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Corrigendum

Corrigendum to "Soil microbial biomass and bacterial diversity in southern European regions vulnerable to desertification" [Ecol. Indicat. 145 (2022) 109725]

V. Catania [a,1], R.S. Bueno [a], R. Alduina [a], E. Grilli [b], T. La Mantia [c], S. Castaldi [b], P. Quatrini [a,*]

[a] Department of Biological, Chemical and Pharmaceutical Sciences and Technologies (STEBICEF), University of Palermo, Viale delle Scienze, blg. 16, 90128 Palermo, Italy

[b] Department of Environmental, Biological and Pharmaceutical Sciences and Technologies (DiSTABIF), University of Campania "Luigi Vanvitelli", via Vivaldi 43, 81100 Caserta, Italy

[c] Department of Agricultural, Food and Forest Sciences (SAAF), University of Palermo, Viale delle Scienze, blg. 4, 90128 Palermo, Italy

The authors regret the incorrect publication of legend for Table 1 and Table 3 in black/white in the original article. The complete legend for Table 1 and Table 3 with colours, indicating degree of significance, are presented below.

Table 1. Summary of the regression testing the effects of SOC, pH, N and CEC on soil microbial biomass (SMB), richness (estimated as observed bacterial OTUs), and diversity (Shannon index) calculated on ARISA profiles and measured as soil extracted dsDNA. R^2 = adjusted fit of the model. Significant p values in bold characters.

Table 3. Spearman correlation coefficients between the relative abundance of the most abundant genera and main soil parameters: cation exchange capacity (CEC), pH, total nitrogen (TN) and soil organic carbon (SOC) obtained in the sampled soils. Only significant correlations (p-value < 0.05) are shown. Blue and red colours indicate negative and positive relationships, respectively, with colour intensity representing the degree of significance ($p < 0.05 > 0.01$, $<0.01 > 0.001$ and < 0.001).

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* Corresponding author.

E-mail addresses: valentina.catania@unipa.it (V. Catania), rafael.dasilveirabueno@unipa.it (R.S. Bueno), rosa.alduina@unipa.it (R. Alduina), eleonora.grilli@unicampania.it (E. Grilli), tommaso.lamantia@unipa.it (T. La Mantia), simona.castaldi@unicampania.it (S. Castaldi), paola.quatrini@unipa.it (P. Quatrini).

[1] Present address: Department of Earth and Marine Science (DiSTeM), University of Palermo, Viale delle Scienze, blg. 16, 90128 Palermo, Italy.

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Phylum	Genera	CEC	pH	TN	SOC
Acidobacteria	Candidatus Koribacter	-0.52	-0.69		
	Candidatus Solibacter	-0.46	-0.78		
Actinobacteria	Arthrobacter		0.66		
	Mycobacterium		-0.48		
	Pseudonocardia		0.68		
	Rubrobacter	0.48	0.84		
	Streptomyces	-0.55		-0.6	-0.6
Alphaproteobacteria	Balneimonas		0.86		
	Bradyrhizobium		-0.66		
	Kaistobacter				-0.54
	Rhodoplanes		-0.66		0.48
	Skermanella		0.88		
Bacteroidetes	Adhaeribacter		0.83		
	Flavisolibacter		0.48		
	Rhodocytophaga	0.57	0.7		
Betaproteobacteria	Burkholderia		-0.82		
Deltaproteobacteria	Candidatus Entotheonella	0.63	0.84		
	Geobacter				
Firmicutes	Alicyclobacillus				
	Ammoniphilus	-0.77			-0.63
	Bacillus	-0.57			-0.71
	Planifilum			-0.47	
	Solibacillus				-0.55
	Sporosarcina	-0.51			-0.52
Gammaproteobacteria	Pseudomonas		0.62		
	Steroidobacter		0.84		
Nitrospirae	Nitrospira		0.73		
Verrucomicrobia	Candidatus Xiphinematobacter				
	DA101	-0.57	-0.51		

The authors would like to apologise for any inconvenience caused.