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The role of ecosystem engineers in shaping the diversity and function of arid soil bacterial communities

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Abstract. Ecosystem engineers (EEs) are present in every environment and are known to strongly influence ecological processes and thus shape the distribution of species and resources. In this study, we assessed the direct and indirect effect of two EEs (perennial shrubs and ant nests), individually and combined, on the composition and function of arid soil bacterial communities. To that end, topsoil samples were collected in the Negev desert highlands during the dry season from four patch types: (1) barren soil; (2) under shrubs; (3) near ant nests; or (4) near ant nests situated under shrubs. The bacterial community composition and potential functionality were evaluated in the soil samples (14 replicates per patch type) using 16S rRNA gene amplicon sequencing together with physico-chemical measures of the soil. We have found that the EEs affected the community composition differently. Barren patches supported a soil microbiome, dominated by *Rubrobacter* and Proteobacteria, while in EE patches Deinococcus-Thermus dominated. The presence of the EEs similarly enhanced the abundance of phototrophic, nitrogen cycle, and stress-related genes. In addition, the soil characteristics were altered only when both EEs were combined. Our results suggest that arid landscapes foster unique communities selected by patches created by each EE(s), solo or in combination. Although the communities' composition differs, they support similar potential functions that may have a role in surviving the harsh arid conditions. The combined effect of the EEs on soil microbial communities is a good example of the hard-to-predict non-additive features of arid ecosystems that merit further research.

1 Introduction

Hot desert environments are characterized by long droughts interspersed by intermittent and unpredictable rain events. Water and nutrients in hot desert environments are scarce and unevenly distributed across the land, resulting in patches of contrasting productivities. High-productivity patches, also called resource islands, are defined by large concentrations of organic matter and nutrients (Bachar et al., 2012; Ben-David et al., 2011; Schlesinger et al., 1996; West, 1981). These resource islands can be formed through the redistribution of nutrients and water by ecosystem engineers (EEs), such as perennial plants or invertebrates (Wilby et al., 2001; Wright et al., 2006). EEs are also known for impacting many components of a given environment, such as soil features, annuals distribution, or community composition of microorganisms (De Graaff et al., 2015; Oren et al., 2007).

An EE is an organism that, directly or indirectly, modifies the availability of resources to other organisms by transforming the physical state of abiotic and/or biotic components of the ecosystem sensu Jones et al. (1994). The im-

pacts of EEs range from physical, through the creation of biogenic structures (e.g. tunnels) (Lavelle, 2002), to chemical, through the production of compounds that have physiological effects (e.g. root exudates) (Lavelle et al., 1992), to biological, through organism behaviour (e.g. seed dispersal) (Lavelle et al., 2006). In drylands, resources, such as nutrients or water, are often concentrated around EEs, boosting the development of diverse populations of annual plants and invertebrates (Wright and Upadhyaya, 1996) as well as microbial communities (Bachar et al., 2012; Ginzburg et al., 2008; Saul-Tcherkas and Steinberger, 2011). This taxonomical response to changes in the physico-chemical conditions is linked to the potential function of the community (Narayan et al., 2020). This implies that the variation in taxonomy by the presence of an EE could potentially be associated with changes in functionality.

In desert ecosystems, ants are a notable example of an EE (Ginzburg et al., 2008). They redistribute resources by tilling the soil, bringing soil from the deep layers to the upper layers (bioturbation), and by gathering, storing, and ejecting food items, such as plant material or dead invertebrates, in and around the nest (Filser et al., 2016; Folgarait, 1998; MacMahon et al., 2000). EEs in arid environments also include perennial shrubs (Callaway, 1995; Schlesinger and Pilmanis, 1998; Segoli et al., 2012; Shachak et al., 2008; Walker et al., 2001). Their root systems create a soil mound that traps litter and seeds, allowing for higher water infiltration. The root exudates increase the content of organic matter and the shrub canopies decrease evaporation, prolonging water availability following a rain event (Bachar et al., 2012). In addition, the presence of shrubs alters the course of water run-off (Oren et al., 2007), which impacts the locations of available water for soil microbial communities. In addition, root systems have their own microbiome, which interacts with the soil microbial community (Steven et al., 2014).

The roles of both ants and perennial shrubs as EEs were reported in various ecosystems (Facelli and Temby, 2002; Farji-Brener and Werenkraut, 2017; Frouz et al., 2003; Gosselin et al., 2016; Pariente, 2002; Schlesinger et al., 1996). However, we know little about their joint effect on arid ecosystems. We hypothesized that each EE would shape a unique soil bacterial community via changes in the soil physico-chemical properties. We further predicted that since shrub canopies and ant nests may affect soil properties differently, their combined effect on the microbial community is non-additive and thus cannot be predicted by the contributing components. To test our hypotheses, we explored arid soil bacterial microbiomes and soil chemical features during the dry season of 2015. We sampled four different patches: under *Hammada scoparia* shrubs; near the nest openings of the harvester ant *Messor ebeninus*; in combined patches of the ants' nests under shrubs; and in barren soil.

2 Materials and methods

2.1 Sampling

The study was conducted in a long-term ecological research (LTER) site in the central Negev, Israel (Zin Plateau, 34°80′ E, 30°86′ N). It is characterized by 90 mm annual rainfall and average monthly temperatures fluctuating from 13 °C (January) to 35 °C (August). Vegetation is scarce and dominated by the perennial shrubs *Hammada scoparia* and *Atriplex halimus* (Gilad et al., 2004).

Sampling was conducted as previously described (Baubin et al., 2019) with slight modifications, such as the inclusion of Shrub & Nest samples. To summarize, we sampled four distinct patch types: (1) barren soil (Barren); (2) under the canopy of *H. scoparia* (Shrub); (3) 20–30 cm from the main opening of the nest of *M. ebeninus* (Nest); and (4) 20–30 cm from an ant nest's opening that was situated under a shrub canopy (Shrub & Nest). Samples were collected in October 2015, after an 8-month drought.

We sampled 14 random experimental blocks from each of the four patches (4 patch types $\times$ 14 blocks = 56 samples). The samples were collected using a scoop that was sterilized between each sampling using 70 % technical ethanol. Soil was collected from the top 5 cm after removal of the crust and debris. Three subsamples of $\sim$ 100 g were collected from each block and pooled together. In the lab, samples from two adjacent blocks were composite and homogenized using a 2 mm sieve. The samples were then separated for consecutive analyses: 15 g of each soil sample was stored in −80 °C for bacterial analysis, 25 g was used to determine the water content in the soil, and the rest was used for the measurements of physico-chemical properties.

2.2 DNA extraction, amplification, and sequencing

Total nucleic acids were extracted from 0.5 g of soil as previously described (Angel, 2012), purified with the ExgeneTM Soil SV kit (GeneAll, Seoul, South Korea) according to the manufacturer's instructions. The 16S rRNA encoding genes V3–V4 region was amplified using 341F and 806R primer (Klindworth et al., 2013). The PCR consisted of 2.5 µL 10× standard buffer, 10 µM primers, 0.8 mM dNTPs, 0.4 µL DreamTaq DNA polymerase, 4 µL template, 1 mM bovine serum albumin (Takara, Kusatsu, Japan), and 12.6 µL Milli-Q water. Triplicate PCR reactions (95 °C for 30 s; 28 cycles of 95 °C for 15 s, 50 °C for 30 s, 68 °C for 30 s; 68 °C for 5 min) were pooled and amplicon concentration and purity were measured by electrophoresis (Nanodrop ND-1000, Thermo Fisher Scientific, Waltham, MA, USA). The amplicon libraries were constructed and sequenced on the Illumina MiSeq platform (2×250, pair-end) at the Research Resources Centre at the University of Illinois.

2.3 Soil physico-chemical analysis

The physico-chemical parameters of the soil samples were assessed following the standard methods (SSSA, 1996). Water content was measured by gravimetry. Other parameters were measured as follows by the Gilat Hasade Services Laboratory (Moshav Gilat, Israel). The pH was measured in saturated soil extract (SSE). Phosphorus (P) was extracted by the Olsen method using a 0.5 M sodium bicarbonate solution ($NaHCO_3$) and the absorbance of the final solution was measured at 880 nm using a spectrophotometer. Nitrate (NO_3^-) and ammonium (NH_4^+) were extracted with a 2 N potassium chloride (KCl) solution and measured at 520 and 660 nm, respectively. Organic matter (OM) content was determined by the Walkley–Black method using a dichromate oxidation ($Cr_2O_7^{-2}$) and the amount of oxidizable OM was measured at 600 nm.

2.4 Bioinformatic analysis

The reads were quality-checked with MultiQC and trimmed using TrimGalore. Briefly, all reads with a quality of less than 20 and shorter than 150 bp were removed, and the rest were analysed further. The reads were then gathered into amplicon sequence variants (ASVs) (99 % identity cutoff) and merged using Dada2 (Callahan et al., 2016) in QIIME2 (Bolyen et al., 2018) following the NeatSeq-Flow pipeline (Sklarz et al., 2018). ASV counts were normalized to equal sampling depth (9100 reads). The taxonomic assignment was done using Silva (version 132) (Quast et al., 2013) through QIIME2 and all non-bacterial data have been characterized as unclassified.

2.5 Statistical analysis

The statistical analysis was done using R (R Core Team, 2016). To visualize the differences between patch types, a non-metric multidimensional scaling (NMDS) plot was created using the Bray–Curtis dissimilarity and the significance of these differences was analysed using a non-parametric analysis of similarity (ANOSIM) ("vegan" package, Oksanen et al., 2014). The envfit function ("vegan" package, Oksanen et al., 2014) was applied on the NMDS data to evaluate the effect of soil parameters on the bacterial community. The NMDS was plotted using the "ggplot2" package (Wickham, 2016) and the arrows representing the effect of each soil parameter as well as the centroids for each patch type, calculated using envfit, were added to the plot. The bacterial data were analysed using the "phyloseq" package (McMurdie et al., 2017). The relative abundance, whenever higher than 0.05 %, of each phylum, class, and order was calculated and then plotted using a stacked bar plot ("ggplot2" package, Wickham, 2016). The significance of difference between patch types was assessed using a non-parametric test: a Kruskal–Wallis test and a post hoc Dunn test (Dinno, 2017; Dunn, 1964; Kruskal and Wallis, 1952). All sequences retrieved in this study were uploaded to BioProject (https://www.ncbi.nlm.nih.gov/bioproject, last access: 30 September 2018) under the submission number PRJNA484096.

2.6 Functional prediction

The prediction of function of the 16S amplicons was done with Piphillin using the KEGG database (October 2018). Piphillin generates a genome abundance table that is normalized to the 16S rRNA copy number for each genome (Iwai et al., 2016; Narayan et al., 2020). To analyse the arid soil microbial functionality, we selected metabolisms and respective genes related to arid soil using groups and genes from the KEGG database (Kaneshisa and Goto, 2000). We selected steps in metabolic pathways for different methods of harvesting energy (organotrophy, lithotrophy, and phototrophy) (Cordero et al., 2019; Greening et al., 2016; León-Sobrino et al., 2019; Tveit et al., 2019), for parts of the nitrogen cycle (Galloway et al., 2004), and for the survival of the individual during a drought (DNA conservation and repair, sporulation, and reactive oxygen species (ROS)-damage prevention) (Borisov et al., 2013; Hansen et al., 2007; Henrikus et al., 2018; Preiss, 1984; Preiss and Sivak, 1999; Rajeev et al., 2013; Repar et al., 2012; Slade and Radman, 2011). Then, we looked for each step in the KEGG database and picked out genes of interest to build our own database. The assignment of function to the KEGG numbers was done in R. The significance of the differences between patch types in predicted functionalities was evaluated using a non-parametric test, a Kruskal–Wallis test and a post hoc Dunn test (Dinno, 2017; Dunn, 1964; Kruskal and Wallis, 1952), and boxplots were created in R.

3 Results

3.1 Soil physico-chemical characteristics

Table 1 depicts the differences in the soil characteristics (full list of values in Table A1) between the patches (barren, nest, shrub, and Shrub & Nest). Shrub & Nest patches have higher concentrations of NO_3^- and P (30 and 54 $mg\,kg^{-1}$, respectively) than the average of the other patches combined (4.7 and 22 $mg\,kg^{-1}$, respectively). When verifying with a Kruskal–Wallis test and a Dunn test on the values of these soil variables (Table A2), we see that the differences between patch types are significant (Shrub & Nest vs. all other patches, $p < 0.05$). Patches with two EEs also have a significantly higher concentration of NH_4^+ (9.72 $mg\,kg^{-1}$) and OM (8.21 %) compared to all other patches (NH_4^+ mean: 5.62 $mg\,kg^{-1}$, p value < 0.05; OM mean: 5.51 %, $p \leq 0.05$). However, the water content and pH did not show significant differences between patches (Table A2).

Table 1. Soil parameters presented as mean ± standard deviation (NO_3^-: nitrate, P: phosphorus, NH_4^+: ammonium, OM: organic matter content, water: water content).

Soil parameter	Barren	Nest	Shrub	Shrub & Nest
NH_4^+ ($mg\,kg^{-1}$)	5.63 ± 1.45	6.39 ± 2.5	4.86 ± 1.15	9.72 ± 2.51
NO_3^- ($mg\,kg^{-1}$)	2.97 ± 1.51	6.47 ± 6.96	4.7 ± 3.71	30.57 ± 35.51
OM (%)	0.56 ± 0.4	0.47 ± 0.13	0.62 ± 0.14	0.82 ± 0.11
pH	8.11 ± 0.15	7.96 ± 0.2	8.24 ± 0.1	7.79 ± 0.12
P ($mg\,kg^{-1}$)	20.11 ± 10.21	20.16 ± 6.45	26.04 ± 19.51	54.1 ± 21.14
Water (%)	1.56 ± 0.09	1.68 ± 0.2	1.56 ± 0.16	1.48 ± 0.09

3.2 Beta diversity

The summary of the sequence analysis can be found in Table A4. Dada2 analysis yielded 2318 ASVs and the ANOSIM results (Fig. 1, Table A3) suggest that there are significant differences in the microbial community between patch types ($R = 0.28$; $p = 0.001$). The envfit function shows that most soil parameters correlated with the barren patches but not with the other three patch types.

3.3 Community composition

The community was mostly composed of Actinobacteria, Proteobacteria, Deinococcus-Thermus, Bacteroidetes, and Firmicutes (Fig. 2). The relative abundance for each phylum is detailed in Table A5. We focused on the results of the three main phyla: Actinobacteria, Deinococcus-Thermus, and Proteobacteria. Using pair-wise comparisons, we saw that shrub patches and nest patches had similar communities (no significant differences, $p > 0.05$); therefore, we considered them to be single EE patches. For these patches, an average relative abundance of nest and shrub patches was used for statistical data. For the Actinobacteria phylum, patches with one EE had significantly lower relative abundance than barren patches (one EE: 9 % vs. Barren patch: 35 % $p < 0.005$) or patches with two EEs (17 %, p value: 0.02). For the Deinococcus-Thermus phylum, barren patches had significantly lower relative abundance than patches with one or two EEs (Barren: 3 % vs. one EE: 25 % vs. two EEs: 9 %, $p < 0.05$). A similar pattern was detected in the Proteobacteria phylum (Barren: 38 % vs. one EE: 44 % vs. two EEs: 39 %, $p < 0.05$). Additionally, we looked at the next three most abundant phyla: Firmicutes, Bacteroidetes, and Chloroflexi. For Firmicutes, the relative abundance of this phylum was significantly higher in the Shrub & Nest patch than in the Barren and Shrub patches. For Bacteroidetes, the Nest patch had a significantly lower relative abundance than the other patches. For Chloroflexi, there was a significant decrease in relative abundance in the Shrub, Nest, and Shrub & Nest patches compared to the Barren patch. All p values can be found in Table A6. The class and order plots show differences between patch types. However, the resolution is not high enough to enable us to draw significant conclusions (Figs. B1 and B2).

3.4 Functional prediction

The abundance of each gene group has been normalized to the 16S rRNA copy number for each genome. The functional prediction results focus on eight distinct gene groups: phototrophy, lithotrophy, organotrophy, DNA conservation, DNA repair, nitrogen cycle, sporulation, and ROS-damage prevention (listed in Table A7). Figure 3 shows the pattern of the obtained functions. It shows higher abundances of the gene group encoding for DNA conservation, DNA repair, nitrogen metabolism, ROS-damage prevention, sporulation, and phototrophy in patches associated with at least one EE compared to the barren patches (Table A8). Therefore, we analysed the results as barren vs. average of the other three patch types that were not significantly different from one another (Table A9), and significant differences ($p < 0.04$) between barren and EE patches were detected. The genes related to lithotrophy only differed between patches with one EE and the barren patches ($p < 0.03$), but patches with two EEs were similar to the barren plots. Finally, for genes related to the organotrophy, there were no significant differences between the patches ($p > 0.05$).

4 Discussion

In desert environments, during the dry season, a large portion of the microbial community is dormant or shows reduced metabolic activity (Bay et al., 2018; Cordero et al., 2019; Lennon and Jones, 2011; Schulze-Makuch et al., 2018). However, the presence of EEs enhances the potential for functions related to metabolism and to survival functions (Fig. 3). EEs create havens of resources and water, which can be affiliated with the concept of resource islands (Schlesinger and Pilmanis, 1998). However, their individual, and combined, effects do not always lead to significant changes in the composition of the soil microbial community (Fig. 2). While the soil parameters might be modified by the presence of both EEs, the microbial community might take a longer time to change due to their slow turnover in the dry season.

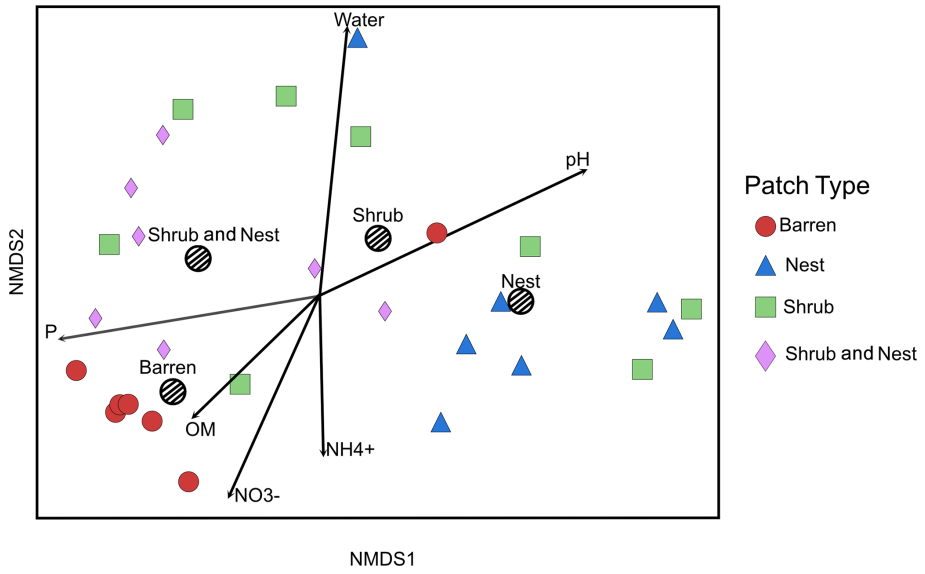

Figure 1. Non-metric multidimensional scaling (NMDS) of the soil 16S microbial communities in the dry season under different patch types. The centroid for each patch type is represented by a dashed circle. The arrow vectors represent the effect of each soil physico-chemical characteristic on the bacterial community calculated with the envfit function. NO_3^-: nitrate, NH_4^+: ammonium, OM: organic matter content, P: phosphorus, water: water content. The patch types are significantly different from each other (ANOSIM, $R = 0.28247$; p value $= 0.001$). P, OM, NO_3^-, and NH_4^+.

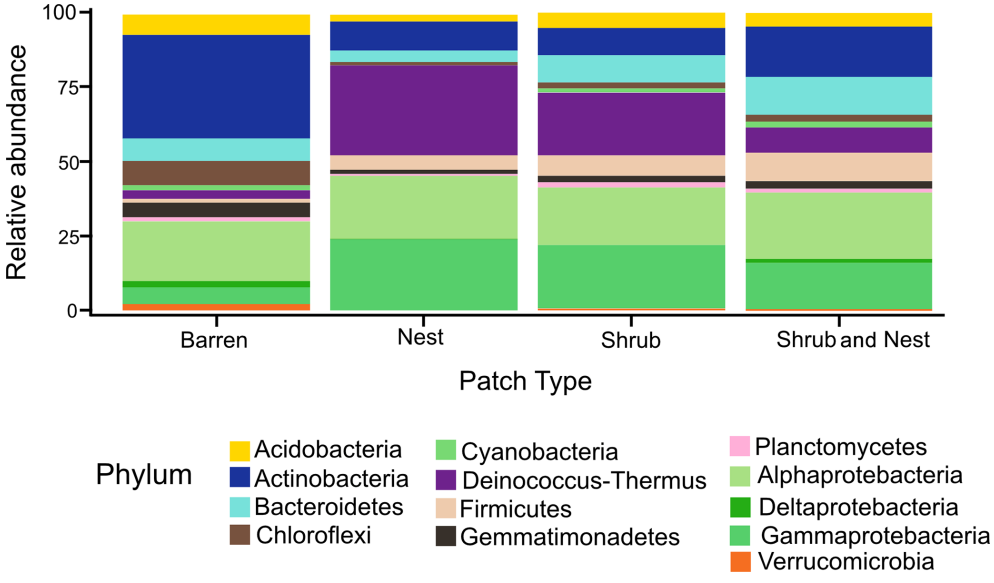

Figure 2. Bar plot of the relative abundance (%) of the most abundant phyla in the soil microbial community in the dry season under different patch types (phyla with a relative abundance > 0.05 %). The Proteobacteria have been separated into their classes (represented here in shades of green). The relative abundance of Deinococcus-Thermus increases when one EE is present, while the population of Actinobacteria decreases.

However, these communities experience more habitable conditions due to the modulating effects of the EEs on the environmental conditions. The increase in the activity of gene groups can be explained by an increase in nutrients in the joint EE patches (Table 1).

Both Actinobacteria and Deinococcus-Thermus were abundant in all patches, but their relative abundances were negatively correlated. Each phylum featured a dominant genus that is well adapted to stressful conditions: *Rubrobacter* dominated the barren soil, while *Deinococcus* dominated the EE patches (Fig. 2 and Table A5). *Rubrobacter* are spe-

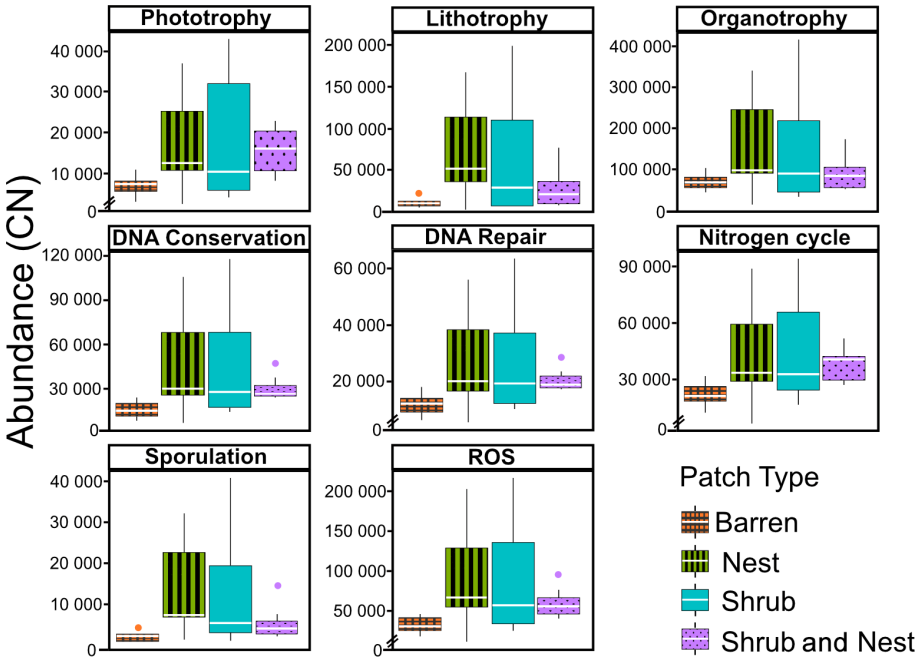

Figure 3. Boxplots of the functional prediction of the 16S sequences. Each panel (boxplot) represents a different group of genes associated with a certain functionality. The full list of genes can be found in Table A7. The patch types are represented by distinct colours and patterns. The *y* axis is the abundance in copy number (CN) normalized to the 16S rRNA copy number for each genome.

cialized in surviving strong desiccation and low nutrients (Bull, 2011; Ferreira et al., 1999), showing high relative abundance in arid barren soils of the Negev desert highlands (Meier et al., 2021). *Deinococcus* are versatile organisms, highly adapted to a wide range of extremes, such as radiations, temperatures, and xerification (Chanal et al., 2006; Prieur, 2007; Slade and Radman, 2011). This versatility allows them to thrive in EE patches as they can better adapt to perturbations compared to *Rubrobacter*.

Only the combination of EEs resulted in significant changes (p values: Table A2) in NO_3^-, P, and, to a lesser extent, NH_4^+, pH, and OM (values: Table A1). When located under a shrub, ants can increase their seed consumption, which enhances the amount of leftovers around the nest (Wagner, 1997) and increases the concentrations of NO_3^- and P. These macronutrients are important drivers of the biological processes, as they are often the limiting factors of microbial growth and activity in the terrestrial environments (FAO et al., 2020). The physico-chemical measures, including soil water content, OM, nitrogen, P, and pH, did not match the changes observed in bacterial composition or function (Tables A1, A2, and A9 and Fig. 1), as was previously reported (Angel et al., 2010; Bachar et al., 2012; Vonshak et al., 2018). Indeed, there was no significant link between the changes in the bacterial communities and the measured soil parameters (Table A10).

The EE patches analysed in this study share the same habitat and resources, but their impacts are distinct (Passarelli et al., 2014), and, thus, their joint impact is non-additive. The behaviour of each EE is important as it becomes a feature of the combined impact of both EEs (Alba-Lynn and Detling, 2008). However, the effect of both EEs together cannot be inferred from their individual environmental impact or from their mutual interaction (Gilad et al., 2004). Here, we investigated a sessile organism with a passive and slow impact (the perennial shrub) and compared it to a motile organism (the ants) with an active and transient impact. Ants may have both a short-term impact, through the seasonal accumulation of seeds and organic matter, and a lasting impact, due to the alternation of the nest mound which remains in the same place for decades (Wagner and Jones, 2004). We have previously proposed that the observed differences in communities could be mediated by microclimatic characteristics under shrub patches (Bachar et al., 2012). It has been reported that the desert dwarf shrubs affect the physical features of their immediate soil patch. Shrubs were shown to divert water flow and reduce evapotranspiration rates following rain events (Segoli et al., 2008; Whitford and Duval, 2002) and reduce temperature and radiation year round (Kidron, 2009). Likewise, ants aerate the soil, thus increasing infiltration during rain events (Berg and Steinberger, 2008), and mix the layers through bioturbation (Folgarait, 1998). Therefore, the prolonged water availability and altered physical conditions from the wet season may have lasting effects on the communities' structure (Baubin et al., 2019), shaping the composition and functions observed here (Figs. 2 and 3).

5 Conclusions

In this study, we focused on two EEs only, but there are many EEs in one ecosystem, and knowing their joint impact would help explain the nutrient turnover and the bacterial communities in this ecosystem. The main stress-resistant phyla (Actinobacteria and Deinococcus-Thermus) react differently to the presence of EEs. The presences of these EEs also lead to a higher potential activity in the microbial communities. However, even though they have similar impacts, when together, EEs have non-additive effects.

Appendix A

Table A1. Soil characteristics data. NH_4^+ and P show the highest discrepancy between Shrub & Nest patches and the other three types.

ID	pH	NH_4^+ ($mg\,kg^{-1}$)	NO_3^- ($mg\,kg^{-1}$)	Water content (%)	OM (%)	P ($mg\,kg^{-1}$)
Barren	7.9	6.2	6.0	1.5	1.5	42.1
Barren	8.1	6.9	1.8	1.8	0.3	20.3
Barren	8.3	4.6	2.7	1.5	0.4	20.8
Barren	8.1	4.1	2.0	1.6	0.5	14.6
Barren	8.0	6.7	3.9	1.6	0.5	15.9
Barren	8.1	7.2	2.0	1.5	0.5	11.7
Barren	8.3	3.8	2.4	1.5	0.3	15.4
Nest	8.2	8.4	4.2	2.0	0.4	23.0
Nest	7.7	10.2	2.9	1.9	0.6	31.1
Nest	7.8	5.4	21.9	1.7	0.6	23.2
Nest	8.0	7.1	2.4	1.6	0.5	15.0
Nest	7.8	6.0	4.0	1.5	0.6	11.4
Nest	8.0	5.4	6.9	1.5	0.4	17.1
Nest	8.2	2.3	3.0	1.5	0.3	20.3
Shrub	8.2	5.2	4.5	1.7	0.6	25.0
Shrub	8.2	6.0	3.8	1.7	0.8	40.2
Shrub	8.2	6.6	12.3	1.3	0.6	62.8
Shrub	8.4	4.3	1.9	1.6	0.7	13.0
Shrub	8.3	3.4	0.9	1.4	0.6	8.4
Shrub	8.3	4.4	3.8	1.5	0.4	10.7
Shrub	8.1	4.0	5.7	1.7	0.7	22.2
Shrub & Nest	8.0	7.6	6.9	1.4	0.6	79.9
Shrub & Nest	7.7	9.5	5.3	1.5	0.8	29.4
Shrub & Nest	7.7	11.6	42.0	1.5	0.7	76.3
Shrub & Nest	7.7	8.5	11.0	1.6	0.9	54.0
Shrub & Nest	7.8	9.6	29.8	1.4	0.9	29.0
Shrub & Nest	7.7	14.3	105.2	1.5	0.8	66.9
Shrub & Nest	7.9	7.0	13.8	1.4	1.0	43.2
Chi2	**16.5**	**13.9**	**13.1**	**4.7**	**13.3**	**11.5**

Table A2. *P* values of the Dunn test between patch types on the soil characteristics variables. Bold numbers are significant (< 0.05).

Comparisons	Water	pH	NO_3^-	NH_4^+	P	OM
Barren–Nest	0.218	0.103	0.084	0.279	0.385	0.500
Barren–Shrub	0.448	0.119	0.194	0.190	0.354	0.067
Nest–Shrub	0.181	**0.007**	0.301	0.072	0.468	0.067
Barren–Shrub & Nest	0.086	**0.004**	**0.0003**	**0.004**	**0.001**	**0.001**
Nest–Shrub & Nest	**0.016**	0.079	0.018	**0.017**	**0.004**	**0.001**
Shrub–Shrub & Nest	0.108	**0.000**	**0.004**	**0.000**	**0.005**	**0.050**

Table A3. Results of the pair-wise adonis test between patch types. Bold numbers are significant (< 0.05).

Comparison	R2	*P* value
Barren vs. Nest	0.38473901	**0.012**
Barren vs. Shrub	0.25759869	**0.006**
Barren vs. Shrub & Nest	0.21665172	**0.048**
Nest vs. Shrub	0.08725184	1.000
Nest vs. Shrub & Nest	0.21988027	0.054
Shrub vs. Shrub & Nest	0.08914105	1.000

Table A4. Number of reads before and after the trimming stage and during the Dada2 stage.

Sample	Patch type	Number of reads				
		Raw	Trimmed	Filtered	Denoised	Non-chimeric
Samples_AD1	Barren	42 089	41 265	36 421	33 675	33 141
Samples_AD2	Barren	28 759	28 008	24 434	21 984	21 507
Samples_AD3	Barren	30 166	29 410	25 782	23 285	22 830
Samples_AD4	Barren	27 024	26 664	23 906	21 545	21 171
Samples_AD5	Barren	48 612	47 548	41 813	38 854	38 352
Samples_AD6	Barren	23 816	23 120	20 084	18 008	17 857
Samples_AD7	Barren	21 806	19 454	16 803	15 532	15 482
Samples_AD8	Nest	22 559	20 965	18 485	17 118	17 118
Samples_AD9	Nest	28 231	26 041	22 688	21 213	21 088
Samples_AD10	Nest	24 428	22 266	19 719	18 340	18 161
Samples_AD11	Nest	39 081	37 713	33 573	31 772	31 124
Samples_AD12	Nest	18 426	17 446	15 756	14 567	14 494
Samples_AD13	Nest	22 881	13 779	10 573	9234	9151
Samples_AD14	Nest	47 080	44 925	39 700	37 254	36 423
Samples_AD15	Shrub	51 183	48 988	43 764	41 558	40 506
Samples_AD16	Shrub	51 519	37 941	30 791	28 403	27 721
Samples_AD17	Shrub	35 494	33 858	29 858	27 875	27 349
Samples_AD18	Shrub	29 615	27 956	24 841	22 947	22 847
Samples_AD19	Shrub	39 011	37 117	32 622	30 293	29 544
Samples_AD20	Shrub	50 894	38 156	30 901	28 515	28 169
Samples_AD21	Shrub	35 365	32 529	28 933	27 200	27 033
Samples_AD22	Shrub	41 660	27 359	21 466	19 924	19 629
Samples_AD23	Shrub & Nest	37 107	35 185	31 099	28 722	28 201
Samples_AD24	Shrub & Nest	55 386	34 724	27 058	24 657	24 136
Samples_AD25	Shrub & Nest	58 632	42 065	34 139	31 435	30 693
Samples_AD26	Shrub & Nest	67 273	47 135	37 618	33 503	33 089
Samples_AD27	Shrub & Nest	35 493	31 891	27 756	26 086	25 915
Samples_AD28	Shrub & Nest	34 645	29 939	26 141	24 533	24 297
Samples_AD29	Shrub & Nest	76 888	53 655	42 659	38 753	38 044

Table A5. Relative abundance (%) of the taxonomic community per patch type.

Phylum	Patch type	Relative abundance
Acidobacteria	Barren	7.02
Acidobacteria	Nest	2.33
Acidobacteria	Shrub	5.10
Acidobacteria	Shrub & Nest	4.52
Actinobacteria	Barren	34.72
Actinobacteria	Nest	9.79
Actinobacteria	Shrub	9.13
Actinobacteria	Shrub & Nest	16.83
Bacteroidetes	Barren	7.41
Bacteroidetes	Nest	3.86
Bacteroidetes	Shrub	9.24
Bacteroidetes	Shrub & Nest	12.42
Chloroflexi	Barren	8.15
Chloroflexi	Nest	1.01
Chloroflexi	Shrub	1.75
Chloroflexi	Shrub & Nest	2.24
Cyanobacteria	Barren	1.59
Cyanobacteria	Shrub	1.48
Cyanobacteria	Shrub & Nest	1.95
Deinococcus-Thermus	Barren	2.77
Deinococcus-Thermus	Nest	30.19
Deinococcus-Thermus	Shrub	20.85
Deinococcus-Thermus	Shrub & Nest	8.69
Firmicutes	Barren	1.20
Firmicutes	Nest	4.89
Firmicutes	Shrub	6.93
Firmicutes	Shrub & Nest	9.12
Gemmatimonadetes	Barren	4.93
Gemmatimonadetes	Nest	1.13
Gemmatimonadetes	Shrub	2.40
Gemmatimonadetes	Shrub & Nest	2.78
Planctomycetes	Barren	1.29
Planctomycetes	Nest	0.55
Planctomycetes	Shrub	1.39
Planctomycetes	Shrub & Nest	1.20
Proteobacteria	Barren	27.67
Proteobacteria	Nest	45.32
Proteobacteria	Shrub	40.44
Proteobacteria	Shrub & Nest	38.77

Table A6. *P* values of the Dunn tests between patch types on the relative abundance of the five most abundant phyla. Bold numbers are significant (< 0.05).

Comparisons	Actinobacteria	Bacteroidetes	Deinococcus-Thermus	Firmicutes	Proteobacteria
Barren–Nest	**0.0004**	**0.0129**	**0.0003**	0.3768	**0.0394**
Barren–Shrub	**0.0004**	0.4774	**0.0009**	0.0718	**0.0120**
Nest–Shrub	0.4661	**0.0124**	0.3352	0.1274	0.3294
Barren–Shrub & Nest	**0.0991**	**0.0836**	**0.0320**	**0.0129**	**0.0042**
Nest–Shrub & Nest	**0.0207**	**0.0002**	0.0583	**0.0278**	0.1897
Shrub–Shrub & Nest	**0.0216**	0.0690	0.1160	**0.200**8	0.3206

Table A7. List of the genes used for function prediction ordered by groups and subgroups.

Group	Metabolic trait	KEGG_ID	Function
DNA conservation	Putative DNA-binding protein	K02524	K10; DNA-binding protein (fs(1)K10, female sterile(1)K10)
	Putative DNA-binding protein	K03111	ssb; single-strand DNA-binding protein
	Putative DNA-binding protein	K03530	hupB; DNA-binding protein HU-beta
	Putative DNA-binding protein	K03622	ssh10b; archaea-specific DNA-binding protein
	Putative DNA-binding protein	K03746	hns; DNA-binding protein H-NS
	Putative DNA-binding protein	K04047	dps; starvation-inducible DNA-binding protein
	Putative DNA-binding protein	K04494	CHD8, HELSNF1; chromodomain helicase DNA-binding protein 8 (EC:3.6.4.12)
	Putative DNA-binding protein	K04680	ID1; DNA-binding protein inhibitor ID1
	Putative DNA-binding protein	K05516	cbpA; curved DNA-binding protein
	Putative DNA-binding protein	K05732	ARHGAP35, GRLF1; glucocorticoid receptor DNA-binding factor 1
	Putative DNA-binding protein	K05787	hupA; DNA-binding protein HU-alpha
	Putative DNA-binding protein	K09061	GCF, C2orf3; GC-rich sequence DNA-binding factor
	Putative DNA-binding protein	K09423	BAA; Myb-like DNA-binding protein BAA
	Putative DNA-binding protein	K09424	REB1; Myb-like DNA-binding protein REB1
	Putative DNA-binding protein	K09425	K09425; Myb-like DNA-binding protein FlbD
	Putative DNA-binding protein	K09426	RAP1; Myb-like DNA-binding protein RAP1
	Putative DNA-binding protein	K10140	DDB2; DNA damage-binding protein 2
	Putative DNA-binding protein	K10610	DDB1; DNA damage-binding protein 1
	Putative DNA-binding protein	K10728	TOPBP1; topoisomerase (DNA) II-binding protein 1
	Putative DNA-binding protein	K10748	tus, tau; DNA replication terminus site-binding protein
	Histone-like protein	K10752	RBBP4, HAT2, CAF1, MIA6; histone-binding protein RBBP4
	Putative DNA-binding protein	K10979	ku; DNA end-binding protein Ku
	Putative DNA-binding protein	K11367	CHD1; chromodomain-helicase-DNA-binding protein 1 (EC:3.6.4.12)
	Histone-like protein	K11495	CENPA; histone H3-like centromeric protein A
	Putative DNA-binding protein	K11574	CBF2, CBF3A, CTF14; centromere DNA-binding protein complex CBF3 subunit A
	Putative DNA-binding protein	K11575	CEP3, CBF3B; centromere DNA-binding protein complex CBF3 subunit B
	Putative DNA-binding protein	K11576	CTF13, CBF3C; centromere DNA-binding protein complex CBF3 subunit C
	Putative DNA-binding protein	K11642	CHD3, MI2A; chromodomain-helicase-DNA-binding protein 3 (EC:3.6.4.12)
	Putative DNA-binding protein	K11643	CHD4, MI2B; chromodomain-helicase-DNA-binding protein 4 (EC:3.6.4.12)
	Histone-like protein	K11659	RBBP7; histone-binding protein RBBP7
	Putative DNA-binding protein	K11685	stpA; DNA-binding protein StpA
	Putative DNA-binding protein	K12965	ZBP1, DAI; Z-DNA-binding protein 1
	Putative DNA-binding protein	K13102	KIN; DNA/RNA-binding protein KIN17
	Putative DNA-binding protein	K13211	GCFC; GC-rich sequence DNA-binding factor
	Putative DNA-binding protein	K14435	CHD5; chromodomain-helicase-DNA-binding protein 5 (EC:3.6.4.12)
	Putative DNA-binding protein	K14436	CHD6; chromodomain-helicase-DNA-binding protein 6 (EC:3.6.4.12)
	Putative DNA-binding protein	K14437	CHD7; chromodomain-helicase-DNA-binding protein 7 (EC:3.6.4.12)
	Putative DNA-binding protein	K14438	CHD9; chromodomain-helicase-DNA-binding protein 9 (EC:3.6.4.12)
	Putative DNA-binding protein	K14507	ORCA2_3; AP2-domain DNA-binding protein ORCA2/3
	Histone-like protein	K15719	NCOAT, MGEA5; protein O-GlcNAcase/histone acetyltransferase (EC:3.2.1.169 2.3.1.48)
	Putative DNA-binding protein	K16640	ssh7; DNA-binding protein 7 (EC:3.1.27.-)
	Putative DNA-binding protein	K17693	ID2; DNA-binding protein inhibitor ID2
	Putative DNA-binding protein	K17694	ID3; DNA-binding protein inhibitor ID3
	Putative DNA-binding protein	K17695	ID4; DNA-binding protein inhibitor ID4
	Putative DNA-binding protein	K17696	EMC; DNA-binding protein inhibitor ID, other
	Histone-like protein	K18710	SLBP; histone RNA hairpin-binding protein

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Putative DNA-binding protein	K18946	gp32, ssb; single-stranded DNA-binding protein
	Putative DNA-binding protein	K19442	ICP8, DBP, UL29; simplex virus major DNA-binding protein
	Histone-like protein	K19799	RPH1; DNA damage-responsive transcriptional repressor/[histone H3]-trimethyl-L-lysine36 demethylase (EC:1.14.11.69)
	Putative DNA-binding protein	K20091	CHD2; chromodomain-helicase-DNA-binding protein 2 (EC:3.6.4.12)
	Putative DNA-binding protein	K20092	CHD1L; chromodomain-helicase-DNA-binding protein 1-like (EC:3.6.4.12)
	Putative DNA-binding protein	K22592	AHDC1; AT-hook DNA-binding motif-containing protein 1
	Putative DNA-binding protein	K23225	SATB1; DNA-binding protein SATB1
	Putative DNA-binding protein	K23226	SATB2; DNA-binding protein SATB2
	Putative DNA-binding protein	K23600	TARDBP, TDP43; TAR DNA-binding protein 43
DNA repair	DNA polymerase PolA (COG0258)	K02320	POLA1; DNA polymerase alpha subunit A (EC:2.7.7.7)
	DNA polymerase PolA (COG0258)	K02321	POLA2; DNA polymerase alpha subunit B
	DNA polymerase PolA (COG0258)	K02335	polA; DNA polymerase I (EC:2.7.7.7)
	DNA polymerase IV	K02346	dinB; DNA polymerase IV (EC:2.7.7.7)
	Exodeoxyribonuclease VII	K03601	xseA; exodeoxyribonuclease VII large subunit (EC:3.1.11.6)
	Exodeoxyribonuclease VII	K03602	xseB; exodeoxyribonuclease VII small subunit (EC:3.1.11.6)
	DNA polymerase IV	K04479	dbh; DNA polymerase IV (archaeal DinB-like DNA polymerase) (EC:2.7.7.7)
	Exodeoxyribonuclease VII	K10906	recE; exodeoxyribonuclease VIII (EC:3.1.11.-)
	DNA polymerase IV	K10981	POL4; DNA polymerase IV (EC:2.7.7.7)
	DNA polymerase IV	K16250	NRPD1; DNA-directed RNA polymerase IV subunit 1 (EC:2.7.7.6)
	DNA polymerase IV	K16252	NRPD2, NRPE2; DNA-directed RNA polymerase IV and V subunit 2 (EC:2.7.7.6)
	DNA polymerase IV	K16253	NRPD7, NRPE7; DNA-directed RNA polymerase IV and V subunit 7
Lithotrophy	NiFe hydrogenase	K00437	hydB; [NiFe] hydrogenase large subunit (EC:1.12.2.1)
	NiFe hydrogenase	K02587	nifE; nitrogenase molybdenum-cofactor synthesis protein NifE
	CO-dehydrogenase CoxM & CoxS	K03518	coxS; aerobic carbon-monoxide dehydrogenase small subunit (EC:1.2.5.3)
	CO-dehydrogenase CoxM & CoxS	K03519	coxM, cutM; aerobic carbon-monoxide dehydrogenase medium subunit (EC:1.2.5.3)
	CO-dehydrogenase large subunit (coxL) Form I	K03520	coxL, cutL; aerobic carbon-monoxide dehydrogenase large subunit (EC:1.2.5.3)
	NiFe hydrogenase	K05586	hoxE; bidirectional [NiFe] hydrogenase diaphorase subunit (EC:7.1.1.2)
	NiFe hydrogenase	K05587	hoxF; bidirectional [NiFe] hydrogenase diaphorase subunit (EC:7.1.1.2)
	NiFe hydrogenase	K05588	hoxU; bidirectional [NiFe] hydrogenase diaphorase subunit (EC:7.1.1.2)
	SOX sulfur-oxidation system	K17218	sqr; sulfide:quinone oxidoreductase (EC:1.8.5.4)
	SOX sulfur-oxidation system	K17222	soxA; L-cysteine S-thiosulfotransferase (EC:2.8.5.2)
	SOX sulfur-oxidation system	K17223	soxX; L-cysteine S-thiosulfotransferase (EC:2.8.5.2)
	SOX sulfur-oxidation system	K17224	soxB; S-sulfosulfanyl-L-cysteine sulfohydrolase (EC:3.1.6.20)
	SOX sulfur-oxidation system	K17225	soxC; sulfane dehydrogenase subunit SoxC
	SOX sulfur-oxidation system	K17226	soxY; sulfur-oxidizing protein SoxY
	SOX sulfur-oxidation system	K17227	soxZ; sulfur-oxidizing protein SoxZ
	NiFe hydrogenase	K18005	hoxF; [NiFe] hydrogenase diaphorase moiety large subunit (EC:1.12.1.2)
	NiFe hydrogenase	K18006	hoxU; [NiFe] hydrogenase diaphorase moiety small subunit (EC:1.12.1.2)
	NiFe hydrogenase	K18008	hydA; [NiFe] hydrogenase small subunit (EC:1.12.2.1)

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Propane monooxygenase (soluble)	K18223	prmA; propane 2-monooxygenase large subunit (EC:1.14.13.227)
	Propane monooxygenase (soluble)	K18224	prmC; propane 2-monooxygenase small subunit (EC:1.14.13.227)
	Propane monooxygenase (soluble)	K18225	prmB; propane monooxygenase reductase component (EC:1.18.1.-)
	Propane monooxygenase (soluble)	K18226	prmD; propane monooxygenase coupling protein
	SOX sulfur-oxidation system	K22622	soxD; S-disulfanyl-L-cysteine oxidoreductase SoxD (EC:1.8.2.6)
	SOX sulfur-oxidation system	K24007	soxD; cytochrome aa3-type oxidase subunit SoxD
	SOX sulfur-oxidation system	K24008	soxC; cytochrome aa3-type oxidase subunit III
	SOX sulfur-oxidation system	K24009	soxB; cytochrome aa3-type oxidase subunit I (EC:7.1.1.4)
	SOX sulfur-oxidation system	K24010	soxA; cytochrome aa3-type oxidase subunit II (EC:7.1.1.4)
	SOX sulfur-oxidation system	K24011	soxM; cytochrome aa3-type oxidase subunit I/III (EC:7.1.1.4)
Organotrophy	ABC sugar transporters	K02025	ABC.MS.P; multiple sugar transport system permease protein
	ABC sugar transporters	K02026	ABC.MS.P1; multiple sugar transport system permease protein
	ABC sugar transporters	K02027	ABC.MS.S; multiple sugar transport system substrate-binding protein
	ABC sugar transporters	K02056	ABC.SS.A; simple sugar transport system ATP-binding protein (EC:7.5.2.-)
	ABC sugar transporters	K02057	ABC.SS.P; simple sugar transport system permease protein
	ABC sugar transporters	K02058	ABC.SS.S; simple sugar transport system substrate-binding protein
	PTS sugar importers	K02777	crr; sugar PTS system EIIA component (EC:2.7.1.-)
	Amino acid transporter	K03293	TC.AAT; amino acid transporter, AAT family
	Peptide transporter	K03305	TC.POT; proton-dependent oligopeptide transporter, POT family
	Amino acid transporter	K03311	TC.LIVCS; branched-chain amino acid:cation transporter, LIVCS family
	Carboxylate transporters	K03326	TC.DCUC, dcuC, dcuD; C4-dicarboxylate transporter, DcuC family
	Amino acid transporter	K03450	SLC7A; solute carrier family 7 (L-type amino acid transporter), other
	Glycosyl hydrolases	K04844	ycjT; hypothetical glycosyl hydrolase (EC:3.2.1.-)
	Amino acid transporter	K05048	SLC6A15S; solute carrier family 6 (neurotransmitter transporter, amino acid/orphan) member 15/16/17/18/20
	Amino acid transporter	K05615	SLC1A4, SATT; solute carrier family 1 (neutral amino acid transporter), member 4
	Amino acid transporter	K05616	SLC1A5; solute carrier family 1 (neutral amino acid transporter), member 5
	Amino acid transporter	K07084	yuiF; putative amino acid transporter
	Carboxylate transporters	K07791	dcuA; anaerobic C4-dicarboxylate transporter DcuA
	Carboxylate transporters	K07792	dcuB; anaerobic C4-dicarboxylate transporter DcuB
	ABC sugar transporters	K10546	ABC.GGU.S, chvE; putative multiple sugar transport system substrate-binding protein
	ABC sugar transporters	K10547	ABC.GGU.P, gguB; putative multiple sugar transport system permease protein
	ABC sugar transporters	K10548	ABC.GGU.A, gguA; putative multiple sugar transport system ATP-binding protein (EC:7.5.2.-)
	Carboxylate transporters	K11689	dctQ; C4-dicarboxylate transporter, DctQ subunit
	Carboxylate transporters	K11690	dctM; C4-dicarboxylate transporter, DctM subunit
	Amino acid transporter	K13576	SLC38A3, SNAT3; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 3
	Carboxylate transporters	K13577	SLC25A10, DIC; solute carrier family 25 (mitochondrial dicarboxylate transporter), member 10

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Amino acid transporter	K13780	SLC7A5, LAT1; solute carrier family 7 (L-type amino acid transporter), member 5
	Amino acid transporter	K13781	SLC7A8, LAT2; solute carrier family 7 (L-type amino acid transporter), member 8
	Amino acid transporter	K13782	SLC7A10, ASC1; solute carrier family 7 (L-type amino acid transporter), member 10
	Amino acid transporter	K13863	SLC7A1, ATRC1; solute carrier family 7 (cationic amino acid transporter), member 1
	Amino acid transporter	K13864	SLC7A2, ATRC2; solute carrier family 7 (cationic amino acid transporter), member 2
	Amino acid transporter	K13865	SLC7A3, ATRC3; solute carrier family 7 (cationic amino acid transporter), member 3
	Amino acid transporter	K13866	SLC7A4; solute carrier family 7 (cationic amino acid transporter), member 4
	Amino acid transporter	K13867	SLC7A7; solute carrier family 7 (L-type amino acid transporter), member 7
	Amino acid transporter	K13868	SLC7A9, BAT1; solute carrier family 7 (L-type amino acid transporter), member 9
	Amino acid transporter	K13869	SLC7A11; solute carrier family 7 (L-type amino acid transporter), member 11
	Amino acid transporter	K13870	SLC7A13, AGT1; solute carrier family 7 (L-type amino acid transporter), member 13
	Amino acid transporter	K13871	SLC7A14; solute carrier family 7 (cationic amino acid transporter), member 14
	Amino acid transporter	K13872	SLC7A6; solute carrier family 7 (L-type amino acid transporter), member 6
	Peptide transporter	K14206	SLC15A1, PEPT1; solute carrier family 15 (oligopeptide transporter), member 1
	Amino acid transporter	K14207	SLC38A2, SNAT2; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 2
	Amino acid transporter	K14209	SLC36A, PAT; solute carrier family 36 (proton-coupled amino acid transporter)
	Amino acid transporter	K14210	SLC3A1, RBAT; solute carrier family 3 (neutral and basic amino acid transporter), member 1
	Carboxylate transporters	K14388	SLC5A8_12, SMCT; solute carrier family 5 (sodium-coupled monocarboxylate transporter), member 8/12
	Carboxylate transporters	K14445	SLC13A2_3_5; solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5
	Peptide transporter	K14637	SLC15A2, PEPT2; solute carrier family 15 (oligopeptide transporter), member 2
	Peptide transporter	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
	Amino acid transporter	K14990	SLC38A1, SNAT1, GLNT; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 1
	Amino acid transporter	K14991	SLC38A4, SNAT4; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 4
	Amino acid transporter	K14992	SLC38A5, SNAT5; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 5
	Amino acid transporter	K14993	SLC38A6, SNAT6; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 6
	Amino acid transporter	K14994	SLC38A7_8; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 7/8
	Amino acid transporter	K14995	SLC38A9; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 9
	Amino acid transporter	K14996	SLC38A10; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 10
	Amino acid transporter	K14997	SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11
	Amino acid transporter	K15015	SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)
	Carboxylate transporters	K15110	SLC25A21, ODC; solute carrier family 25 (mitochondrial 2-oxodicarboxylate transporter), member 21

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Amino acid transporter	K16261	YAT; yeast amino acid transporter
	Amino acid transporter	K16263	yjeH; amino acid efflux transporter
	Peptide transporter	K17938	sbmA, bacA; peptide/bleomycin uptake transporter
Phototrophy	RuBisCO	K01601	rbcL; ribulose-bisphosphate carboxylase large chain (EC:4.1.1.39)
	Chlorophyll synthesis	K01669	phrB; deoxyribodipyrimidine photo-lyase (EC:4.1.99.3)
	Chlorophyll synthesis	K02689	psaA; photosystem I P700 chlorophyll *a* apoprotein A1
	Chlorophyll synthesis	K02690	psaB; photosystem I P700 chlorophyll *a* apoprotein A2
	Chlorophyll synthesis	K02691	psaC; photosystem I subunit VII
	Chlorophyll synthesis	K02692	psaD; photosystem I subunit II
	Chlorophyll synthesis	K02693	psaE; photosystem I subunit IV
	Chlorophyll synthesis	K02694	psaF; photosystem I subunit III
	Chlorophyll synthesis	K02695	psaH; photosystem I subunit VI
	Chlorophyll synthesis	K02696	psaI; photosystem I subunit VIII
	Chlorophyll synthesis	K02697	psaJ; photosystem I subunit IX
	Chlorophyll synthesis	K02698	psaK; photosystem I subunit X
	Chlorophyll synthesis	K02699	psaL; photosystem I subunit XI
	Chlorophyll synthesis	K02700	psaM; photosystem I subunit XII
	Chlorophyll synthesis	K02701	psaN; photosystem I subunit PsaN
	Chlorophyll synthesis	K02702	psaX; photosystem I 4.8kDa protein
	Chlorophyll synthesis	K02703	psbA; photosystem II P680 reaction centre D1 protein (EC:1.10.3.9)
	Chlorophyll synthesis	K02704	psbB; photosystem II CP47 chlorophyll apoprotein
	Chlorophyll synthesis	K02705	psbC; photosystem II CP43 chlorophyll apoprotein
	Chlorophyll synthesis	K02706	psbD; photosystem II P680 reaction centre D2 protein (EC:1.10.3.9)
	Chlorophyll synthesis	K02707	psbE; photosystem II cytochrome b559 subunit alpha
	Chlorophyll synthesis	K02708	psbF; photosystem II cytochrome b559 subunit beta
	Chlorophyll synthesis	K02709	psbH; photosystem II PsbH protein
	Chlorophyll synthesis	K02710	psbI; photosystem II PsbI protein
	Chlorophyll synthesis	K02711	psbJ; photosystem II PsbJ protein
	Chlorophyll synthesis	K02712	psbK; photosystem II PsbK protein
	Chlorophyll synthesis	K02713	psbL; photosystem II PsbL protein
	Chlorophyll synthesis	K02714	psbM; photosystem II PsbM protein
	Chlorophyll synthesis	K02716	psbO; photosystem II oxygen-evolving enhancer protein 1
	Chlorophyll synthesis	K02717	psbP; photosystem II oxygen-evolving enhancer protein 2
	Chlorophyll synthesis	K02718	psbT; photosystem II PsbT protein
	Chlorophyll synthesis	K02719	psbU; photosystem II PsbU protein
	Chlorophyll synthesis	K02720	psbV; photosystem II cytochrome c550
	Chlorophyll synthesis	K02721	psbW; photosystem II PsbW protein
	Chlorophyll synthesis	K02722	psbX; photosystem II PsbX protein
	Chlorophyll synthesis	K02723	psbY; photosystem II PsbY protein
	Chlorophyll synthesis	K02724	psbZ; photosystem II PsbZ protein
	Chlorophyll synthesis	K03157	LTB, TNFC; lymphotoxin beta (TNF superfamily, member 3)
	Chlorophyll synthesis	K03159	TNFRSF3, LTBR; lymphotoxin beta receptor TNFR superfamily member 3
	Chlorophyll synthesis	K03541	psbR; photosystem II 10kDa protein
	Chlorophyll synthesis	K03542	psbS; photosystem II 22kDa protein
	Chlorophyll synthesis	K03716	splB; spore photoproduct lyase (EC:4.1.99.14)
	Chlorophyll synthesis	K05468	LTA, TNFB; lymphotoxin alpha (TNF superfamily, member 1)
	Chlorophyll synthesis	K06315	splA; transcriptional regulator of the spore photoproduct lyase operon
	Chlorophyll synthesis	K06876	K06876; deoxyribodipyrimidine photolyase-related protein
	Chlorophyll synthesis	K08901	psbQ; photosystem II oxygen-evolving enhancer protein 3

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Chlorophyll synthesis	K08902	psb27; photosystem II Psb27 protein
	Chlorophyll synthesis	K08903	psb28; photosystem II 13kDa protein
	Chlorophyll synthesis	K08904	psb28-2; photosystem II Psb28-2 protein
	Chlorophyll synthesis	K08905	psaG; photosystem I subunit V
	Chlorophyll synthesis	K08928	pufL; photosynthetic reaction centre L subunit
	Chlorophyll synthesis	K08929	pufM; photosynthetic reaction centre M subunit
	Chlorophyll synthesis	K08940	pscA; photosystem P840 reaction centre large subunit
	Chlorophyll synthesis	K08941	pscB; photosystem P840 reaction centre iron–sulfur protein
	Chlorophyll synthesis	K08942	pscC; photosystem P840 reaction centre cytochrome c551
	Chlorophyll synthesis	K08943	pscD; photosystem P840 reaction centre protein PscD
	Chlorophyll synthesis	K11524	pixI; positive phototaxis protein PixI
	Chlorophyll synthesis	K13991	puhA; photosynthetic reaction centre H subunit
	Chlorophyll synthesis	K13992	pufC; photosynthetic reaction centre cytochrome c subunit
	Chlorophyll synthesis	K13994	pufX; photosynthetic reaction centre PufX protein
	Chlorophyll synthesis	K14332	psaO; photosystem I subunit PsaO
	Chlorophyll synthesis	K19016	IMPG1, SPACR; interphotoreceptor matrix proteoglycan 1
	Chlorophyll synthesis	K19017	IMPG2, SPACRCAN; interphotoreceptor matrix proteoglycan 2
	Chlorophyll synthesis	K20715	PHOT; phototropin (EC:2.7.11.1)
	Chlorophyll synthesis	K22464	FAP; fatty acid photodecarboxylase (EC:4.1.1.106)
	Chlorophyll synthesis	K22619	Aequorin; calcium-regulated photoprotein (EC:1.13.12.24)
	Chlorophyll synthesis	K24165	PCARE; photoreceptor cilium actin regulator
ROS-damage prevention	Cytochrome C oxidase	K00404	ccoN; cytochrome c oxidase cbb3-type subunit I (EC:7.1.1.9)
	Cytochrome C oxidase	K00405	ccoO; cytochrome c oxidase cbb3-type subunit II
	Cytochrome C oxidase	K00406	ccoP; cytochrome c oxidase cbb3-type subunit III
	Cytochrome C oxidase	K00407	ccoQ; cytochrome c oxidase cbb3-type subunit IV
	Cytochrome bd ubiquinol oxidase	K00424	cydX; cytochrome bd-I ubiquinol oxidase subunit X (EC:7.1.1.7)
	Cytochrome C oxidase	K00424	cydX; cytochrome bd-I ubiquinol oxidase subunit X (EC:7.1.1.7)
	Cytochrome bd ubiquinol oxidase	K00425	cydA; cytochrome bd ubiquinol oxidase subunit I (EC:7.1.1.7)
	Cytochrome C oxidase	K00425	cydA; cytochrome bd ubiquinol oxidase subunit I (EC:7.1.1.7)
	Cytochrome bd ubiquinol oxidase	K00426	cydB; cytochrome bd ubiquinol oxidase subunit II (EC:7.1.1.7)
	Cytochrome C oxidase	K00426	cydB; cytochrome bd ubiquinol oxidase subunit II (EC:7.1.1.7)
	Cytochrome C oxidase	K00428	E1.11.1.5; cytochrome c peroxidase (EC:1.11.1.5)
	Cytochrome C oxidase	K02256	COX1; cytochrome c oxidase subunit 1 (EC:7.1.1.9)
	Cytochrome C oxidase	K02258	COX11, ctaG; cytochrome c oxidase assembly protein subunit 11
	Cytochrome C oxidase	K02259	COX15, ctaA; cytochrome c oxidase assembly protein subunit 15
	Cytochrome C oxidase	K02260	COX17; cytochrome c oxidase assembly protein subunit 17
	Cytochrome C oxidase	K02261	COX2; cytochrome c oxidase subunit 2
	Cytochrome C oxidase	K02262	COX3; cytochrome c oxidase subunit 3
	Cytochrome C oxidase	K02263	COX4; cytochrome c oxidase subunit 4
	Cytochrome C oxidase	K02264	COX5A; cytochrome c oxidase subunit 5a
	Cytochrome C oxidase	K02265	COX5B; cytochrome c oxidase subunit 5b
	Cytochrome C oxidase	K02266	COX6A; cytochrome c oxidase subunit 6a
	Cytochrome C oxidase	K02267	COX6B; cytochrome c oxidase subunit 6b
	Cytochrome C oxidase	K02268	COX6C; cytochrome c oxidase subunit 6c

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Cytochrome C oxidase	K02269	COX7; cytochrome c oxidase subunit 7
	Cytochrome C oxidase	K02270	COX7A; cytochrome c oxidase subunit 7a
	Cytochrome C oxidase	K02271	COX7B; cytochrome c oxidase subunit 7b
	Cytochrome C oxidase	K02272	COX7C; cytochrome c oxidase subunit 7c
	Cytochrome C oxidase	K02273	COX8; cytochrome c oxidase subunit 8
	Cytochrome C oxidase	K02274	coxA, ctaD; cytochrome c oxidase subunit I (EC:7.1.1.9)
	Cytochrome C oxidase	K02275	coxB, ctaC; cytochrome c oxidase subunit II (EC:7.1.1.9)
	Cytochrome C oxidase	K02276	coxC, ctaE; cytochrome c oxidase subunit III (EC:7.1.1.9)
	Cytochrome C oxidase	K02277	coxD, ctaF; cytochrome c oxidase subunit IV (EC:7.1.1.9)
	Cytochrome C oxidase	K02297	cyoA; cytochrome o ubiquinol oxidase subunit II (EC:7.1.1.3)
	Cytochrome C oxidase	K02298	cyoB; cytochrome o ubiquinol oxidase subunit I (EC:7.1.1.3)
	Cytochrome C oxidase	K02299	cyoC; cytochrome o ubiquinol oxidase subunit III
	Cytochrome C oxidase	K02300	cyoD; cytochrome o ubiquinol oxidase subunit IV
	Cytochrome C oxidase	K02826	qoxA; cytochrome aa3-600 menaquinol oxidase subunit II (EC:7.1.1.5)
	Cytochrome C oxidase	K02827	qoxB; cytochrome aa3-600 menaquinol oxidase subunit I (EC:7.1.1.5)
	Cytochrome C oxidase	K02828	qoxC; cytochrome aa3-600 menaquinol oxidase subunit III (EC:7.1.1.5)
	Cytochrome C oxidase	K02829	qoxD; cytochrome aa3-600 menaquinol oxidase subunit IV (EC:7.1.1.5)
	Mn2+ catalase	K07217	K07217; Mn-containing catalase
	Cytochrome C oxidase	K15408	coxAC; cytochrome c oxidase subunit I+III (EC:7.1.1.9)
	Cytochrome C oxidase	K15862	ccoNO; cytochrome c oxidase cbb3-type subunit I/II (EC:7.1.1.9)
	Cytochrome C oxidase	K18173	COA1; cytochrome c oxidase assembly factor 1
	Cytochrome C oxidase	K18174	COA2; cytochrome c oxidase assembly factor 2
	Cytochrome C oxidase	K18175	CCDC56, COA3; cytochrome c oxidase assembly factor 3, animal type
	Cytochrome C oxidase	K18176	COA3; cytochrome c oxidase assembly factor 3, fungi type
	Cytochrome C oxidase	K18177	COA4; cytochrome c oxidase assembly factor 4
	Cytochrome C oxidase	K18178	COA5, PET191; cytochrome c oxidase assembly factor 5
	Cytochrome C oxidase	K18179	COA6; cytochrome c oxidase assembly factor 6
	Cytochrome C oxidase	K18180	COA7, SELRC1, RESA1; cytochrome c oxidase assembly factor 7
	Cytochrome C oxidase	K18181	COX14; cytochrome c oxidase assembly factor 14
	Cytochrome C oxidase	K18182	COX16; cytochrome c oxidase assembly protein subunit 16
	Cytochrome C oxidase	K18183	COX19; cytochrome c oxidase assembly protein subunit 19
	Cytochrome C oxidase	K18184	COX20; cytochrome c oxidase assembly protein subunit 20
	Cytochrome C oxidase	K18185	COX23; cytochrome c oxidase assembly protein subunit 23
	Cytochrome C oxidase	K18189	TACO1; translational activator of cytochrome c oxidase 1
	Cytochrome bd ubiquinol oxidase	K22501	appX; cytochrome bd-II ubiquinol oxidase subunit AppX (EC:7.1.1.7)
	Cytochrome C oxidase	K22501	appX; cytochrome bd-II ubiquinol oxidase subunit AppX (EC:7.1.1.7)
	Cytochrome C oxidase	K24007	soxD; cytochrome aa3-type oxidase subunit SoxD
	Cytochrome C oxidase	K24008	soxC; cytochrome aa3-type oxidase subunit III
	Cytochrome C oxidase	K24009	soxB; cytochrome aa3-type oxidase subunit I (EC:7.1.1.4)
	Cytochrome C oxidase	K24010	soxA; cytochrome aa3-type oxidase subunit II (EC:7.1.1.4)
	Cytochrome C oxidase	K24011	soxM; cytochrome aa3-type oxidase subunit I/III (EC:7.1.1.4)
Sporulation	Glycogen synthesis	K00693	GYS; glycogen synthase (EC:2.4.1.11)
	Sporulation (Actinobacteria)	K02490	spo0F; two-component system, response regulator, stage 0 sporulation protein F
	Sporulation (Actinobacteria)	K02491	kinA; two-component system, sporulation sensor kinase A (EC:2.7.13.3)
	Glycogen synthesis	K03083	GSK3B; glycogen synthase kinase 3 beta (EC:2.7.11.26)
	Sporulation (Actinobacteria)	K03091	sigH; RNA polymerase sporulation-specific sigma factor
	Sporulation (Actinobacteria)	K04769	spoVT; AbrB family transcriptional regulator, stage V sporulation protein T
	Sporulation (Actinobacteria)	K06283	spoIIID; putative DeoR family transcriptional regulator, stage III sporulation protein D
	Sporulation (Actinobacteria)	K06348	kapD; sporulation inhibitor KapD

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Sporulation (Actinobacteria)	K06359	rapA, spo0L; response regulator aspartate phosphatase A (stage 0 sporulation protein L) (EC:3.1.-.-)
	Sporulation (Actinobacteria)	K06371	sda; developmental checkpoint coupling sporulation initiation to replication initiation
	Sporulation (Actinobacteria)	K06375	spo0B; stage 0 sporulation protein B (sporulation initiation phosphotransferase) (EC:2.7.-.-)
	Sporulation (Actinobacteria)	K06376	spo0E; stage 0 sporulation regulatory protein
	Sporulation (Actinobacteria)	K06377	spo0M; sporulation-barren protein
	Sporulation (Actinobacteria)	K06378	spoIIAA; stage II sporulation protein AA (anti-sigma F factor antagonist)
	Sporulation (Actinobacteria)	K06379	spoIIAB; stage II sporulation protein AB (anti-sigma F factor) (EC:2.7.11.1)
	Sporulation (Actinobacteria)	K06380	spoIIB; stage II sporulation protein B
	Sporulation (Actinobacteria)	K06381	spoIID; stage II sporulation protein D
	Sporulation (Actinobacteria)	K06382	spoIIE; stage II sporulation protein E (EC:3.1.3.16)
	Sporulation (Actinobacteria)	K06383	spoIIGA; stage II sporulation protein GA (sporulation sigma-E factor processing peptidase) (EC:3.4.23.-)
	Sporulation (Actinobacteria)	K06384	spoIIM; stage II sporulation protein M
	Sporulation (Actinobacteria)	K06385	spoIIP; stage II sporulation protein P
	Sporulation (Actinobacteria)	K06386	spoIIQ; stage II sporulation protein Q
	Sporulation (Actinobacteria)	K06387	spoIIR; stage II sporulation protein R
	Sporulation (Actinobacteria)	K06388	spoIISA; stage II sporulation protein SA
	Sporulation (Actinobacteria)	K06389	spoIISB; stage II sporulation protein SB
	Sporulation (Actinobacteria)	K06390	spoIIIAA; stage III sporulation protein AA
	Sporulation (Actinobacteria)	K06391	spoIIIAB; stage III sporulation protein AB
	Sporulation (Actinobacteria)	K06392	spoIIIAC; stage III sporulation protein AC
	Sporulation (Actinobacteria)	K06393	spoIIIAD; stage III sporulation protein AD
	Sporulation (Actinobacteria)	K06394	spoIIIAE; stage III sporulation protein AE
	Sporulation (Actinobacteria)	K06395	spoIIIAF; stage III sporulation protein AF
	Sporulation (Actinobacteria)	K06396	spoIIIAG; stage III sporulation protein AG
	Sporulation (Actinobacteria)	K06397	spoIIIAH; stage III sporulation protein AH
	Sporulation (Actinobacteria)	K06398	spoIVA; stage IV sporulation protein A
	Sporulation (Actinobacteria)	K06399	spoIVB; stage IV sporulation protein B (EC:3.4.21.116)
	Sporulation (Actinobacteria)	K06401	spoIVFA; stage IV sporulation protein FA
	Sporulation (Actinobacteria)	K06402	spoIVFB; stage IV sporulation protein FB (EC:3.4.24.-)
	Sporulation (Actinobacteria)	K06403	spoVAA; stage V sporulation protein AA
	Sporulation (Actinobacteria)	K06404	spoVAB; stage V sporulation protein AB
	Sporulation (Actinobacteria)	K06405	spoVAC; stage V sporulation protein AC
	Sporulation (Actinobacteria)	K06406	spoVAD; stage V sporulation protein AD
	Sporulation (Actinobacteria)	K06407	spoVAE; stage V sporulation protein AE
	Sporulation (Actinobacteria)	K06408	spoVAF; stage V sporulation protein AF
	Sporulation (Actinobacteria)	K06409	spoVB; stage V sporulation protein B
	Sporulation (Actinobacteria)	K06412	spoVG; stage V sporulation protein G
	Sporulation (Actinobacteria)	K06413	spoVK; stage V sporulation protein K
	Sporulation (Actinobacteria)	K06414	spoVM; stage V sporulation protein M
	Sporulation (Actinobacteria)	K06415	spoVR; stage V sporulation protein R
	Sporulation (Actinobacteria)	K06416	spoVS; stage V sporulation protein S
	Sporulation (Actinobacteria)	K06417	spoVID; stage VI sporulation protein D
	Sporulation (Actinobacteria)	K06437	yknT; sigma-E barren-led sporulation protein
	Sporulation (Actinobacteria)	K06438	yqfD; similar to stage IV sporulation protein
	Sporulation (Actinobacteria)	K07697	kinB; two-component system, sporulation sensor kinase B (EC:2.7.13.3)
	Sporulation (Actinobacteria)	K07698	kinC; two-component system, sporulation sensor kinase C (EC:2.7.13.3)
	Sporulation (Actinobacteria)	K07699	spo0A; two-component system, response regulator, stage 0 sporulation protein A
	Sporulation (Actinobacteria)	K08293	SMK1; sporulation-specific mitogen-activated protein kinase SMK1 (EC:2.7.11.24)
	Sporulation (Actinobacteria)	K08384	spoVD; stage V sporulation protein D (sporulation-specific penicillin-binding protein)
	Glycogen synthesis	K08822	GSK3A; glycogen synthase kinase 3 alpha (EC:2.7.11.26)

Table A7. Continued.

Group	Metabolic trait	KEGG_ID	Function
	Sporulation (Actinobacteria)	K12576	SPO12; sporulation-specific protein 12
	Sporulation (Actinobacteria)	K12771	SPA; sporulation-specific protein 1 (EC:2.7.11.1)
	Sporulation (Actinobacteria)	K12772	SPD; sporulation-specific protein 4
	Sporulation (Actinobacteria)	K12773	SPR3; sporulation-regulated protein 3
	Sporulation (Actinobacteria)	K12783	SSP1; sporulation-specific protein 1
	Sporulation (Actinobacteria)	K13532	kinD; two-component system, sporulation sensor kinase D (EC:2.7.13.3)
	Sporulation (Actinobacteria)	K13533	kinE; two-component system, sporulation sensor kinase E (EC:2.7.13.3)
	Glycogen synthesis	K16150	K16150; glycogen synthase (EC:2.4.1.11)
	Exopolysaccharide synthesis	K16566	exoY; exopolysaccharide production protein ExoY
	Exopolysaccharide synthesis	K16567	exoQ; exopolysaccharide production protein ExoQ
	Exopolysaccharide synthesis	K16568	exoZ; exopolysaccharide production protein ExoZ
	Sporulation (Actinobacteria)	K16947	SPR28; sporulation-regulated protein 28
	Glycogen synthesis	K20812	glgA; glycogen synthase (EC:2.4.1.242)

Table A8. Abundance (in copy number (CN)) of each patch type within each group of gene.

Group	Patch type	Abundance (in CN)
DNA conservation	Barren	16 153.38
DNA conservation	Nest	47 287.31
DNA conservation	Shrub	46 252.92
DNA conservation	Shrub & Nest	30 860.48
DNA repair and degradation	Barren	12 091.56
DNA repair and degradation	Nest	27 516.74
DNA repair and degradation	Shrub	27 102.20
DNA repair and degradation	Shrub & Nest	20 810.48
Lithotrophs	Barren	11 856.26
Lithotrophs	Nest	73 242.15
Lithotrophs	Shrub	65 602.91
Lithotrophs	Shrub & Nest	29 183.05
Nitrogen	Barren	14 971.68
Nitrogen	Nest	29 265.84
Nitrogen	Shrub	30 326.47
Nitrogen	Shrub & Nest	25 184.32
Organotrophs	Barren	69 296.86
Organotrophs	Nest	16 1271.21
Organotrophs	Shrub	15 0159.89
Organotrophs	Shrub & Nest	90 170.34
Phototrophy	Barren	6949.817
Phototrophy	Nest	17 722.912
Phototrophy	Shrub	19 736.83
Phototrophy	Shrub & Nest	15 555.43
ROS-damage prevention	Barren	33 660.03
ROS-damage prevention	Nest	93 064.68
ROS-damage prevention	Shrub	88 543.76
ROS-damage prevention	Shrub & Nest	60 566.25
Sporulation capsule & C storage	Barren	2129.44
Sporulation capsule & C storage	Nest	14 338.20
Sporulation capsule & C storage	Shrub	12 904.33
Sporulation capsule & C storage	Shrub & Nest	5514.04

Table A9. Chi-square values and p values of the Dunn tests between patches done on the functional prediction results. Bold numbers are significant (< 0.05).

Comparisons	Nitrogen	ROS-damage	Sporulation	Phototrophy
Barren–Nest	**0.0278**	**0.0046**	**0.0014**	**0.0207**
Control–Shrub	**0.0271**	**0.0212**	**0.0073**	**0.0235**
Nest–Shrub	0.4790	0.2545	0.2623	0.4516
Barren–Shrub & Nest	**0.0140**	**0.0207**	**0.0421**	**0.0164**
Nest–Shrub & Nest	0.3888	0.2860	0.1046	0.4625
Shrub–Shrub & Nest	0.3653	0.4693	0.2545	0.4134
Chi-square	6.1179803	7.80073892	10.0155172	6.28472906
Comparisons	Organotrophy	DNA conservation	DNA repair	Lithotrophy
Barren–Nest	0.0513	**0.0038**	**0.0110**	**0.0066**
Barren–Shrub	0.2267	**0.0121**	**0.0227**	**0.0320**
Nest–Shrub	0.1746	0.3077	0.3577	0.2391
Barren–Shrub & Nest	0.2549	**0.0060**	**0.0085**	0.1165
Nest–Shrub & Nest	0.1653	0.4376	0.4625	0.0991
Shrub–Shrub & Nest	0.4725	0.3668	0.3221	0.2676
Chi-square	2.69926108	9.30837438	7.53793103	6.68743842

Table A10. Results of the adonis analysis of the impact of soil parameters on the bacterial community.

Soil parameter	R2	P value
NH_4^+	0.03383	0.451
pH	0.01542	0.948
NO_3^-	0.03141	0.512
OM	0.04244	0.263
Water	0.03851	0.355
P	0.03863	0.343

Appendix B

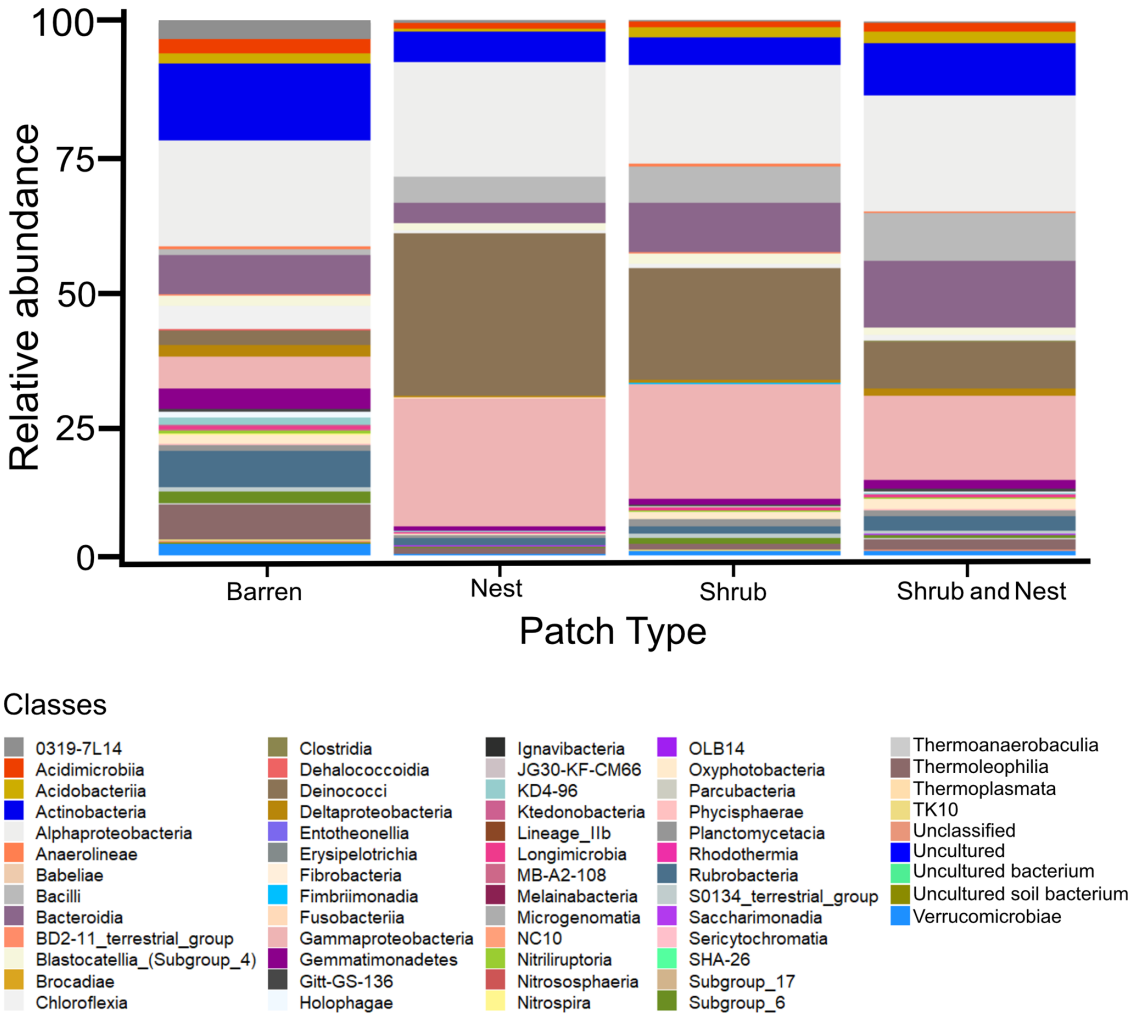

Figure B1. Bar plot of the relative abundance (%) of the most abundant classes in the soil microbial community in the dry season under different patch types (classes with a relative abundance > 0.05 %). The resolution is too low to draw significant conclusions.

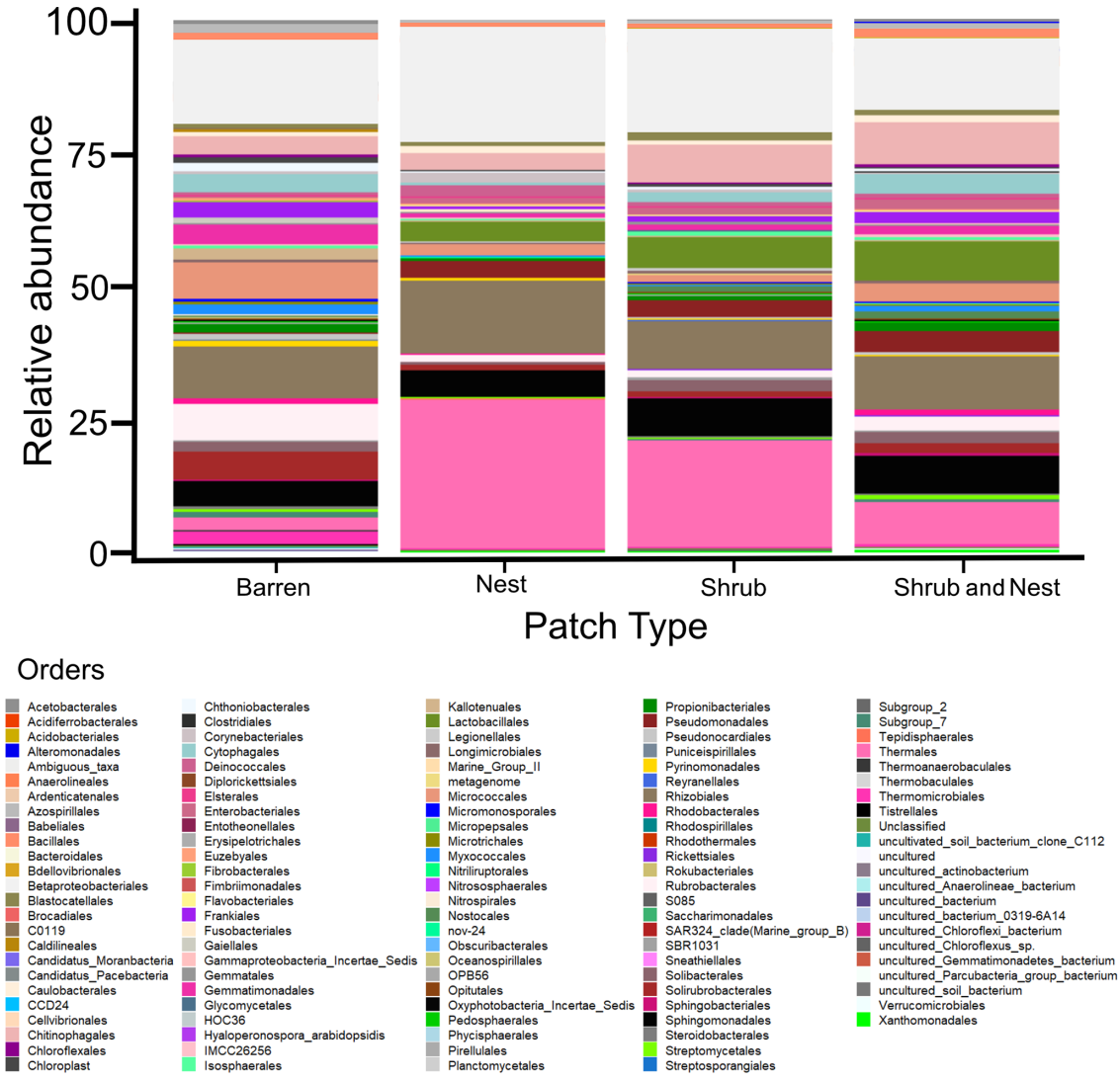

Figure B2. Bar plot of the relative abundance (%) of the most abundant orders in the soil microbial community in the dry season under different patch types (orders with a relative abundance > 0.05 %). The resolution is too low to draw significant conclusions.

Data availability. The data (raw reads) are available in BioProject under the submission number PRJNA484096 at https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA484096 (Baubin, 2018).

Author contributions. IG, OG, and AMF conceptualized and designed the methodology; AMF and AS collected the samples and metadata; LG and AMF did the laboratory work and sequencing; CB did the formal analysis, visualization, and data curation and wrote the manuscript; IG, OG, and CB did the reviewing and editing of the manuscript.

Competing interests. The authors declare that they have no conflict of interest.

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