

OPONENT REVIEW ON Ph.D. THESIS

Ensyeh Sarikhani - Soil microbial communities in agroecosystems and natural habitats contributing to resistance and resilience of the soil environment

The thesis is represented by “long” form of Ph.D. thesis and contains classical divisions as Aims, Introduction, Materials and methods, Results, Discussion and Conclusions.

Even though the thesis has logical structure, and theme is interesting with practical impacts to one of the most important agricultural crop, there are some formal discrepancies. Here are from my point of view the most significant problems: The text of thesis is very extensive (the recommended length is about 100 pages) and there are no explanatory figures which can be helpful at least in the introductory part. Overall text formatting is not nice and some of the graphs are not edited properly. List of abbreviations is containing just a trace of the real amount of abbreviation in the thesis. The structure of individual chapters is non consistent and both “Material and Methods” and “Results” have the same chapter number. All of those formal problems makes the thesis hard to read and makes difficult for reader to orient within the text.

Scientific side of study seems to be well done, introduction contains extensive amount of information about the potato scab and all the methods used in the experiments. The thesis is presenting various experiments based on current molecular methods (qPCR, 16S rRNA gene-based taxonomic microarray and Illumina amplicon sequencing) which are amended by experiments with isolated aktinobacterial strains from potato scab suppressive soils. Author participated on sample and experiments preparation, results analysis, paper writing and she introduced a method for eukaryotic community analysis by Illumina sequencing. Author wrote the thesis mainly based on two successfully published papers and part of the thesis contains large overlap with those papers.

Sarikhani, E., Sagova-Mareckova, M., Omelka, M., & Kopecky, J. (2016). The effect of peat and iron supplements on the severity of potato common scab and bacterial community in tuberosphere soil. *FEMS microbiology ecology*, 93(1), fiw206.

Whole paragraphs on pages: 52-54, 59, 95, 96, 129 ...

Kopecky, J., Samkova, Z., Sarikhani, E., Kyselková, M., Omelka, M., Kristufek, V., Divis, J., Grundmann, G., Moenne-Loccoz, Y., & Sagova-Mareckova, M. (2019). Bacterial, archaeal and micro-eukaryotic communities characterize a disease-suppressive or conducive soil and a cultivar resistant or susceptible to common scab. *Scientific Reports* (9: 14883).

Whole paragraphs on pages: 54-56, 60-61, 100-112 ...

Here are some minor comments:

Page 13: Same abbreviation for peat and phosphorus – “P”

Page 92- 94: Figures 30, 31, 32 hard to read

Page 29: What is “Burgundy mixture”?

Page 32: Missing citation - “(citation)”

Page 32, 37, 45, 52, 55: Introductory part should not contain references to own work representing the results.

Page 60: Table 1. No explanation of treatment names e.g.: “VH-1 to” vs “VH” etc.

Page 111: Unclear legend of Figure 39.

Conclusion

In general the thesis has logical structure, it is based on current methodology and the results are appropriately processed and analyzed and I recommend it for defense.

Questions

- 1) In community analysis studies the group of Achaea is quite depreciated in the agricultural soils. Why do you think they should be important in potato scab disease development/suppression?
- 2) In your study you showed higher eukaryotic diversity in conducive soil/susceptible cultivar than in suppressive soil/resistant cultivar, even though it was not so significant. Do you have any hypothesis why the lower diversity can be connected with disease resistant conditions?
- 3) In the materials and methods chapter you are writing about processing of Illumina sequences: “A taxonomical assignment of sequence libraries was performed in Mothur using the Silva Small Subunit rRNA Database, release 128 (Yilmaz et al., 2014), adapted for use in Mothur (https://mothur.org/w/images/b/b4/Silva.nr_v128.tgz) as the reference database. Sequences of plastids, mitochondria, and those not classified in the domain Bacteria were discarded.” Part of the study were also Archaeal and Eukaryotic sequences, but I did not found how they were treated. Could you explain how it was done?

In Prague, 4.2.2020

Tomáš Větrovský