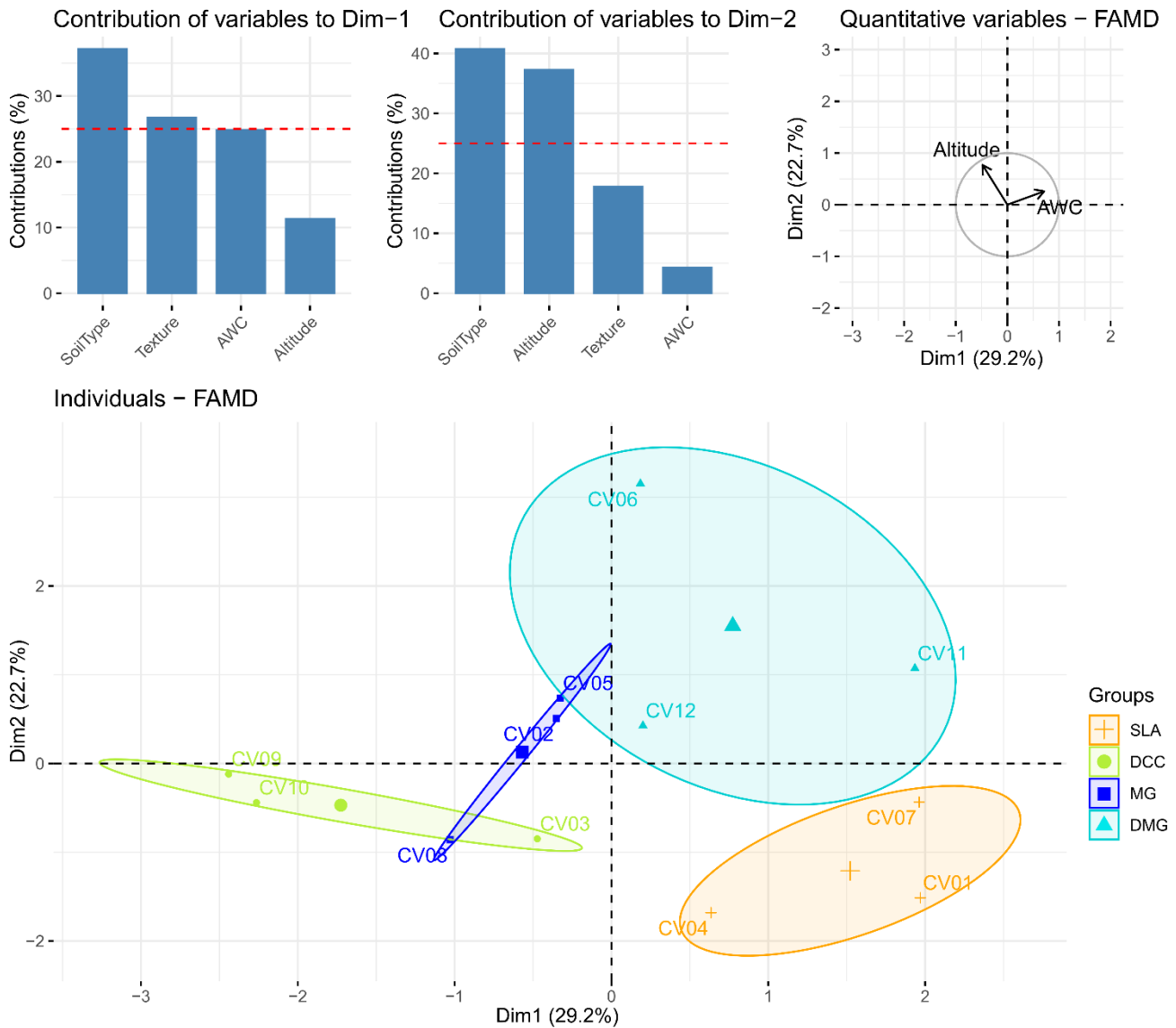


SUPPLEMENTARY DATA

Morelli, R., Zanzotti, R., Pindo, M., Donati, C., Cestaro, A., & Colter, E. (2025). Pedological origin and edaphic factors drive biota in vineyard soils of Northeast Italy. *OENO One*, 59(2).  
<https://doi.org/10.20870/oeno-one.2025.59.2.9288>

**Figure S1.** FAMD analysis of site characteristics in the four soil types investigated.



**SUPPLEMENTARY DATA**

Morelli, R., Zanzotti, R., Pindo, M., Donati, C., Cestaro, A., & Coller, E. (2025). Pedological origin and edaphic factors drive biota in vineyard soils of Northeast Italy. *OENO One*, 59(2).

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**Figure S2.** Geographical positions of the investigated sites from Google Earth Pro.



**SUPPLEMENTARY DATA**

Morelli, R., Zanzotti, R., Pindo, M., Donati, C., Cestaro, A., & Collier, E. (2025). Pedological origin and edaphic factors drive biota in vineyard soils of Northeast Italy. *OENO One*, 59(2).  
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**Table S1.** Geographical, meteorological (mean ± SD) and agronomic details of vineyards studied.

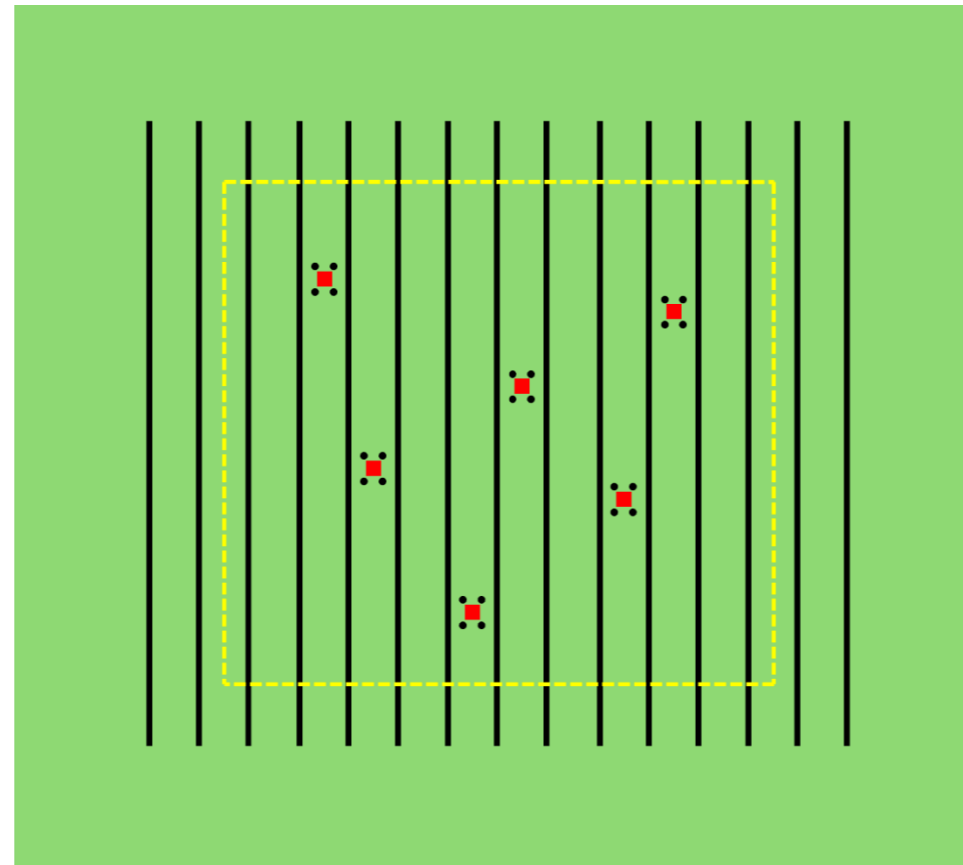
Site	Municipality	Soil type	Vineyard planting year	Agronomic management	Previous Crop	Texture	AWC (mm)	Altitude (mm a.l.s.)	Autumn		Winter		Spring		Summer	
									Rain (mm)	T <sub>mean</sub> (°C)	Rain (mm)	T <sub>mean</sub> (°C)	Rain (mm)	T <sub>mean</sub> (°C)	Rain (mm)	T <sub>mean</sub> (°C)
CV01	Roverè della Luna	SLA	1984	Integrated	Vineyard (V)	Silt loam	132	209	36.6 ± 3.7	12.7 ± 0.5	22.3 ± 3.0	2.7 ± 0.2	28.6 ± 2.8	13.9 ± 0.4	34.8 ± 3.0	22.5 ± 0.2
CV04	Zambana	SLA	2000	In conversion	Orchard (O)	Loam	132	201	41.3 ± 3.7	12.2 ± 0.5	26.0 ± 3.5	2.2 ± 0.2	27.2 ± 2.8	13.9 ± 0.4	34.0 ± 2.8	22.7 ± 0.2
CV07	Aldeno	SLA	2001	In conversion	Orchard (O)	Sandy loam	212	199	37.6 ± 3.4	12.1 ± 0.5	25.5 ± 3.4	2.5 ± 0.2	29.7 ± 3.2	13.2 ± 0.4	35.7 ± 3.1	22.0 ± 0.2
CV03	Mezzolombardo	DCC	2016	Integrated	Vineyard (V)	Loam	203	232	40.0 ± 4.0	12.9 ± 0.5	24.5 ± 3.5	2.9 ± 0.2	27.0 ± 2.7	13.7 ± 0.4	30.5 ± 2.7	22.5 ± 0.2
CV09	Covelo	DCC	2009	Organic	Vineyard (V)	Loam	40	517	39.7 ± 3.6	10.8 ± 0.5	24.2 ± 3.2	0.7 ± 0.2	29.9 ± 3.0	11.0 ± 0.4	37.1 ± 3.1	20.4 ± 0.2
CV10	Terlago	DCC	2005	Integrated	Corn (C)	Loam	40	444	39.7 ± 3.6	10.8 ± 0.5	24.2 ± 3.2	0.7 ± 0.2	29.9 ± 3.0	11.0 ± 0.4	37.1 ± 3.1	20.4 ± 0.2
CV02	Faedo	MG	2001	Integrated	Vineyard (V)	Loam	213	447	39.8 ± 3.8	10.9 ± 0.5	22.5 ± 3.0	2.0 ± 0.2	28.7 ± 2.8	10.8 ± 0.4	35.8 ± 3.1	19.6 ± 0.2
CV05	Tenno	MG	1993	In conversion	Vineyard (V)	Sandy loam	99	356	31.2 ± 2.9	14.6 ± 0.5	23.8 ± 3.1	5.6 ± 0.2	23.6 ± 2.4	13.0 ± 0.4	30.2 ± 2.4	22.7 ± 0.2
CV08	Ravina	MG	1995	Integrated	Vineyard (V)	Loam	64	246	38.4 ± 3.6	12.8 ± 0.5	26.4 ± 3.5	2.8 ± 0.2	30.1 ± 3.3	13.6 ± 0.4	32.9 ± 2.9	22.7 ± 0.2
CV06	Vigo Caventine	DMG	2001	Integrated	Grassland (G)	Sandy loam	171	648	44.4 ± 4.5	11.3 ± 0.5	25.7 ± 3.5	2.2 ± 0.2	31.0 ± 3.4	11.1 ± 0.4	39.7 ± 3.2	20.2 ± 0.2
CV11	Mesiano	DMG	1998	Integrated	Vineyard (V)	Silt loam	215	340	40.2 ± 3.7	12.4 ± 0.5	23.6 ± 3.2	2.6 ± 0.2	29.9 ± 3.1	13.0 ± 0.4	35.6 ± 3.0	21.9 ± 0.2
CV12	Villazzano	DMG	1978	In conversion	Vineyard (V)	Loam	146	274	40.2 ± 3.7	12.4 ± 0.5	23.6 ± 3.2	2.6 ± 0.2	29.9 ± 3.1	13.0 ± 0.4	35.6 ± 3.0	21.9 ± 0.2

**SUPPLEMENTARY DATA**

Morelli, R., Zanzotti, R., Pindo, M., Donati, C., Cestaro, A., & Coller, E. (2025). Pedological origin and edaphic factors drive biota in vineyard soils of Northeast Italy. *OENO One*, 59(2).

<https://doi.org/10.20870/oeno-one.2025.59.2.9288>

**Figure S3.** Example scheme of sampling applied in the studied sites (vineyards).



**LEGEND**

black vertical lines = rows of vines

yellow dotted lines = sampling area of the vineyard

red squares = soil cube sampled for microarthropod analysis

black points = soil cores sampled for chemical and metataxonomic analyses

**Table S2.** Analysis of similarity (ANOSIM) among communities of the investigated soil types.

<b>Kingdom</b>	<b>Comparison</b>	<b>R</b>	<b>Pvalue</b>
fungi	SLA-DCC	0.6747	0.0001
fungi	SLA-DMG	0.5172	0.0001
fungi	SLA-MG	0.7129	0.0001
fungi	DCC-DMG	0.3324	0.0001
fungi	DCC-MG	0.2852	0.0001
fungi	DMG-MG	0.3207	0.0001
bacteria	SLA-DCC	0.4385	0.0001
bacteria	SLA-DMG	0.5303	0.0001
bacteria	SLA-MG	0.6504	0.0001
bacteria	DCC-DMG	0.2953	0.0002
bacteria	DCC-MG	0.3453	0.0002
bacteria	DMG-MG	0.3542	0.0001
microarthropods	SLA-DCC	0.1617	0.0033
microarthropods	SLA-DMG	0.0297	0.1720
microarthropods	SLA-MG	0.0852	0.0300
microarthropods	DCC-DMG	0.0708	0.0504
microarthropods	DCC-MG	0.1070	0.0189
microarthropods	DMG-MG	0.0777	0.0486

**SUPPLEMENTARY DATA**

Morelli, R., Zanzotti, R., Pindo, M., Donati, C., Cestaro, A., & Coller, E. (2025). Pedological origin and edaphic factors drive biota in vineyard soils of Northeast Italy. *OENO One*, 59(2).  
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**Table S3.** NMDS coordinates of environmental factors and their significance. Permutation: free. Number of permutations: 999. Significance codes: 0 “\*\*\*”, ≤0.001 “\*\*”, ≤0.01 “\*”, ≤0.05 “.”, ≤0.1 “ ”.

Fungi						Bacteria						Microarthropods					
Variables	NMDS1	NMDS2	R <sup>2</sup>	p <sub>value</sub>	Significance	Variables	NMDS1	NMDS2	R <sup>2</sup>	p <sub>value</sub>	Significance	Variables	NMDS1	NMDS2	R <sup>2</sup>	p <sub>value</sub>	Significance
Cd	-	-	0.4055	0.001	***	Cd	0.57337	-0.8193	0.4203	0.001	***	Total carbonates	0.92855	-	0.2755	0.001	***
Total carbonates	0.92994	0.36771	0.3464	0.001	***	Total carbonates	0.96363	0.26725	0.3257	0.001	***	pH	0.99669	-	0.2052	0.003	**
pH	-	0.60579	0.2021	0.001	***	Zn	0.99911	-0.0422	0.2213	0.001	***	Pb	0.31505	0.94907	0.2033	0.001	***
Total N	0.72178	0.69213	0.1472	0.004	**	Total N	0.53158	-	0.1761	0.001	***	SOM	0.75441	-	0.1575	0.003	**
SOM	-	0.56428	0.1447	0.003	**	SOM	0.54977	-	0.1635	0.002	**	Total N	0.697	-	0.1465	0.007	**
Zn	0.82558	0.52153	0.1352	0.006	**	pH	0.61914	0.78528	0.0721	0.068	.	C/N	0.86477	0.50217	0.1337	0.007	**
Pb	0.91223	0.40969	0.075	0.072	.	C/N	0.27282	0.96207	0.039	0.265		Cd	0.45138	-	0.1311	0.008	**
silt	0.20263	0.97926	0.0662	0.093	.	Cu	0.17619	0.98436	0.0318	0.294		silt	0.29607	-	0.065	0.112	
C/N	0.74453	0.66759	0.0605	0.107		Pb	0.92916	-	0.0307	0.324		clay	-0.597	0.80224	0.0539	0.148	
Cu	0.48333	0.87544	0.0469	0.193		clay	-	-0.825	0.017	0.54		Cu	0.06771	0.9977	0.0499	0.155	
sand	0.03847	0.99926	0.0281	0.376		sand	0.56513	0.95244	0.0156	0.58		Zn	0.90607	-	0.0392	0.246	
clay	0.73805	0.67475	0.0184	0.508		silt	-	-	0.0081	0.743		sand	-	0.42313	0.0188	0.554	
	0.764	0.64521					0.14836	0.98893					0.08469	0.99641			

**Table S4.** Relative frequencies (%) of bacterial (a) and fungal (b) functional groups (mean ± SE) in the investigated soil types.

FUNCTION	SLA	DCC	MG	DMG
<b>a)</b>				
<b>C cycle</b>				
aromatic compound degradation	0.18±0.02	0.28±0.04	0.2±0.01	0.22±0.02
aromatic hydrocarbon degradation	0.01±0	0.01±0	0.01±0	0.01±0
cellulolysis	0.12±0.03 (b)	0.24±0.03 (a)	0.1±0.01 (b)	0.07±0.01 (b)
aliphatic non methane hydrocarbon degradation	0.01±0	0.01±0	0.01±0	0.01±0
hydrocarbon degradation	0.13±0.01 (c)	0.36±0.05 (a)	0.3±0.04 (ab)	0.2±0.03 (b)
chitinolysis	0.06±0.01 (b)	0.1±0.01 (a)	0.05±0.01 (b)	0.05±0.01 (b)
ureolysis	0.19±0.02	0.34±0.05	0.2±0.01	0.61±0.38
xylanolysis	0.07±0.01 (b)	0.12±0.01 (a)	0.07±0.01 (b)	0.04±0.01 (c)
methanogenesis	0.01±0 (a)	0.01±0 (a)	0±0 (b)	0±0 (b)
methanogenesis by CO <sub>2</sub> reduction with H <sub>2</sub>	0±0 (b)	0.01±0 (a)	0±0 (b)	0±0 (b)
methanogenesis by disproportionation of methyl groups	0±0 (b)	0.01±0 (a)	0±0 (b)	0±0 (b)
methanogenesis by reduction of methyl compounds with H <sub>2</sub>	0.01±0	0±0	0±0	0±0
methanol oxidation	0.02±0 (b)	0.07±0.01 (a)	0.03±0 (b)	0.01±0 (b)
methanotrophy	0.12±0.01 (b)	0.35±0.05 (a)	0.28±0.04 (ab)	0.19±0.03 (b)
methylotrophy	0.14±0.01 (b)	0.41±0.06 (a)	0.3±0.04 (ab)	0.19±0.03 (b)
hydrogenotrophic methanogenesis	0.01±0 (a)	0.01±0 (a)	0±0 (b)	0±0 (b)
reductive acetogenesis	0±0	0±0	0±0	0±0
fermentation	0.4±0.03 (b)	0.87±0.12 (a)	0.73±0.06 (a)	0.51±0.03 (b)
anoxygenic photoautotrophy	0.02±0 (b)	0.04±0.01 (ab)	0.05±0.01 (a)	0.02±0 (b)
chloroplasts	0.14±0.05	0.21±0.05	0.16±0.04	0.13±0.02
iron respiration	0.1±0.01 (a)	0±0 (c)	0.03±0.01 (b)	0.03±0.01 (b)
photoautotrophy	0.02±0 (b)	0.04±0.01 (ab)	0.05±0.01 (a)	0.02±0 (b)
<b>N cycle</b>				
denitrification	0.02±0 (b)	0.05±0.01 (a)	0.05±0.01 (a)	0.02±0 (b)
nitrate denitrification	0.02±0 (b)	0.05±0.01 (a)	0.05±0.01 (a)	0.02±0 (b)
nitrite denitrification	0.02±0	0.05±0.01	0.05±0.01	0.02±0
nitrification	7.17±0.28	10.1±0.76	10.16±0.69	11.36±0.32
aerobic ammonia oxidation	6.58±0.28 (b)	9.71±0.8 (a)	9.68±0.7(a)	11.07±0.31 (a)
aerobic nitrite oxidation	0.59±0.02 (a)	0.39±0.06 (bc)	0.49±0.03 (b)	0.29±0.01 (c)
nitrate reduction	0.18±0.01 (c)	0.52±0.06 (a)	0.34±0.03 (ab)	0.3±0.02 (c)
nitrate respiration	0.06±0.01 (b)	0.08±0.01 (ab)	0.1±0.01 (a)	0.05±0.01 (b)
nitrite respiration	0.02±0	0.05±0.01	0.05±0.01	0.02±0
nitrogen fixation	0.26±0.02 (b)	0.4±0.04 (ab)	0.35±0.02 (b)	0.62±0.07 (a)
nitrogen respiration	0.06±0.01 (b)	0.08±0.01 (ab)	0.1±0.01 (a)	0.05±0.01 (b)
<b>S cycle</b>				
respiration of sulfur compounds	0.03±0.01 (a)	0±0 (c)	0±0 (c)	0.01±0 (b)
sulfate respiration	0±0	0±0	0±0	0±0

sulfur respiration	0.02±0.01 (a)	0±0 (b)	0±0 (b)	0±0 (b)
thiosulfate respiration	0±0	0±0	0±0	0±0
dark oxidation of sulfur compounds	0.01±0	0.02±0	0.01±0	0.01±0
dark sulfide oxidation	0±0	0±0	0±0	0±0
anoxygenic photoautotrophy S oxidizing	0.02±0 (b)	0.04±0.01 (ab)	0.05±0.01 (a)	0.02±0 (b)
<b>Parasites/Pathogens</b>				
human pathogens all	0.02±0 (b)	0.03±0 (a)	0.02±0.01 (b)	0.02±0 (b)
human pathogens pneumonia	0.01±0	0.01±0	0±0	0.01±0
intracellular parasites	0.13±0.01 (a)	0.09±0.01 (b)	0.1±0.01 (ab)	0.11±0.01 (ab)
predatory or exoparasitic	0.02±0 (a)	0.04±0.01 (a)	0.02±0 (a)	0.01±0 (b)
<b>Other</b>				
aerobic chemoheterotrophy	4.44±0.3 (b)	8.2±0.68 (a)	6.99±0.39 (a)	6.72±0.29 (a)
anaerobic chemoheterotrophy	0.79±0.07 (b)	1.13±0.08 (a)	0.69±0.03 (b)	0.6±0.03 (b)
chemoheterotrophy	5.23±0.33 (b)	9.33±0.75 (a)	7.68±0.41 (a)	7.33±0.31 (a)
photoheterotrophy	0.02±0 (b)	0.04±0.01 (ab)	0.05±0.01 (a)	0.03±0 (b)
phototrophy	0.02±0 (b)	0.04±0.01 (ab)	0.05±0.01 (a)	0.03±0 (b)
animal parasites or symbionts	0.03±0 (b)	0.06±0.01 (a)	0.04±0.02 (b)	0.03±0 (b)
dark hydrogen oxidation	0.01±0 (b)	0.06±0.02 (ab)	0.01±0 (b)	0.12±0.04 (a)
human associated	0.02±0 (b)	0.06±0.01 (a)	0.03±0.01 (b)	0.02±0 (b)
human gut	0±0 (b)	0.03±0.01 (a)	0.01±0 (b)	0.01±0 (b)
mammal gut	0±0 (b)	0.03±0.01 (a)	0.01±0 (b)	0.01±0 (b)
manganese oxidation	0±0	0±0	0.01±0	0±0

b)

FUNCTION	SLA	DCC	MG	DMG
<b>Endophytes</b>	21.63±1.34 (b)	25.92±1.97 (ab)	25.44±1.35 (ab)	30.17±2.06 (a)
<b>Epiphytes</b>	0.73±0.13 (b)	2.94±0.47 (a)	4.36±0.43 (a)	6.34±1.23 (a)
<b>Saprotrophs/decomposers</b>				
dung saprotroph	1.6±0.21	2.25±0.39	2.56±0.46	1.69±0.37
leaf saprotroph	0.63±0.13	1.09±0.35	0.51±0.19	0.67±0.21
litter saprotroph	14.64±0.93	12.86±1.05	12.33±1.62	11.75±1.77
pathotroph	19±0.95 (b)	24.47±1.98 (ab)	23.65±1.35 (ab)	27.67±1.75 (a)
plant saprotroph	0.21±0.03	0.32±0.07	0.38±0.12	0.25±0.05
root associated biotroph	0±0	0±0	0±0	0±0
saprotroph	46.66±1.87	48.15±1.68	51.84±2.47	50.77±2.38
soil saprotroph	14.79±0.95	13.61±1.03	14.41±1.76	12.06±1.82
symbiotroph	27.46±1.33 (b)	29.81±2.08 (ab)	29.54±1.18 (ab)	35.11±1.96 (a)
wood saprotroph	7.28±0.78 (b)	12.77±1.63 (a)	10.73±0.88 (a)	13.56±1.25 (a)
<b>Parasites/Pathogens</b>				
fungal parasite	5.74±0.55 (b)	6.85±1.37 (ab)	7.47±0.6 (ab)	8.37±0.64 (a)
lichen parasite	4.04±0.35 (b)	5.31±1.36 (b)	6.56±0.79 (ab)	6.77±0.51 (a)
plant parasite	0.49±0.12	1.08±0.35	0.44±0.2	0.58±0.2

plant pathogen	13.33±0.93	15.99±1.89	14.44±0.81	16.81±1.2
animal pathogen	9.27±0.88 (b)	14.75±1.68 (a)	15.76±1.52 (a)	20.44±1.63 (a)
bryophyte parasite	1.28±0.24	1.28±0.36	1.03±0.25	0.75±0.21
<b>Mycorrhizae</b>				
ectomycorrhizal	0.99±0.18	1.4±0.39	0.87±0.27	1.12±0.25
endomycorrhizal	0.82±0.32	1.46±0.56	0.69±0.25	0.44±0.12
arbuscular mycorrhizal	3.93±0.75 (a)	0.58±0.1 (c)	1.76±0.5 (c)	2.75±0.48 (ab)
ericoid mycorrhizal	0±0	0.03±0.02	0.24±0.15	0±0
orchid mycorrhizal	0±0	0±0	0±0	0±0
<b>Other</b>				
animal endosymbiont	0.16±0.04	0.13±0.07	0.19±0.11	0.06±0.02
clavicipitaceous endophyte	0.12±0.04	0.08±0.03	0.12±0.08	0.02±0.01
lichenized	0.08±0.03	0.25±0.08	0.71±0.44	0.08±0.02