

PUTATIVE ECOLOGICAL CATEGORIES IN PLANT-FUNGAL INTERACTIONS REVEALED BY DIFFERENTIAL NETWORK ANALYSIS

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We present with **pride** an automated clusters analysis workflow of *Tilia cordata* rhizosphere mycobiomes. NGS data was obtained from nursery pots and seedlings established *in situ*, a year after planting in the forest. FUNGuild tool was used to divide species into six highly probable life styles: Bcn - biocontrol agents, End - endophytes, Myc - mycorrhizas, Nop - non plant-oriented, Pat - pathogens, Sap - saprophytes.

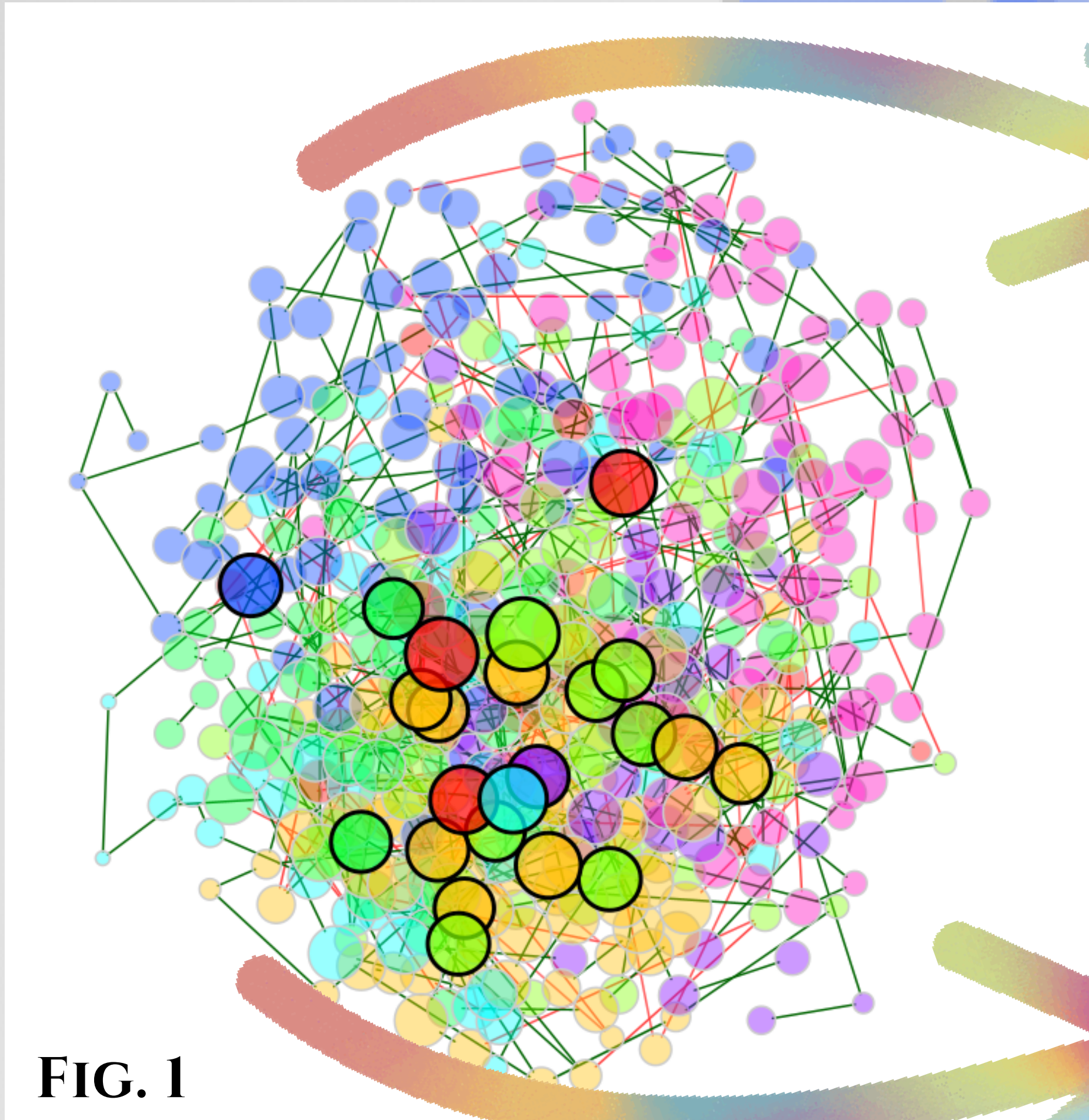


FIG. 1

NetCoMi [1] network analysis of 452 species (cut_off = 75) identified in pots and field samples. SpiecEasi method [2] - the measure reliable for large communities was chosen due to reliably high modularity (0.36 for this graph).

CONCLUSIONS

The identified clusters appear to represent putative syntrophic-like [3] interactions between ecological groups:

- Only cluster_1 is dominated by co-occurrence of pathogenic fungi
- Clusters 2 and 5 represent cooperating saprotrophs
- Cluster_8 reveals putative interactions between mycorrhiza and their helper fungi, which may supply them crucial nutrients

FUTURE PERSPECTIVES

Guided by our approach one could study the available genomes (including MAGs) of taxa from highlighted clusters to search for genes functional to their lifestyle[4].

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LITERATURE

1. Peschel et al. (2021). NetCoMi: network construction and comparison for microbiome data in R. Briefings in bioinformatics 22 (4), doi:10.1093/bib/bbaa290
2. Kurtz et al. (2015). Sparse and compositionally robust inference of microbial ecological networks. PLoS computational biology 11(5), doi: 10.1371/journal.pcbi.1004226.
3. Morris et al. (2013). Microbial syntrophy: interaction for the common good. FEMS microbiology reviews 37(3), doi: 10.1111/1574-6976.12019
4. Djemiel et al. (2022) Inferring microbiota functions from taxonomic genes: a review, GigaScience 11, doi:10.1093/gigascience/giab090

	Bcn	ENA	End	Myc	Nop	Pat	Sap
cluster_1	0.0	0.18	0.0	0.0	0.0	0.79	0.02
cluster_2	0.0	0.43	0.0	0.01	0.02	0.12	0.43
cluster_3	0.0	0.58	0.0	0.07	0.0	0.2	0.14
cluster_4	0.0	0.56	0.0	0.11	0.17	0.07	0.09
cluster_5	0.0	0.46	0.0	0.01	0.05	0.12	0.36
cluster_6	0.0	0.67	0.0	0.01	0.05	0.12	0.15
cluster_7	0.0	0.64	0.0	0.2	0.0	0.04	0.12
cluster_8	0.0	0.21	0.01	0.33	0.27	0.02	0.15

FIG. 2

The automated pipeline divided clusters of different sizes from Fig. 1 by ecological categories contribution. This approach helps to understand the community composition and propose biological functions, including taxa not ecologically assigned (ENA) by FUNGuild.

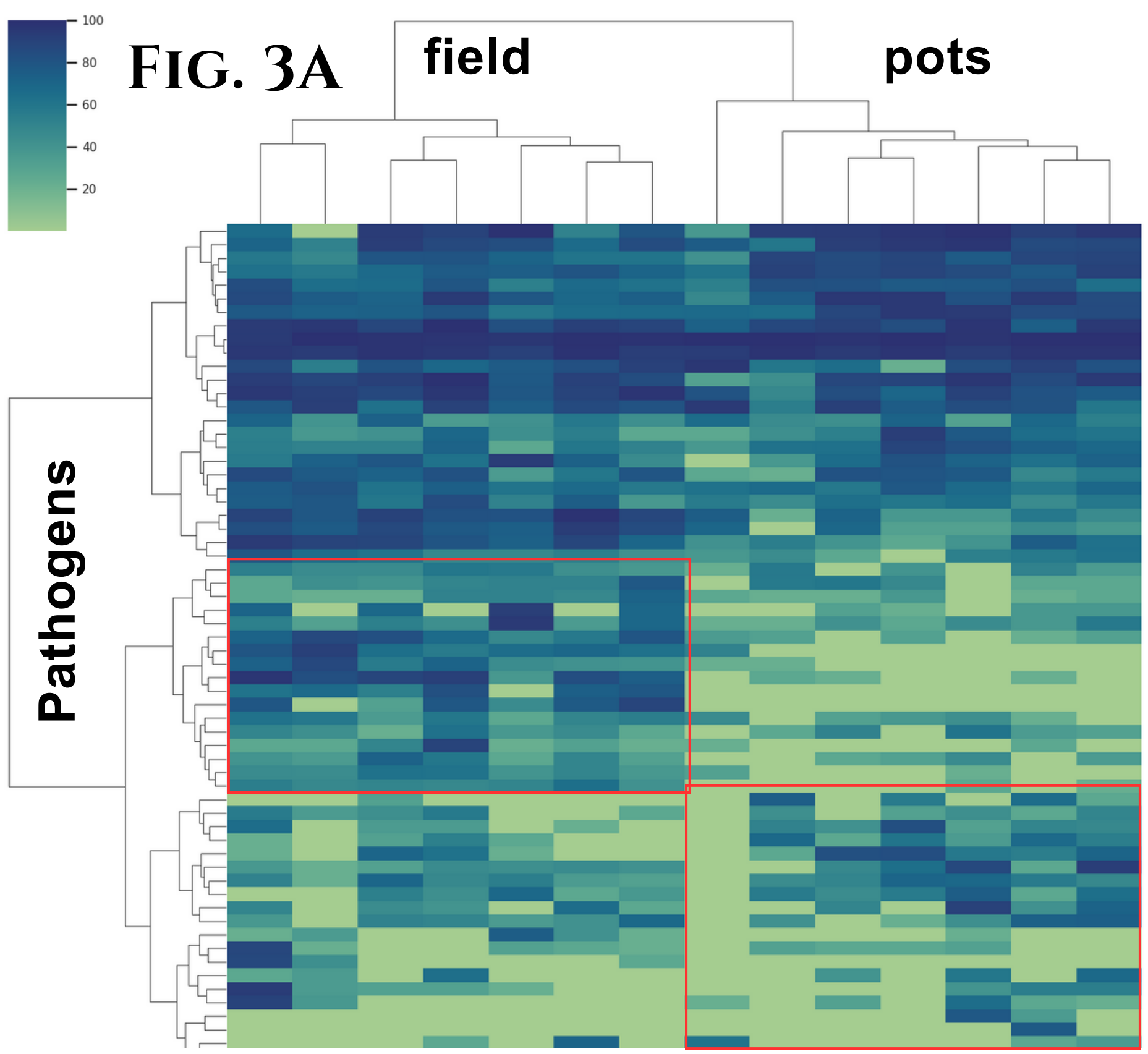


FIG. 3A

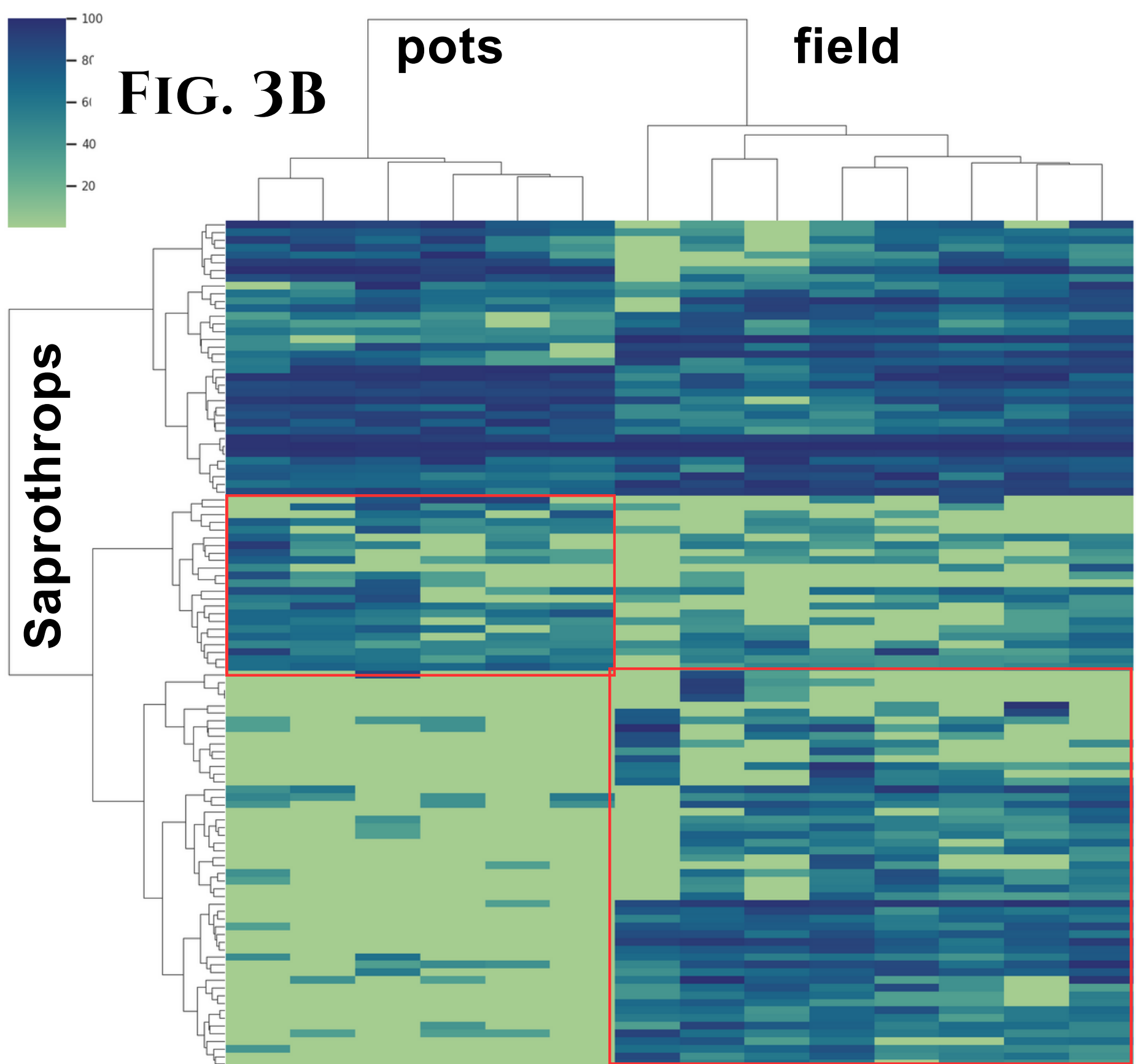


FIG. 3B

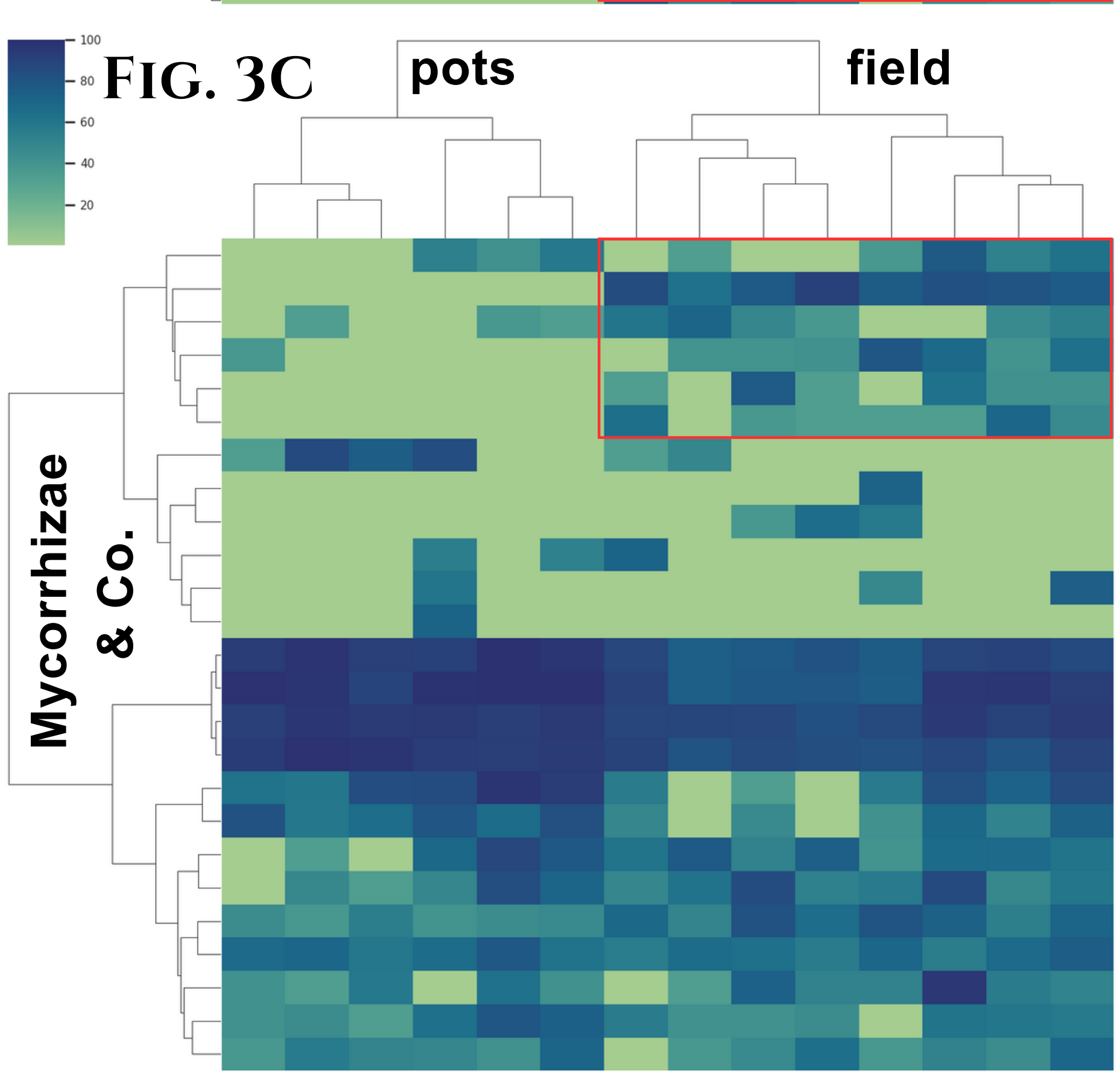


FIG. 3C

Tilia cordata root soil samples

Field and pots mycobiota form distinct dendrogram units (red boxes) obtained by pairwise clustering. It reflects different transition rates of exogenous taxa to the rhizosphere of those two groups - clearly an effect of pots' isolation.