

SUPPLEMENTARY MATERIAL

for

Argan and pine stands comparably improve soil organic matter levels and microbiome structure and function under semi-arid Mediterranean conditions.

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The supplementary material includes Figure S1-S4 and Table S1-S7.

Fig. S1. Representative pyrograms (Py-GC/MS) of total ion count (TIC) of SOM in soil influenced by argan or pine, and the bare soil, respectively. Labels on the chromatographic peaks identify the most abundant compounds. Selected ion chromatograms at m/z : 55 and 57 representing n -alkenes/alkanes, and m/z : 73 and 74 representing of the presence of n -fatty acids. s. Analytical pyrolysis was conducted as described in materials and methods. Lignin derived methoxyphenols: G, guaiacol; MG, methylguaiacol; EG, ethylguaiacol; VG, vinylguaiacol; AG, acetoguaiacol; SA, syringylacetone.

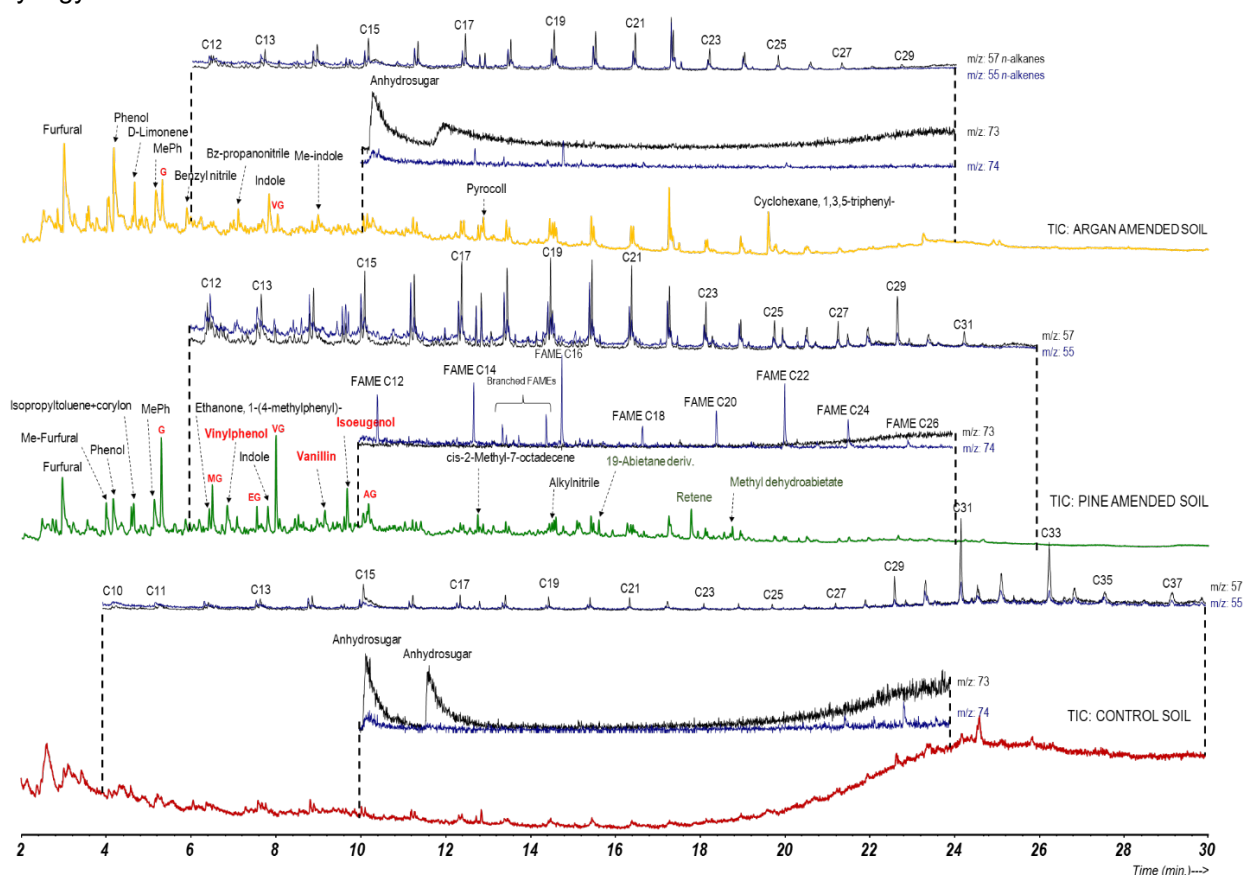


Fig. S2. Heatmap showing the relative abundance of the top-30 compounds, obtained by analytical pyrolysis, contributing the most to the differences between treatments according to SIMPER analysis. Compounds are ordered in decreasing contribution to the differences between treatments. Percentages to the right of each compound indicate the percent dissimilarity contributed by each compound. Different letters within the row of each compound indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA). Color legend and scale (%) are provided in the figure.

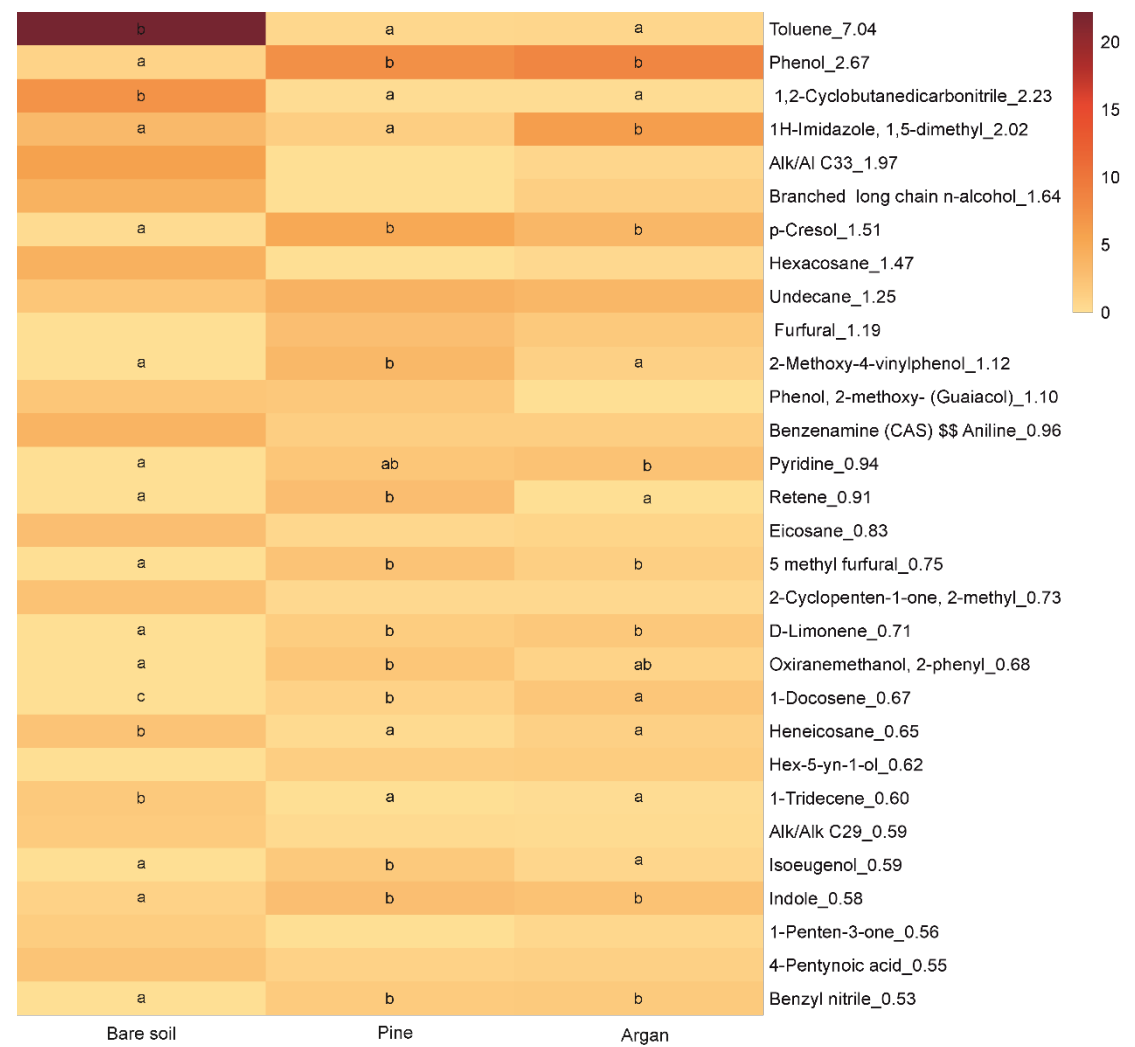


Fig. S3. Taxonomic (genus number) and functional (number of KEGG functional genes) richness in the bare soil and soil influenced by pine or argan, respectively, as determined by shotgun metagenomics. Different letters above each bar indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

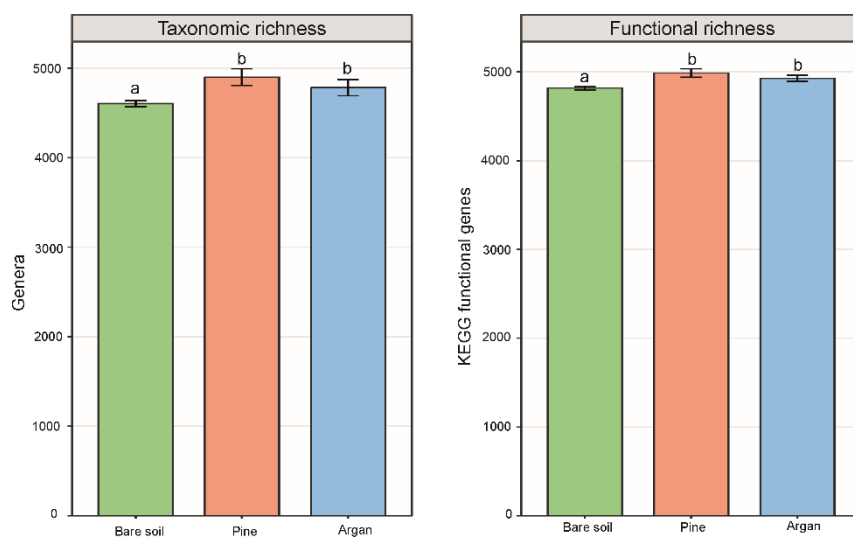


Fig. S4. Relative abundance of P cycling pathways categories showing significant differences between treatments. For each category, different letters above each bar indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

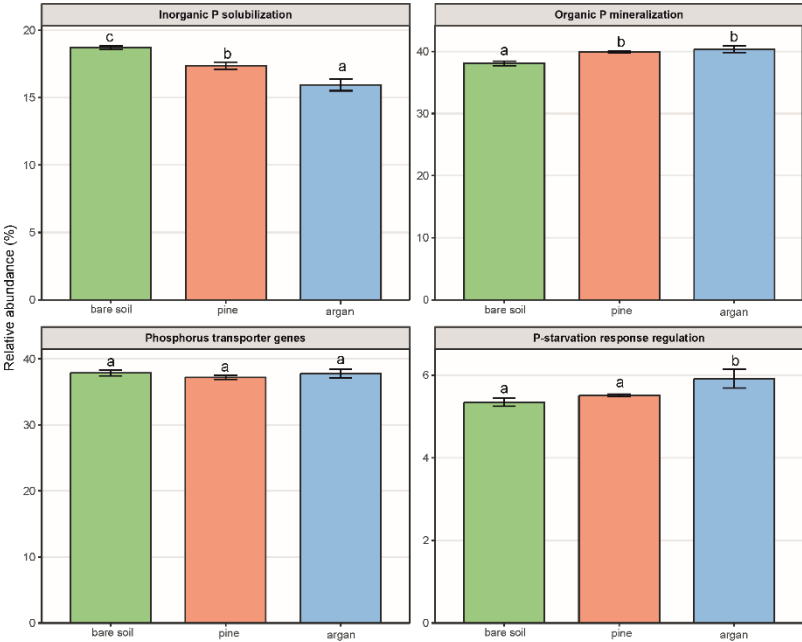


Table S1. Fatty acids used for the quantification of bacterial and fungal biomass.

Bacterial biomass	Fungal biomass
i15:0	18:2 ω 6,9t
a15:0	18:2 ω 6,9c
i16:0	
16:1 ω 9c	
10Me16:0	
i17:0	
cy17:0	
10Me18:0	
cy19:0	

Table S2. Total carbon, nitrogen and phosphorus contents in pine needles and argan leaves in spring season. Different letters within each row indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

	Total C (g/100g)	Total N (g/100g)	Total P (g/100g)	C/N	N/P	C:N:P ratio
Argan	45.43 a	2.11 b	0.07 b	21.53	30.14	649:30:1
Pine	51.28 b	0.96 a	0.05 a	53.42	19.2	1026:19:1

Table S3. Relative abundance (%) at domain level of the microbial communities in bare soil and soil influenced by pine or argan, respectively, as determined by shotgun metagenomics. Values are means (n=4) with the standard deviations in parentheses. Different letters within each row indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

Domain	Bare soil	Pine	Argan
Archaea	3.9885 (0.2034) b	2.3479 (0.3864) a	2.7285 (0.2375) a
Bacteria	95.8149 (0.2137) a	97.3651 (0.3583) b	97.078 (0.2406) b
Eukaryota	0.1927 (0.0112) a	0.271 (0.0598) b	0.1789 (0.0051) a
Viruses	0.0037 (0.0003) a	0.0158 (0.0055) b	0.0144 (0.0056) b

Table S4. Relative abundance (%) of the main bacterial, archaeal, and fungal phyla found in bare soil and soil influenced by pine or argan, respectively, as determined by shotgun metagenomics. Values are means (n=4) with the standard deviations in parentheses. Different letters within each row indicate significance of differences at p<0.05 (Tukey's HSD test and ANOVA).

Domain	Phylum	Bare soil	Pine	Argan
Bacteria	Actinobacteria	61.368 (0.323) a	61.966 (1.481) a	60.660 (0.253) a
Bacteria	Proteobacteria	18.164 (0.139) a	20.067 (1.290) b	20.170 (0.400) b
Bacteria	Chloroflexi	4.765 (0.023) b	3.718 (0.097) a	3.311 (0.081) a
Bacteria	Acidobacteria	2.384 (0.033) a	2.607 (0.143) b	2.774 (0.360) c
Bacteria	Gemmatimonadetes	2.086 (0.013) a	1.546 (0.288) a	2.553 (1.203) a
Bacteria	Planctomycetes	1.884 (0.011) a	2.095 (0.128) b	2.139 (0.105) b
Bacteria	Firmicutes	1.242 (0.016) b	1.138 (0.048) a	1.294 (0.061) b
Bacteria	Cyanobacteria	1.096 (0.023) b	0.933 (0.063) a	0.875 (0.028) a
Bacteria	Candidatus Tectomicrobia	0.625 (0.015) a	0.989 (0.151) b	0.798 (0.059) a
Bacteria	Bacteroidetes	0.562 (0.010) a	0.62 (0.036) b	0.630 (0.018) b
Bacteria	Nitrospirae	0.382 (0.004) a	0.43 (0.053) ab	0.463 (0.023) b
Bacteria	Verrucomicrobia	0.275 (0.005) a	0.297 (0.005) a	0.335 (0.029) b
Archaea	Thaumarchaeota	3.658 (0.199) b	2.063 (0.361) a	2.341 (0.325) a
Archaea	Euryarchaeota	0.291 (0.001) a	0.253 (0.022) a	0.297 (0.033) a
Eukaryota	Ascomycota	0.028 (0.001) a	0.080 (0.022) b	0.032 (0.001) a
Eukaryota	Basidiomycota	0.022 (0.001) a	0.056 (0.025) b	0.019 (0.007) a
Eukaryota	Mucoromycota	0.012 (0.001) a	0.012 (0.001) a	0.013 (0.001) a
Eukaryota	Streptophyta	0.068 (0.004) b	0.060 (0.016) ab	0.046 (0.006) a
Eukaryota	Arthropoda	0.012 (0.001) a	0.011 (0.001) a	0.014 (0.002) a
	Others	1.065 (0.013)	1.048 (0.065)	1.225 (0.155)

Table S5. Relative abundance (%) of the genera contributing the most to the differences among bare soil and soil influenced by pine or argan. Values are means (n=4) with the standard deviations in parentheses. Different letters within each row indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

Phylum	Genus	Bare soil	Pine	Argan
Actinobacteria	<i>Rubrobacter</i>	23.837 (0.077) c	13.424 (2.335) b	7.214 (3.391) a
Actinobacteria	<i>Solirubrobacter</i>	7.885 (0.142) a	10.077 (0.076) b	10.978 (0.334) c
Actinobacteria	<i>Thermoleophilum</i>	2.421 (0.031) a	3.104 (0.662) ab	4.109 (0.785) b
Actinobacteria	<i>Pseudonocardia</i>	2.272 (0.108) a	3.871 (0.604) b	2.612 (0.050) a
Actinobacteria	<i>Conexibacter</i>	3.814 (0.041) a	4.485 (0.460) a	5.381 (0.535) b
Thaumarchaeota	<i>Nitrososphaera</i>	2.772 (0.136) b	1.436 (0.299) a	1.580 (0.253) a
Actinobacteria	<i>Streptomyces</i>	1.416 (0.007) a	1.977 (0.059) b	2.724 (0.181) c
Actinobacteria	<i>Mycobacterium</i>	0.610 (0.015) a	1.85 (0.967) b	0.996 (0.022) ab
Actinobacteria	<i>Gaiella</i>	2.567 (0.052) ab	1.965 (0.547) a	3.086 (0.667) b
Actinobacteria	<i>Nocardioides</i>	1.331 (0.009) a	1.569 (0.226) a	2.561 (0.360) b
Chloroflexi	<i>Kallotenue</i>	1.869 (0.013) c	1.088 (0.139) b	0.689 (0.250) a
Actinobacteria	<i>Mycolicibacterium</i>	0.411 (0.015) a	1.388 (0.699) b	0.784 (0.015) ab
Proteobacteria	<i>Microvirga</i>	2.119 (0.016) b	1.521 (0.414) ab	1.275 (0.356) a
Proteobacteria	<i>Rubrivivax</i>	1.082 (0.015) b	0.463 (0.054) a	0.423 (0.148) a
Gemmatimonadetes	<i>Undefined Gemmatimonadetes</i>	0.840 (0.008) a	0.690 (0.126) a	1.278 (0.685) a
Acidobacteria	<i>Luteitalea</i>	0.842 (0.010) a	1.185 (0.062) b	1.347 (0.012) c
Actinobacteria	<i>Blastococcus</i>	1.099 (0.018) b	0.684 (0.119) a	0.631 (0.041) a
Actinobacteria	<i>Actinophytocola</i>	0.268 (0.015) a	0.718 (0.156) c	0.470 (0.071) b
Proteobacteria	<i>Mesorhizobium</i>	0.569 (0.028) a	0.896 (0.162) b	0.964 (0.073) b
Proteobacteria	<i>Steroidobacter</i>	0.187 (0.007) a	0.611 (0.124) b	0.371 (0.121) a

Table S6: Relative abundance of selected KEGG level 2 categories in bare soil, soil influenced by argan or pine, respectively, as determined by shotgun metagenomics. Values are means (n=4) with the standard deviations in parentheses. Different letters within each row indicate significance of differences at $p < 0.05$ (Tukey's HSD test and ANOVA).

KEGG Level 2	Bare soil	Pine	Argan
Protein families: signalling and cellular processes	6.359 (0.029) a	6.516 (0.030) b	6.586 (0.028) c
Amino acid metabolism	5.658 (0.011) a	5.614 (0.038) a	5.721 (0.008) b
Energy metabolism	3.362 (0.014) a	3.449 (0.039) b	3.484 (0.007) b
Membrane transport	2.482 (0.014) a	2.822 (0.122) b	2.836 (0.022) b
Lipid metabolism	1.799 (0.007) a	1.966 (0.057) b	1.936 (0.012) b
Glycan biosynthesis and metabolism	0.880 (0.009) a	0.929 (0.011) b	0.954 (0.012) c

Table S7: P cycling pathways and relative abundance of functional genes related to each pathway in bare soil, soil influenced by pine or argan, respectively, as determined by shotgun metagenomics. Values are means (n=4) with the standard deviations in parentheses. Different letters within each row indicate significance of differences at p<0.05 (Tukey's HSD test and ANOVA).

	Bare soil	Pine	Argan
Organic P mineralization			
<i>phoA</i>	1.8 (0.15)	1.63 (0.34)	1.29 (0.34)
<i>3-phytase</i>	1.29 (0.12) a	1.79 (0.31) ab	2.44 (0.56) b
<i>phoD</i>	12.83 (0.34) a	13.82 (0.41) b	13.59 (0.64) ab
<i>phoX</i>	12.03 (0.18)	11.8 (0.22)	11.93 (0.24)
<i>phnW</i>	0.2 (0.04) a	0.27 (0.04) ab	0.33 (0.07) b
<i>phnX</i>	0.08 (0.04)	0.11 (0.03)	0.14 (0.05)
<i>phnN</i>	0.09 (0.03)	0.07 (0.05)	0.06 (0.02)
<i>phnM</i>	0.49 (0.03)	0.73 (0.23)	0.62 (0.13)
<i>phnJ</i>	0.2 (0.03)	0.3 (0.09)	0.2 (0.04)
<i>phnI</i>	0.32 (0.07)	0.42 (0.15)	0.39 (0.08)
<i>phnH</i>	0.13 (0.04)	0.08 (0.03)	0.12 (0.03)
<i>phnG</i>	0.18 (0.04)	0.25 (0.1)	0.24 (0.04)
<i>phnP</i>	1.33 (0.09) b	1.1 (0.08) a	1.21 (0.11) ab
<i>phnA</i>	0.03 (0.01)	0.04 (0.02)	0.05 (0.03)
<i>Phosphotriesterase</i>	0.22 (0.03)	0.26 (0.07)	0.27 (0.08)
<i>phoN</i>	0.04 (0.01)	0.05 (0.03)	0.02 (0.01)
<i>ugpQ</i>	6.51 (0.13) a	6.93 (0.2) b	7.24 (0.2) b
<i>phnF</i>	0.06 (0.02)	0.04 (0.02)	0.04 (0.02)
<i>phnL</i>	0.09 (0.02)	0.07 (0.01)	0.09 (0.02)
<i>phnK</i>	0.16 (0.02)	0.16 (0.08)	0.12 (0.04)
Inorganic P solubilization			
<i>Ppa</i>	13.28 (0.16) c	11.73 (0.12) b	10.79 (0.36) a
<i>pqqC</i>	5.43 (0.07) b	5.64 (0.15) b	5.16 (0.09) a
P-starvation response regulation			
<i>phoR</i>	0.85 (0.09) c	0.62 (0.13) a	0.69 (0.06) b
<i>phoB</i>	0.02 (0.02)	0.03 (0.01)	0.05 (0.02)
<i>phoU</i>	4.48 (0.13) a	4.86 (0.1) b	5.17 (0.21) c
Phosphorus transporter genes			
<i>pstB</i>	7.89 (0.11) b	6.97 (0.16) a	7.55 (0.57) ab
<i>pstC</i>	3.21 (0.09) b	2.9 (0.15) a	3.12 (0.08) b
<i>pstA</i>	3.79 (0.13)	3.63 (0.23)	3.56 (0.1)
<i>pstS</i>	17.26 (0.49)	17.08 (0.47)	17.55 (0.75)
<i>phnE</i>	2.13 (0.23)	2.57 (0.72)	2.28 (0.15)
<i>ugpB</i>	0.39 (0.08)	0.36 (0.05)	0.32 (0.06)
<i>ugpA</i>	0.14 (0.02)	0.16 (0.02)	0.12 (0.03)
<i>ugpE</i>	0.2 (0.04)	0.19 (0.03)	0.24 (0.02)
<i>phnC</i>	0.43 (0.05) a	0.63 (0.09) b	0.39 (0.05) a
<i>phnD</i>	1.84 (0.12)	1.98 (0.34)	1.61 (0.21)
<i>Pit</i>	0.6 (0.04) a	0.73 (0.16) a	1.04 (0.02) b

