



# WG1



## Methods

# Functional characterisation of beneficial microorganism diversity

### Aim:

**Tapping into existing knowledge & resources to define common principles regarding the recruitment of the different beneficial microorganisms**

***335 members representing 48 countries,  
from Albania to United States***



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## Functional characterisation of beneficial microorganism diversity

### RELEVANT DELIVERABLES [...*a bit late in delivering*...]

***D2. A comprehensive meta-analysis of the currently available sequencing information particularly focused on beneficial root-associated microorganisms (publication, M18)***

***D7. A dataset of microbial taxa and functions associated to beneficial services conserved across plant lineages (dataset, M30)***

***D12. Ad hoc computational scripts to integrate, analyse and interpret distinct sequencing datasets (dataset, M42)***

**=> WG1 members remember to fill in the survey for the review!  
[you've received an email just before the meeting]**



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## Showcasing WG1 STSMs: from concept ideas to collaborative results

**Micol Guaschino**  
[CREA, Italy visiting  
Dunudee Plant Sciences  
last summer]

⇒ **Don't miss Micol talk on  
Wednesday!**





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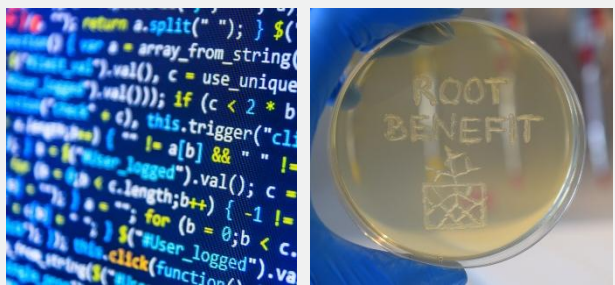


## WG1 “core group”

**Davide (UK), Hanna (Austria), Natalija (North Macedonia), Steffen (Germany) & Stuart (Türkiye)**

**Liaising & coordinating the activities of WG1**

**Monthly meetings to monitor progressions**



**Methods**



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## Contacts

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**Vacant position for deputy WP leader:**  
**your name could be here!**

