

Kill'em all?

Interactions of predatory Myxobacteria with soil microbes – an in vitro and microcosm perspective on their role in the soil microbial food-web Piecha¹, Marc; Streblow¹, Morten ;Woyde¹, Jonas; Groß¹, Verena; Borg Dahl¹, Mathilde; Reinhard, Anne¹; Wang¹, Haitao; Tamang², Mandip; Pester², Michael; van Bommel³, Miriam; Rueß³, Liliane; Urich¹, Tim University Greifswald, Greifswald¹; DSMZ Braunschweig, Braunschweig²; Humboldt Universität, Berlin³





Introduction:

Soils hosts one of the most **complex** communities on Earth and are vital resources providing food and essential ecosystem services [1]. The **high complexity** of the soil food web and the intricate organismic diversity hindered the creation of explicit links functional) taxonomical between (and microbiome composition microbial and physiology, especially for Myxobacteria. We want to shed light on their **predatory life style** their **influence** on **microbial death**, and growth and turnover in the soil microbial food web.



Aims:

- unravel **role** of **Myxobacteria** in the soil food web
- investigate **predation patterns** and prey preferences for Myxobacteria
 - utilizing *in vitro* predation assays
- Interactions of **Myxobacteria** with bacteriovorous **competition** in *in vivo* mesocosms

prokaryotic
community
composition

• utilizing **metatranscriptomics** for **3-Domain SSU rRNA** community profiling



- 16 soil bacteria as prey
- first time that Gemmatimonodata and Verrucomicrobia were
- testing predatory behavior of *Myxococcus fulvus*, Myxococcus virescens, Haliangium ochraceum and Corallococcus coralloides





Figure 3: Mesocosm setup with main soil chamber and connected CO₂ traps [3]



In vivo mesocosms

- Experiments with **fertilized Dikopshof** soil over 32 days
- Three consecutive Experiments with higher trophic level predators added:
- No nematodes, bacterivorous or fungivorous nematodes
- organic matter manipulation: no carbon source, maize litter and 13Clabelled maize litter
- Soil samples taken on **five** different **time** points
 - extracted **DNA** and **RNA**

Figure 2: (A) Predation assay setup over eight days for *M. fulvus* on *N. terrae*, (B) Results of the in vitro predation Assays, showing lysis diameter in cm for corresponding predator-prey paring

4: 3-Domain SSU rRNA community profiles of the microcosm Figure experiment. Depicted are taxon relative abundance [%], C-source manipulation, the addition of nematodes and the sampling dates (D0-D32) for selected groups: (A) Myxococcota (order level), (B) Fungi (kingdom level), (C) predatory Protists (phylum level).

- All prey was lysed by at least one Myxobacterium
- Myxobacteria had different prey preferences
- Haliangium ochraceum has the broadest spectrum
- predation susceptibility of prey organisms differs greatly

Conclusion:

- Myxobacteria killed all prey bacteria in in vitro assays
- Myxobacteria are highly abundant in soil and resistant to higher trophic level predation in the *in vivo* mesocosms
 - suggest an **important role** in agricultural **soil micro food web**

[1] Thompson, L.R., Sanders, J.G., McDonald, D., Amir, A., Ladau, J., Locey, K.J., et al. (2017) A communal catalogue reveals Earth's multiscale microbial diversity. Nature 551: 457–463

[2] Stefan Geisen, Robert Koller, Maike Hünninghaus, Kenneth Dumack, Tim Urich, Michael Bonkowski, The soil food web revisited: Diverse and widespread mycophagous soil protists, Soil Biology and Biochemistry, Volume 94, 2016, Pages 10-18, ISSN 0038-0717, https://doi.org/10.1016/j.soilbio.2015.11.010. modified by Gross, 2020

[3] Curtesy of Miriam van Bommel, Humboldt Universität, Berlin.

[4] Petters, S., Groß, V., Söllinger, A. et al. The soil microbial food web revisited: Predatory myxobacteria as keystone taxa?. ISME J 15, 2665–2675 (2021). https://doi.org/10.1038/s41396-021-00958-2

Quantitative metatranscriptomics:

- **Bacteria** are the most **abundant** domain (90 %)
- **Myxobacteria** highly **abundant** (11-20 %) in microbiome and **not** strongly affected by Nematode grazing
- **Predatory bacterivorous Protists** were the most **abundant Eukaryotes** (5-6 %) \rightarrow large, but rather unresponsive bacterial channel
- **Fungi** had a **low** relative **abundance** (1%) in soils **without** additional **C-source** relative **abundance doubled** with addition of **maize litter**
 - \rightarrow Small fungal channel, but responsive to C-source manipulation
- They were **prone** to **predation** by **fungivorous Nematodes**

