

community composition can cascade through the ecosystem, potentially affecting the abundance and diversity of other organisms (Pradhan et al., 2022). Long-term studies are needed to assess the broader ecological impacts of SynComs and ensure that they do not negatively affect biodiversity (Shayanthan et al., 2022).

## 6 Long-term Case Studies on SynCom applications

### 6.1 Long-term effects of SynCom on soil microorganisms

Arnault et al. (2023) developed and proposed a simple, repeatable, and effective method for seedling microbiota engineering, which involves inoculating SynCom on seeds (Figure 1). This method utilizes a wide variety of SynCom components and bacterial strains representing common bean seed microbial communities. This method can regulate the composition and community size of seed microbial communities. Then, SynComs significantly surpassed the local seed and potted soil microbial communities, contributing an average of 80% of the seedling microbial community. In addition, the engineering seed microbiota altered the recruitment and assembly of seedling and rhizosphere microbiota through preferential effects, indirectly affecting the diversity and function of soil microorganisms.

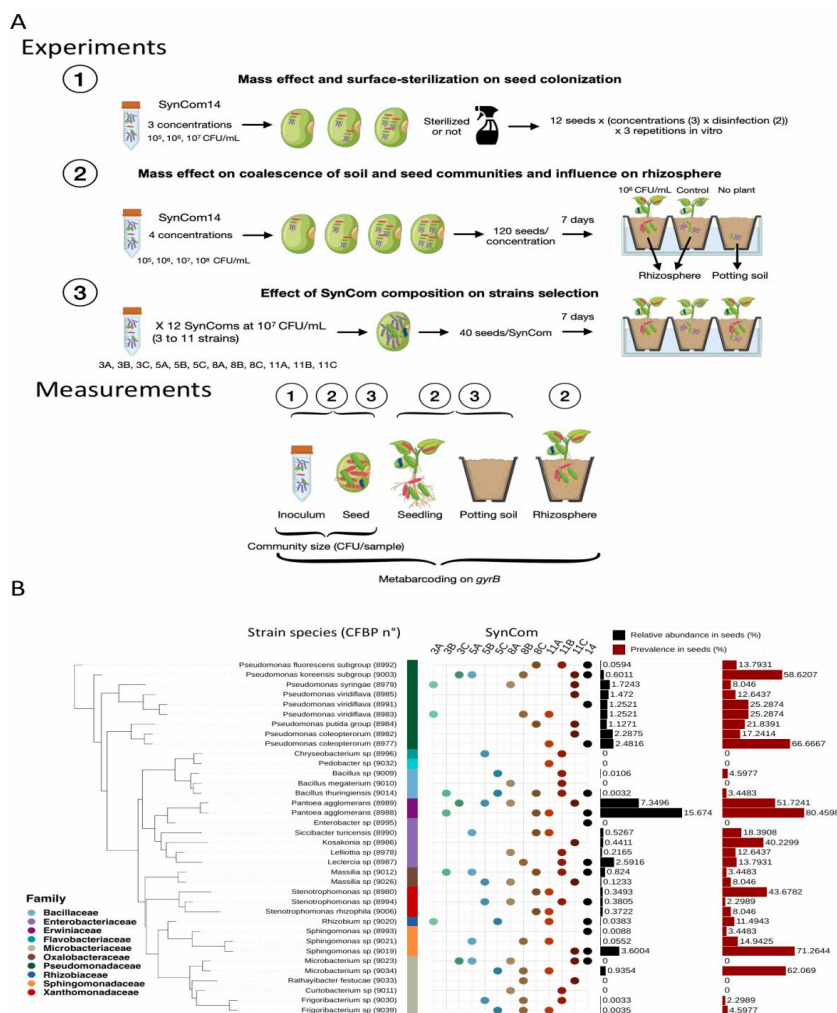


Figure 1 Design of the different experiments, strain selection and SynCom compositions (Adopted from Arnault et al., 2023)

Image caption: A) Overview of the different experiments; In Experiment 1, inoculation of SynCom14 (composed of 14 bacterial strains) on surface-sterilized and unsterilized seeds at different concentrations; In Experiment 2, influence of SynCom14 inoculation at different concentrations on seed and seedling microbiota assembly; In Experiment 3, influence of the inoculation of 12 different SynComs (with 3, 5, 8 or 11 bacterial strains) on seed and seedling microbiota assembly; B) Phylogenetic tree of the 36 strains selected and composition of the 13 SynComs; SynCom14 was studied in experiments 1 and 2 and the others in experiment 3; The number in SynCom names indicates the SynCom richness; Relative abundance and prevalence of each strain in the original seed samples are plotted on the right side; Seven strains were selected while they were not detected using the metabarcoding approach (Adopted from Arnault et al., 2023)