

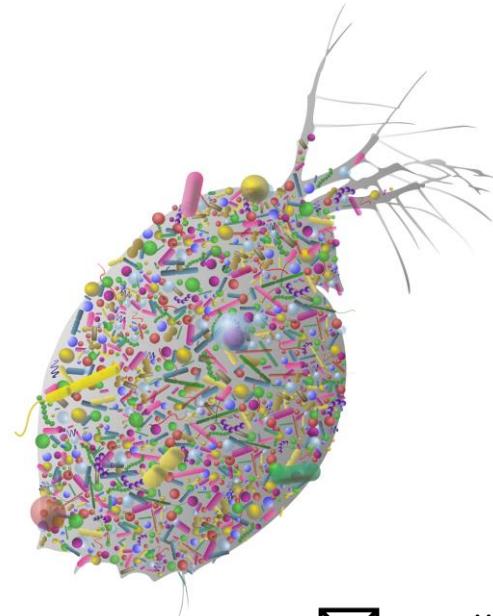
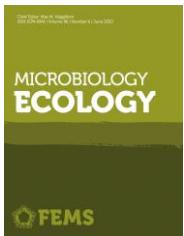
The role of the microbiome in eco-evolutionary dynamics

Daphnia and its microbiome as a model



Ellen Decaestecker – KU Leuven

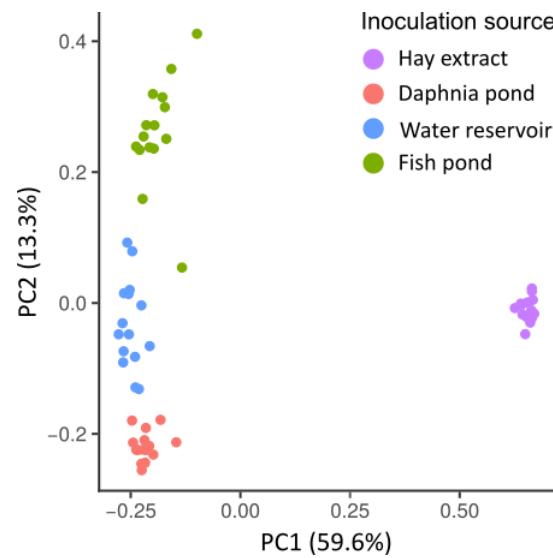
The bacterioplankton community composition and a host genotype dependent occurrence of taxa shape the *Daphnia magna* gut bacterial community



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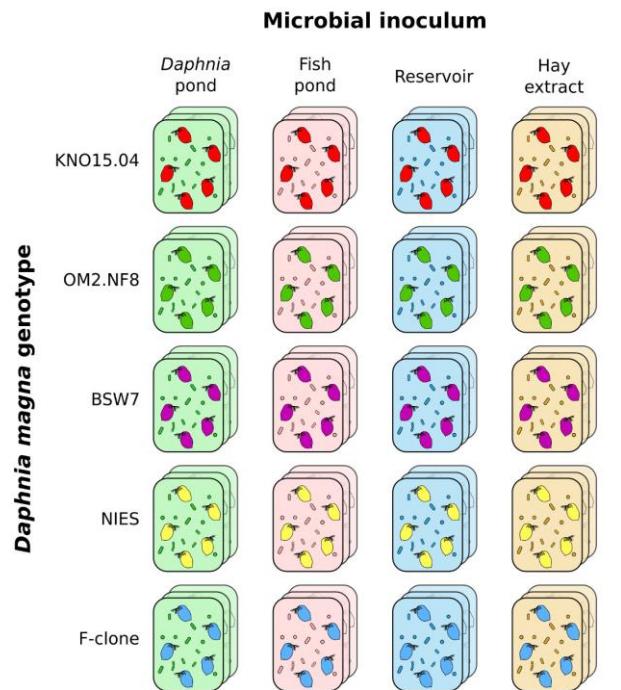
FEMS Microbiology Ecology, Volume 96, Issue 8, August 2020, fiaa128, <https://doi.org/10.1093/femsec/fiaa128>

Experimental setup



Four distinct bacterioplankton communities

Experimental setup

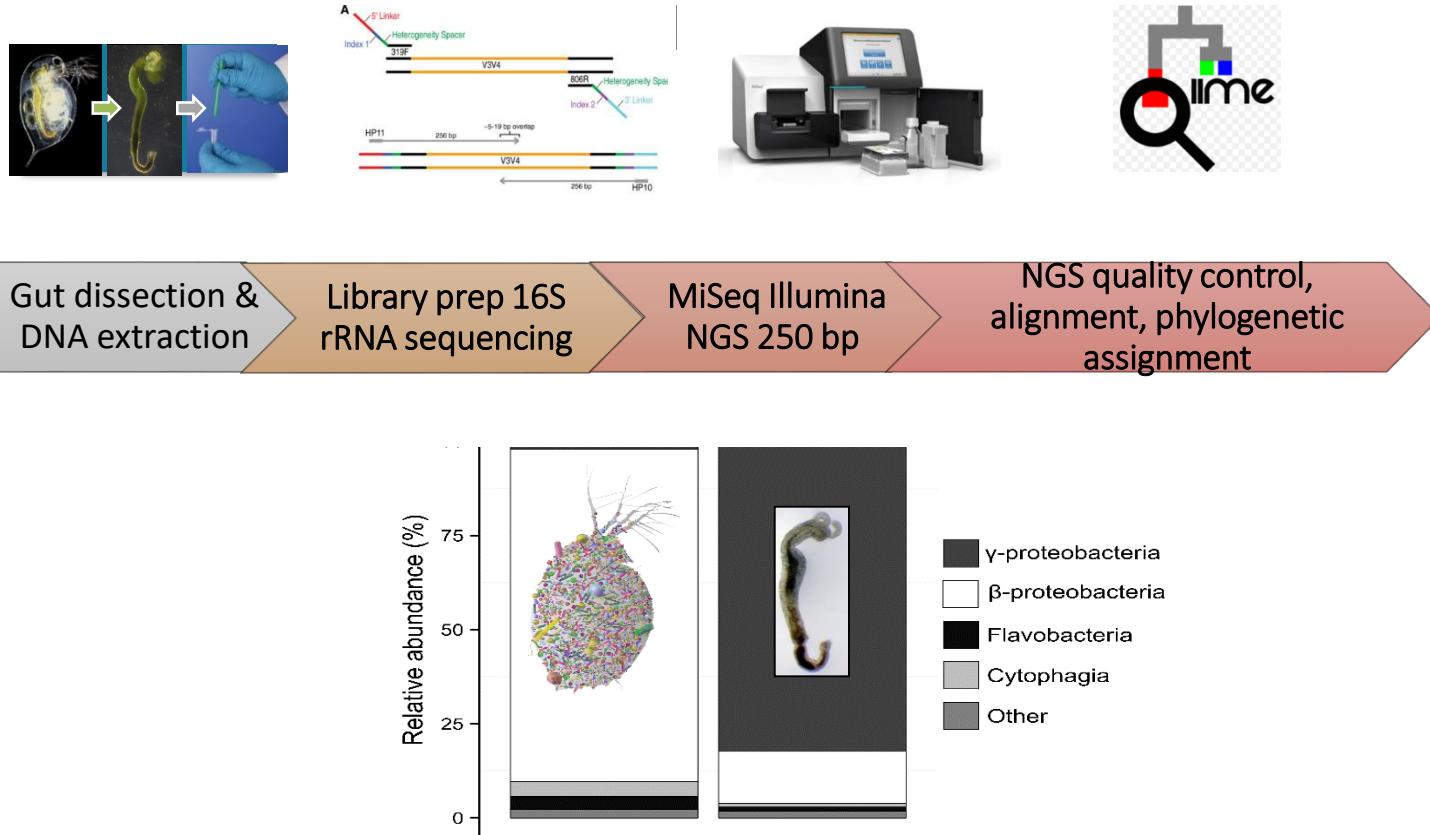


→ Five *Daphnia magna* genotypes

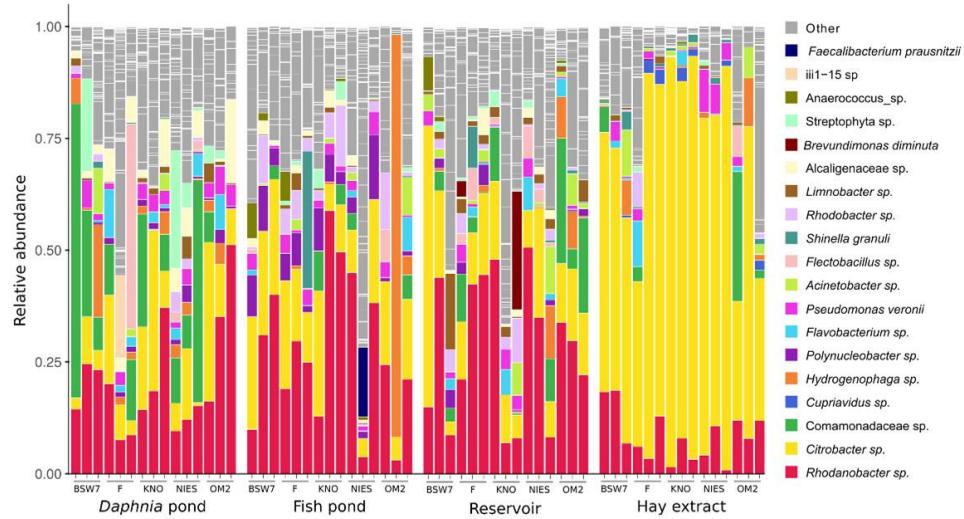
→ Guts colonized by bacterioplankton

What is the relative impact of the **bacterioplankton** and the **host genotype** on the gut bacterial community?

Daphnia gut microbiome community



Influence of bacterioplankton on gut bacteria

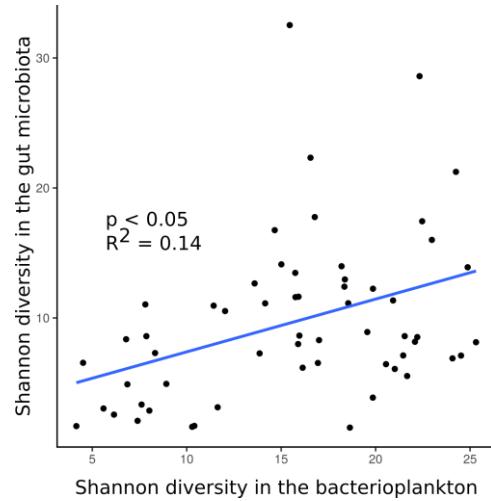


30.6% of variation explained by
bacterioplankton treatment

Quantitative metrics*
→ relative abundance

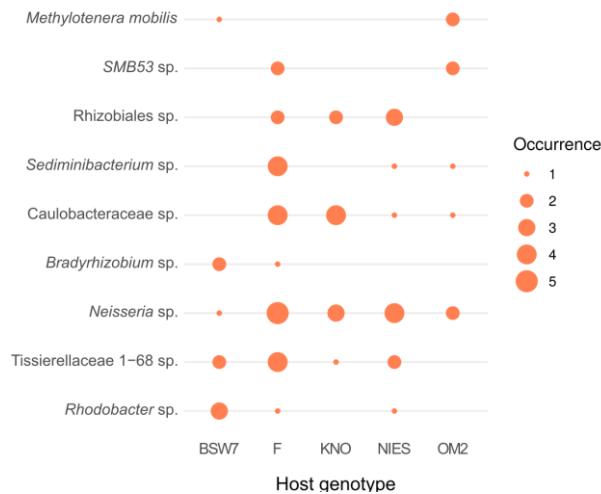
Qualitative metrics*
→ presence/absence

Influence of bacterioplankton on gut bacteria



Correlation between bacterioplankton and gut diversity

Influence of bacterioplankton on gut bacteria

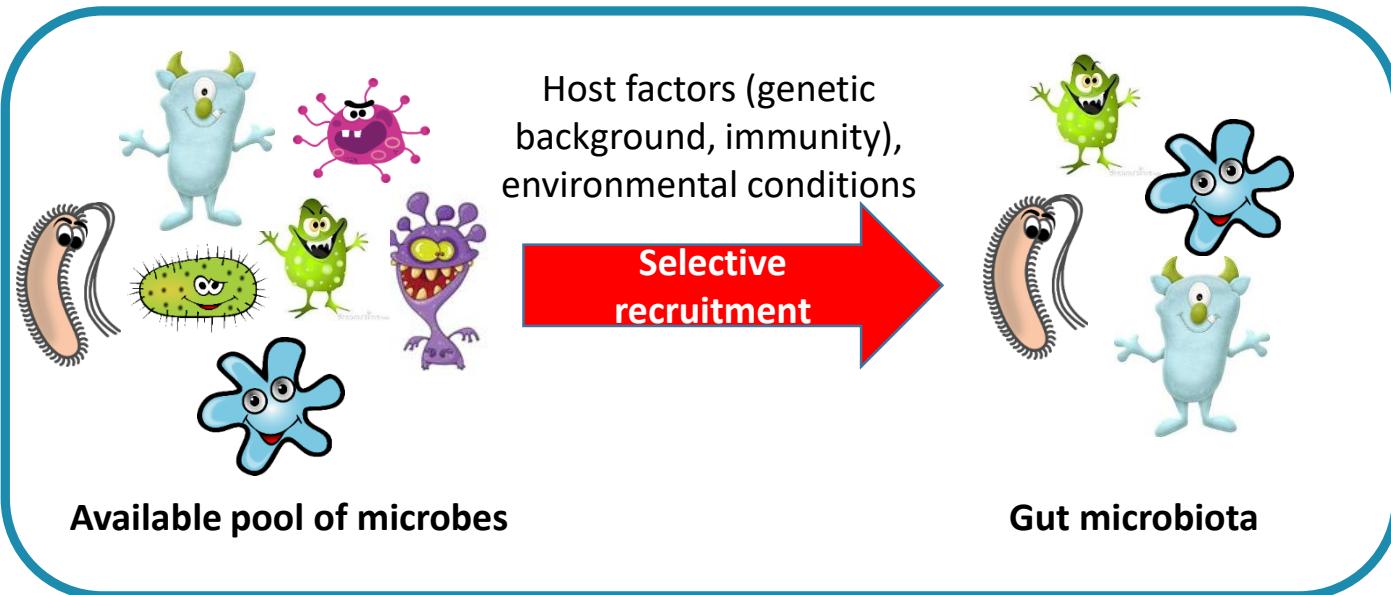


Differentially abundant taxa
according to host genotype

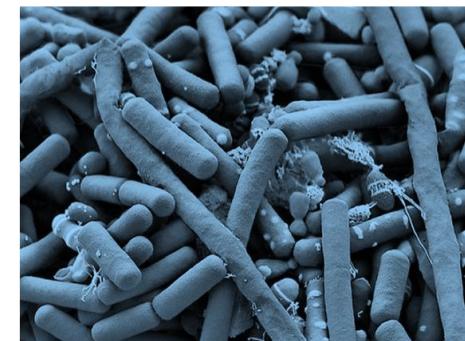
Perspectives

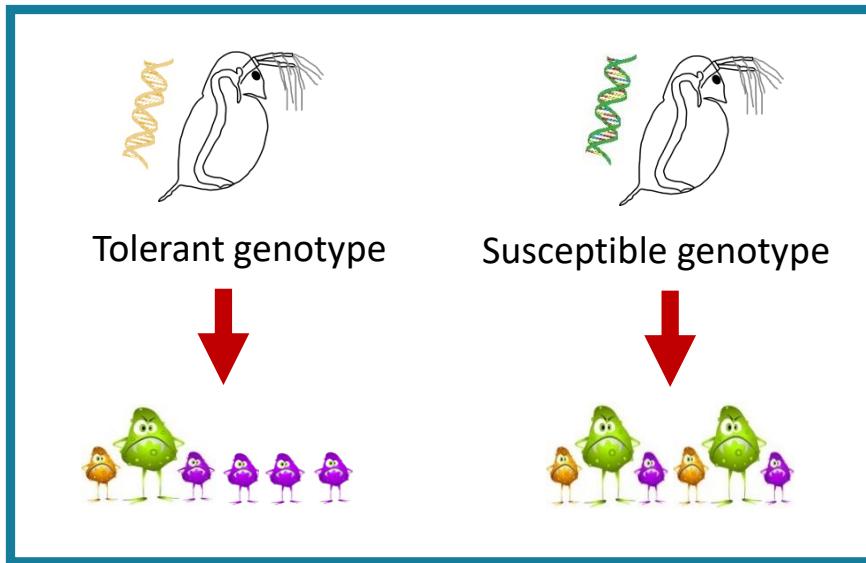
- Ecological interactions between gut microbiota members?
- Biological mechanism of host genotype effect on gut microbiota?

Transmission and acquisition of the gut microbiome

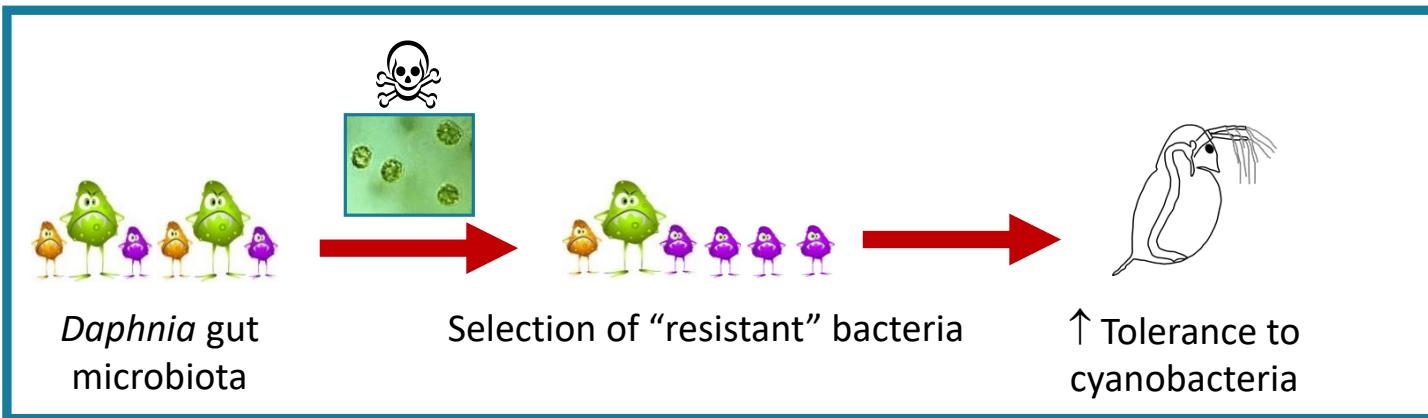


Host genotype shapes the assembly of the gut microbiota and the surrounding bacterioplankton



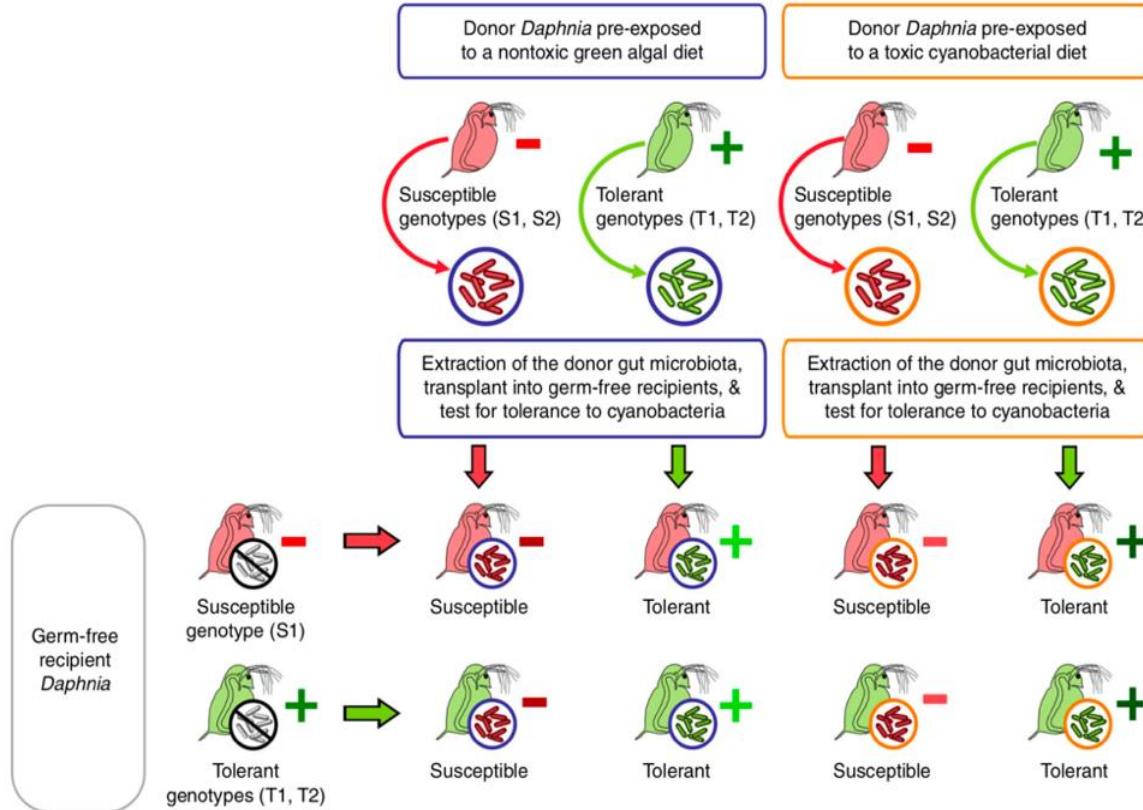


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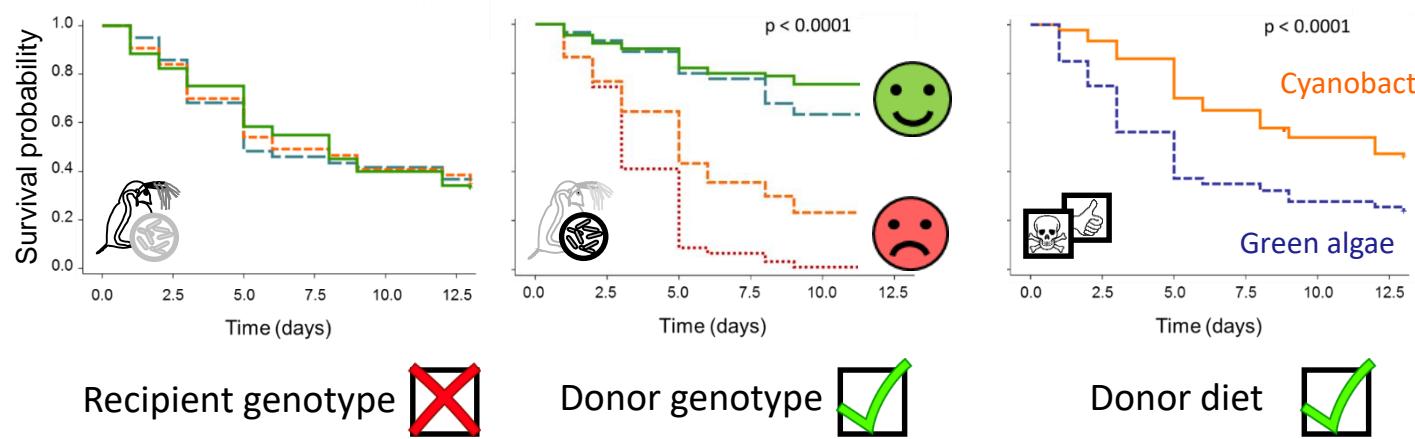
?

Gut microbiome transplant : Donor and recipient experiment



Gut microbiome adaptation and *Daphnia* acclimatization to toxic cyanobacteria

Results on phenotype of the recipients

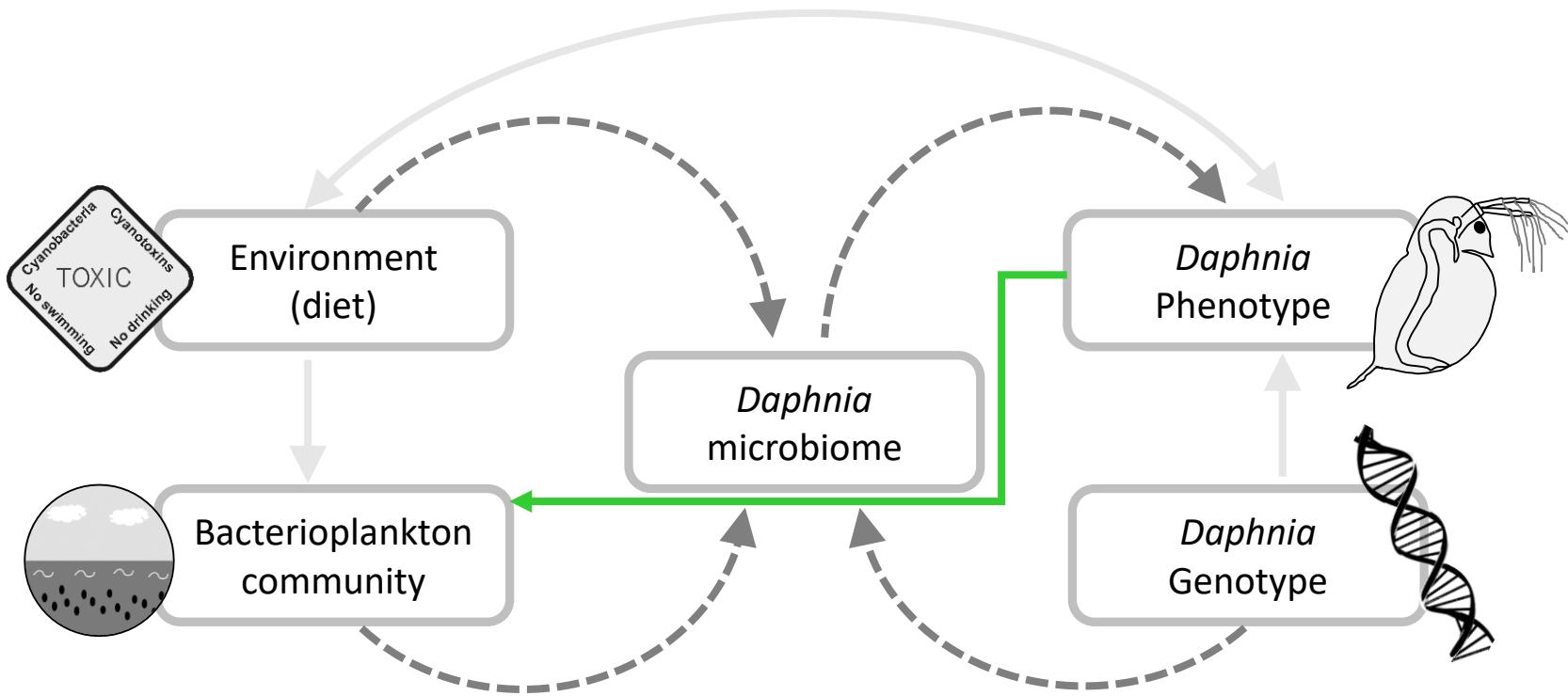


Resistance to cyanobacteria is mainly mediated by the gut microbiota

Genetic variation in the functionality of the microbiota

Pre-exposure to cyanobacteria increases the protective effect of the microbiota

Daphnia microbiome: scope for eco-evolutionary dynamics?

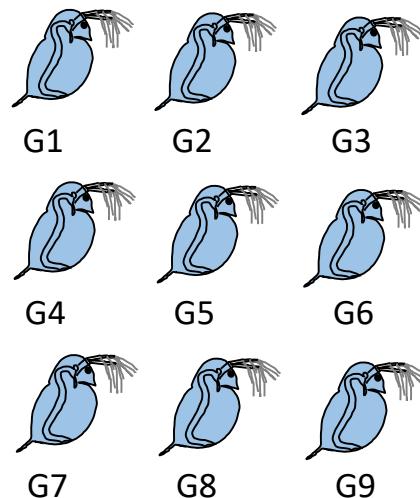


Follow up Experiment 1

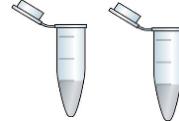
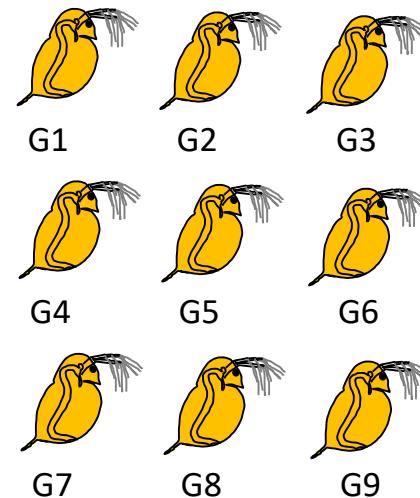
Exposure to
wide bacterial
community
(field inoculum)



Genotypes exposed to a
green algae diet

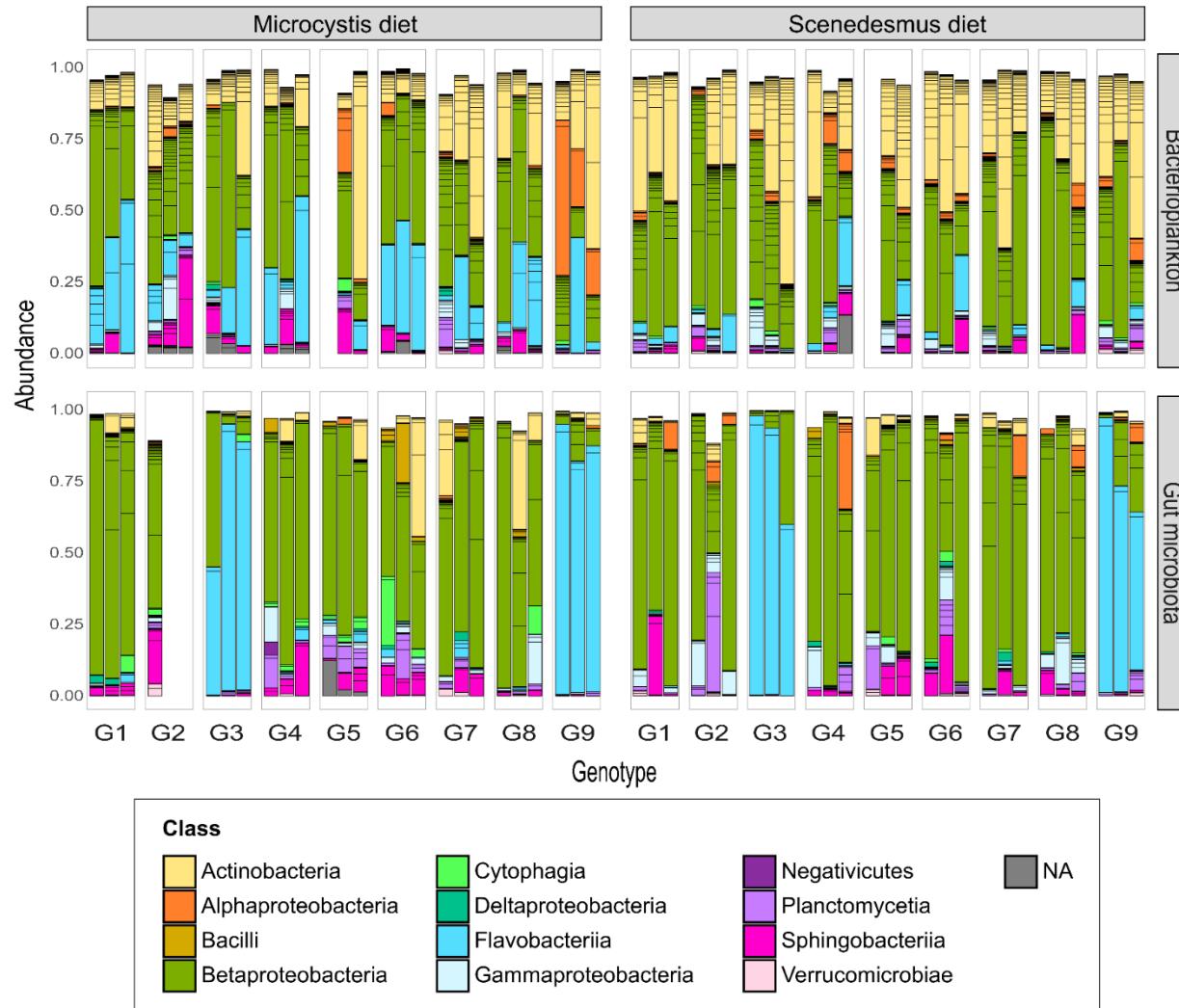


Genotypes exposed to a
cyanobacteria diet



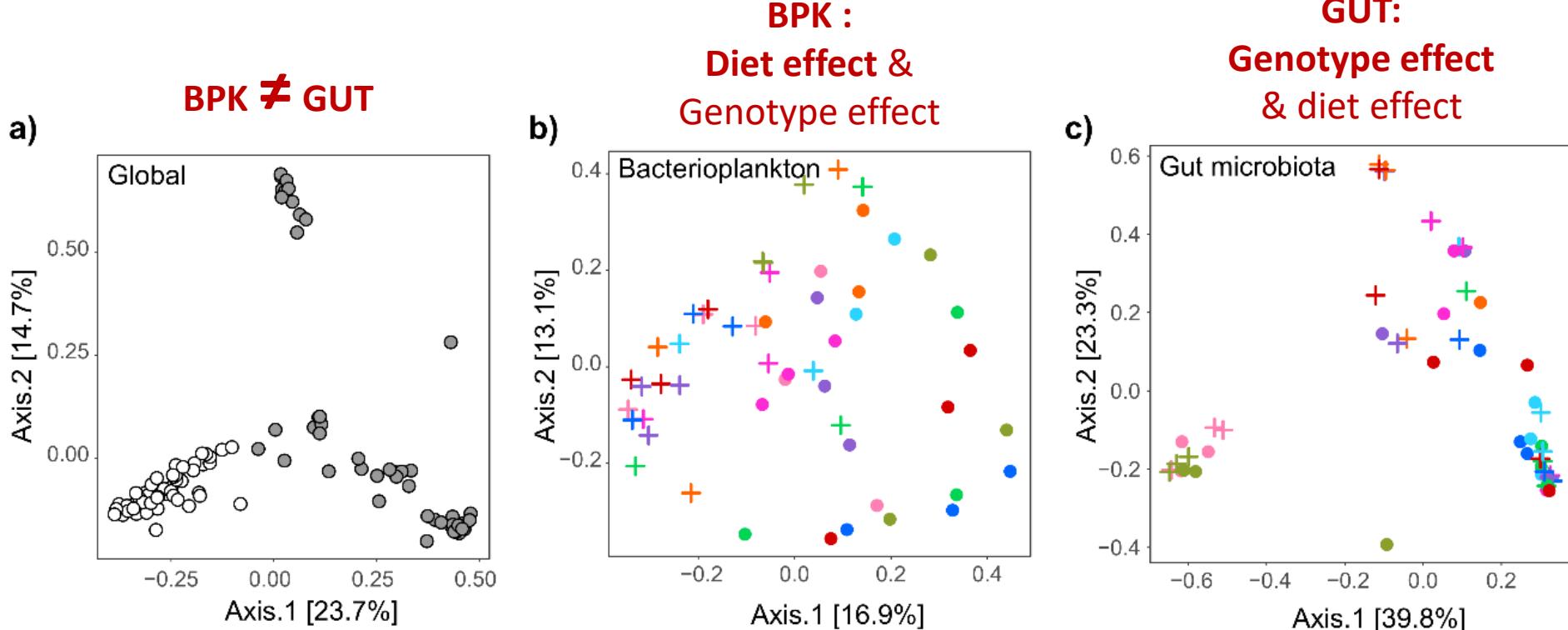
After 1 year of exposure:
Sequencing on
gut microbiota +
BACTERIOPLANKTON

Characterization microbiota of the donors inclusive BPK



- Gut microbiome and bacterioplankton: genotype and diet dependent composition

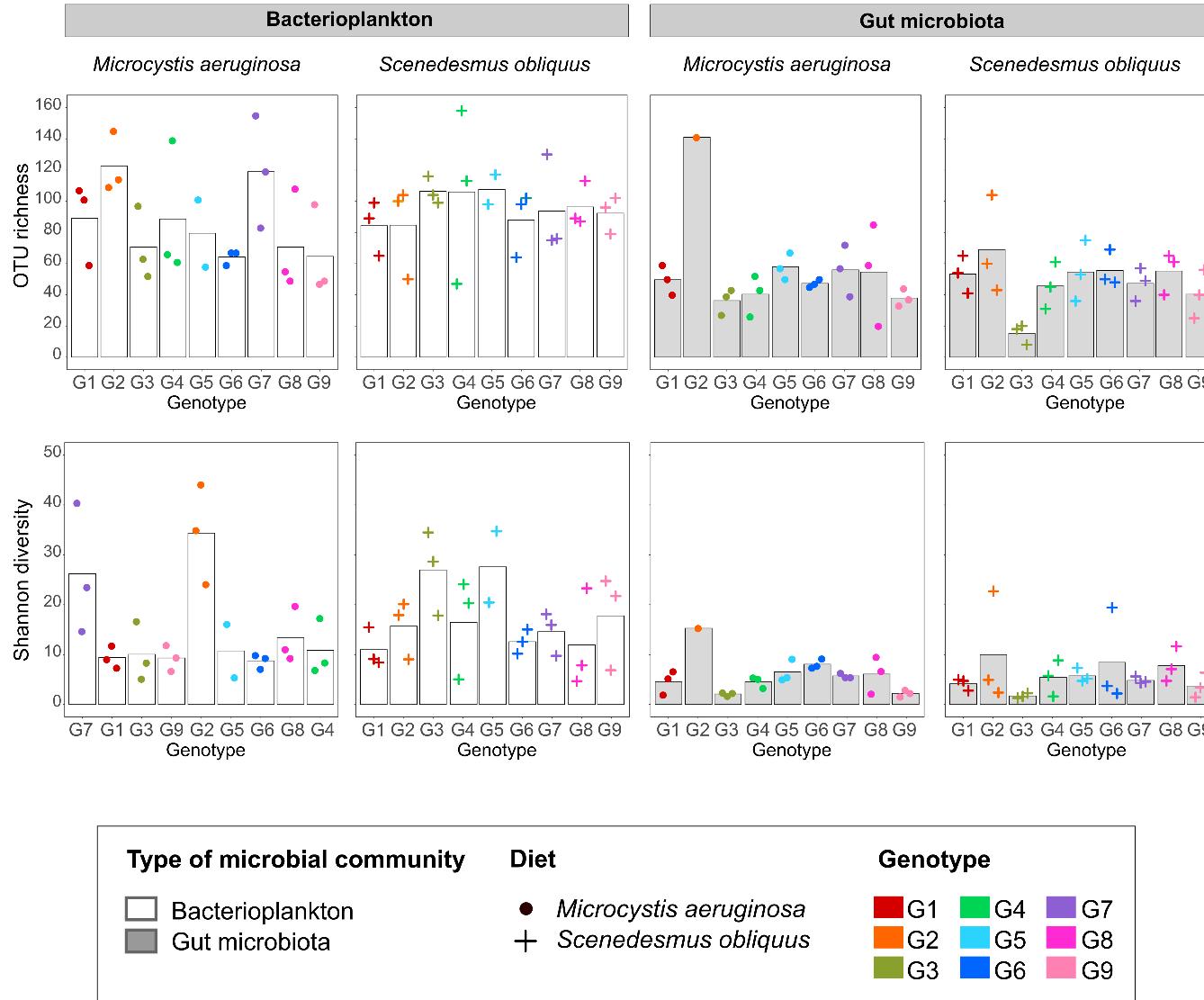
Characterization microbiota of the donors inclusive BPK



Type of microbial community	Diet	Genotype
□ Bacterioplankton ■ Gut microbiota	● <i>Microcystis aeruginosa</i> + <i>Scenedesmus obliquus</i>	G1 G4 G7 G2 G5 G8 G3 G6 G9

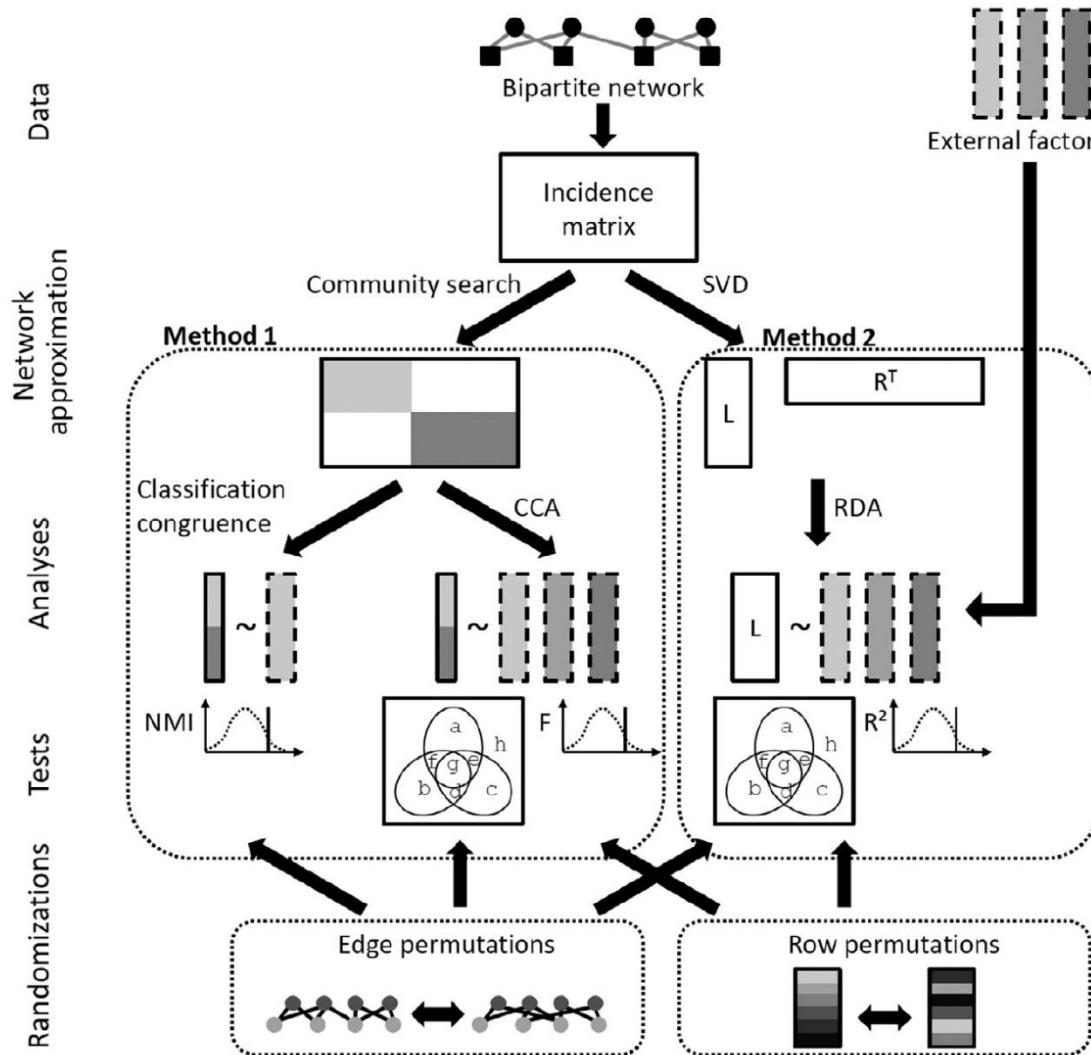
- Gut microbiome differed from bacterioplankton

Characterization microbiota of the donors inclusive BPK



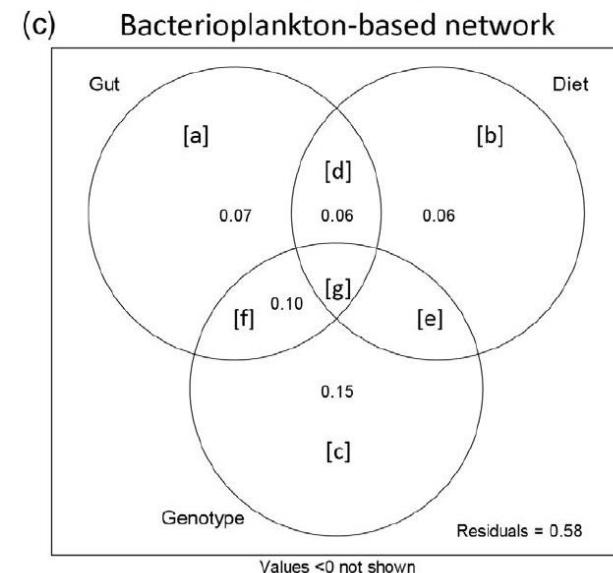
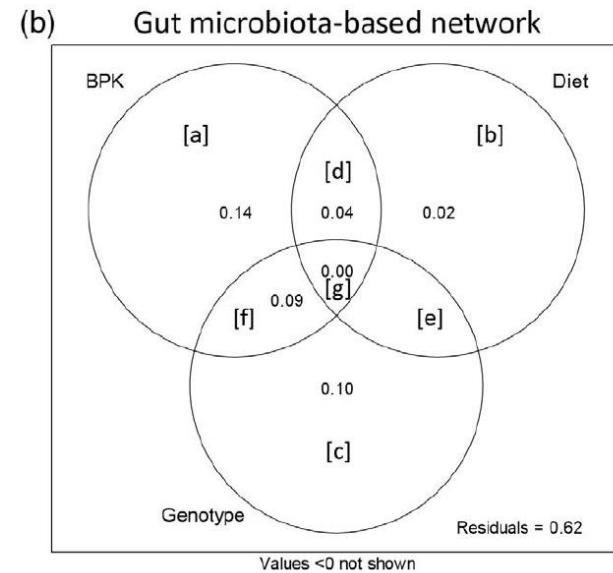
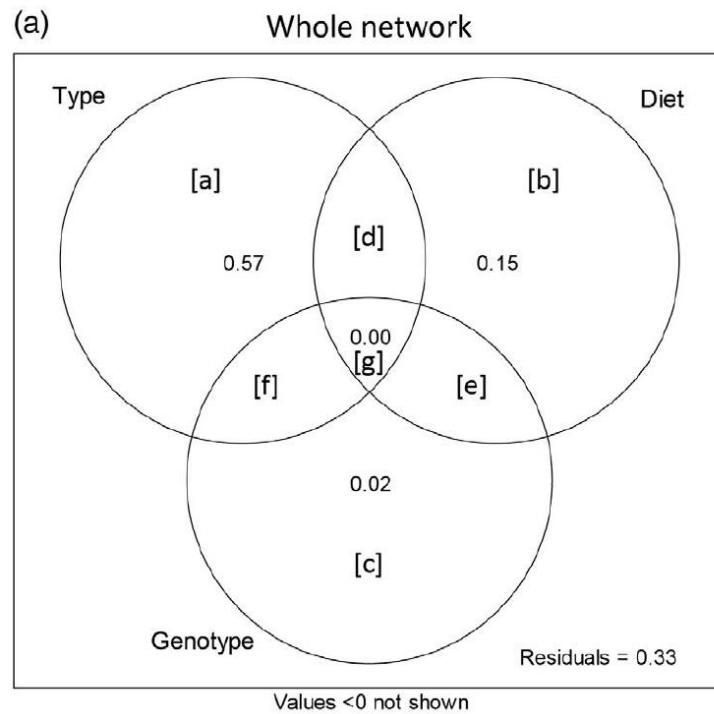
- α-diversity GM < BPK :
suggesting selective rejecting of bacteria from regional species pool

Analysis of determinants of gut microbiota using ecological network methods

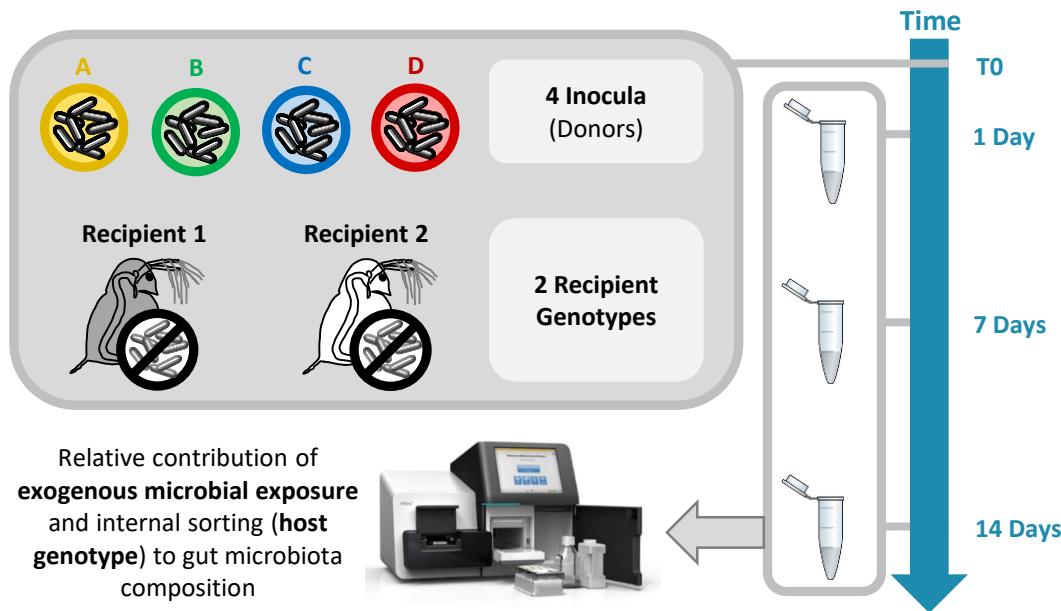


Analysis of determinants of gut microbiota using ecological network methods

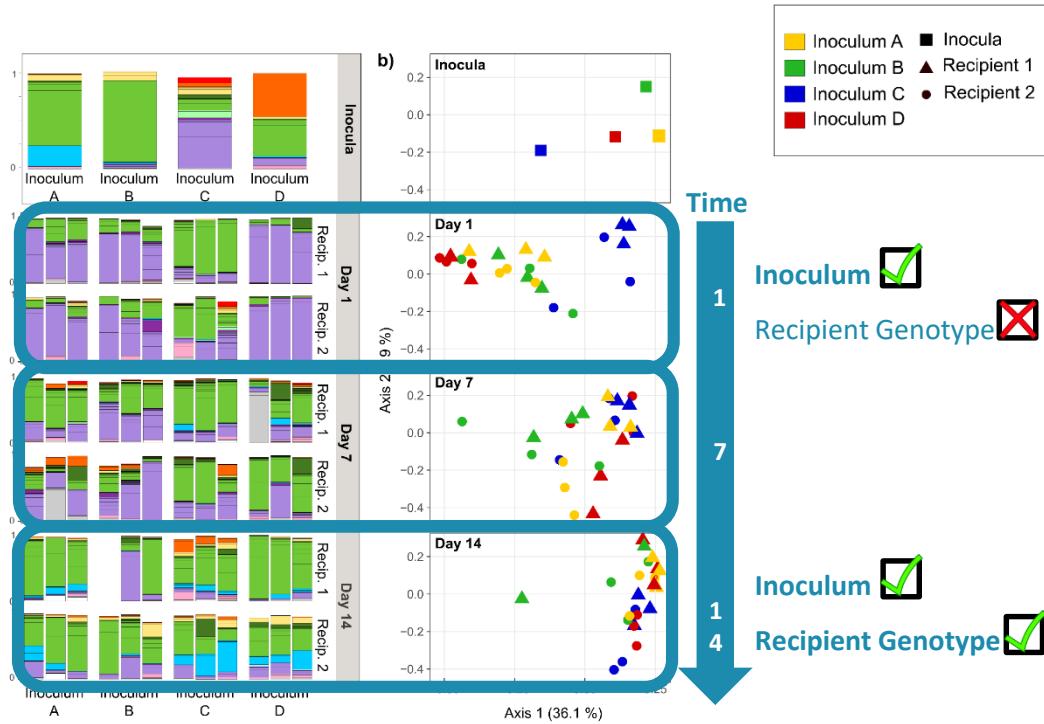
Gut-BPK reciprocal influences?



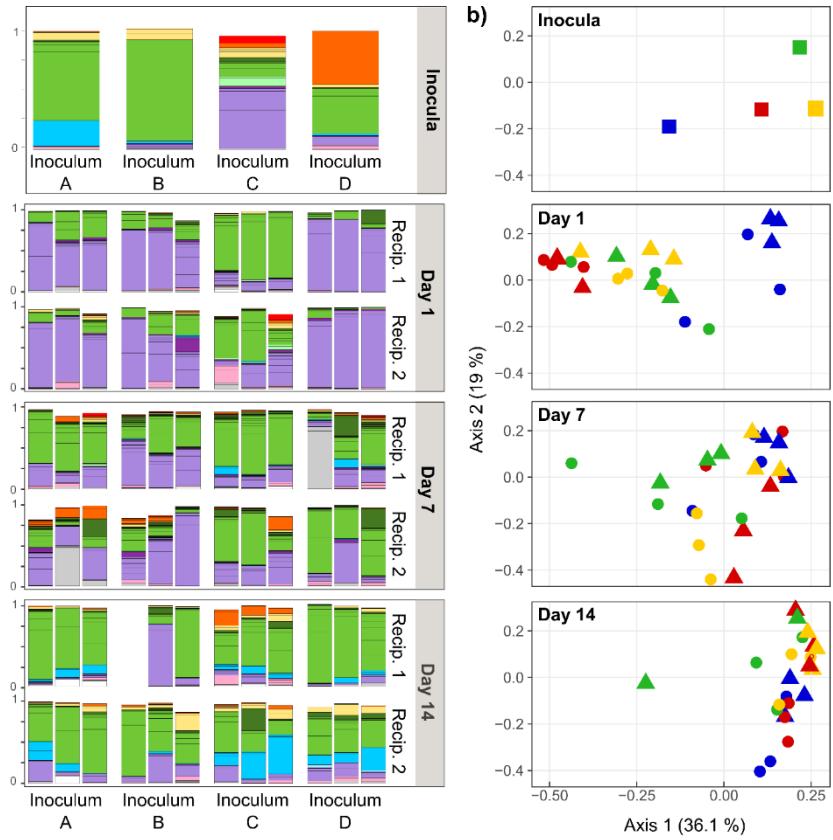
Follow up Experiment 2



Assembly of the gut microbiota in the recipients

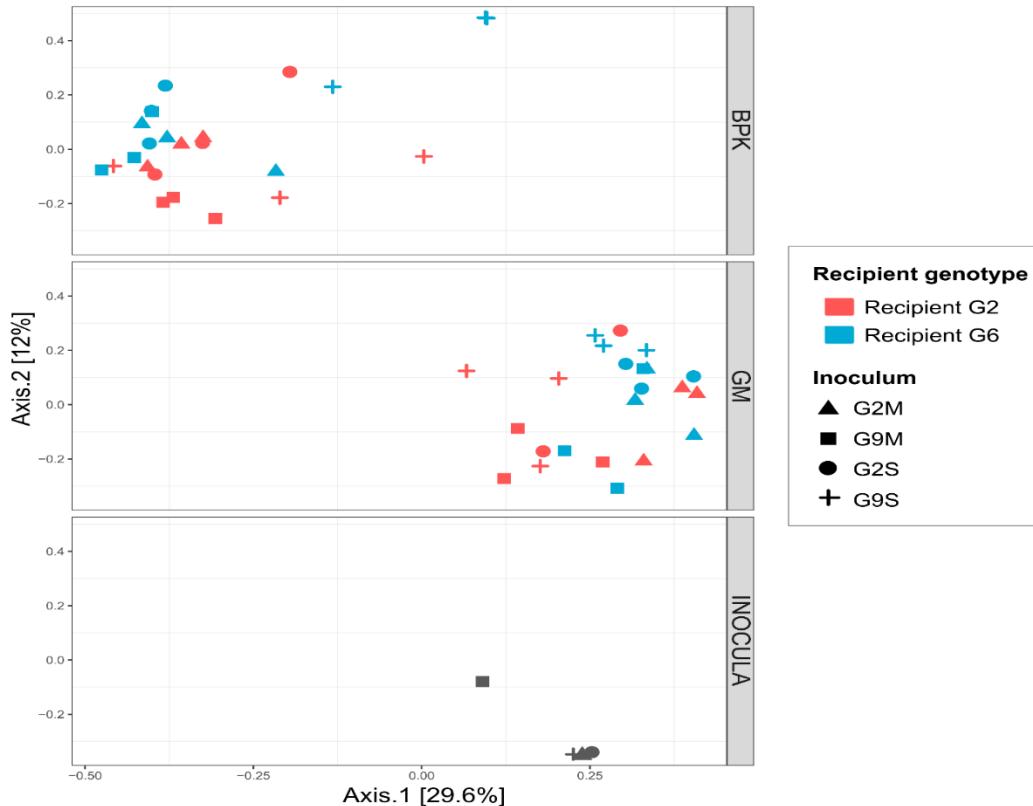


Assembly of the gut microbiota in the recipients



- Composition in recipient is different from the inocula → **selective recruitment**
- **Variation over time** → Ecological succession ? Response to variations in metabolic demand over the *Daphnia* life cycle ?
- Recipient genotype and inoculum x genotype interaction in adults → **genotype-dependent internal sorting**

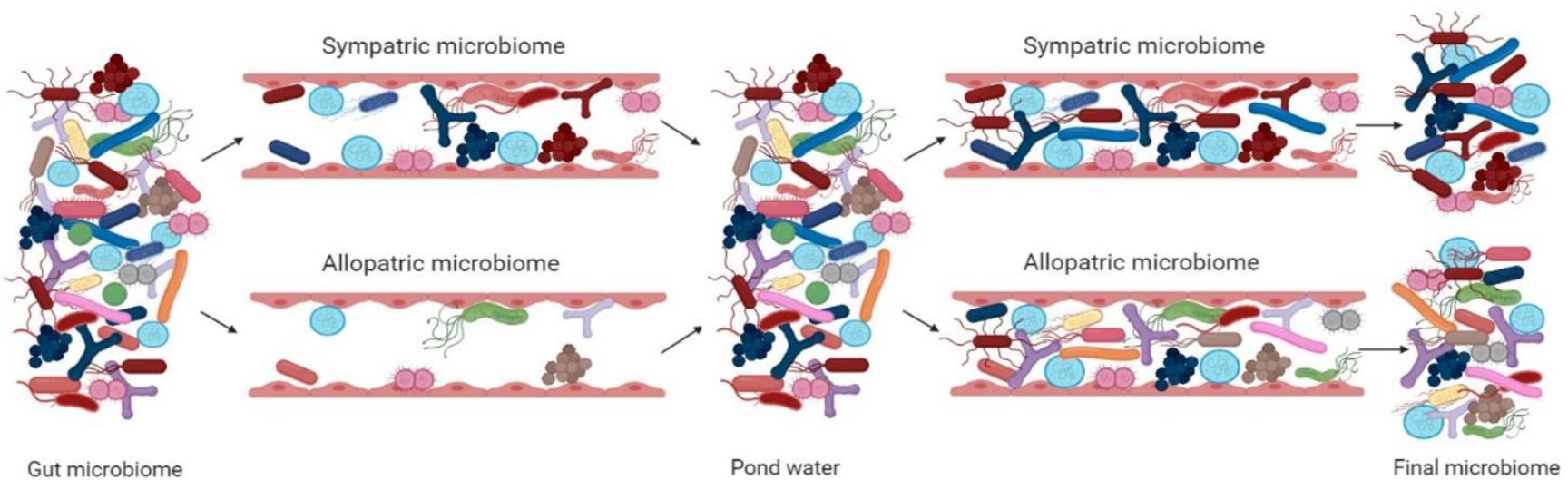
Characterization of gut microbiota and bacterioplankton after 14 days



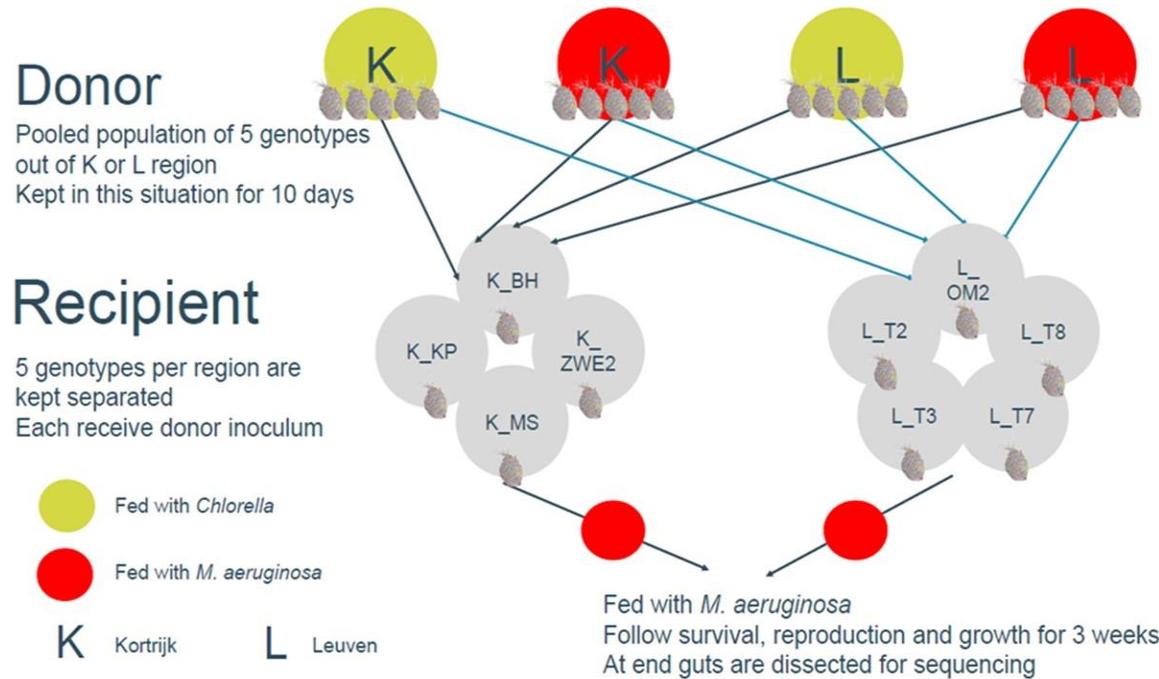
Analysis of determinants of gut microbiota using network methods

- Bacterioplankton and Gut microbiota are different communities
- *Daphnia* genotype affects Gut microbiota through a diversity effect and selects BPK
- BPK and gut microbiota have little reciprocal effects
- Different modules confirm these results, but suggest some possible correspondence between groupings by BPK and gut microbiota

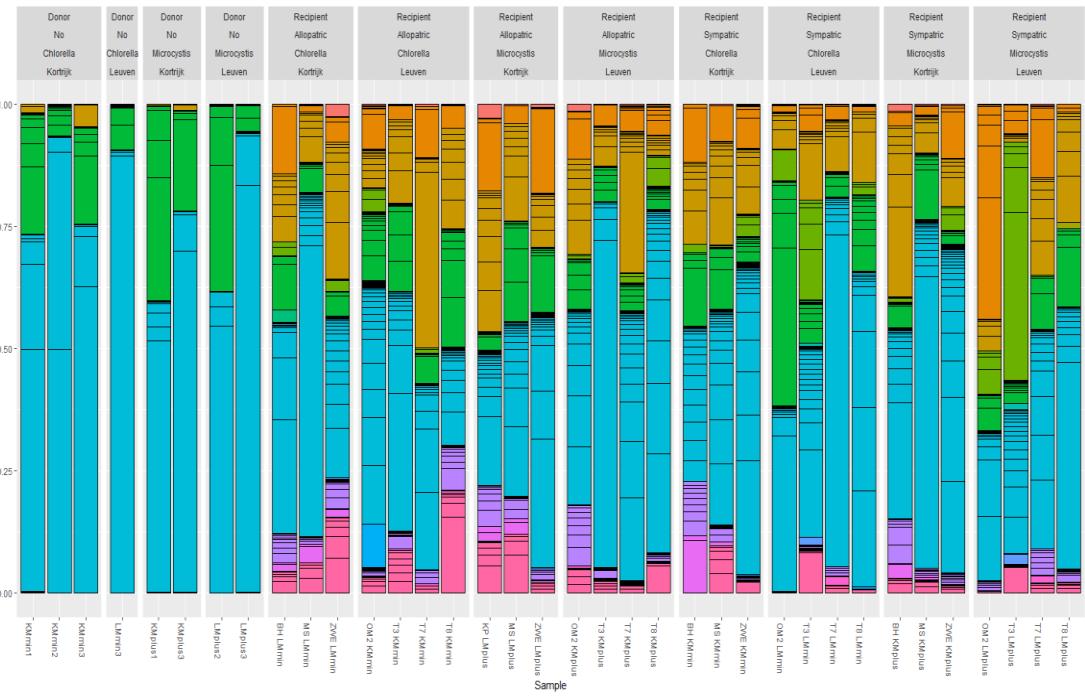
Role of local versus foreign microbiome in cyanobacterial tolerance



Role of local versus foreign microbiome in cyanobacterial tolerance



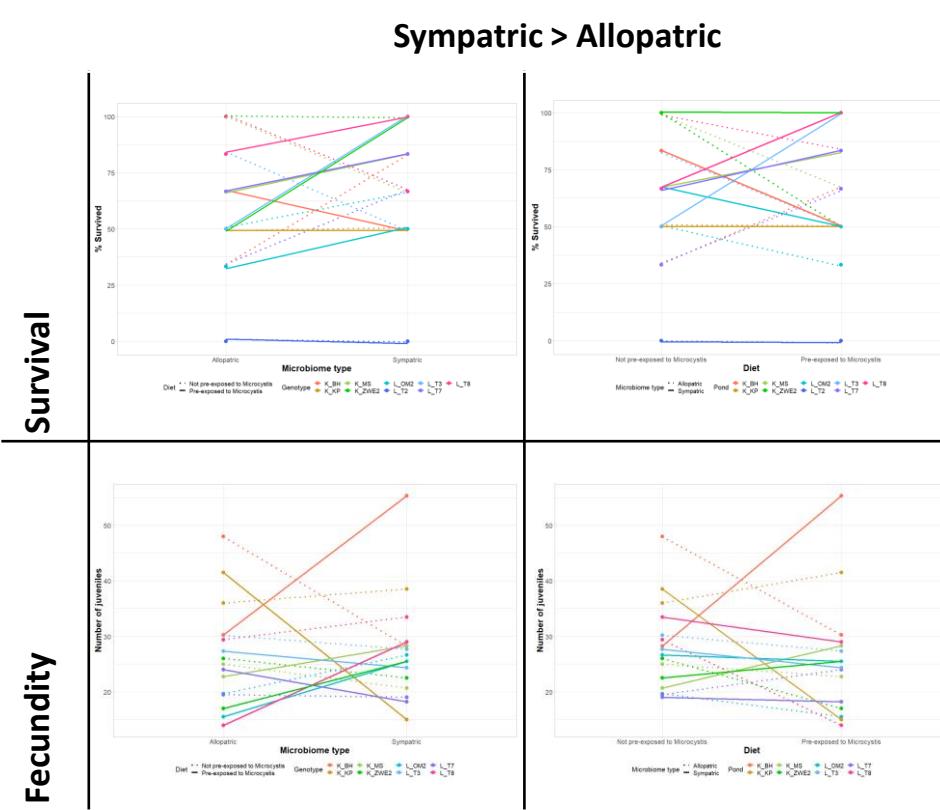
Role of local versus foreign microbiome in cyanobacterial tolerance



Factor	p-value
Donors vs Recipients	0,001



Role of local versus foreign microbiome in cyanobacterial tolerance?

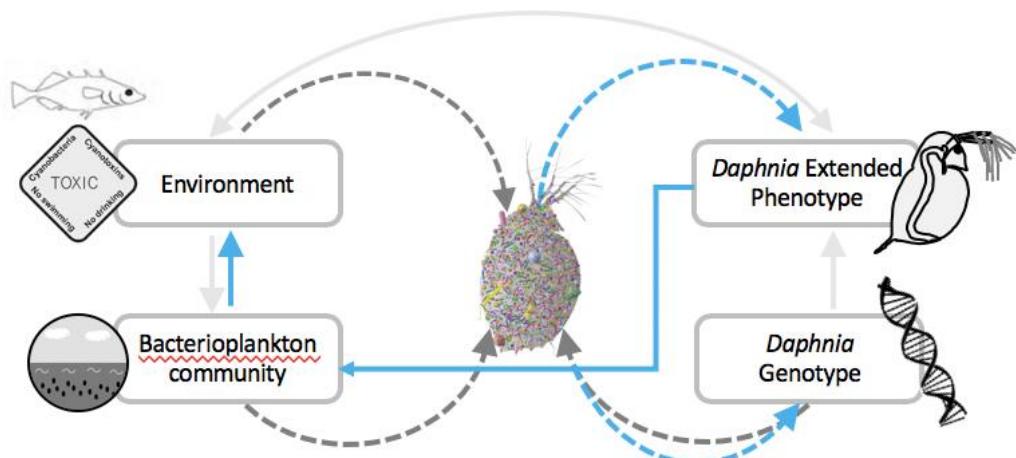


Factor	p-value
Diet	0,05 (*)
Diet x Pond	0,03 *
Microbiome type x Pond	<0,0001 ***
Diet x Genotype	0,06 (*)
Microbiome type x Genotype	<0,0001 ***
Diet x Microbiome type x Pond	<0,0001 ***
Diet x Microbiome type x Genotype	<0,0001 ***

Factor	p-value
Diet x Microbiome type	0,036 *
Diet x Region	0,033 *
Diet x Microbiome type x Pond	0,01*

Conclusions

- GM resembled when assembled from different microbial resources:
GM is assembled non-randomly
- Interactions between the *Daphnia* genotype, GM and BPK
- GxE interactions are structured by the local microbiome
- There is scope for eco-evo dynamics mediated by the gut microbiome in *Daphnia*



Eco-evo and microbiome-mediated dynamics across timescales

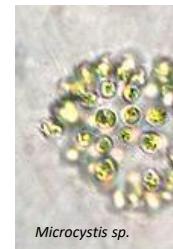
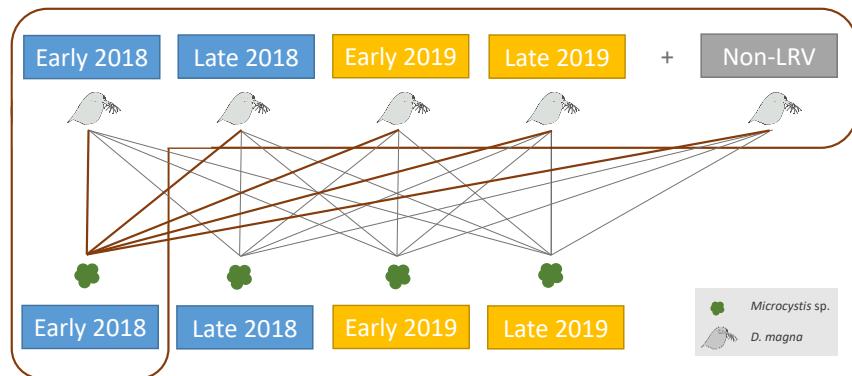


- What are the *Daphnia*/cyanobacteria-dynamics **across different timescales** (within seasons, over different years, over decades) in **natural settings**?

Transplant experiments

Reconstruction/resurrection of *Daphnia* sp. and cyanobacteria from sediments

- What is the **role of the microbiome** on these dynamics?



Microcystis sp.



Daphnia magna



Unravelling the role of miRNAs associated with the host microbiome, epigenetics and transposable elements under stress tolerance



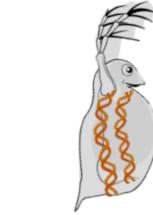
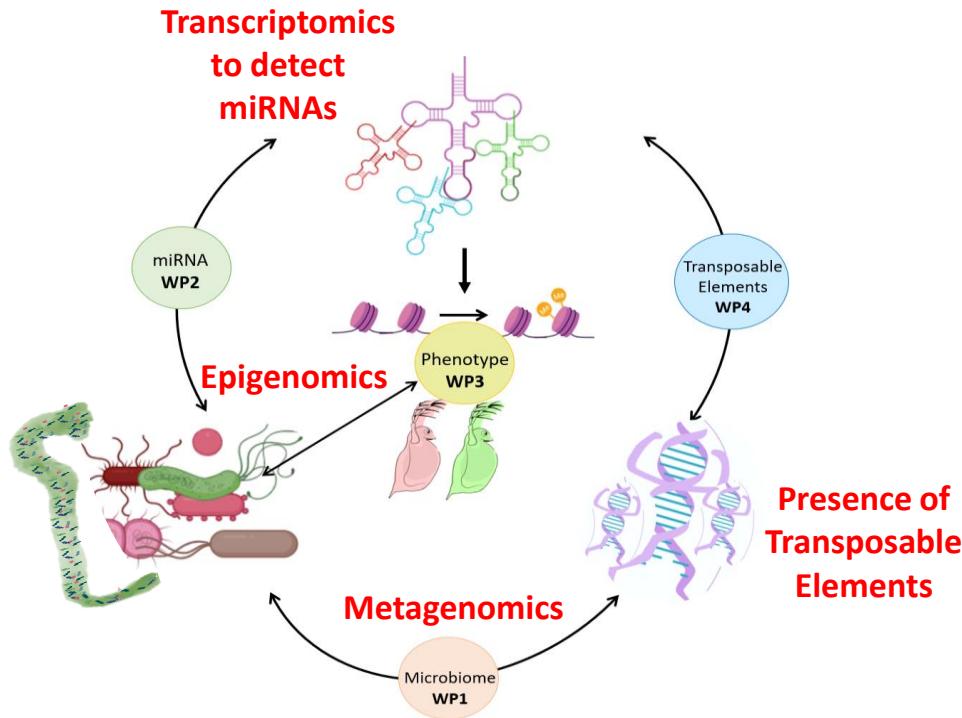
Stressors



Microcystis aeruginosa



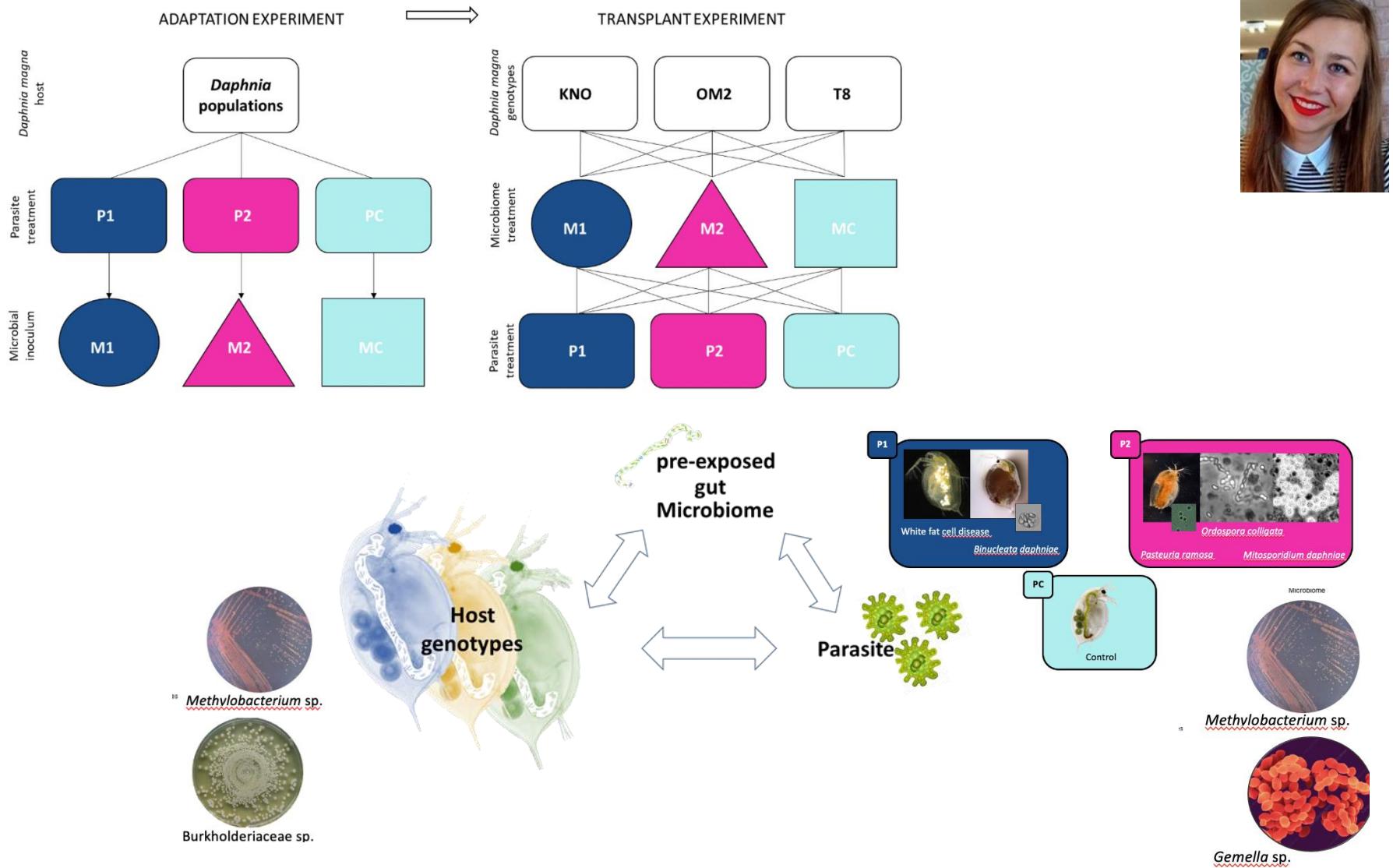
Iridoviral infection
White Fat Cell
Disease



Daphnia magna

Host-microbiota interactions ?
Causal and effect relationship ?
Gut as a stress tolerant organ ?

You can choose your microbiome, but you can't choose your genotype: Gut microbiota – host genotype – parasite interactions



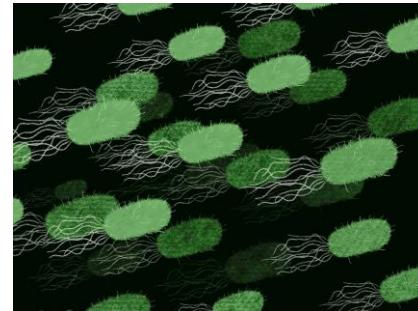
MicroResist – The influence of snail host microbiome in trematode parasite resistance



Snail



Trematode
parasite

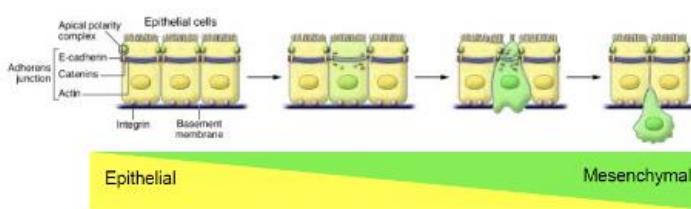
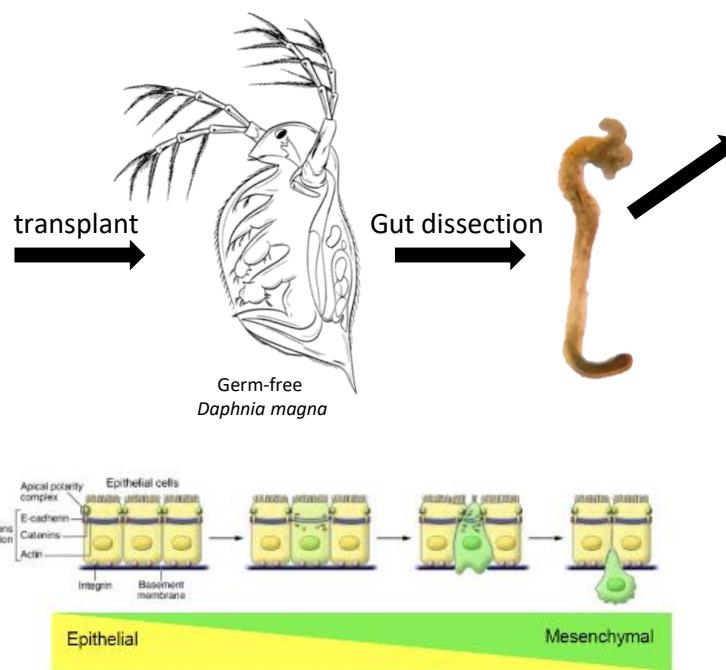
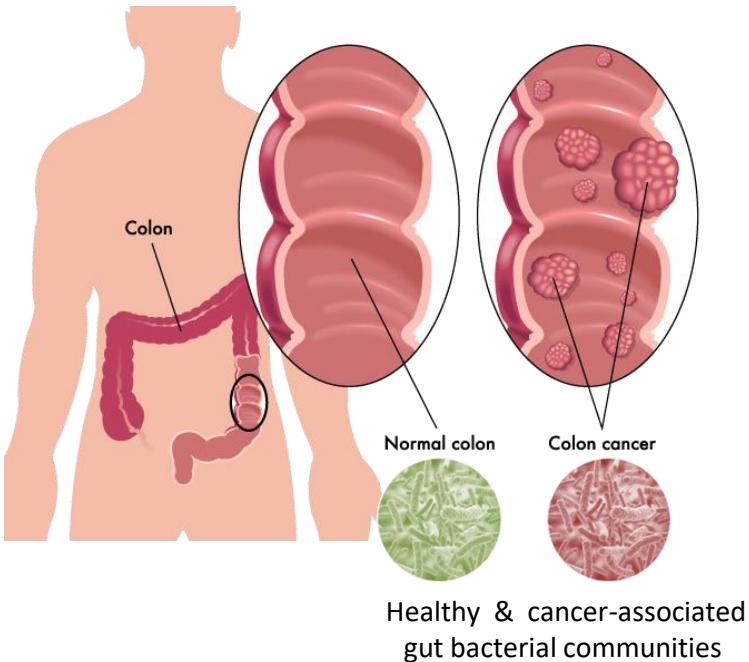


Microbiome

AFRICA
museum



The influence of the gut microbiome on basic processes of tumorigenesis in *Daphnia magna*



Unravel the molecular underpinnings of EMT

Link it with Epigenetics

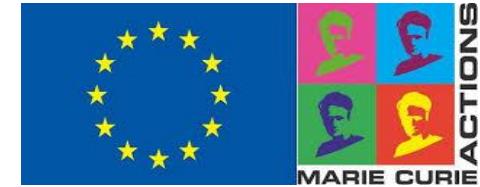
Identify biomarkers

Study the effect of single CRC associated bacterial strains

Mono-association experiments

Acknowledgements

microbiome and eco-evo dynamics



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