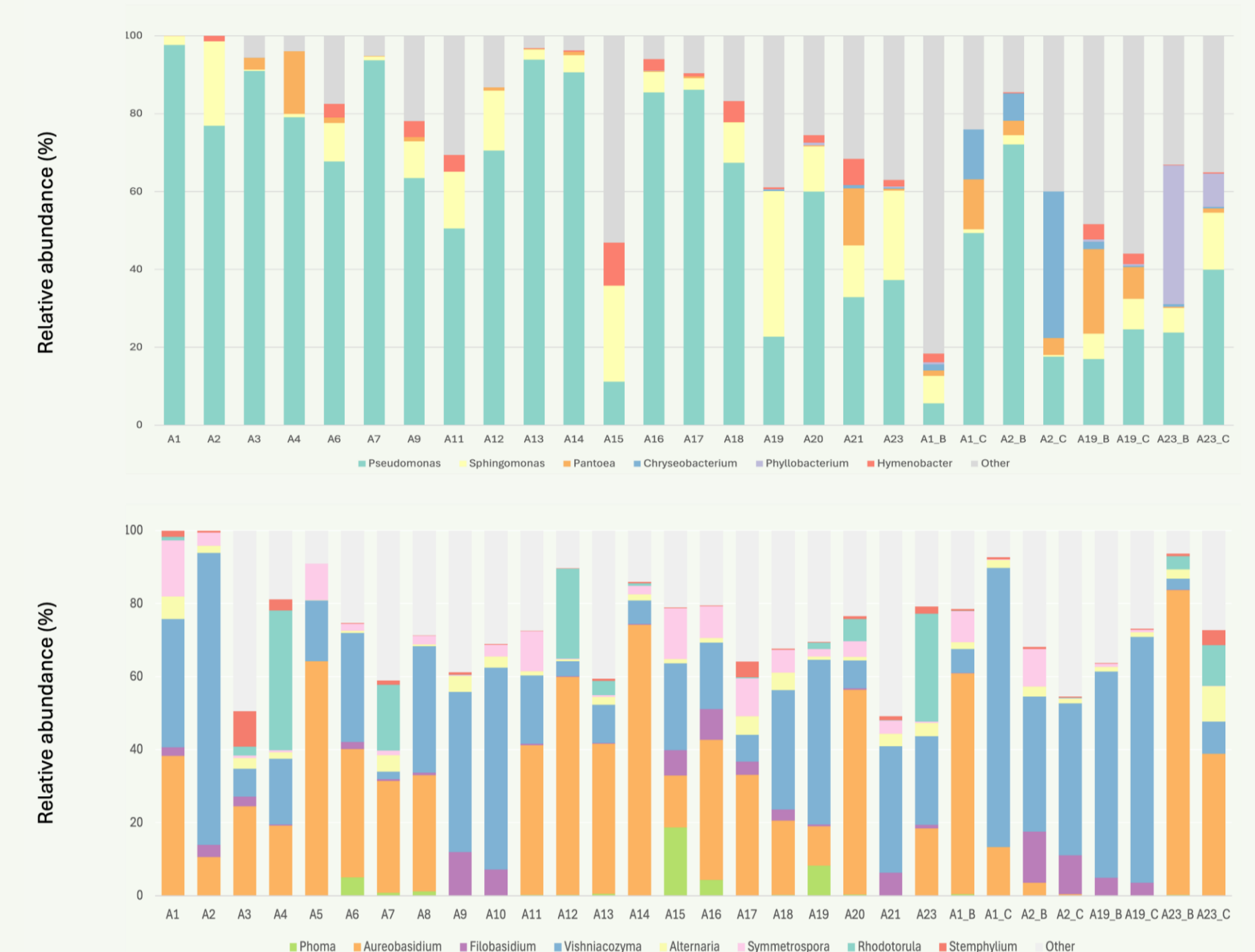
## Introduction

- Pear brown spot, caused by the Ascomycete fungus *Stemphylium vesicarium*, is a major economic threat to pear production in northern Italy leading to considerable crop loss and reduced fruit quality.
- This study investigated the influence of microbial communities on brown spot development and the impact of disease management strategies on these communities.
- The specific objectives are: A) Compare microbial communities on pear surfaces in orchards under organic management and IPM; B) Investigate potential correlations between *S. vesicarium* and the adopted disease control strategy, *S. vesicarium* abundance and brown spot incidence, specific microbial taxa and *S. vesicarium* abundance.

## Results



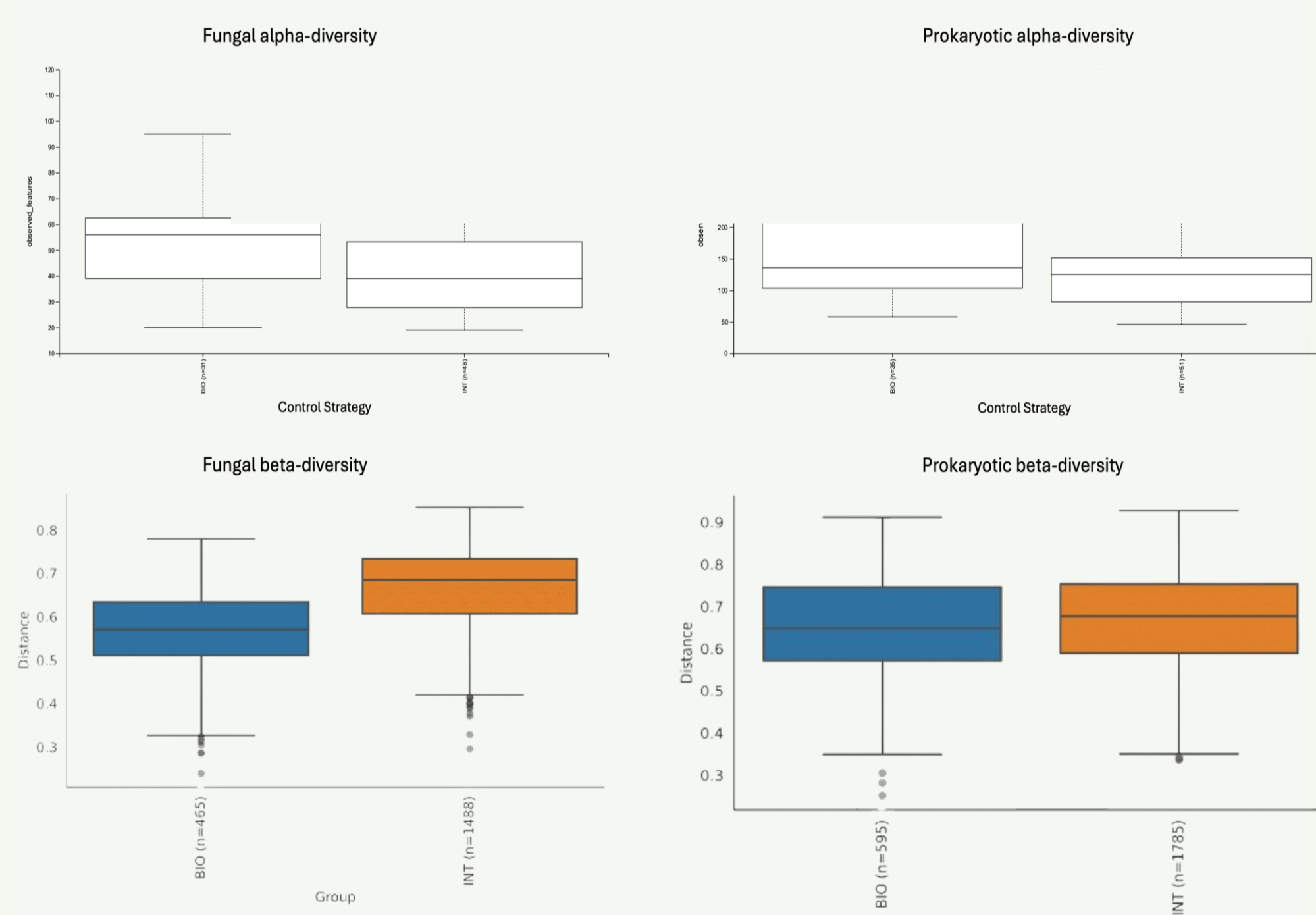
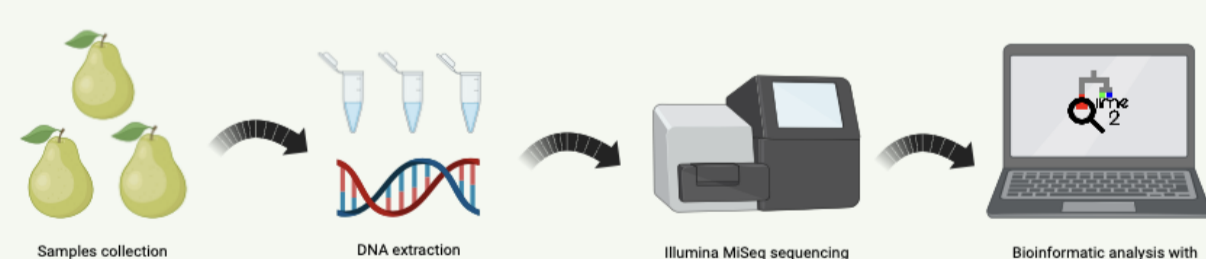
A total of 23 orchards were sampled across five different provinces: Bologna, Ravenna, Modena, Ferrara and Forlì-Cesena. The bar charts displayed on the map illustrate the relative frequency of *S. vesicarium* in the sampled orchards.



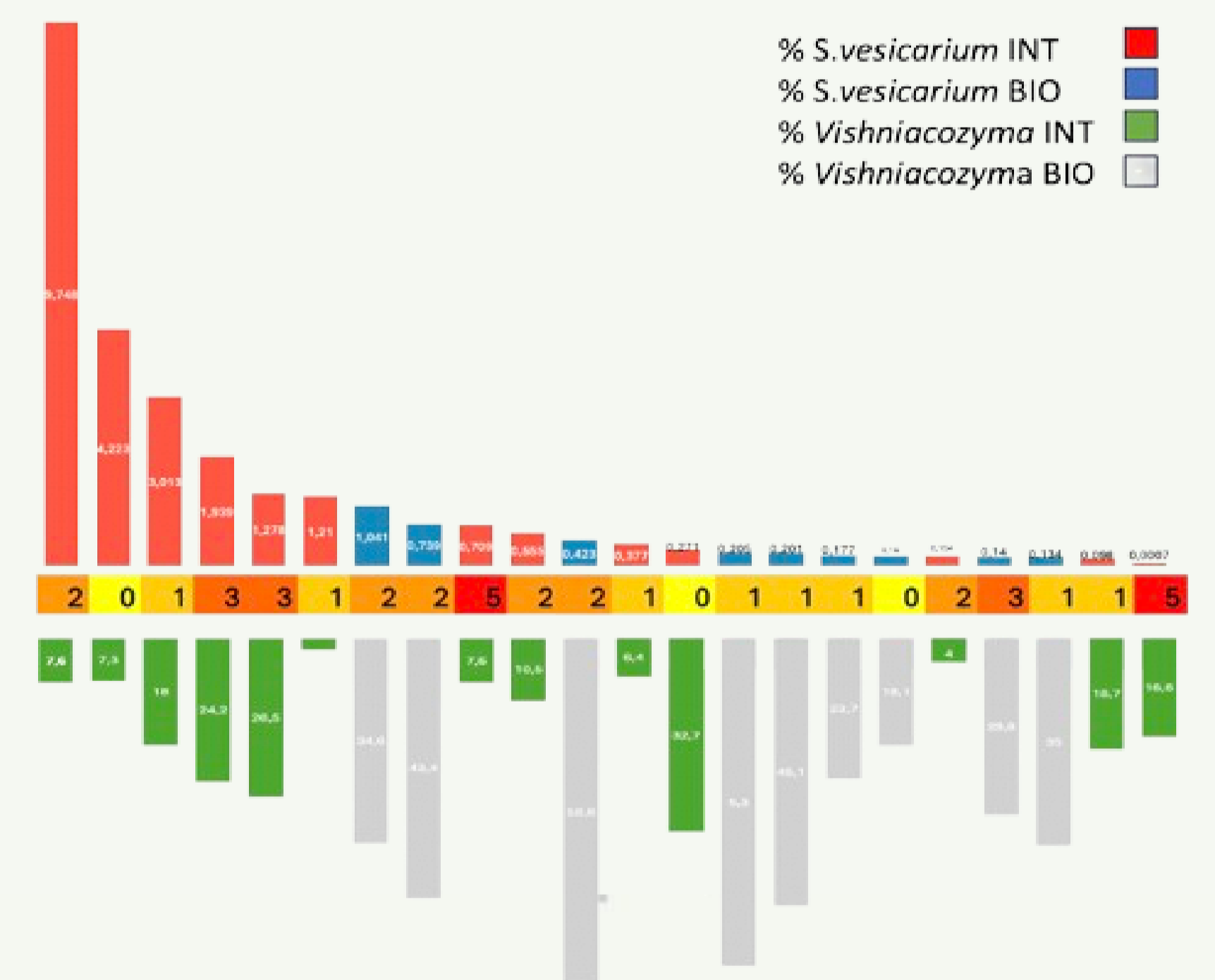
Taxonomic analysis have shown that *Aureobasidium*, *Vishniacozyma*, and *Rhodotorula* were the most abundant fungal taxa while *Pseudomonas*, *Sphingomonas*, and *Pantoea* dominated the bacterial population.

## Methods

- Pear samples (Abate fétel) were collected between June and August 2023 from orchards of five different provinces of Emilia-Romagna;
- DNA of microbiome was extracted from pear carposphere using a modified CTAB method;
- Metabarcoding with high-throughput sequencing was employed to analyze the microbial communities. We targeted the V3-V4 region of the 16S rRNA gene for prokaryotes and the ITS2 region for fungi;
- QIIME 2, a bioinformatic pipeline, was used for data analysis.



Our preliminary results revealed significant differences ( $p$ -value  $< 0.05$ ) in fungal and bacterial beta-diversity (community composition) and fungal alpha-diversity (species richness) between organic and integrated orchards.



The results of our study indicated a slight negative correlation between the presence of *S. vesicarium* and *Vishniacozyma*. However, further statistical analyses are required to confirm this hypothesis.

## Conclusions and perspectives

This study revealed differences in microbial composition between organic and integrated orchards. Further analyses are needed to confirm correlations between *S. vesicarium* and disease incidence. Investigating potential negative correlations between previously identified abundant taxa (e.g., *Pseudomonas*) and *S. vesicarium* abundance or disease severity is warranted, considering their reported biocontrol potential.

## ACKNOWLEDGEMENTS