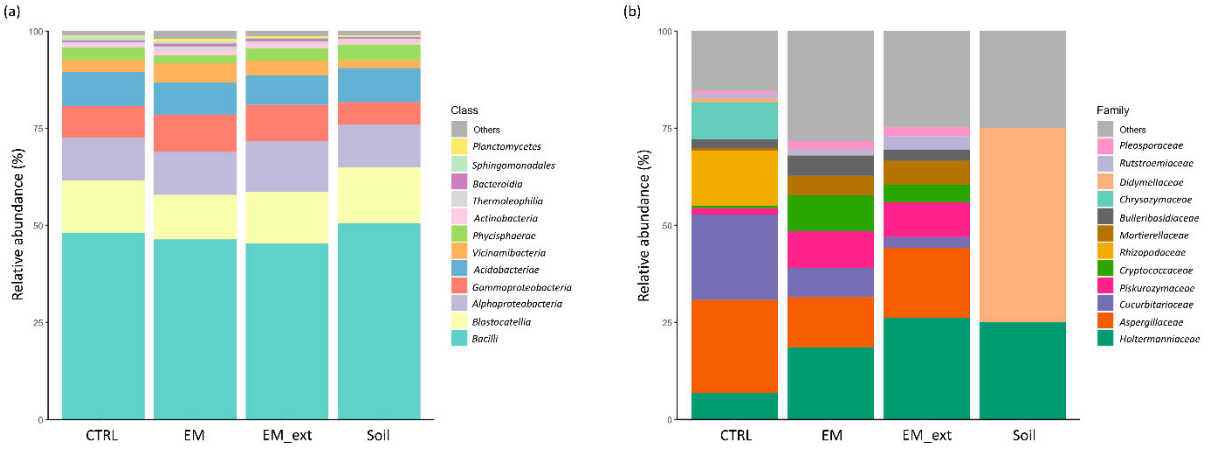


Figure S2. Relative abundance of bacterial (16S) and fungal (ITS) communities across treatments.
(a) Relative abundance of bacterial Classes obtained through 16S rRNA gene metabarcoding, aggregated by treatment using the *groupmean = "Type"* option in the microeco package. Taxonomic assignment was performed at the Class level. Samples are grouped into four treatments: CTRL, EM, EM_ext, and Soil. Overall, the bacterial community structure appears highly similar across treatments, with major Classes (e.g., *Bacilli*, *Blastocatellia*, *Alphaproteobacteria*, *Gammaproteobacteria*) showing only minor fluctuations. Notably, no major differences emerge between Soil and the planted treatments, indicating that the presence of zucchini had a limited impact on bacterial community composition at this taxonomic resolution.
(b) Relative abundance of fungal Families obtained through ITS metabarcoding and taxonomic assignment against the UNITE reference database. Data were likewise aggregated by treatment using *groupmean = "Type"*. Although some shifts among Families (e.g., *Holtermanniaceae*, *Aspergillaceae*, *Didymellaceae*, *Piskurozymaceae*) can be observed between treatments, these differences should be interpreted with caution because the ITS dataset is characterized by a relatively low number of reads, which reduces the robustness of the inferred community profiles. Overall, the relative abundance profiles indicate a stable bacterial community across treatments, while the fungal community shows apparently larger fluctuations that are, however, not supported by high sequencing depth.