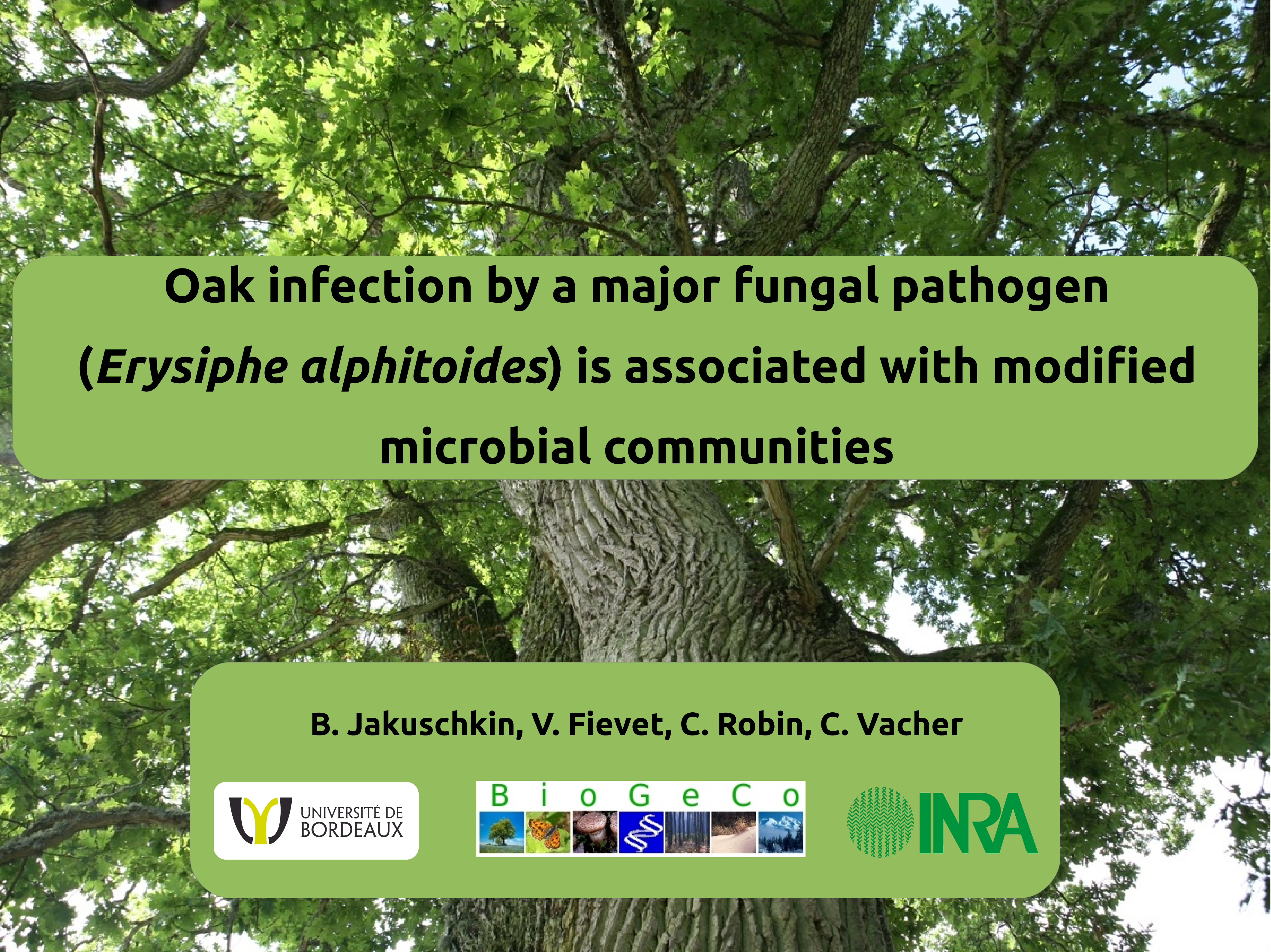


Oak infection by a major fungal pathogen (*Erysiphe alphitoides*) is associated with modified microbial communities

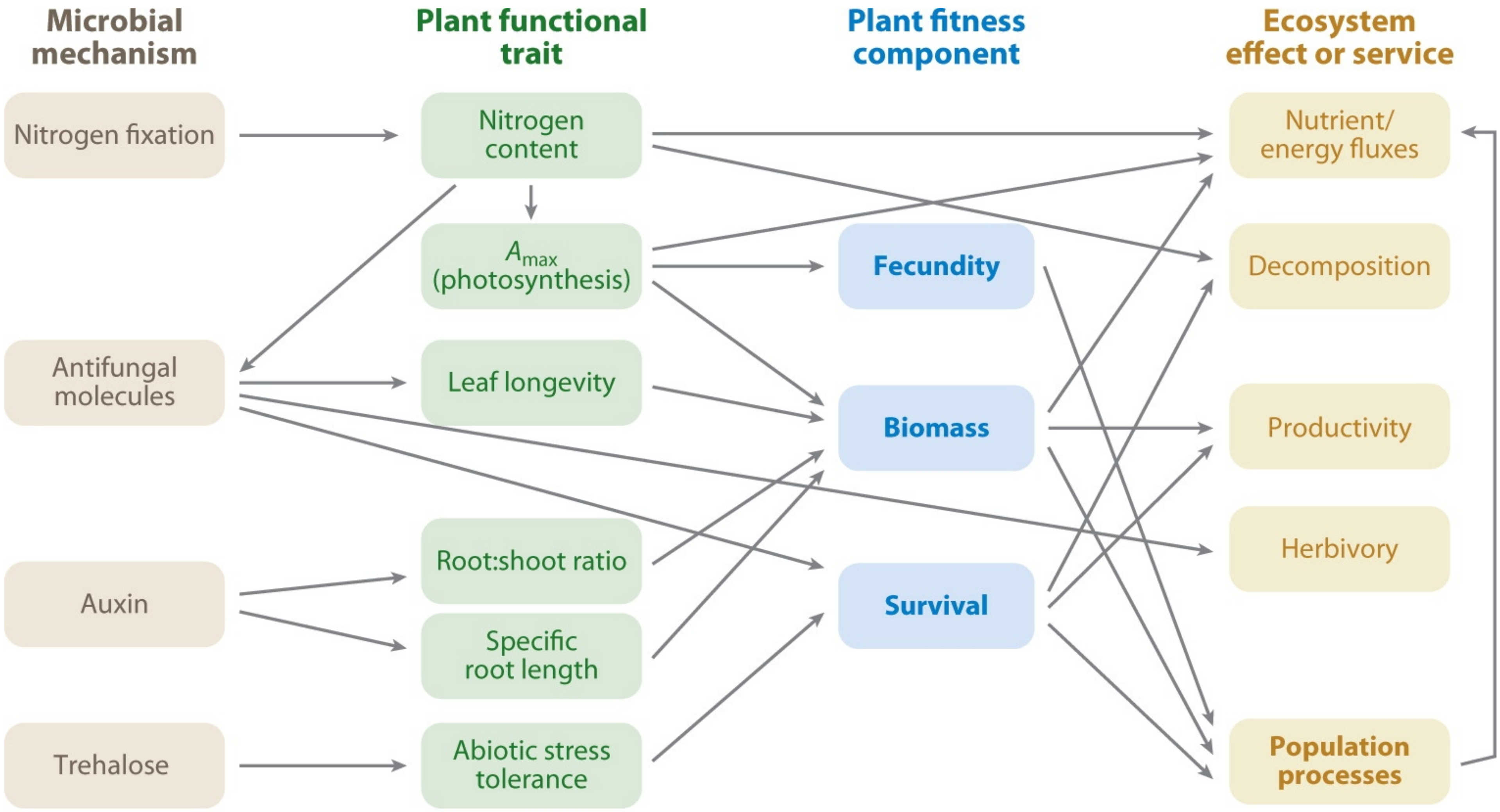
B. Jakuschkin, V. Fievet, C. Robin, C. Vacher

UNIVERSITÉ DE BORDEAUX

BioGeCo

INRA

Microbially mediated plant functional traits:



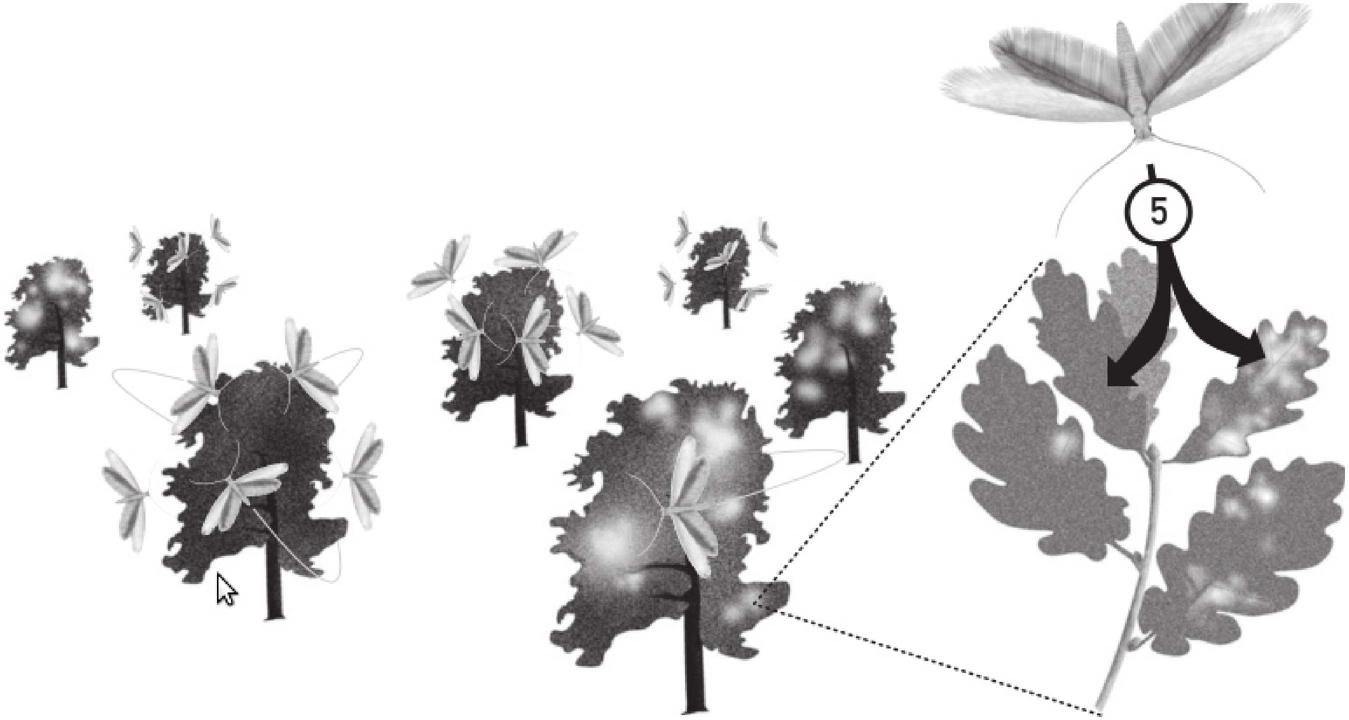
Friesen M.L. et al. 2011

Ecology Letters, (2012) **15**: 177–185 doi: 10.1111/j.1461-0248.2011.01724.x

LETTER

Cross-kingdom interactions matter: fungal-mediated interactions structure an insect community on oak

Ayco J. M. Tack,[1]* Sofia Gripenberg[1,2] and Tomas Roslin[3]



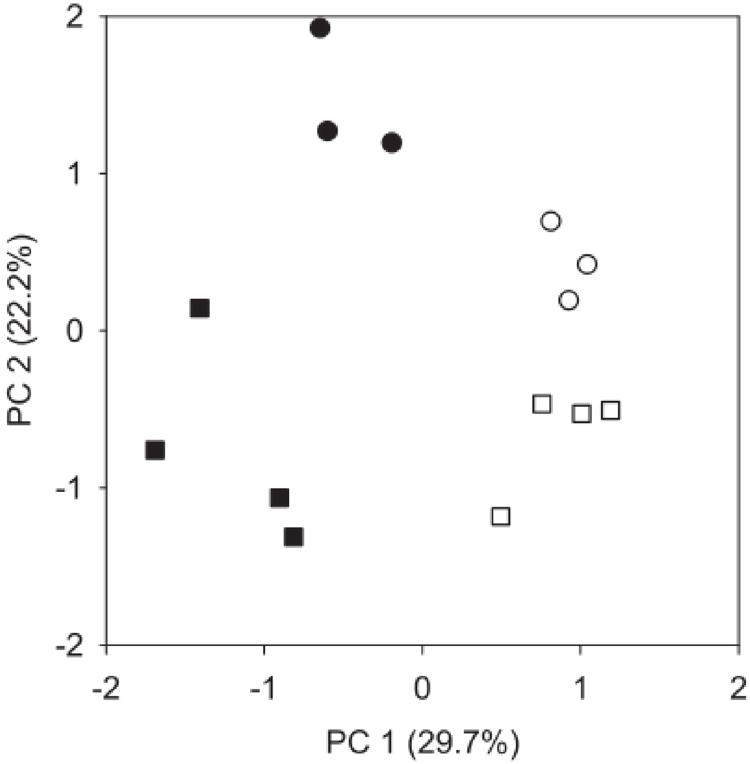
The oak powdery mildew is one of the most common infectious diseases in European forests

- is caused by *Erysiphe alphitoides*
- reduces the life-span of infected leaves
- decreases carbon uptake over growing season
- increases seedling mortality
- causes tree decline

Powdery Mildew-Infection Changes Bacterial Community Composition in the Phyllosphere

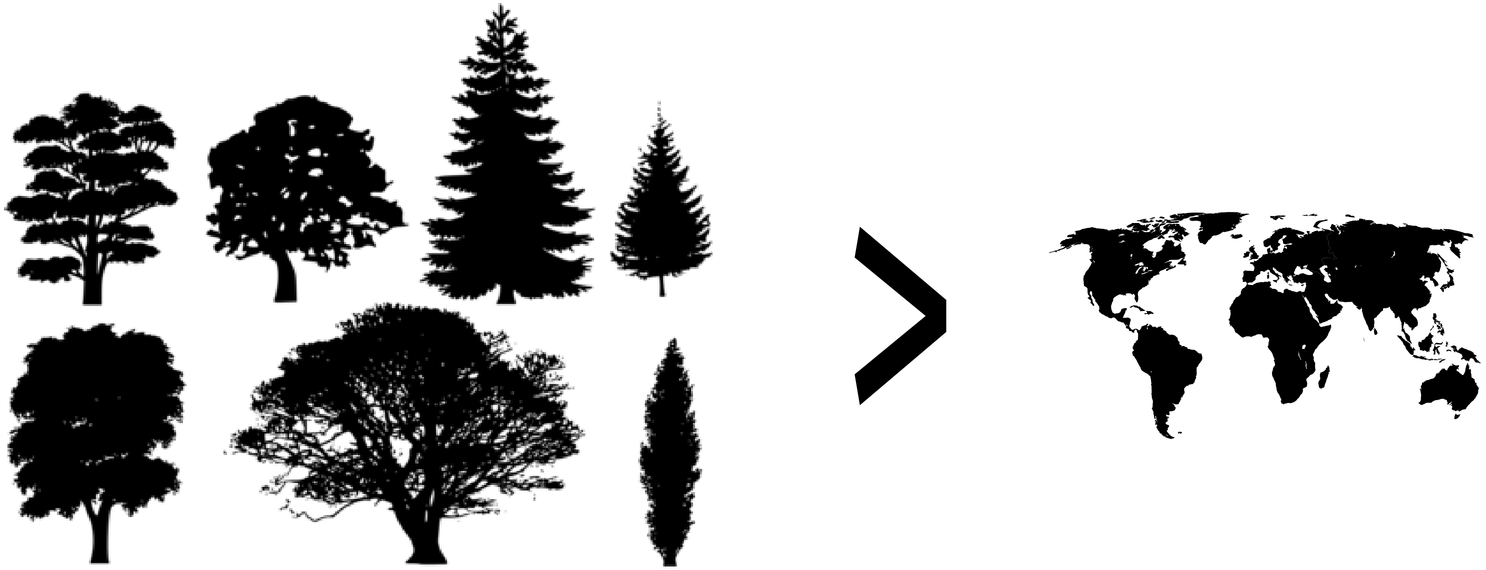
WATARU SUDA[1], ASAMI NAGASAKI[1], and MASAHIRO SHISHIDO[1]*

- pm infection of cucumber and Japanese spindle leaves results in
  - structural changes in bacterial community
  - larger bacterial population
  - greater bacterial diversity and
  - greater richness



Suda et al. 2009

The phyllosphere is one of the largest microbial habitats on Earth



Terrestrial leaf surface 2-4 times larger than Earth's land surface

Morris C. E.; Kinkel L. L. 2002

Microbial diversity and community structure are influenced by:

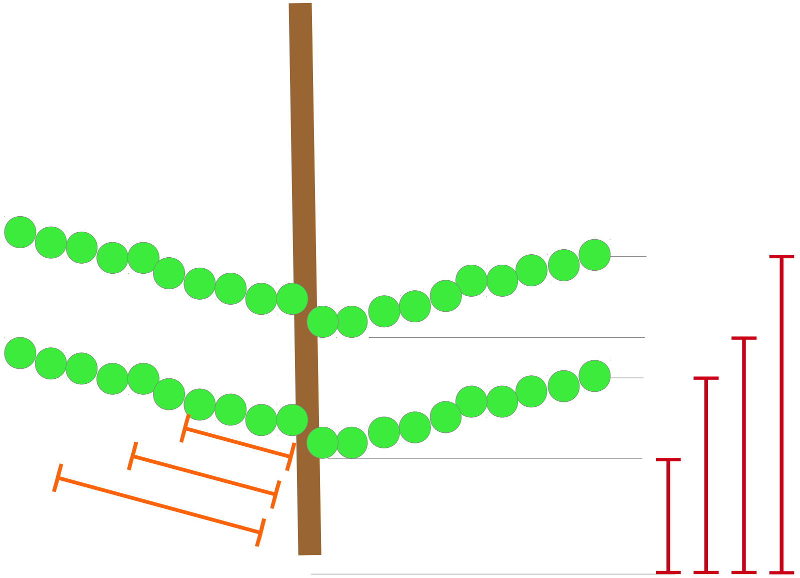
- environment
  - solar radiation, rainfall, wind, air spora, nearby vegetation, temperature, soil
- plant
  - leaf morphology, leaf chemistry, phenology, metabolism

Yadav R.K.P. 2005; Compant 2005; Kinkel L.L. 1997; Cordier T. et al. 2012

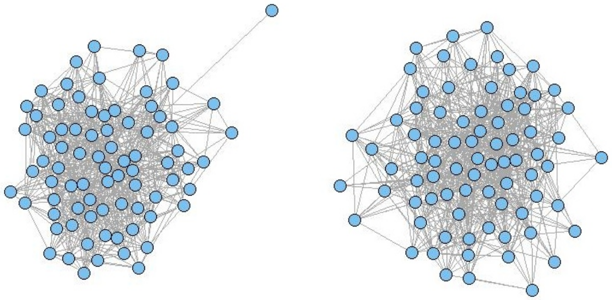
Aims and questions

- We want to examine the relationship between *E. alphitoides* and the structure of residential microbial community
  - reduction of fungal community diversity?
  - increase of bacterial community diversity?
- Is the phyllosphere dominated by antagonistic interactions between microbial inhabitants due to the high level of competition?

Experimental setup



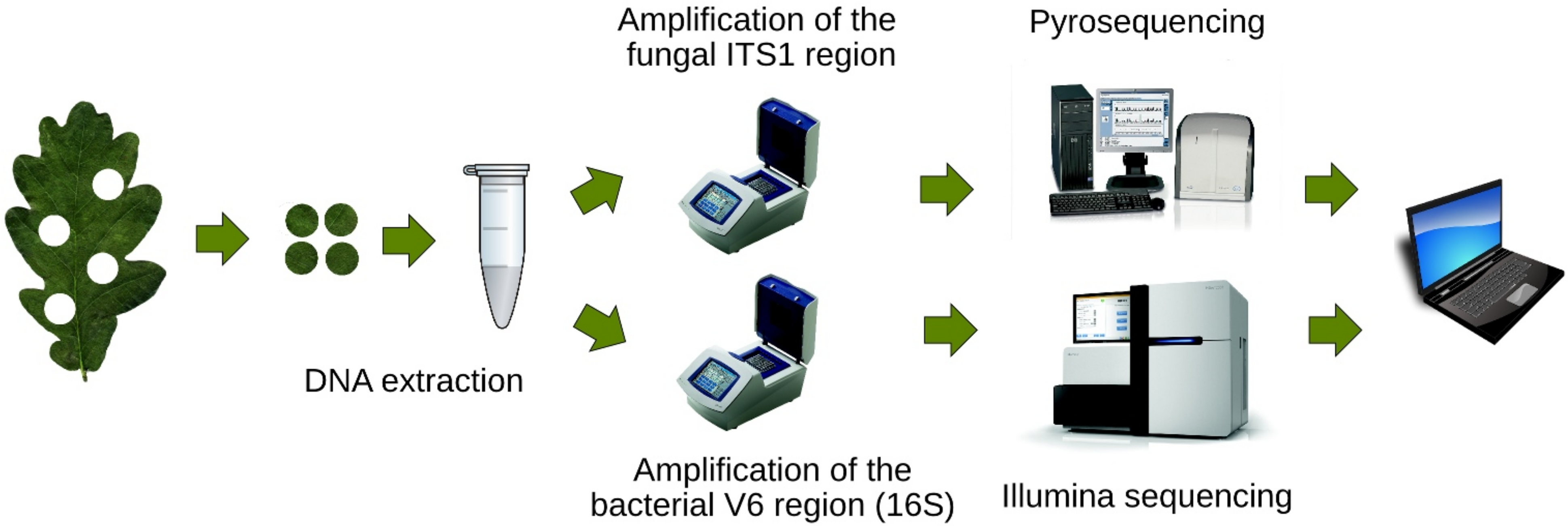
3 trees
4 branches/tree
10 leaves /branch



bacteria
fungi

powdery mildew

Workflow



DNA extraction

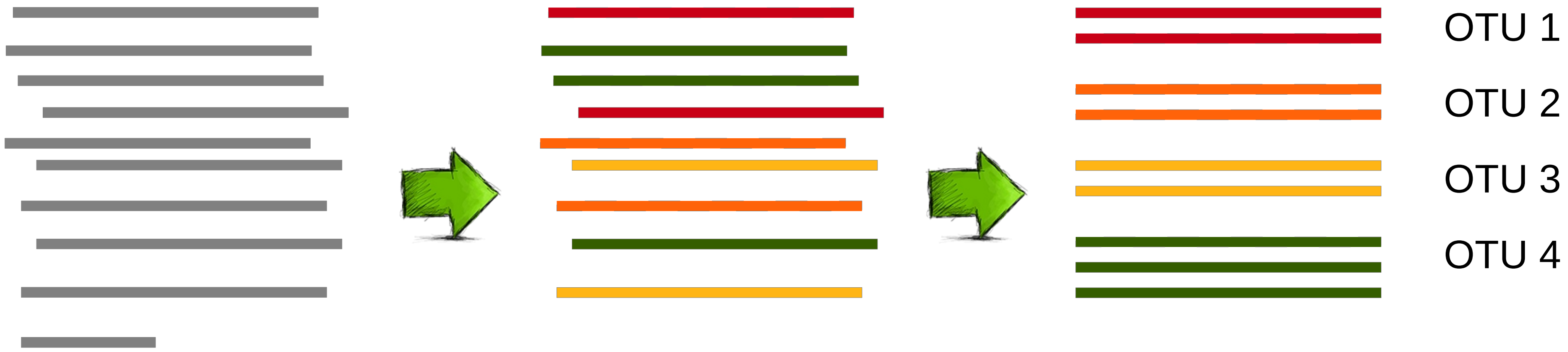
Amplification of the fungal ITS1 region

Amplification of the bacterial V6 region (16S)

Pyrosequencing

Illumina sequencing

Processing of high throuput sequencing data



quality filtering
+ demultiplexing

clustering

OTU 1 → *Species 1*

OTU 2 → *Species 2*

OTU 3 → No blast hit

OTU 4 → No blast hit

taxonomy
assignment

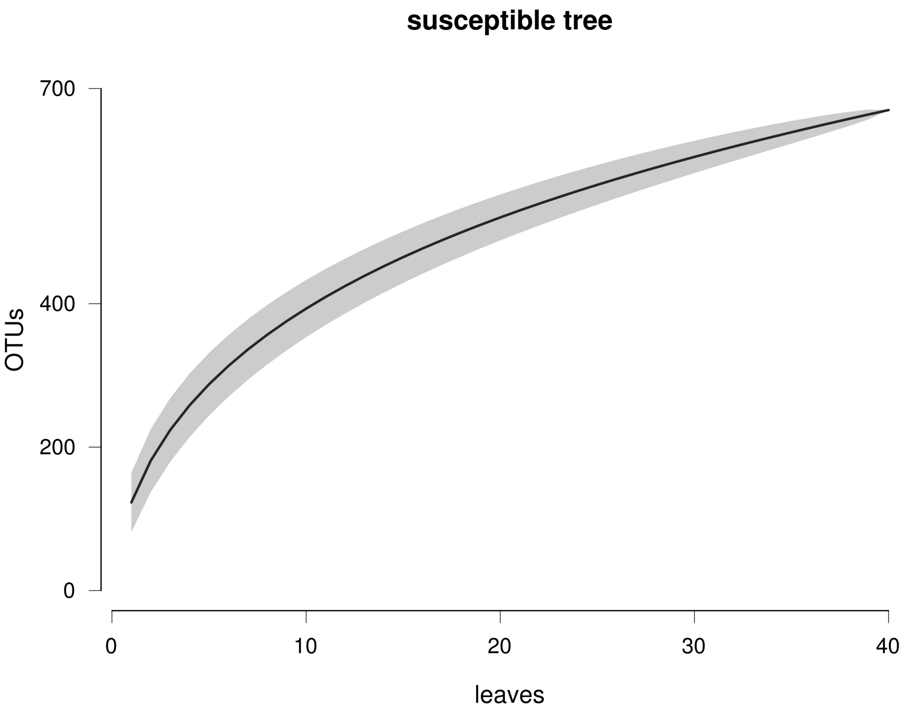
OTU table

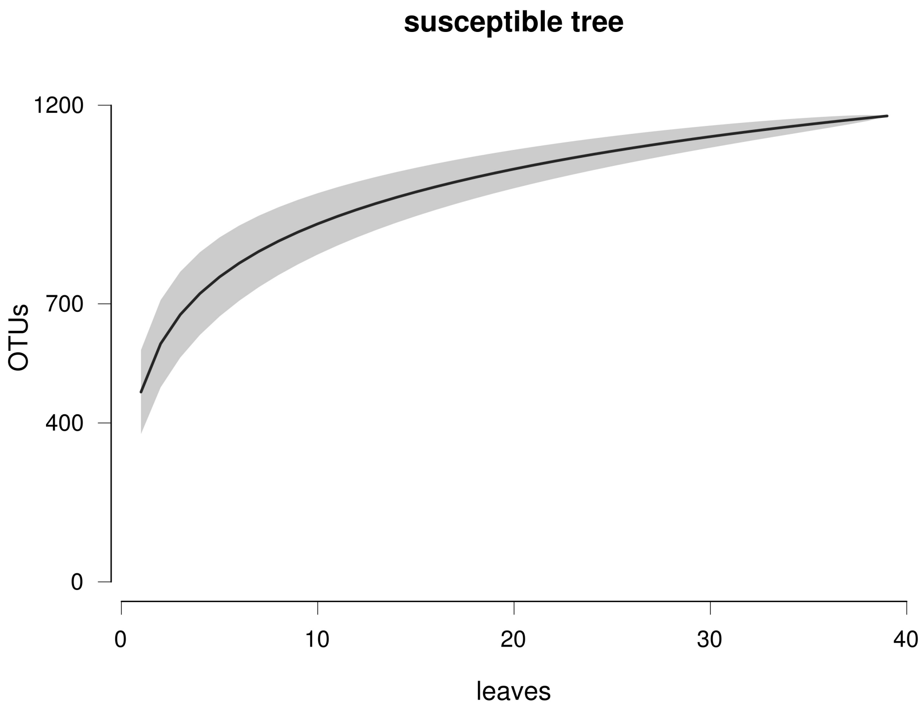
	Sample 1	Sample 2	Taxonomy
OTU1	1	1	Species 1
OTU2	2	0	Species 2
OTU3	0	2	No blast hit
OTU4	1	2	No blast hit

The oak phyllosphere harbors very rich microbial communities

- **Fungi:**
- 251,000 sequences
- 2,100 per sample
- 1,081 OTUs

- **Bacteria:**
- $2.4 \cdot 10^6$ sequences
- 20,000 per sample
- 1,507 OTUs


susceptible tree


susceptible tree

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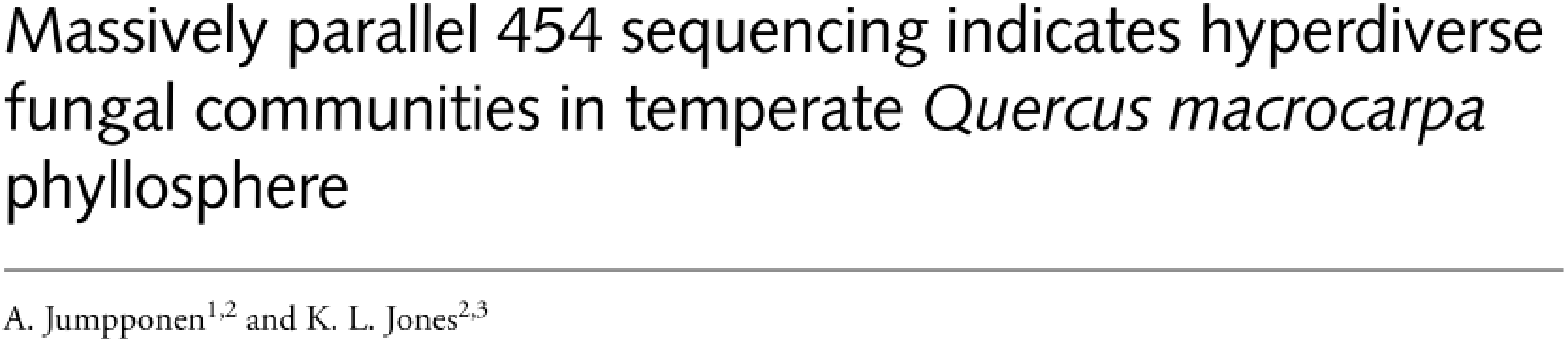


Massively parallel 454 sequencing indicates hyperdiverse fungal communities in temperate *Quercus macrocarpa* phyllosphere

A. Jumpponen[1,2] and K. L. Jones[2,3]

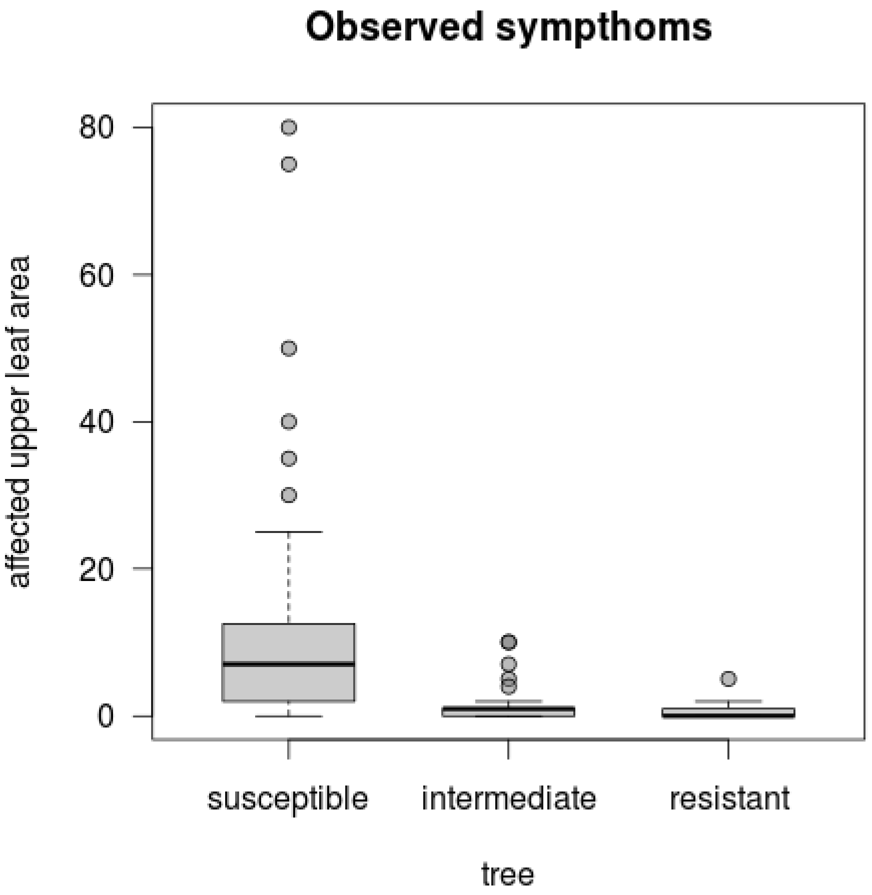
Microbial richness and diversity differ among the trees

		p-value	results
Richness	Fungi	<0.001	u2=u3>u1
	Bacteria	<0.001	u2>u1=u3
Simpson diversity	Fungi	<0.001	u2=u1>u3
	Bacteria	<0.001	u2>u1=u3

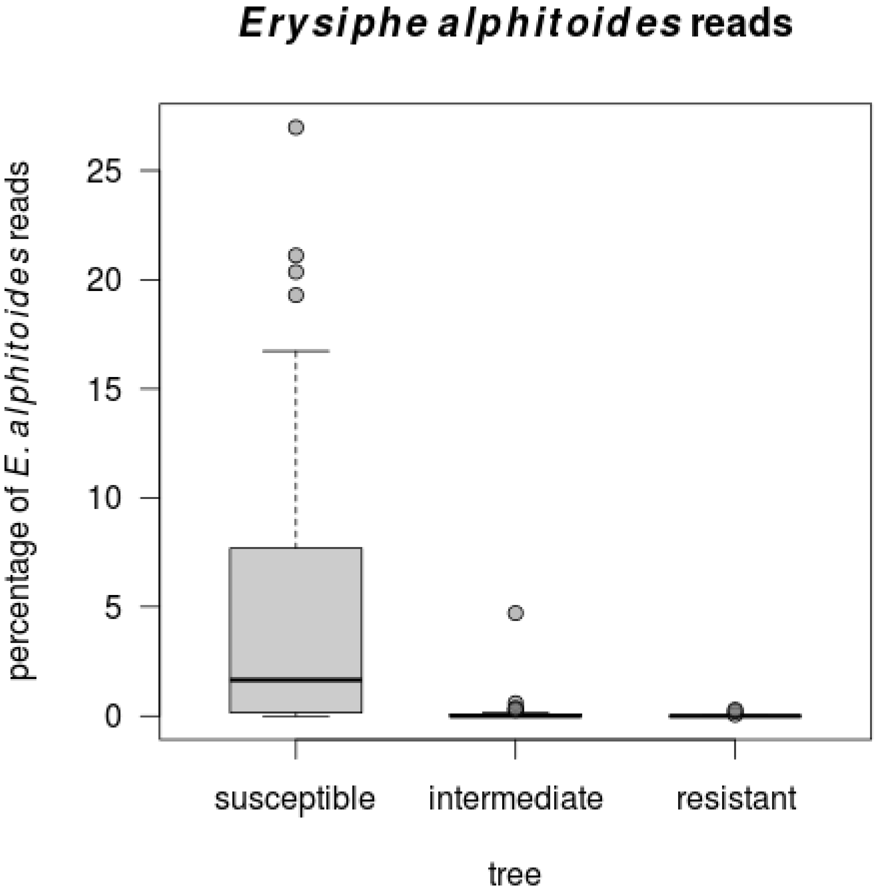
➡ The mean levels for bacterial diversity and richness are highest for the intermediately susceptible tree.

(NBGLM for richness; GLM for diversity)

Susceptible tree shows the highest variation in the number of reads and the level of observed symptoms

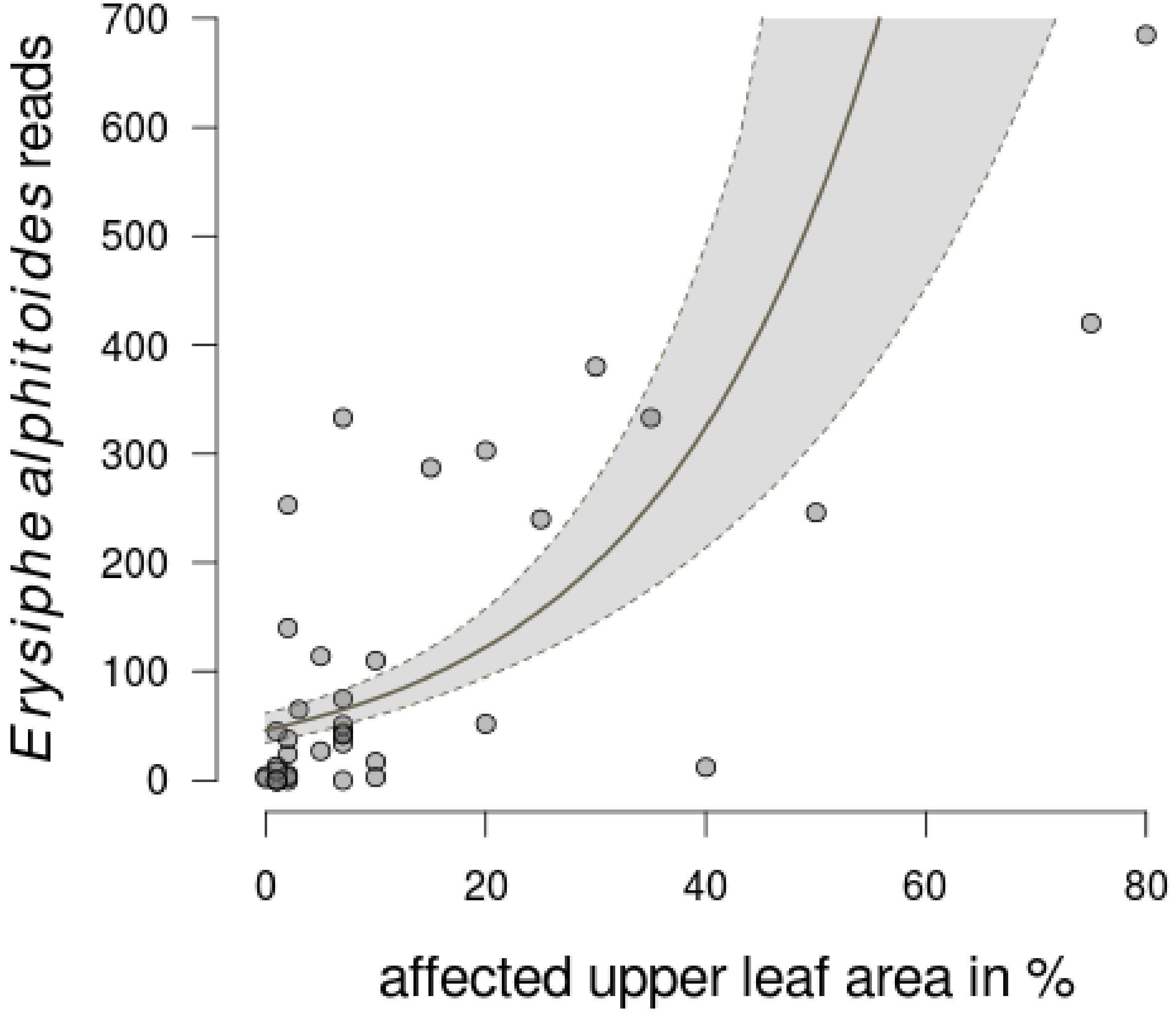


Observed sympthoms



***Erysiphe alphitoides* reads**

Number of reads correlates with observed PM symptoms

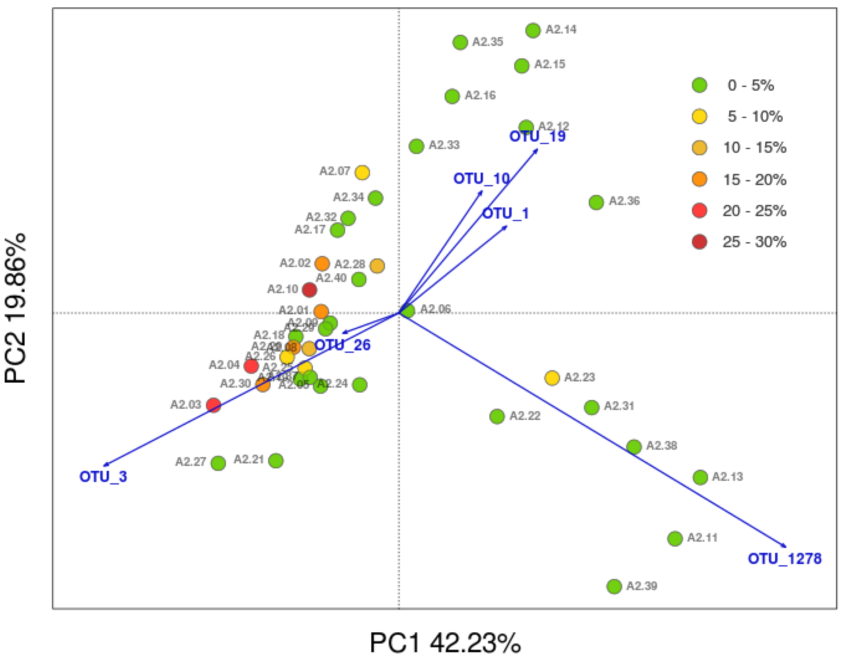


Powdery mildew does not influence the microbial diversity

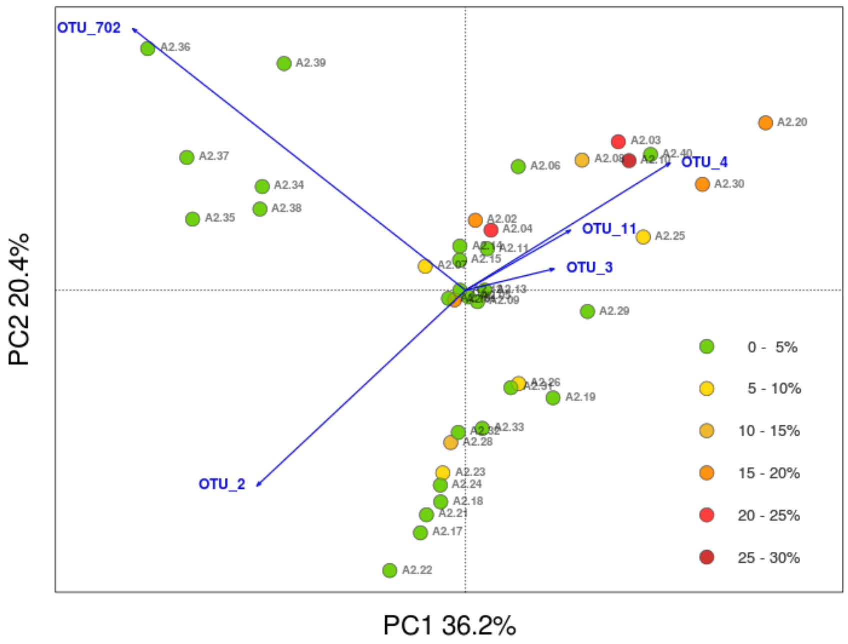
			coefficient	p-value
Richness	observed PM symptoms	Fungi	0.00667	**0.002**
		Bacteria	-0.00256	0.202
	%-age of *E. alphitoides reads*	Fungi	0.02213	**<0.001**
		Bacteria	-0.00204	0.697
Diversity	observed PM symptoms	Fungi	0.00070	0.051
		Bacteria	0.00034	0.618
	%-age of *E. alphitoides reads*	Fungi	0.00153	0.097
		Bacteria	0.00134	0.448

The powdery mildew-infection is associated with modified microbial community composition

Fungi; susceptible tree



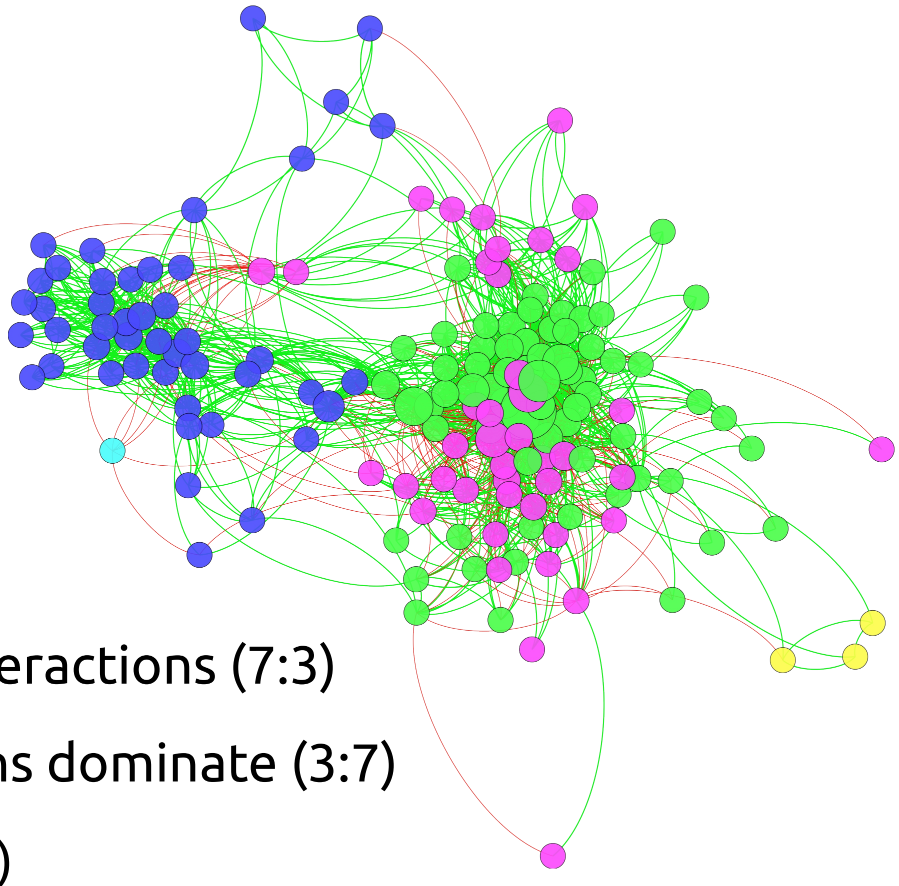
Bacteria; susceptible tree



What are the underlying mechanisms?

- PM directly affects bacterial composition by secreting certain metabolites
- PM infection alters the chemical and/or physiological conditions of leaves which influences the colonization and growth of epiphytic bacteria
- PM itself can harbor diverse bacteria and represent a new microbial habitat
- the residential microbiota differs among the leaves in the first place, which either facilitates or hinders the leaf colonization by PM

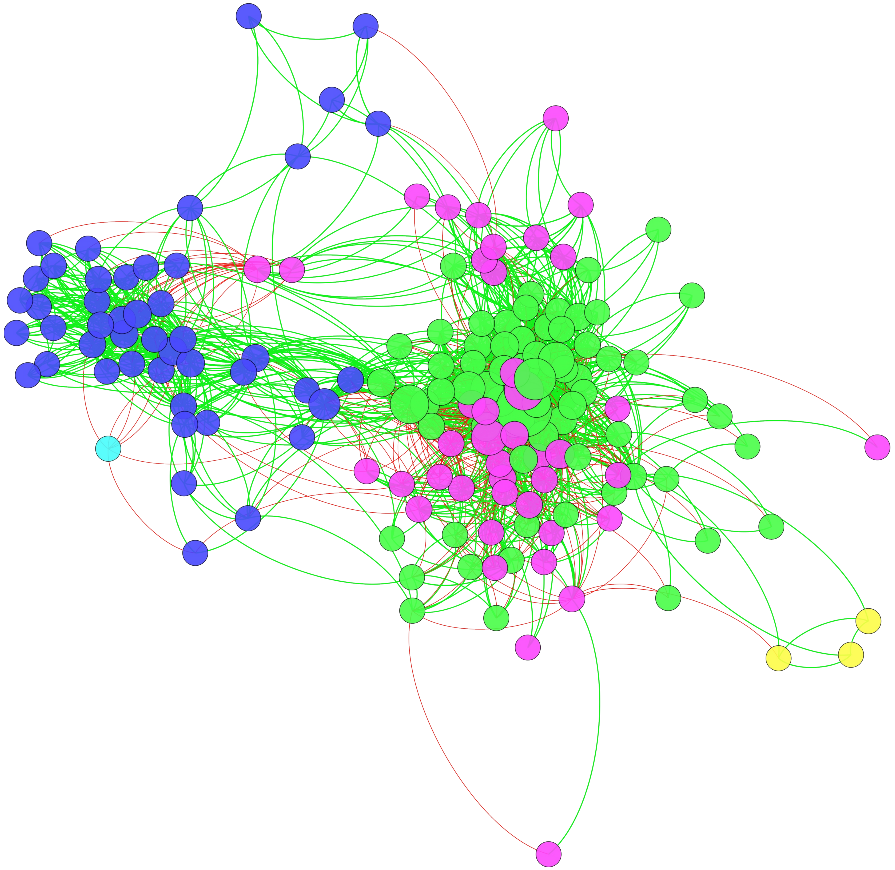
Inference of correlations from compositional data



- SparCC (Friedman & Alm 2012)

- positive interactions > negative interactions (7:3)
- fungi-bacteria: negative interactions dominate (3:7)
- not for the PM-susceptible tree (6:4)
- *E. alphitoides*: negative interactions dominate (3:7)

Inference of correlations from compositional data



➡ cooperation, not competition, is more prevalent in microbial phyllosphere community (?)

➡ Polz et al. (2013) → strong niche-specific selection pressure and massive local gene-exchange promote stable functional networks, which increases the robustness of communities to perturbation.

Merci!