**Soil-microbes-mediated invasional meltdown in plants**

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Codes, reports and data

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We experimentally tested whether and how a third plant species affected the competitive outcomes between alien and native plants through its soil legacy. We first conditioned soil with one of ten species (six natives and four aliens; these are the soil-conditioning species) or without plants. Then, we grew on these 11 soils, five aliens and five natives (these are the test species) without competition, or with intra- or interspecific competition.

* The files started with ‘01’ are the codes.
  + ‘**01functions.R**’ is the functions that are used in ‘01plant\_NEE.Rmd’ and ‘01soil\_NEE.Rmd’.
  + ‘**01plant\_NEE.Rmd**’ is the code for plant data, and it calls ‘03plant\_dat.csv’ (see below for details of ‘03plant\_dat.csv’). If you want to re-run the analyses, please run ‘01plant\_NEE.Rmd’ before ‘01soil\_NEE.Rmd’, as it will export data that will be used in ‘01soil\_NEE.Rmd’
  + ‘**01soil\_NEE.Rmd**’ is the code for the soil-microbe data, and it calls ‘04phyloseq\_16s\_its.RData’ and ‘05dfr\_funguild\_guilds.csv’ (see below for details).
* The files started with ‘02’ are the reports of ‘01xxx.Rmd’ (I think, in most cases, reading these two reports will solve your questions.).
* The file ‘**03plant\_dat.csv**’ is the biomass data of test plants.
  + - The variable ‘fix’ is identity of unit (pot), i.e. the plants with same ‘fix’ number were grown in the same pot.
    - The variables ‘sp\_p1’, ‘family\_p1’ and ‘origin\_p1’ are the species, family and origin (native or alien, or empty if no soil-conditioning plant) of the soil-conditioning plant, respectively.
    - The variable ‘bio\_p1’ is the aboveground biomass of soil-conditioning plant when harvest, and in ‘bio\_p1\_0’, we set the biomass as 0 for pots without plants.
    - The variables ‘target’, ‘family’ and ‘origin\_p2’ are the species, family and origin of the focal test plant, respectively.
    - The variable ‘biomass’ is the aboveground biomass of focal test plant, and ‘root’ is the belowground biomass of focal test plant that was grown alone.
    - The variables ‘comp’ and ‘family\_comp’ are the species and family of competitor test plant, respecitively.
    - ‘competition’ describe whether the focal test plant was grown alone, or with intra- or interspecific competition.
    - The variable ‘trans\_date\_c’ is the transplanting date [day as the unit]. The plants that are transplanted first are set as 0.
    - The variable ‘comb’ is the ID of the test species pair (e.g. A1 indicates that *Dactylis glomerata* was grown alone, H15 indicates that *Plantago media* and *Lolium multiflorum* were grown together).
* The file ‘**04phyloseq\_16s\_its.RData**’ include two *phyloseq* objects of 16S (bacteria) and ITS (fungi). It contains the cleaned sequencing data for each soil sample, which was sampled when we harvested the soil-conditioning plants. We used three tables of each *phyloseq* object:
  + otu\_table: a sample-by-ASV [Amplicon sequence variant] matrix, with number of reads as entries.
  + tax\_table: a table of the taxonomy of each ASV.
  + sam\_data: a table of sample information.
    - ‘fix’ can linked with the ‘03plant\_dat.csv’.
    - ‘status’ is the origin of the soil-conditioning plant (n: native, a: alien, ck: no soil-conditioning plant).
    - ‘ster.not’ indicate whether soil inoculum was sterilized or not before the soil-conditioning.
* The file ‘**05dfr\_funguild\_guilds.csv**’ is the FUNGuild (<http://www.funguild.org/>) information of all ITS ASVs, which is used to determine the functional groups of fungi (according to the ‘Guild’ variable.). The FUNGuild was accessed on 2019-10-30.
* The file ‘**06tree.tre**’ is the phylogenetic tree of all species in the project.
* The rest six files are the csv versions of ‘04phyloseq\_16s\_its.RData’, which are for who do not use R. ‘otu\_table\_xx’, ‘tax\_table\_xx’ and ‘sam\_table’ correspond to otu\_table, tax\_table and sam\_data in the ‘04phyloseq\_16s\_its.RData’, respectively.