

PROGRAMME

09:00 – 10:00	REGISTRATION AND COFFEE
10:00 – 10:30	WELCOME AND INTRODUCTION BY CHAIR (Paul Bodelier, Netherlands Institute of Ecology)
10:30 – 11:10	MICROBES AND INSECTS – DARWINIAN AGRICULTURE – INSPIRED BY AN ANCIENT FARMING MUTUALISM (Duur Aanen, Wageningen University)
11:10 – 11:40	COFFEE / TEA
11:40 – 12:20	MICROBES AND SOILS – CAUSES AND CONSEQUENCES OF SOIL MICROBIAL DIVERSITY (Joana Falcão Salles, University of Groningen)
12:20 – 13:00	MICROBES AND PLANTS – THE PLANT MICROBIOME AND PLANT HEALTH (Corné Pieterse, Utrecht University)
13:00 – 14:00	LUNCH
14:00 – 14:40	MICROBES AND HUMANS – THE ECOLOGY OF THE HUMAN MICROBES IN HEALTH AND DISEASE (Eric Alm, Massachusetts Institute of Technology)
14:40 – 15:20	MICROBES AND WATER – MARINE VIRUSES: FROM THE INDIVIDUAL LEVEL TO LARGE SCALE EFFECTS (Corina Brussaard, Royal Netherlands Institute for Sea Research)
15:20 – 15:50	COFFEE / TEA
15:50 – 16:30	MICROBES AND CLIMATE – TERRESTRIAL N₂O REDUCING MICROBES AND THEIR IMPORTANCE AS N₂O SINKS (Sara Hallin, Swedish University of Agricultural Sciences)
16:30 – 17:00	PLENARY DEBATE
17:00 – 18:00	DRINKS

Microbial Power
***Impact of microbial communities:
from gut to globe***

Thursday 19 November 2015

Conference Centre de Werelt
Westhofflaan 2, Lunteren, The Netherlands

ORGANISERS:

Dr. Paul Bodelier (Netherlands Institute of Ecology)
Prof. Wietse de Boer (Netherlands Institute of Ecology)
Dr. Claudius van de Vijver (NERN)
Dr. Lennart Suselbeek (NERN)

SUPPORTED BY:

Netherlands Ecological Research Network (NERN)
NWO Aard- en Levenswetenschappen (NWO-ALW)
Graduate Schools PE&RC, RSEE, and SENSE



ABSTRACTS

10:30 MICROBES AND INSECTS – DARWINIAN AGRICULTURE – INSPIRED BY AN ANCIENT FARMING MUTUALISM

Duur Aanen, Wageningen University

In nature, individual-level selection prevails, often preventing the evolution of cooperative strategies and leading to tragedies of the commons. Examples are over-investment in roots and stems, decreasing collective performance of plants. Recently, the insight that selecting for lower individual competitiveness may increase yield has been applied to human agriculture in a developing field called "Darwinian Agriculture". In my presentation, I will discuss what we may learn from an ancient, *non-human*, form of agriculture, the mutualistic symbiosis between fungus-growing termites and *Termitomyces* fungi. In contrast to the –evolutionarily– recent human agriculture, this agricultural symbiosis has been shaped by millions of years of evolution and may thus conceal undiscovered principles of sustainable agriculture. The termites cultivate fungi by continuously inoculating spores, which form a colony of hyphae, cooperating in plant degradation and production of fungal biomass and new spores. Analogous to the challenges human farmers face, I will discuss, i) how termites select productive crop varieties to start a fungus farm; ii) by which cultivation mode they maximize yield; and iii) how they maintain crops of high genetic quality during long-term clonal propagation. I will argue that continuous 'artificial' selection of the fungus by termites during a colony's life time is required in order to keep the fungus productive.

11:40 MICROBES AND SOILS – CAUSES AND CONSEQUENCES OF SOIL MICROBIAL DIVERSITY

Joana Falcão Salles, University of Groningen

Soil microbial communities are extremely diverse, with values ranging from 1,000 to 1,000,000 unique taxa per gram of soil. These communities of overwhelming diversity are responsible for the provision of many ecosystem services. Yet, our understanding of the mechanisms controlling this sheer microbial diversity and whether changes in microbial diversity influence ecosystem functioning is limited. In the first part of my talk I will discuss how we are using soil primary and secondary succession to understand the mechanisms leading to the establishment of soil microbial communities – the causes of microbial diversity. The focus here will be on a recently developed a framework that unravels the trajectories of microbial communities through succession along a stochastic / deterministic continuum. Collectively, this study gives a fundamental contribution to the understanding and predictability of microbial community assembly and succession. The second part of my talk will focus on a key paradigm in microbial ecology, which is unravelling how soil microbial diversity drives ecosystem functioning – the consequences of microbial diversity. By focusing on two functions, denitrification and invasion resistance, I will demonstrate that soil microbial communities follow the expected biodiversity-ecosystem functioning relationships, i.e. that more diverse systems perform better than less diverse ones. Importantly, by using the concept of community niche, we provide evidence that efficiency in resource use – via resource complementarity and partitioning among resident species – is the overarching mechanism promoting the positive effects of diversity. Overall, in a time where global change is a reality and biodiversity loss is expected to accelerate, understanding the mechanisms controlling the diversity of soil microorganisms is crucial to predict the responses of microbial driven process to global change scenarios and to sustain soil ecosystem services.

12:20 MICROBES AND PLANTS – THE PLANT MICROBIOME AND PLANT HEALTH

Corné Pieterse, Utrecht University

Plants nurture a large community of plant growth-promoting rhizobacteria (PGPR) that provide them with essential services, such as enhanced mineral uptake, nitrogen fixation, growth promotion, and protection from pathogens. These plant microbiota are predominantly hosted by the root system, and can be selected for by the plant via root exudates. Selected PGPR promote plant health by stimulating the plant's immune system, a phenomenon called induced systemic resistance (ISR). The molecular mechanisms underpinning ISR have been intensively studied in the interaction between the model plant *Arabidopsis thaliana* (*Arabidopsis*) and the PGPR strain *Pseudomonas fluorescens* WCS417 (WCS417). WCS417-mediated ISR is effective against a broad variety of pathogens and even insect herbivores. Rhizobacteria-induced immunity requires action of the plant hormones

jasmonic acid and ethylene, as well as the defence regulatory proteins NPR1 and MYC2. Large scale gene expression analyses of plants of which the roots were colonized by WCS417 revealed that ISR in foliar tissues is not associated with major changes in gene expression. Instead, ISR-expressing leaves are primed for accelerated defence gene expression, which only becomes apparent after pathogen attack. This phenomenon is known as priming and provides a cost-effective mechanism of protection against pathogens and pests. In contrast to leaves, roots reprogram the expression of a large set of genes in response to colonization by WCS417. The root-specific R2R3-type MYB transcription factor MYB72 emerged as an important early regulator in the onset of rhizobacteria-ISR. Recently, we demonstrated that MYB72 is essential for both ISR and the production of phenolic compounds that are excreted in the rhizosphere to mobilize iron. Our recent work highlights the role of rhizobacterial volatiles in this process and provides a thus far unidentified mechanistic link between the ability of rhizobacteria to stimulate systemic immunity and iron uptake mechanisms in host plants.

14:00 MICROBES AND HUMANS – THE ECOLOGY OF THE HUMAN MICROBES IN HEALTH AND DISEASE

Eric Alm, Massachusetts Institute of Technology

The microbiome is emerging as a major contributor to human health, impacting diseases ranging from obesity to autism. I will present results from several studies characterizing the microbiome from an ecological perspective. In particular, I will discuss looking at the infectious disease *Clostridium difficile* as an invasive species, and how it can be prevented or cured by faecal transplantation. Finally, I will show how data generated on the human microbiome can be used to address basic questions about the diversity and stability of ecosystems.

14:40 MICROBES AND WATER – MARINE VIRUSES: FROM THE INDIVIDUAL LEVEL TO LARGE SCALE EFFECTS

Corina Brussaard, Royal Netherlands Institute for Sea Research

Viruses are the most numerically dominant life form in the oceans and infect in large numbers microbial hosts. Host sensitivity and physiology, in combination with viral decay determine the overall success of the marine viruses. With unicellular species as main host, their action most often results in rapid host mortality and consequently viral action promotes a more regenerative system. Overall, viral lysis rates are found to be at least comparable to the more traditional loss factor grazing and their impact goes beyond the individual level. During this presentation I will illustrate and discuss how marine viruses are a driving force behind host population dynamics, biodiversity, ecosystem functioning and biogeochemical cycling.

15:50 MICROBES AND CLIMATE – TERRESTRIAL N₂O REDUCING MICROBES AND THEIR IMPORTANCE AS N₂O SINKS

Sara Hallin, Swedish University of Agricultural Sciences

Nitrous oxide is reduced by bacteria and archaea harbouring the N₂O reductase. The phylogeny of this enzyme is split into two major clades, with the previously undetected Clade II being equally abundant as Clade I. However, the conditions that select for different N₂O reducers, and how such differences affect N₂O emissions, are poorly understood. Here, recent findings based on comparative genomics, experimental work and field studies indicating niche differentiation between the two clades and their roles in regulating N₂O emissions are summarized. A comparison of 652 genomes illustrated the modularity of the denitrification pathway, which underpin the importance of community structure for N₂O emissions. Further, variations of the pathway were not randomly distributed across taxa or amongst habitats, with N₂O reduction occurring more frequently among aquatic organisms. Analysis of 47 soils across Europe showed that the soil N₂O sink capacity is mostly explained by the abundance and diversity of Clade II, and that niche differentiation or even competitive interactions exist between organisms with either type of N₂O reductase. Interestingly, plant roots selected for clade I rather than clade II. Altogether, the results indicate that Clade II organisms are important N₂O sinks, favoured by other factors than those within clade I.