LegumBiome Innovations: Climate-Resilient Agriculture via Desert Legume Microbiota

João Barnabé [1,2]; Isabel Videira e Castro[2]; Juan Ignacio Vílchez[1]

[1] Green IT, ITQB, Universidade Nova de Lisboa, Portugal [2]NIAV, Instituto Nacional de Investigação Agrária e Veterinária, Portugal.

Abstract

In response to climate change, the LegumBiome Project investigates microbiota in desert-adapted legumes in the Mediterranean's Iberian Peninsula. Our 2023 study sampled 60 sites, identifying common legumes like *Medicago sativa* and *Bituminaria bituminosa*. Early 16S rRNA gene sequencing identified 460 bacterial isolates, including potential Plant Growth-Promoting Bacteria (PGPB) like *Bacillus subtilis*. Noteworthy was *Paenarthrobacter nitroguajacolicus*, suggesting nitrogen-fixing traits. This initiative highlights sustainable biotechnology's role in addressing climate-induced agricultural challenges.

Introduction

Confronted with climate change and resource depletion, the Mediterranean's Iberian Peninsula is where our focus lies. The LegumBiome Project explores the microbiota in desert-adapted legumes, seeking sustainable solutions within their microbial interactions to bolster agricultural resilience.



Figure 1. Iberian Peninsula heat map.

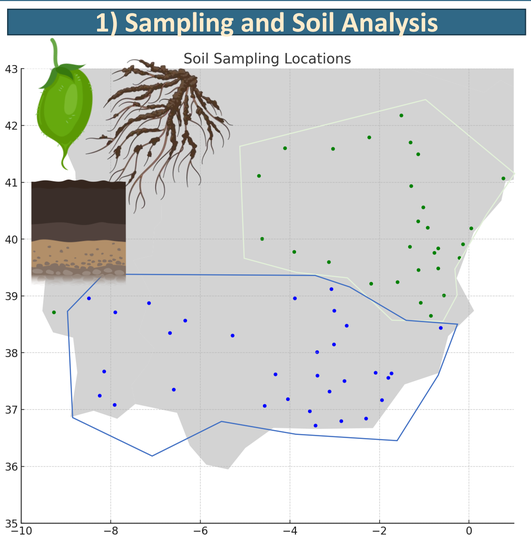


Figure 2. PGPB's stress mitigation effects.

PGPB, identified in wild legumes such as *Medicago sativa* (alfalfa), show potential to enhance commercial crop growth and resilience. These bacteria represent a promising, sustainable shift in agricultural practices, pending further research.

Methods and Tasks

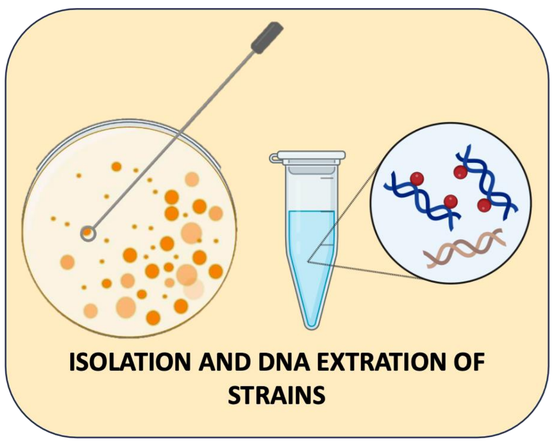
1) Sampling and Soil Analysis

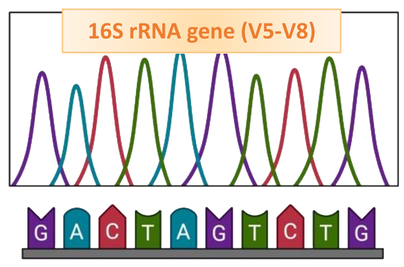




Samples of seeds, roots, soil, and nodules from wild legumes like *Bituminaria bituminosa* and *Medicago* sp. were gathered at 60 Iberian sites. This collection, crucial for spatial and contextual strain analysis, leverages soil data, climate, and regional patterns, setting the stage for ensuing population assays

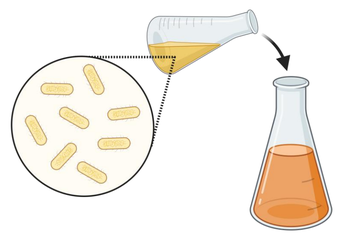
2) Population assay and molecular identification





In Task 2, primers 799F and 1392R were employed to amplify the 16S rRNA gene, profiling bacterial communities in our samples.

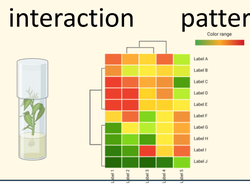
3) Functional screening of Identified Bacteria



Following bacterial identification, planned assays will assess functions including colonization, hormone production (e.g., auxins), siderophore presence, and antioxidant activity.

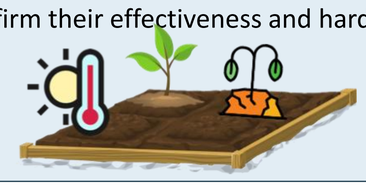
4) In Vitro Assay

Post-screening, chosen PGPB strains will undergo in vitro testing on legumes under diverse abiotic stresses, with stress markers and RNA sequencing slated to uncover interaction patterns and responses.



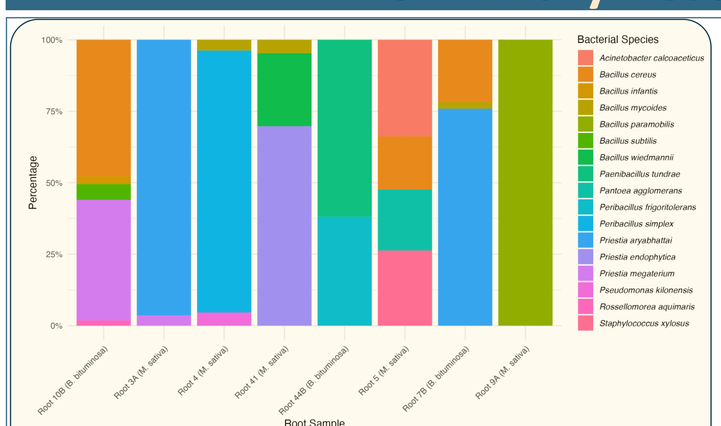
5) Field Trial Analysis

PGPB strains, successful in vitro, will next be tested in actual field conditions. Observing plant behaviors and environmental interactions aims to confirm their effectiveness and hardiness.



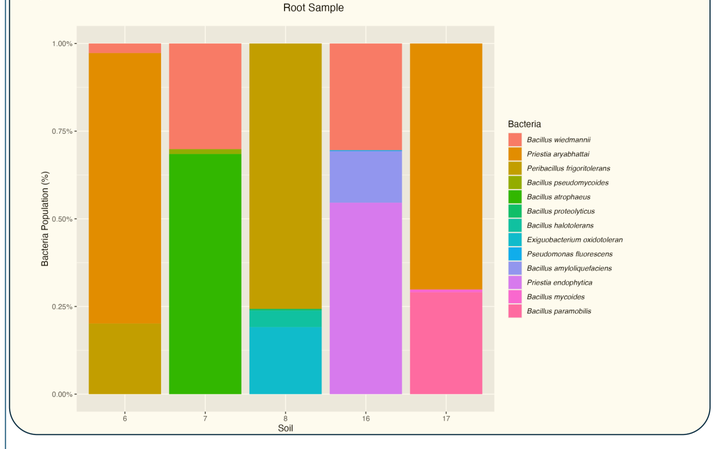
This project explores beneficial microbes in wild legumes, merging microbial profiling and molecular studies, set to culminate in field trial validations. We aim to boost legume resilience using an integrative, applied method.

Preliminary Results

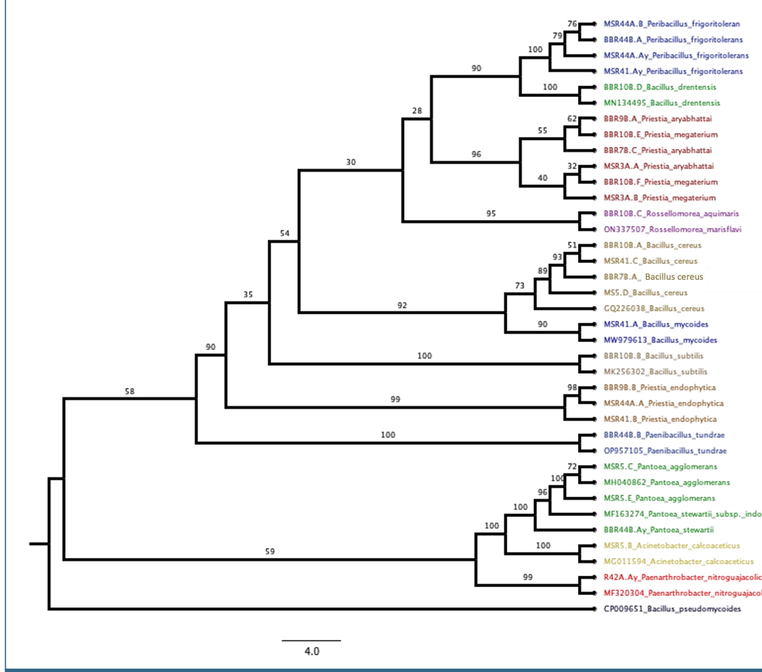




Morphological Characteristics: *Pantoea agglomerans* (R5C) and *Bacillus mycoides* (S19A) presented



We often find Priestia aryabhattai and *Bacillus cereus* in wild legume roots. Similarly, soil samples frequently show *Priestia aryabhattai* and *Bacillus wiedmannii*, revealing a rich mix of microorganisms in these natural areas



Early phylogenetic analyses indicate potential species validation, with initial data aligning with model strain sequences

Conclusions

In summary, our early exploration into the microbes living with desert legumes, particularly *Bituminaria bituminosa*, shows promising potential. The path ahead is challenging, requiring detailed studies of seeds and plant populations. Through dedicated research, we aim to make significant contributions to current agricultural challenges.

Contact

João Barnabé
Instituto de Tecnologia Química e Biológica (ITQB)
Email: joao.barnabe@itqb.unl.pt

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