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There is emerging realisation that every plant is endowed with its own adaptable microbiome. A growing literature shows plant health, growth, and biomass production are influenced by microbiomes. In *Arabidopsis thaliana*, for example, fungal endophyte communities vary with host genotype and show strong interactions between microbial species. Interaction between host plant and microbiome has already been successfully used by application of selected bacteria or fungal strains on crops to enhance stress resilience to drought in grapevine, generally promoting plant growth and stress resistance in wheat and increase yield in nutrient stressed barley cultivars. This suggests the potential for engineering beneficial microbial communities. We recently observed dramatic within-species, population-level differences in resilience to extreme saline and serpentine environments in several tractable *Brassicaceae* species. We hypothesise that differences in plant microbiomes may influence the remarkable resilience contrasts we observe. In particular, a subset of *Arabidopsis arenosa* populations grow in drought prone serpentine sites while a subset of *Brassica fructiculosa* populations are locally adapted to high salt conditions, whereas other populations in both species are not adapted to these challenges. Thus, we are constructing microbiome atlases to investigate whether microbiome communities may facilitate adaption to extreme environments. Additionally, because serpentine and high saline soil populations have a common characteristic of being very drought prone, we will test for shared drought specific patterns of community change between the plant and microbial genomes. We focus on populations that are adapted to high saline soils and populations adapted to serpentine soils, as both present stringent challenges that are directly relevant to growing worldwide agricultural need.

Keywords: *Brassica fructiculosa*, *Arabisdopsis arenosa*, salt stress, serpentine adaption, microbiome

P13. The impact of genotype and warming on the leaf fungal patho- and microbiome.

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The leaf surface of plants is a habitat to many fungal species. The leaf surface fungal species communities can be structured by both abiotic and biotic factors, such as host genetic identity and elevated temperatures. However, only few manipulative experiments were conducted to assess the impact of these two factors on above-ground microbial communities. We set up a warming experiment to investigate how foliar fungal pathogens and endophytes are affected by elevated temperatures and host genetic identity. In this study, we particularly focused on: 1) the impact of host genetic identity and warming on the resistance of the host tree to a specialist pathogen, the powdery mildew *Erysiphe alphitoides*, and 2) the impact of host genetic identity and warming on the composition of foliar fungal communities of *Quercus robur*. Preliminary results show that powdery mildew was more abundant in the non-heating treatment, but the effect also differed among the host genetic identities. This suggests that effects of temperatures on host-pathogen systems may be mediated by the interaction of environment and the genetic identity of the host, and may therefor lead to changes in host-pathogen interactions.
Keywords: Endophytes, pathogens, species interactions, fungal-climate interactions, host genotype

P14. A library preparation optimized for RNA virus metagenomics allows

sensitive detection of an arbovirus in wild-caught vectors.

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The study of viral communities has recently been boosted by the use of the so-called high-throughput sequencing (HTS) technologies. Coupled with random amplification of nucleic acids, HTS allows the identification of viral species present in a given sample without a-priori knowledge on their identity but their resemblance to known viruses. The huge interest of this approach for virus ecology and diagnostics has triggered several technical improvements in most steps required in virus metagenomics, from nucleic-acid extraction to bioinformatics analysis of sequencing results. Surprisingly, there is yet a key step that has received little attention, that of library preparation. Here, we describe a library preparation for exploring viral diversity in a large number of samples with the use of high-throughput sequencing. This method uses custom adaptors that are PCR ligated, allowing low cost, high multiplexing and fully exploitable read lengths. After validation of our method with artificial viral communities, we have tested it with two samples set from wild-caught arthropod vectors showing that our approach allows to identify an arbovirus in highly-degraded samples with a relatively high sensitivity.

Keywords: Metagenomics; arbovirus; arthropod vectors.

P15. Conserved virome diversity and structure in the mosquito vector *Culex pipiens*.

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Recent epidemics caused by different mosquito-borne viruses underline the viral diversity associated to mosquitoes. However, beyond human viral pathogens, we know little on other viruses of the

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