



HODNOCENÍ KVALIFIKAČNÍ PRÁCE POSUDEK OPONENTA PRÁCE

Studijní program: Zemědělské inženýrství

Studijní obor: Agroekologie – Ekologické zemědělství

Akademický rok: 2021/2022

Název práce: Bacterial life history strategies in gamma-irradiated arable soil receiving different microbial inocula

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Katedra: Agroekosystémů

Vedoucí práce: doc. Ing. Jan Moudrý, Ph.D.

Oponent: doc. Ing. Jiří Bárta, Ph.D.

Pracoviště oponenta: Jihočeská univerzita v Českých Budějovicích

Hlediska	Stupeň hodnocení						Nelze hodnotit
	A	B	C	D	E	F	
1 Splnění požadavků zadání	X						
2 Práce s informacemi a odbornou literaturou	X						
3 Vhodnost metodiky řešení	X						
4 Využití metod zpracování výsledků	X						
5 Interpretace výsledků, diskuse			X				
6 Formulace závěrů práce			X				
7 Jazykové zpracování a práce s odborným jazykem	X						
8 Odborná úroveň práce		X					
9 Formální úprava práce			X				
10 Zhodnocení možnosti praktického využití výsledků							X

Hodnocení vyznačte X (slouží pro stanovení výsledné klasifikace; A = 1, B = 1-, C = 2, D = 2-, E = 3, F = 4)



Konkrétní připomínky a otázky k obhajobě:

The thesis deals with the current issue of microbial biodiversity (both taxonomic and functional) of soils and how it is affected by introduced microorganisms, e.g. present in manure.

The introductory section describes both the soil environment in general and the biological component (from bacteria to invertebrates), describing the relationship between the phylogenetics of microorganisms, their functional traits and how these traits affect the quality and biodiversity of soils. In the second part, methodological approaches to study microorganisms are described and the 16S rRNA gene sequencing method is mainly highlighted. This method was also used in the actual work. The literature search is written in readable English and contains all the information, highlights the research gaps and appropriately discusses suggestions to fill them.

The objectives of the thesis are clearly defined and follow logically from the introduction and build on the knowledge gaps.

The methodological part, including current bioinformatics tools, is very nicely, clearly and detailed. The results are well presented in the form of graphs and tables. However, for some data, the data are presented in a double way (table and graph).

The discussion could have gone more in-depth and discussed individual traits in more detail. I find the conclusions too general and some apply only to a particular treatment.

Overall, I think that the paper has provided valuable data in understanding the effect of different inoculum on the development of soil microorganisms and could form the basis for a good publication after fine-tuning some of the content and formality.

Questions:

A total of almost 33k ASVs were identified, which is a relatively high number. Is this number common in soil and analyses based on sequence clustering with 3% dissimilarity tend to be much lower. Could you comment on this relatively high number and how you explain it or what might be influencing it?

I think it would be interesting to do a trait analysis also for different functional groups (e.g. denitrifying, diazotrophic bacteria, etc.). Have you tried this analysis? Functional guilds can be predicted using e.g. PICRUST2, FAPROTAX or FUNguild algorithms/databases.

Comments (content and formal)

The methodology states that all sequences assigned to the Archaea domain were filtered out. Figure 4.1 shows the Crenarchaeota strain from the Archaea domain.

I would have preferred a better colour palette (some of the colour shades of the classes are difficult to distinguish)

The data are presented in both a table and a graph. I would choose only one option. I would put a description of the abbreviations in the tables or choose the same description for the graph and the table.

Závěrečnou práci doporučuji k obhajobě (ANO/NE):

ANO



Navrhovaná výsledná klasifikace práce (slovně):

výborn



(výborně, velmi dobře, dobře, nevyhověl/a)

Datum: 05. 09. 2022

Podpis: