

Slope aspect influences soil microbial community structure and composition in the Israel arid Mediterranean

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Supplementary material

Table S1 The estimated richness OTUs in the dataset as measured by (Chao, Jack1, Jack2, and Bootstrap) with variance (\pm) indicating number of unseen OTUs.

Taxon	OTUs	Chao	Jack1	Jack2	Bootstrap
Bacteria	8558	16376.84 \pm 325.8619	12945.6 \pm 1182.724	15958.32	10406.95 \pm 485.2659
Fungi	16381	55931.12 \pm 1204.895	27724.73 \pm 3056.108	36855.5	20933.9 \pm 1131.046

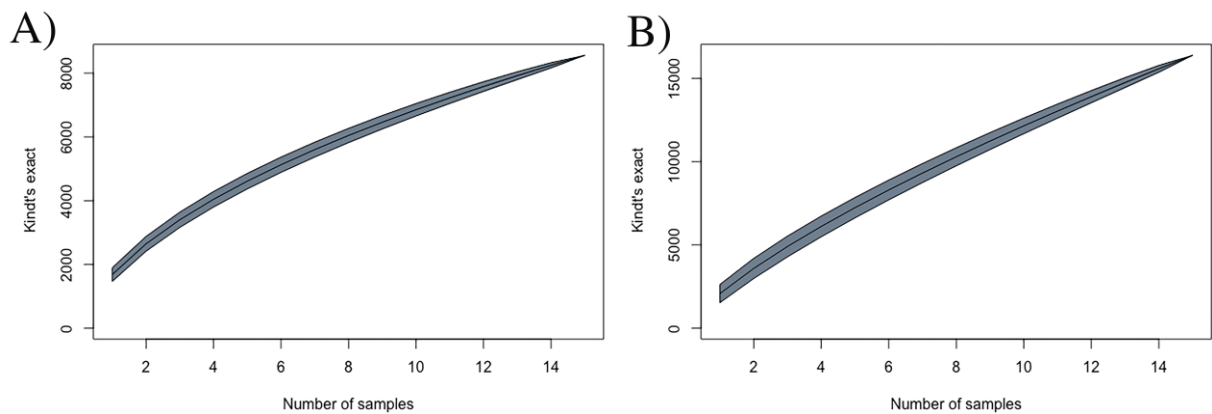


Figure S1 Species accumulation curve with A) bacteria and B) fungi both curves indicating high abundance of recovered OTUs. In total, 6 031 124 bacterial (8558 OTUs) and 7 132 381(16381 OTUs) fungal reads were obtained.

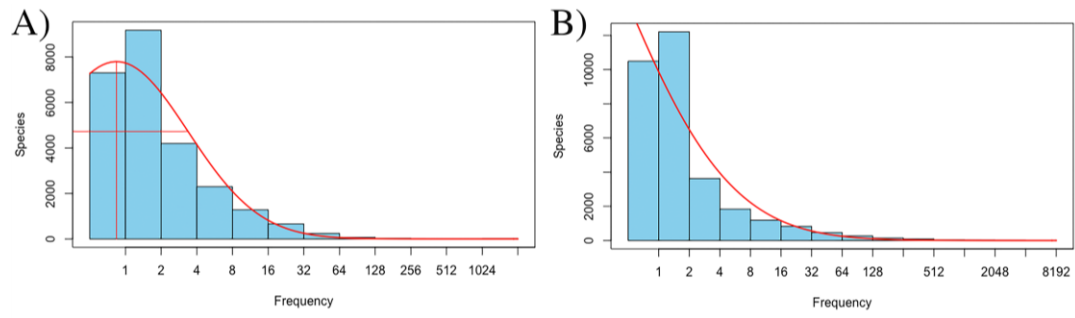


Figure S2 Preston log normal curve indicating the proportion of rare OTUs and the expected OTUs (area under the curve) with A) indicating few rare OTUs (truncation point far below the mode) and B) indicating increased number of unique OTUs.

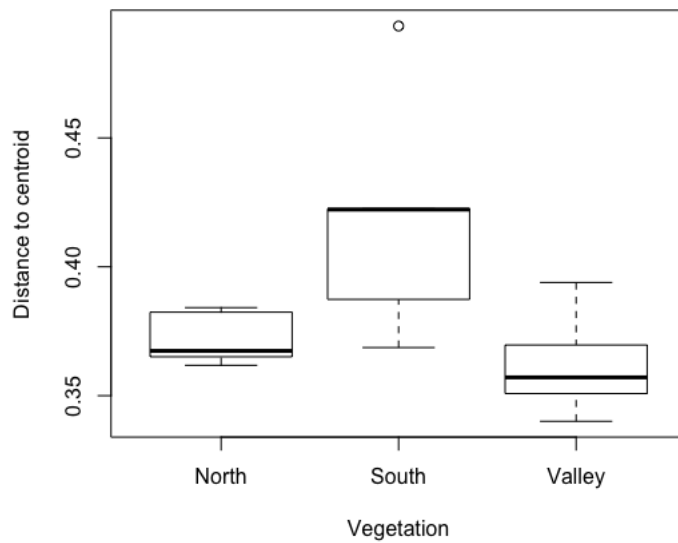


Figure S3 Homogeneity and multivariate dispersion within bacterial community.

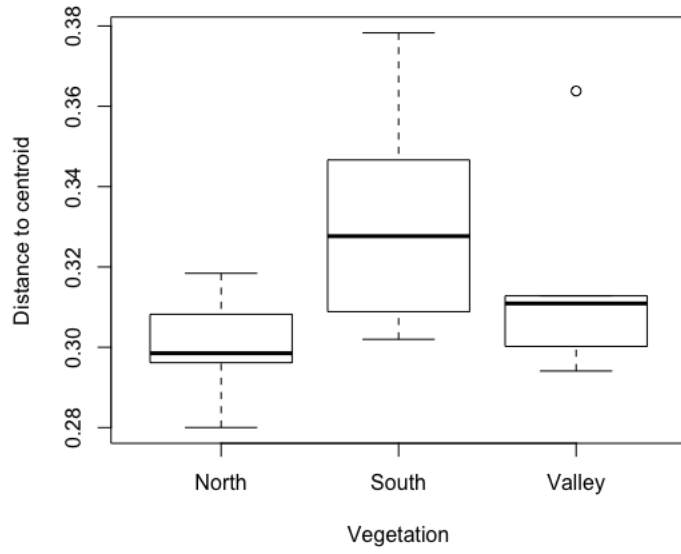


Figure S4 Homogeneity and multivariate dispersion within fungal community.

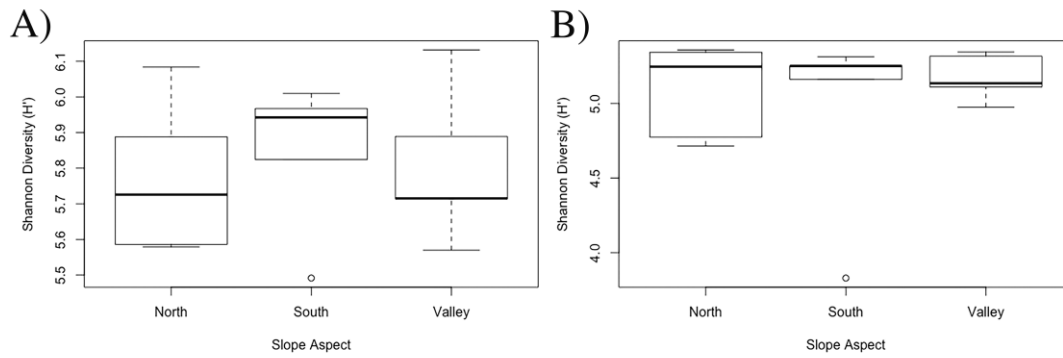


Figure S5 Shannon diversity with A) bacteria and B) fungi across the different slope aspects.

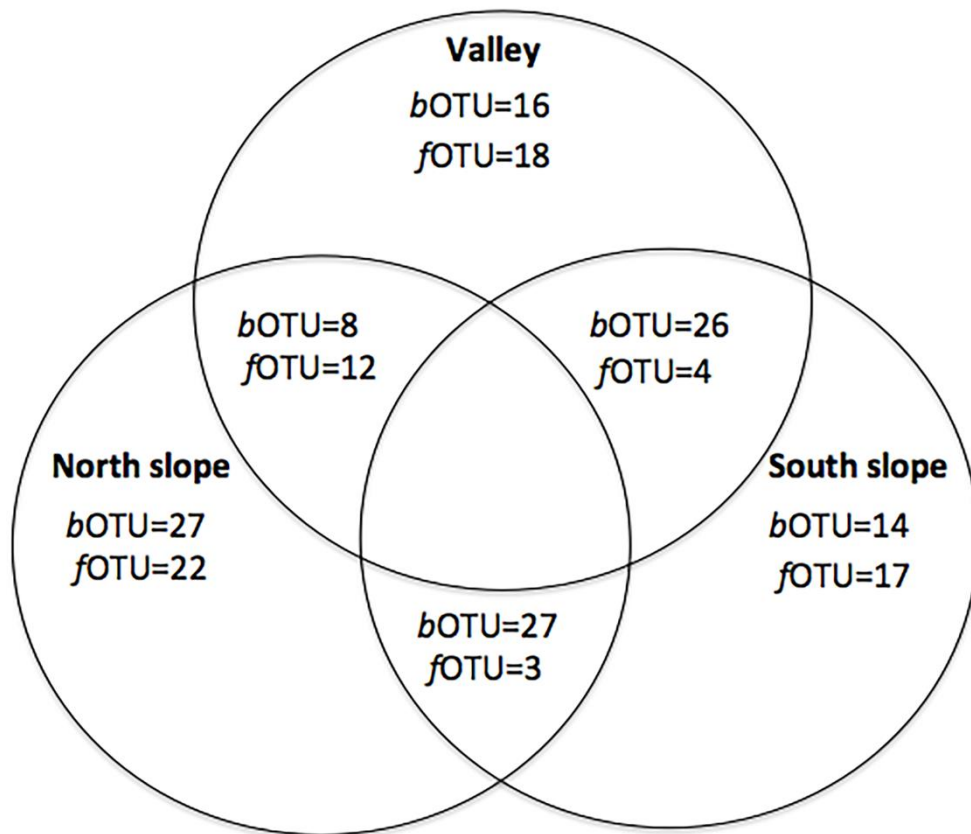


Figure S6 Indicator OTUs and their association with the specific sites with *bOTU* indicating bacterial OTUs and *fOTU* indicating fungal OTUs. There were more shared *bOTU* than *fOTU*.