

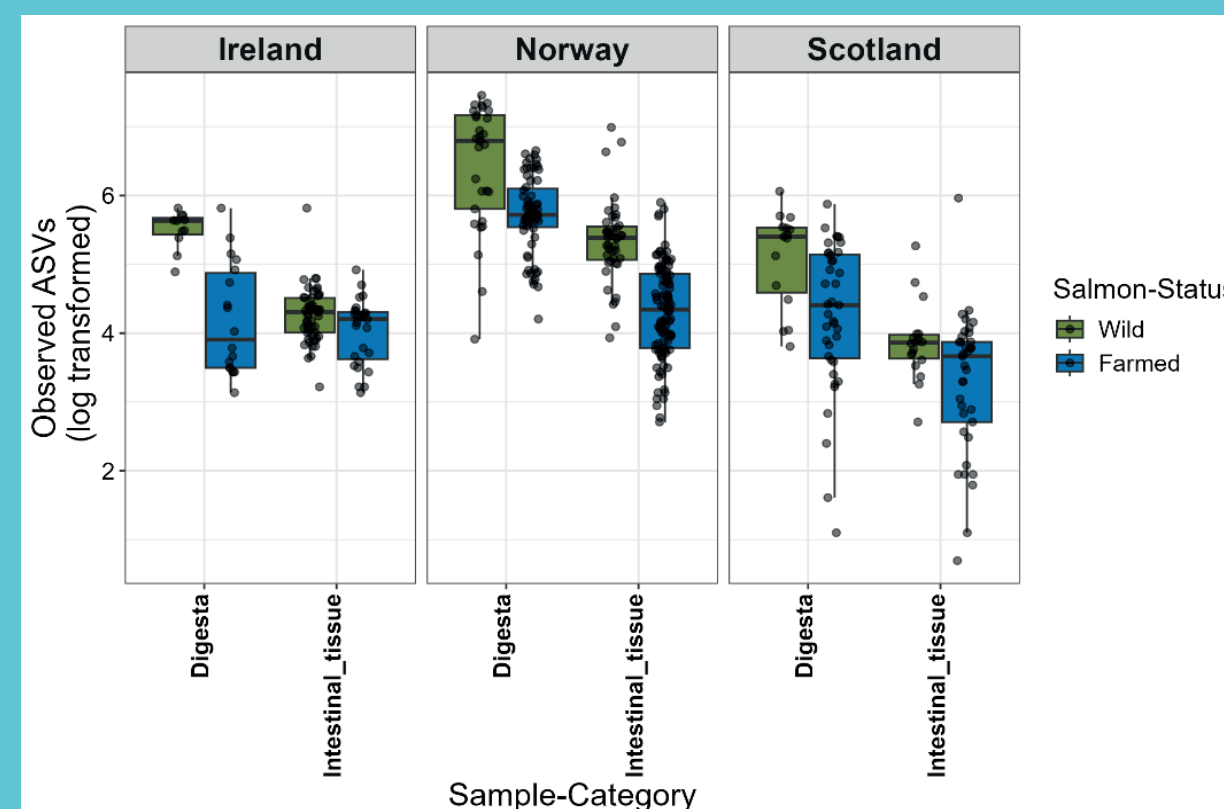


Insights into the dynamics of Atlantic Salmon Gut Microbiomes

A comparative analysis of wild and farmed Salmon gut microbiomes across life-stages and countries

Questions Asked:

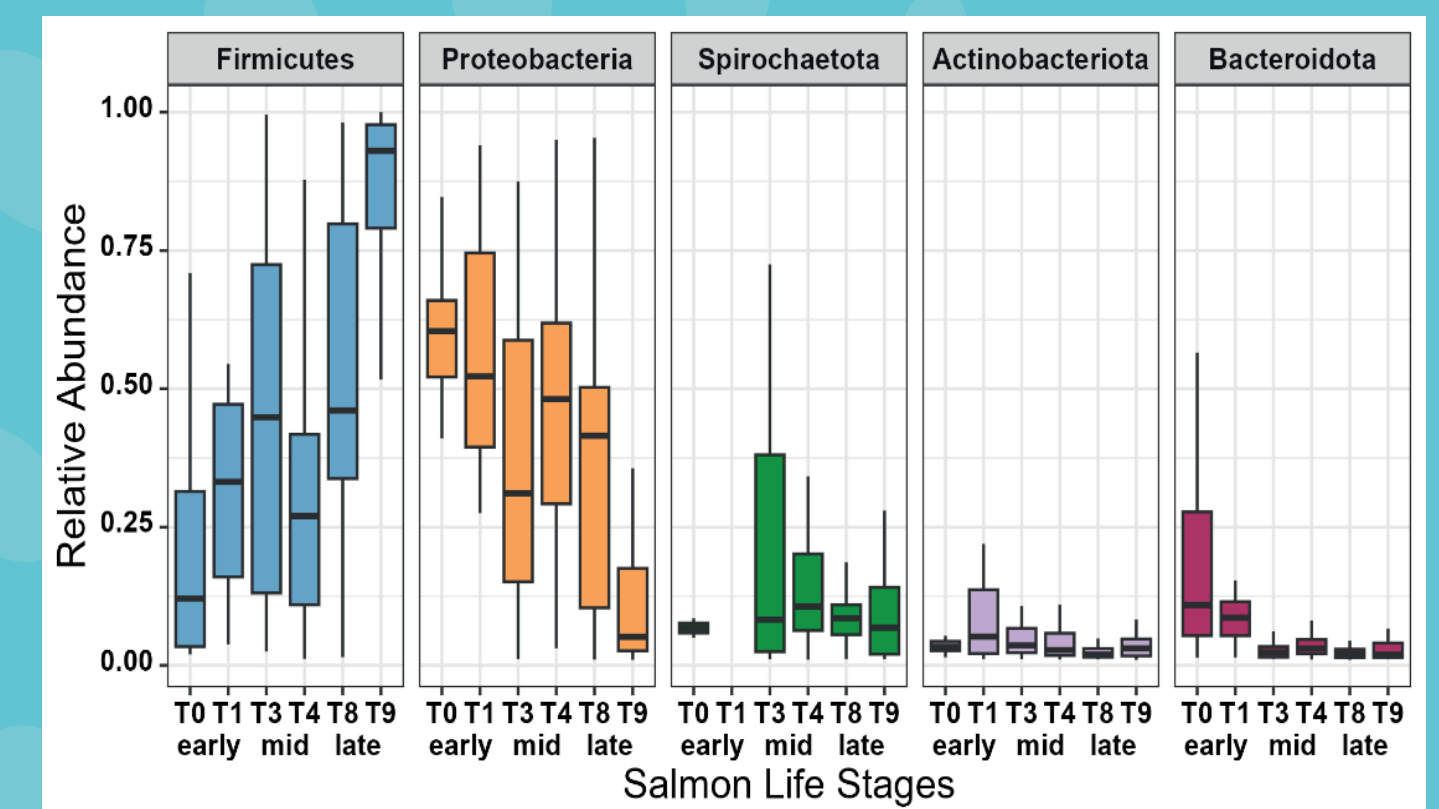
- Characterizing gut microbiome of wild and farmed Atlantic Salmon?
- Identifying factors shaping the gut microbiome of Atlantic Salmon?
- Knowledge gained to improve Salmon aquaculture?



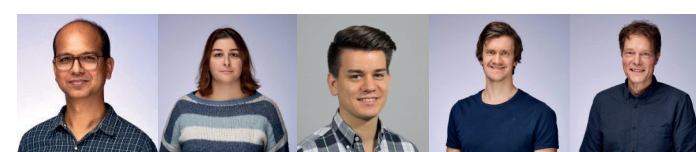
Higher gut microbiome richness (ASV count, $p=0.003$) in wild Salmon compared to farmed Salmon, with variations by country.

Results:

- Atlantic Salmon gut microbiome diversity and community composition vary by country and between wild and farmed Salmon.
- Life-stages, diet, and environment together shape the gut microbiome of farmed Atlantic Salmon.
- Specific bacterial taxa (e.g., *Aliivibrio* spp.) can be leveraged to improve Salmon aquaculture



Top five bacterial phylum ($>0.1\%$ abundance) significantly different ($p \leq 0.05$) for Salmon life-stages.



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Zonation of the *Vitis vinifera* microbiome in Vino Nobile di Montepulciano PDO production area

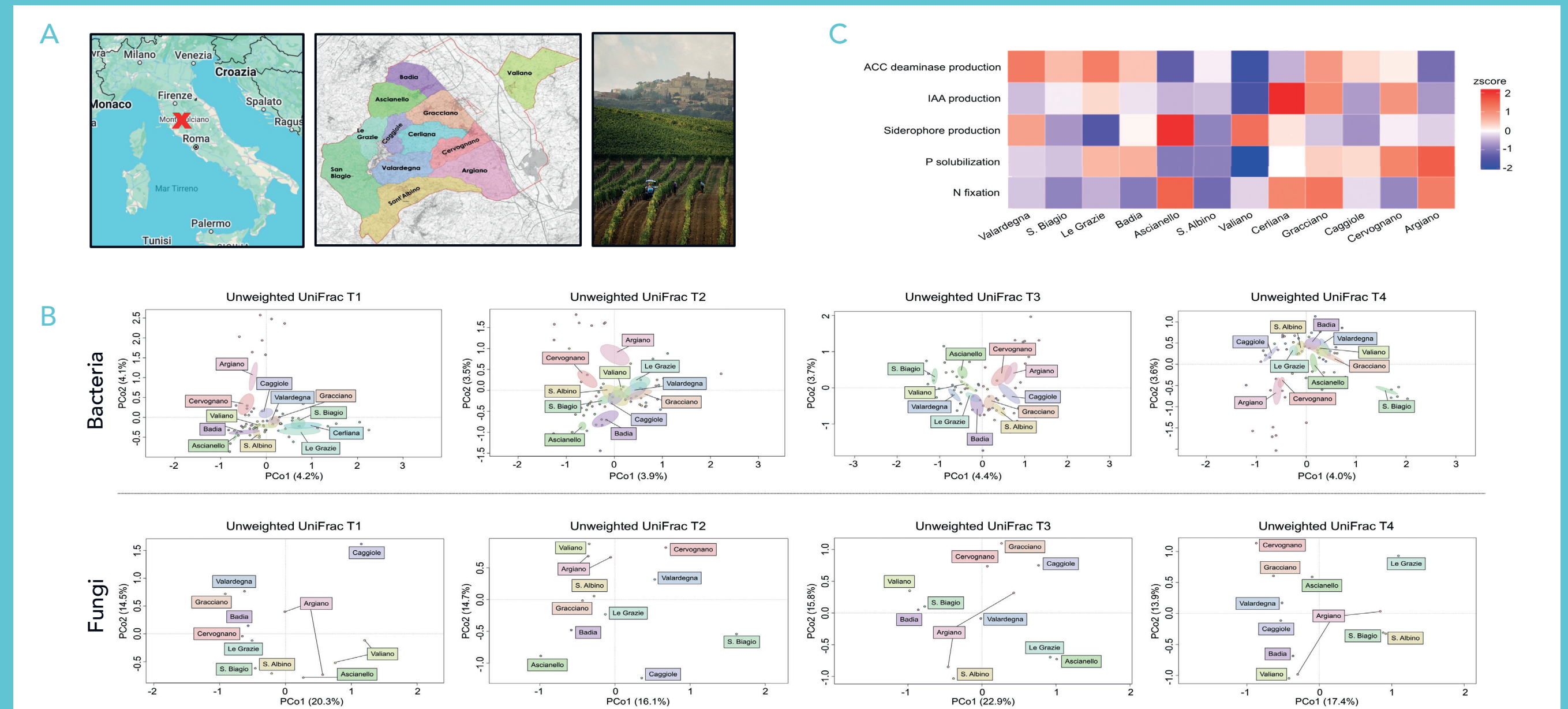


Figure 1. **A** - Map of the 12 production areas (i.e. Additional Geographical Units - AGUs) recognized by the Consorzio del Vino Nobile di Montepulciano DOCG (Tuscany, Italy). The production areas have different colors: Valiano, Valardegna, San Biagio, Sant'Albino, Le Grazie, Gracciano, Cervognano, Cerliana, Caggiole, Badia, Ascianello and Argiano. **B** - PCoAs of bacterial and fungal composition of rhizospheric soil samples in Montepulciano AGUs at different time points (T1 to T4). **C** - Functional Plant Growth Promoting (PGP) profile of AGU rhizosphere microbiomes.

In the framework of the Circles project, we defined the microbial terroir of vineyards distributed in the 12 subzones (Additional Geographical Units - AGU) of the Consorzio del Vino Nobile di Montepulciano DOCG (Italy, Figure 1A), a world-famous wine region, with the aim of identifying those characteristics that represent microbiological aspects to be protected because they are related to plant health. To this end, rhizospheres of *Vitis vinifera* cultivar Sangiovese and soil samples were collected during the 2022 and 2023 vintages and analyzed using an integrated metabarcoding/shotgun metagenomic approach targeting both bacteria and fungi. While highlighting a peculiar taxonomic configuration of the Vino Nobile di Montepulciano terroir compared to other Italian and global vineyards, our data show that microbiomes are "AGU-specific" in terms of taxonomic abundances and plant growth-promoting functions (Figure 1B and 1C). The reconstructed metagenome-assembled genomes confirmed a high potential for plant growth promotion, with differences related to AGU, thus confirming the importance of protecting microbial terroir and biodiversity to ensure the production of high quality traditional wines.



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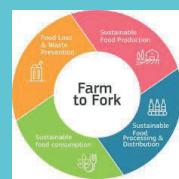


Developing new circular tools for wheat microbiome modulation as an innovative contribution for a sustainable, healthy, and resilient food production system

World population growth: 10 billion by 2050



- Biodiversity loss
- Hunger & malnutrition
- Resource depletion
- Human impact on the environment



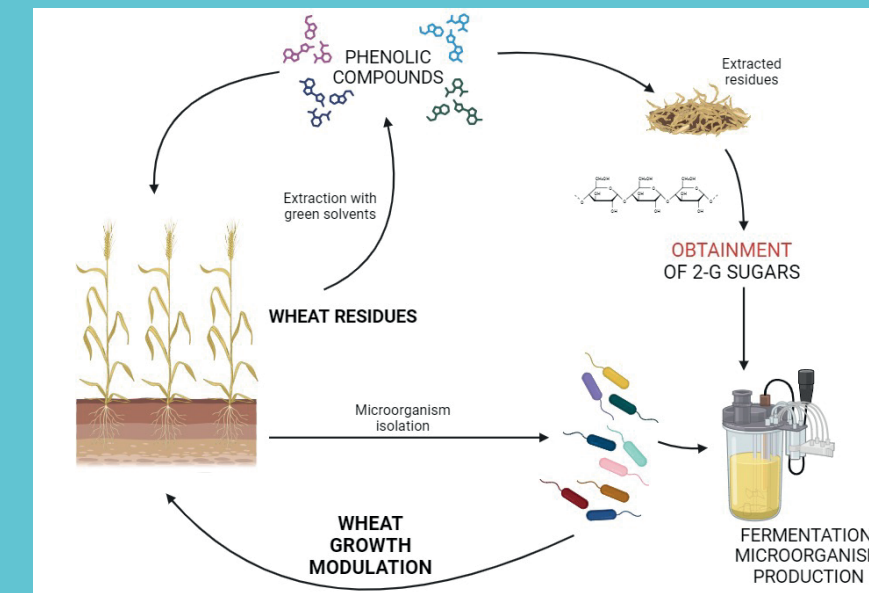
To reduce net emissions of GHGs to zero by 2050, while ensuring the prosperity of the European economy and the well-being of its citizens.



- 20% reduction in the use of agrochemicals for fertilization
- 50% reduction in the use of chemical pesticides
- 50% reduction in nutrient losses
- 50% reduction in the use of antibiotics for farm animals



This policy provides a framework for transforming food systems into resilient systems to ensure that everyone has access to affordable and healthy food.



Methodology and Results

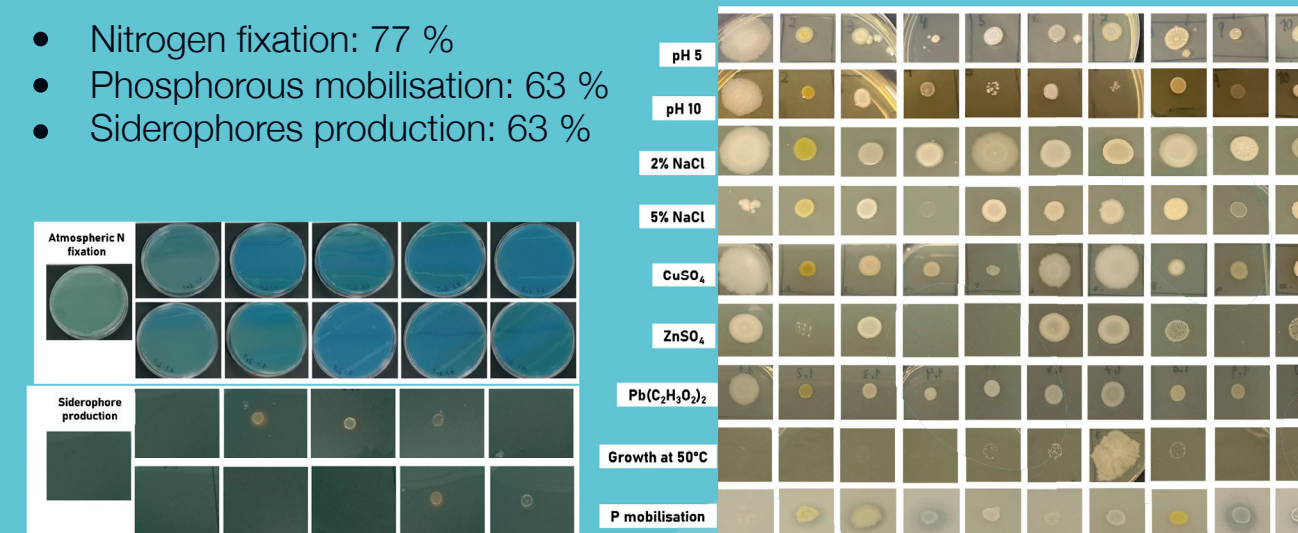
Circularity and sustainable practices

- Isolation of specific microorganisms with PGP activity as wheat modulators
- Enzymatic hydrolysis of wheat residues to release 2G sugars
- Use of wheat hydrolysates as fermentation medium for the microbial modulators. Process development and scaling-up

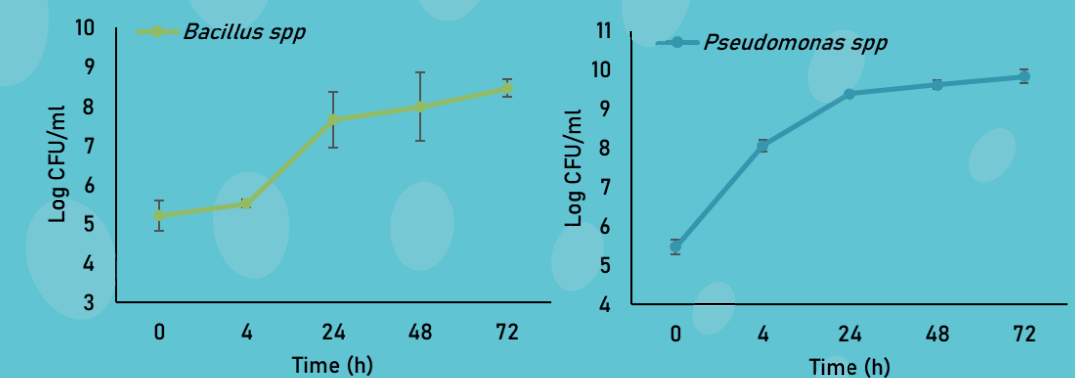
Microbial isolation & evaluation of Plant Growth Promoting (PGP) activities

From the 154 isolates, 122 were selected to screen PGP activities according to their biosafety (BSL1)

- Nitrogen fixation: 77 %
- Phosphorous mobilisation: 63 %
- Siderophores production: 63 %



2 PGP microorganisms have been selected for optimisation of microbial culture: *Pseudomonas* sp and *Bacillus* sp. Both microorganisms show high cell viability in growth-kinetic studies when cultured in LB medium:



Objectives

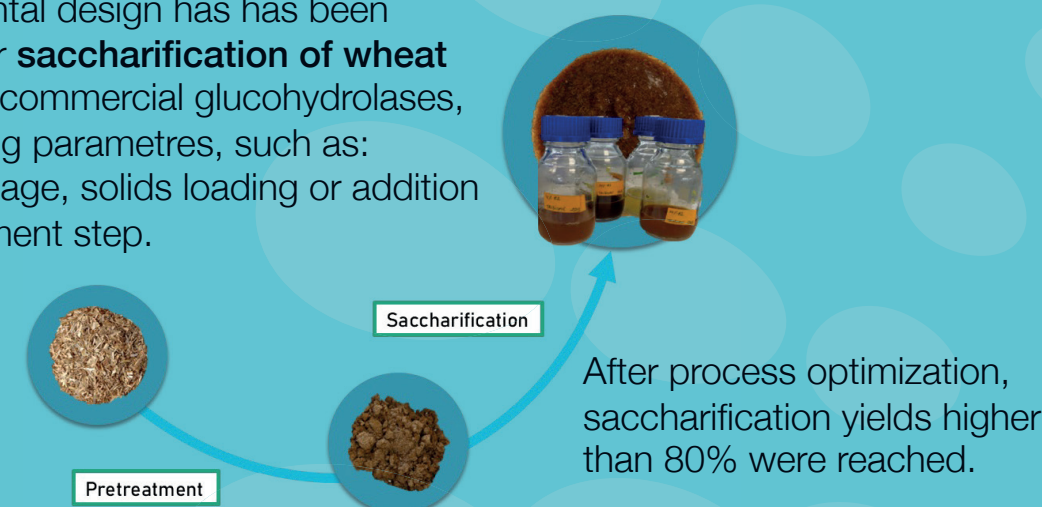
The overall objective of the project is to deep the knowledge of the **microbiome of the soil & plant**, studying the variability under different biotic and abiotic stresses, with the aim of carrying out a modelling that will allow further research into new tools for **modulating and improving crop yields**, as well as to improve agricultural production to obtain **advanced, improved & more nutritional food with a direct positive impact** on the **microbiome in both animals & humans**. In this work, we aim to isolate potential microorganisms for wheat crop modulation from wheat residues and soil samples and to develop and optimise bioconversion processes for the production of 2 microorganisms and wheat waste fermented media as modulators.

Conclusions and Next Steps

The work presented here shows that we are on the right way of gathering best practices related to microbiomes in food production systems. Next steps are related to:

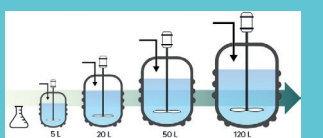
- Conditioning and integration of obtained products with fertilizers for validation in pot trials and in field.
- Develop and optimise extraction processes with high efficiency for the production of 2 phenolic extracts from wheat residues and/or other botanical extracts.

An experimental design has been performed for **saccharification of wheat straw**, using commercial glucosylhydrolases, and optimizing parametres, such as: enzymes dosage, solids loading or addition of a pretreatment step.



Ongoing experimental sets:

- Evaluation of additional PGP properties: indol, organic acid and plant hormones production, as well as ACC deaminase activity.
- Optimisation of microbial growth conditions from 2G-sugars derived from wheat residues at lab scale.
- Scaling-up of the selected bioprocesses, obtaining the required amounts of modulators for conditioning and validation.



Advanced tools for integration and synergistic inTeRconnection of microBIOMes in resilient food systems



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Rosa Doménech, Enrique Cubas, Annabel Serpico & Yaiza Gómez. ITENE Research Center, Spain