

Interactive comment on “Microbial communities and their predictive functional profiles in arid soil of Saudi Arabia” by Munawwar A. Khan and Shams T. Khan

Anonymous Referee #2

Received and published: 18 June 2020

From reviewer’s point of view the work presented in this study is an important piece of work filling in the Knowledge gap about the microbial community in the soil of arid regions in Saudi Arabia. This study also provides substantial ground to carry out many future projects related to improving soil fertility in these regions. It will be interesting to confirm in future studies that the addition of carbon sources with single carbon like butanoate and dimethylformamide can enrich certain groups of bacteria mentioned in this study. And to monitor the survival and role of these microorganisms in these arid soils. Authors are also requested to ask add some discussion as to why the microbial community in the soil from Hafral-batin was so different.

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What are the possible reasons for the high population of Bacterioidetes bacteria in Abha region. Very recently published study “Desert plant bacteria reveal host influence and beneficial plant growth properties” by Eida shows microbial communities in the rhizospheric soil in Jizan region. Authors should consider including this report for comparing microbial community.

Please correctly calculate how many times $5.5 \pm 1.9 \times 10^5$ is higher than $1.1 \pm 0.9 \times 10^4$. I think it is 50 times?

Manuscripts also needs some minor corrections listed below

In title better to use “in the arid”

Line 15, delete “in” from the sentence, change samples in containing

Line 16, The presence of “in the arid soil”.

Line 18, Add analysis after PICRUST.

Line 18, environmental conditions.; shows an abundance of genes

Line 41, Asir reion and arid regions same change in line 47

Line 77, use hyphen between t and test

Line 86, the weather of the city

Line 96, remove an before 8.1

Line 112, the population of proteobacteria was

Line 115 was observed

Line 130, these sequences have been

Line 151, the arid conditions

Line 155, are known to oxidize

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Line 169, dimethylformamide

Line 178, Figures 5 and 6

Line 190, consider “indicating the”

Mark A and B clearly in figure 1.

Interactive comment on SOIL Discuss., <https://doi.org/10.5194/soil-2020-31>, 2020.

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