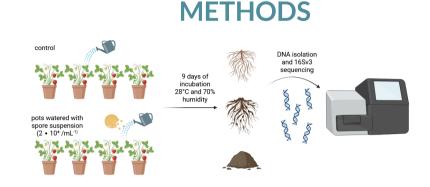
The Anna Karenina Principle in the microbiome: How Pilidium Iythri destabilizes bacterial communities in soil

Dominika Siegieda¹*, Jacek Panek¹, Emilia Hannula², Magdalena Frąc¹

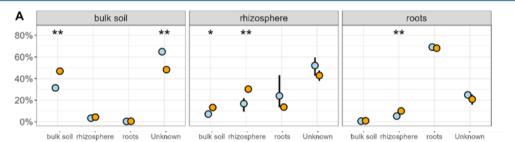
¹Institute of Agrophysics, Polish Academy of Sciences, Doświadczalna 4 St., 20-290 Lublin, Poland ²Leiden University, Institute of Environmental Sciences, Department of Environmental Biology, Leiden, The Netherlands *e-mail: d.siegieda@ipan.lublin.pl

INTRODUCTION

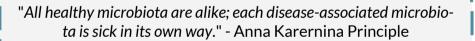
- ⇒ Global warming causes spreadnig of thermotolerant fungal pathogens to new areas
- ⇒ *Pilidium lythri*-phytopathogen affecting many agriculturally important plants (olive, cornelian cherry, European plum, grapevine) and many ornamental flowers; with **strawberries as the primary host**
- ⇒ First recognised as a strawberry pathogen in Iran and China; now **expanding geographical distribution** to temperate climate, with recent identification in organic strawberry plantations in Poland
- \implies Non-host specific, capable of infecting both wounded and intact fruits
- ⇒ Despite its accelerated spread due climate change, significant knowledge gap remains regarding its influence on native microbiome structure



- DNA was isolated with EURx GeneMATRIX Soil DNA Purification Kit
- \implies Libraries were sequenced on Illumina MiSeq with Reagent Kit v3 (2x300)
- Downstream analyses: QIIME2, Silva 138, microeco, SourceTracker



To elucidate the influence of *Pilidium lythri* on microbial migration between the niches, we SourceTracker. Samples from sampling at 0 days were used as a source, and samples from sampling at 9 days as sinks. In bulk soil, bacterial community revealed significantly higher share of microorganisms in bulk soil and a lower portion from unknown source in infected samples (Fig. A). Furthermore, we observed migration of bacteria from bulk soil to rhizosphere in infected communities, but also from rhizosphere to rhizosphere for bacteria in infected communities. Finally, analysis revealed increased migration from rhizosphere to roots in infected samples in bacterial community.



Arnault, G., Mony, C., & Vandenkoornhuyse, P. (2023). Plant microbiota dysbiosis and the Anna Karenina Principle. Trends in Plant Science, 28(1), 18–30



The βNRI results revealed a dominance of stochastic processes in both healthy and infected rhizosphe-

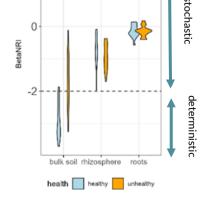
RESULTS

SourceTracker is a Bayesian tool used to estimate the proportions of microbial communities that come from various known sources (like soil, rhizosphere, roots, etc.). It utilizes Gibbs sampler. (doi: 10.1038/nmeth.1650)

Beta Net Relatedness Index (β NRI) is a phylogenetic beta-diversity metric. It measures how different two communities are in terms of the evolutionary relationships among the species they contain. It tells us whether two microbial communities are made up of species that are more or less closely related than expected by chance. If the communities are made up of very distantly related species, β NRI will be higher than |2| (suggesting different environmental filtering or evolutionary histories). (doi: 10.1038/ismej.2013.93)

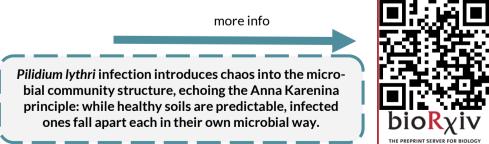
CONCLUSIONS

- ⇒ In healthy bulk soil, microbial communities were shaped by deterministic processes suggesting similar, stable, and predictable communities across replicates. This aligns with the AKP's idea of "all healthy microbiomes are alike."
- → In infected bulk soil, we observed a shift toward stochastic processes, meaning more random and variable communities — a hallmark of <u>"each dysbiotic microbiome is dysbiotic in its own way."</u>
- This shift implies that <u>Pilidium lythri infection disrupts environmental fil-</u> tering, leading to less control over which microbes establish – causing greater divergence between infected samples.
- \Rightarrow The increased microbial migration between niches in infected plants may



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re and root samples of strawberry (betaNRI values between -2 and 2). Furthermore, we observed differences in community assembly processes between healthy and infected bulk soil, with a shift from deterministic processes (characterized by lower turnover) in healthy bulk soil to a dominance of stochastic processes in infected soil (Fig. B). further contribute to dysbiosis and the individualized trajectories of each infected microbiome.







DS's 3-month visit at the Institute or Environmental Sciences, Leiden University, was financed by the Polish National Agency for Academic Exchange, contract number: BPN/BEK/2023/1/00125/ U/00001

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This project was funded in whole by National Science Centre, Poland. Grant Number 2022/45/NZ9/02089