Soil microbiota promotes early developmental stages of *Phelipanche ramosa* (L.) Pomel during plant parasitism on *Brassica napus* (L.)

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Supplementary tables

Supp. Table S3 Relative proportion of species within the *Aspergillus* genus, detected in the rapeseed study soil. Several amplicon sequence variant (ASV) corresponded to the same species. No differences were found between the three biological replicates (p-value >0.05%; pairwise comparisons of proportions).

Aspergillus spp. 20.00%			
ASV identifier	**UNITE assignation**	**Abundance (mean %)**	**sd**
ASV 853	*Aspergillus unidentified*	76.07	1.14
ASV 1804	*Aspergillus_protuberus*	18.50	1.33
ASV 107	*Aspergillus_candidus*	2.98	0.35
ASV 1	*Aspergillus_pseudodeflectus*	1.18	0.56
ASV 3301	*Aspergillus_alliaceus*	0.77	0.97
ASV 914	*Aspergillus_flavipes*	0.55	NA
ASV 2326	*Aspergillus_candidus*	0.46	NA
ASV 844	*Aspergillus_penicillioides*	0.24	0.09
ASV 3819	*Aspergillus_unidentified*	0.15	NA
ASV 2187	*Aspergillus_flavipes*	0.08	0.06
ASV 1621	*Aspergillus_flavus*	0.08	0.04
ASV 178	*Aspergillus_affinis*	0.08	NA

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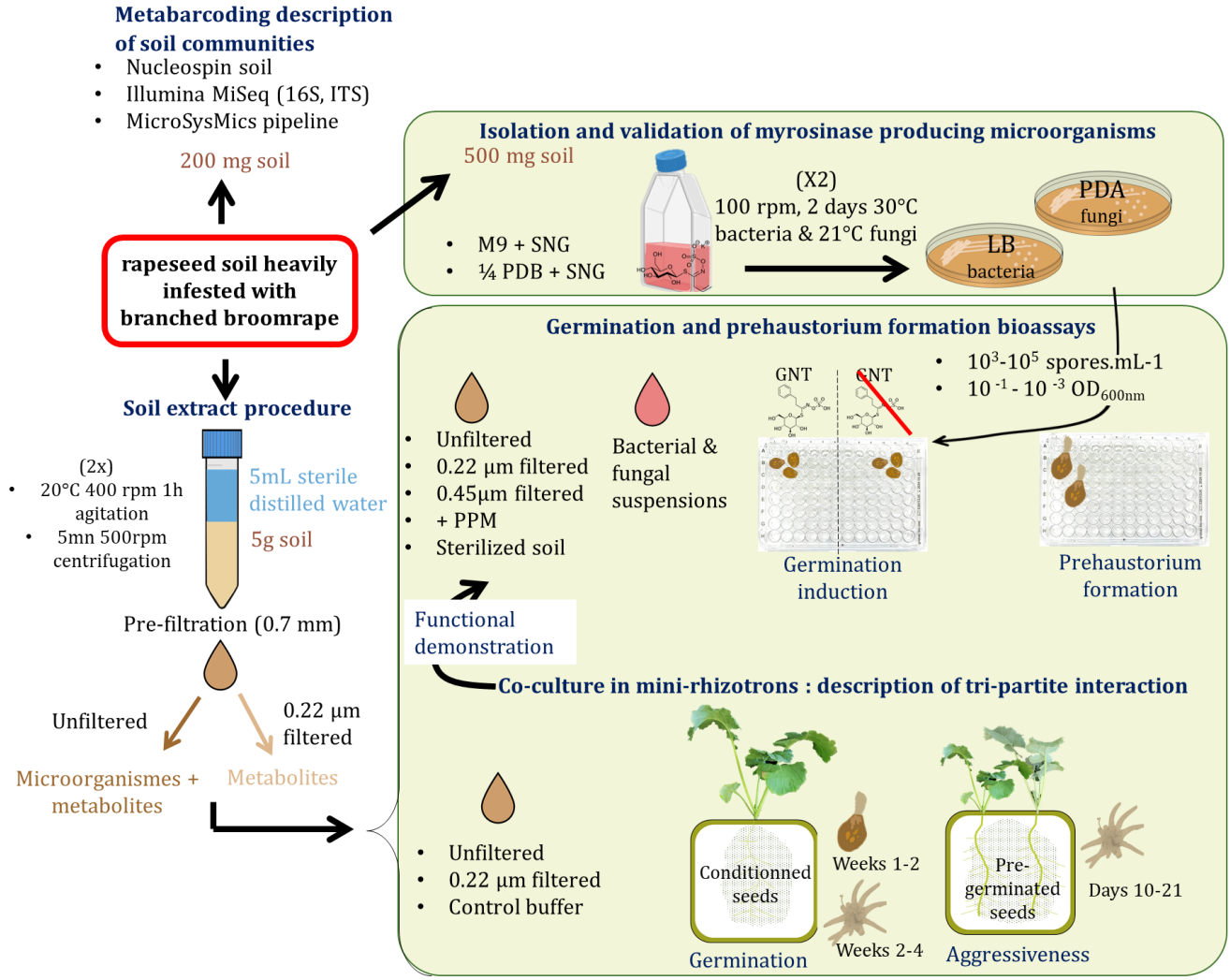
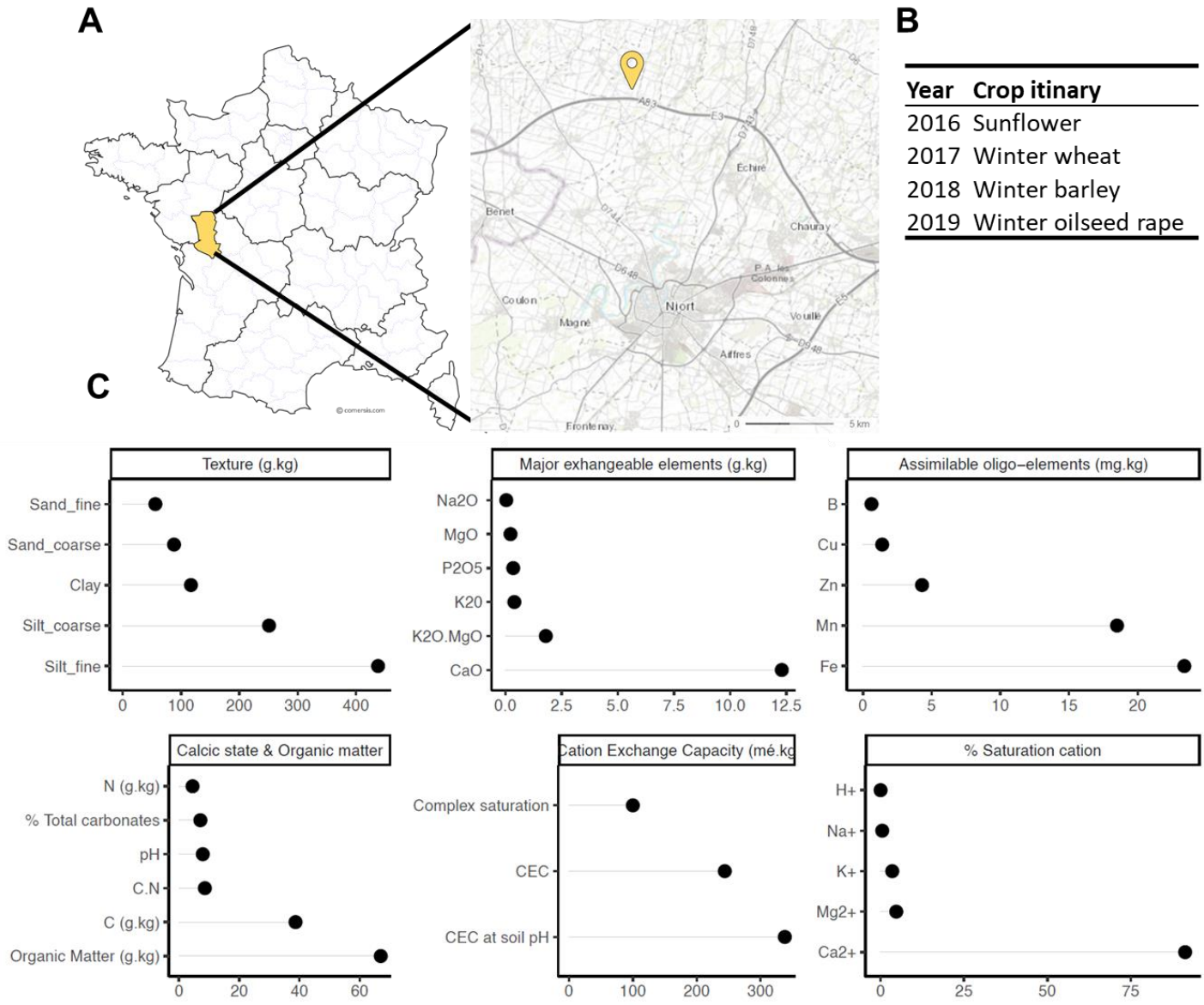
Supplementary figures



Supp. Fig.S1 Summary of experimental design conducted for this study. A rapeseed soil was used to functionally demonstrate the promoting role of microorganisms in plant parasitism. Minirhizotron Co-cultures were first used to validate the contribution of microorganisms while plate bioassays further characterized direct and indirect production of signal metabolites. Isolation of active strains reinforced the hypotheses.



Supp. Fig.S2 Additional information about the study sol with **A** localization on France map, **B** crop itinerary from 2016 to 2019, and **C** complete result of physicochemical analyses.

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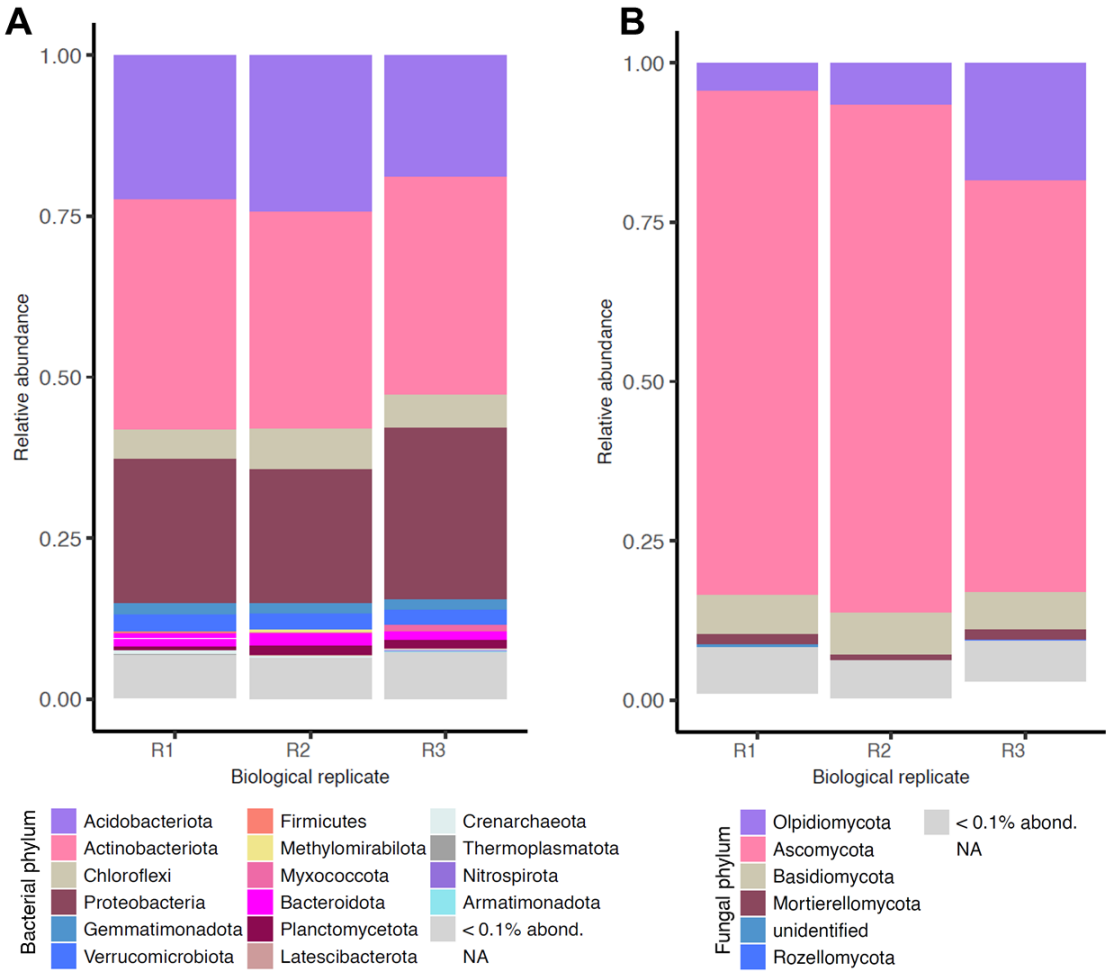
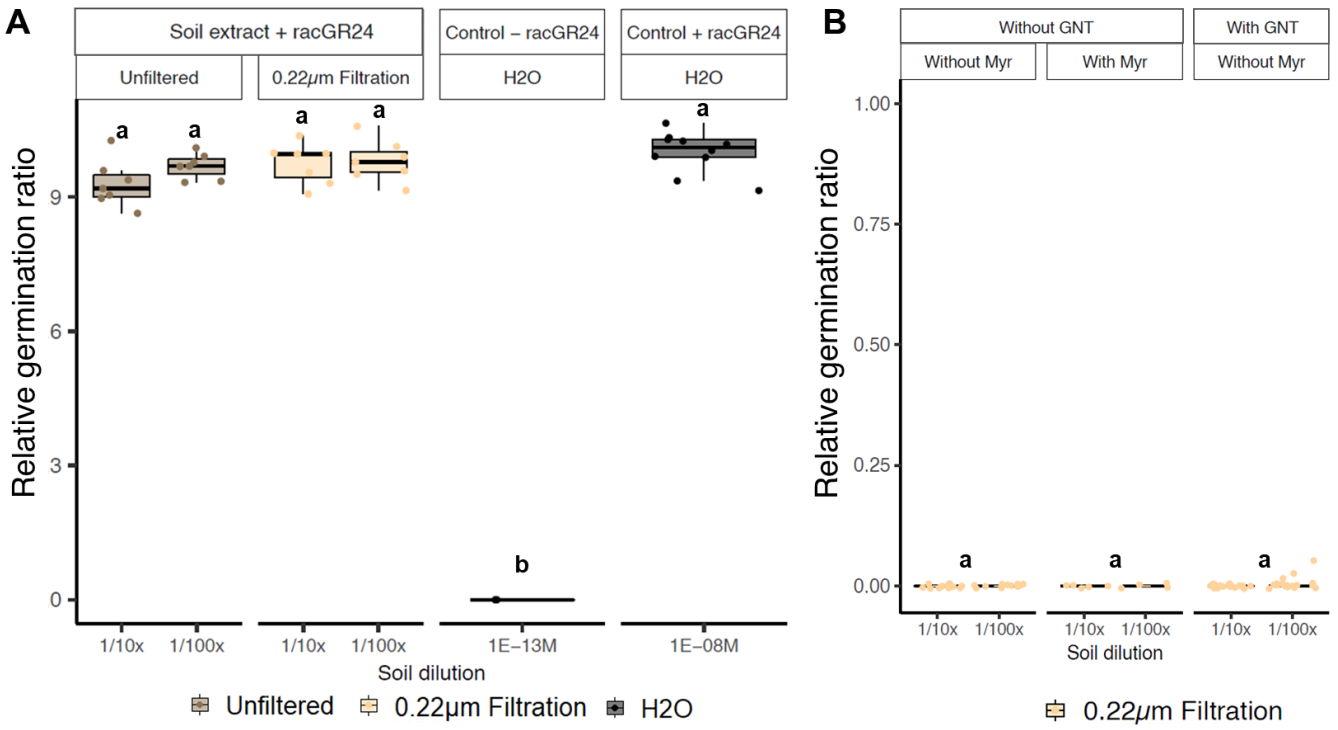
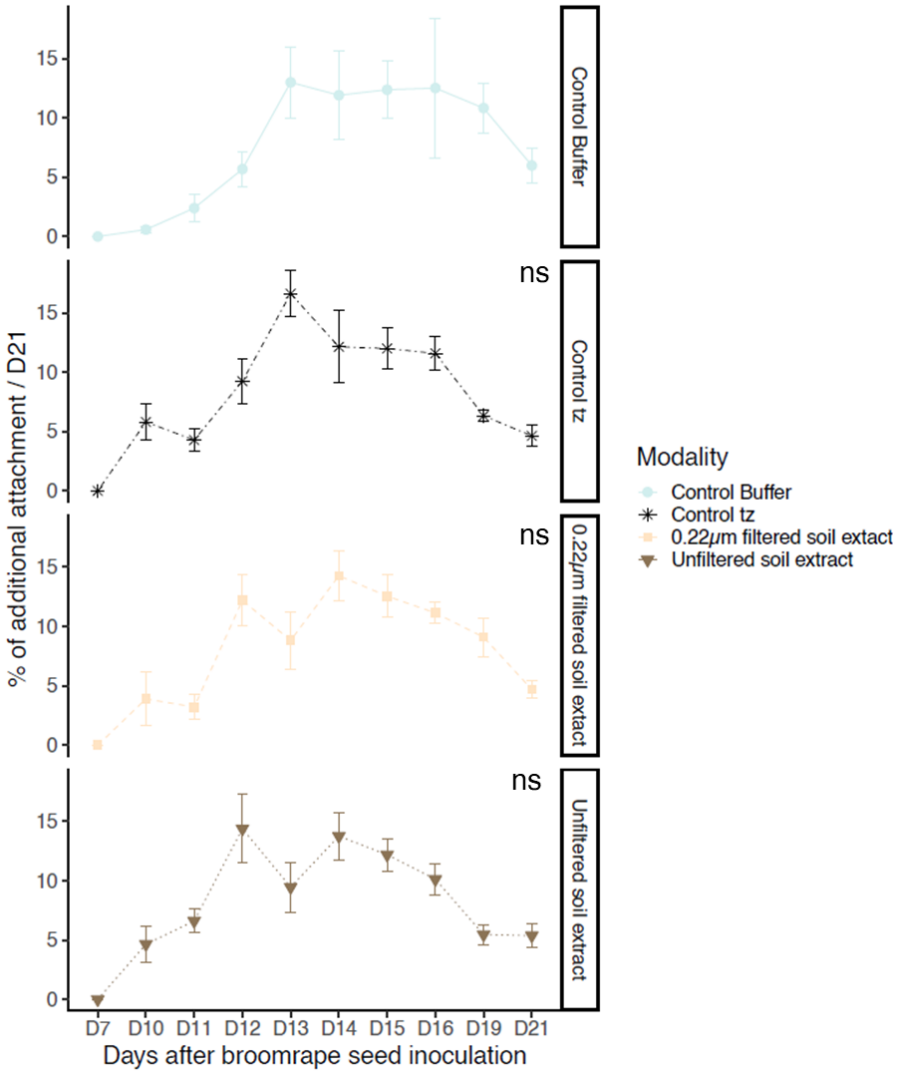


Supp. Fig. S3 Relative abundance levels of bacterial **A** and fungal **B** phyla, expressed as percentages of all Amplicon sequence variant (ASVs) detected in the broomrape infested soil. DNA extraction was performed on three soil samples and amplification targeted the V4 region of the 16S rRNA genes. Taxa less than 0.1% abundant were grouped into the "< 0.1% abond." class, and taxa with no family assignation of family level were grouped into the "NA" class (not available).



Supp. Fig.S4 Germination of broomrape seeds after **A** a co-treatment with unfiltered soil extracts at a 10-fold or 100-fold dilution and germination stimulation with racGR24 (10^{-8} *M*) to test for germination inhibition or **B** a co-treatment with 0.22µm filtered soil extracts and myrosinase enzymes (5 $mU.mL^{-1}$) or gluconasturtiin (GNT 1.10^{-3} *M*) to test for presence of residuals GNT or extracellular enzymes. For both figures, ratios are expressed as the number of germinated seeds on total seeds, relatively to the average ratio obtained with the positive control (racGR24 10^{-7} *M*, a synthetic strigolactone, maximum germination ratio = 1 ≈ 71.35±7.50% of germinated seeds). Germinated seeds were colored in purple after MTT reduction, and non-germinated seeds appeared in yellow. Significant differences are represented by different lowercase letters (p-value <0.05), and determined by a Kruskal-Wallis rank sum test (non-normal data) and multiple pairwise comparison.



Supp. Fig.S5 Daily increase of parasitic attachments to rapeseed roots compared to final monitoring in day 21. Aggressiveness assays were conducted on 9 subsample replicates using germinated and 48 h pre-treated seeds with either control buffer solution, unfiltered soil extract (containing soil microorganisms and soil metabolites), or 0.22µm filtered soil extract (containing soil metabolites only) or cytokinin (*t*Z 10^{-7} *M*). Values are displayed as mean with standard deviation as error bars. Significant differences between treatment was determined by ANOVA on generalized model with a quasi-law for Poisson regression. There was no effect of the treatment on daily attachment increase (p-value =0.83)