Final report

1., Introduction, aims

My main objectives in attending the conference were getting an insight into the current trends in the field of plant-microbe interactions, to network and to present my own results.

2., Results

2.1. Current trends in plant-microbe interactions

It became clear to me that the current trends include large-scale screening studies and making the most use of whole-genome sequencing. The latter is being driven by new bioinformatic approaches and new available sequencing methods of excellent value. This was well exemplified by a lecture on screening genes responsible for resistance to nematodes: about 500 accessions of *Arabidopsis thaliana* were infected with nematodes, daily photos were prepared from all cultures, and the data were evaluated against the whole-genome sequences of the accessions to yield about 12 gene candidates for further study.

I obtained clues about what current molecular biology considers to be a sufficient experimental setup to prove hypotheses. Regarding plant-microbe interactions, mutant and rescue phenotypes and/or addition of pure compounds is becoming essential.

These lessons will certainly influence our research methods and approaches in the near future.

2.2. Networking and presentation

Researchers using untargeted metabolomics as core methodology and plant microbiome studies were relatively under-represented. The conference was dominated by colleagues with microscopy and genetic and transcriptomic backgrounds. One of the exceptions was a colleague from the Swammerdam Institute for Life Sciences (SILS, The Netherlands), with whom I was able to discuss methodological details on exudate analysis and metabolomics. I intend to visit the group in the near future.

The poster I presented was prepared from the results of a metabolome - microbiome network study in a cultivated plant, *Armoracia rusticana* (horseradish). The poster is available as a shared PDF online at http://bit.ly/SGonda_posters. The ones interested wanted to know the most about the methods for annotation of compounds. This is indeed a bottleneck in current high-throughput chemical analysis, yet, interestingly most colleagues were surprised that semi-automated algorithms already exist to make the process more efficient (which we routinely use). I've already started networking along this observation in hope of contributing to the research of groups working in plant-microbe or microbe-microbe interactions by adding a chemical layer.

There were opportunities to talk with the Editorial Board of the official journal of the organizers. It was a great experience to have a discussion with these editors on issues like peer review quality and issues in scientific publishing in general.

Overall, I think the attendance was a great success, and I am grateful for the support that made this visit possible.

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