

## **Comment on soil-2021-130**

Anonymous Referee #1

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Referee comment on "Dynamic and migration characteristics of soil free amino acids during the whole growth period of rice after application of milk vetch" by Jing Yang et al., SOIL Discuss., <https://doi.org/10.5194/soil-2021-130-RC1>, 2022

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### General comments:

The paper showed an experiment to study the fate of free amino acids in a paddy soil, considering the bacterial communities structure fluctuations during different plant growth stages. The study of free amino acids in soil to understand their impact on N dynamics in soil could be very interesting for soil scientists to have information about the microbial activities and organic input can alterate the N cycle processes and this information could help to achieve information on N dynamics in soil. Unfortunately the paper showed problems in the text, in particular many information about the methods used are absent or incomplete in Materials and methods, and the presentation of results and the discussion are poor. The authors in many cases did not support the methods proposed or their statements by references. Specific comments:

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#### Materials and methods

The materials and methods requires a deep revision. The application of Chinese milk vetch in soil and the fertilization are not clear and many information are absent: e.g. the soil sampling methods for 20-40 cm and 40-60cm were not described, the method for free amino acids extraction is not clearly described or any references were not reported. The free amino acids extraction and quantification is the core of the paper, therefore it's important to include the details about the method you used to quantify the FAA in soil.

It's not clear if the authors performed the plasmid extraction, the protocol used is not well described and however the benefit to include this analysis is not explained.

In results section the authors reports some soil parameters (e.g. pH, SOM, urease, protease, bacterial biomass), but the protocols they used are not reported in materials and methods.

In Statistical analysis the authors could support the structural equation model analysis by appropriate references and I suggest including a description of the method to permit the reproducibility.

## Results

The description of FAA result is not sufficiently clear. The authors should indicate the statistical significant differences (by ANOVA) between CK and each different treatment to highlight the effect of different treatment. The description of the trend of FAA under different treatment during the different plant growth stages could help the reader to understand the information provided by the experiment. Moreover, I suggest in legend of figure 1 including the description of different treatment acronyms.

The authors should better describe the results reported in PCA plot. Moreover, the authors should explain why in the PCA plot are reported 8 dots: how many replicates in the experiment? The authors should consider the fertilization effect, too.

A correlation between soil parameters and free amino acids by a structural equation model analysis was measured but the model and the coefficients they used are not clearly described and not supported by references.

## Discussion

The discussion section is not well supported by appropriate references in particular regarding the fate of free amino acids in soil. Moreover, the link between the presence of amino acids and bacterial communities is not well discussed and the potential impact of plant roots in the dynamics (degradation, transport, rhizodeposition and so on) are neglected. The bacterial communities (by 16sRNA) but not the fungal communities are analyzed, but the authors declared that the degradation and production of free amino acids are affected by microbial communities, including the fungal community. The authors could justify their choice in discussion section.