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Soil organic carbon fractions and their associated bacterial and fungal abundance in alpine ecosystems

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Soil organic matter (SOM) has a key role in the carbon (C) cycle and consists of particulate organic matter (POM) and mineral-associated organic matter (MAOM), which differ in stability and turnover. This study investigates C dynamics and microbial abundance at two alpine sites (1526 and 2500 m a.s.l). Soil samples were fractionated, and the C:N ratio, pH, and microbial abundances were analysed. While the MAOM/POM ratio remained stable across sites, the higher-elevation soil, dominated by N-poor alpine graminoids, showed an increased C:N ratio, consistent with reduced decomposition and transfer of litter into mineral-associated pools under colder, more acidic conditions. Bacteria predominated in MAOM, supporting their role in SOM stabilisation, whereas fungal abundance was highest in MAOM only at 2500 m. Fungal abundance remained stable across sites, indicating greater tolerance to low temperatures and pH compared to bacteria, which declined at higher altitudes. This suggests fungi play a key role in decomposition in colder environments. Correlations between fungi and bacteria were context-dependent: negative in MAOM and positive in POM, but only at 2500 m. These findings highlight how the composition and stability of SOM and microbial abundance differ between fractions and at different elevations, underscoring the value of integrating microbial data with SOM fractionation to better understand alpine soil C dynamics.

Keywords Carbon fractions, POM, MAOM, Soil ecology, Fungal abundance, Bacterial abundance

Soils store approximately 74% of the global terrestrial carbon (C) pool[1–4], making soil organic matter (SOM) a fundamental component of the C cycle. As both a reservoir and a source of C, SOM influences CO_2 fluxes, contributing to C storage regulation and release[5]. Furthermore, C stability depends on its partitioning within SOM fractions, which respond differently to environmental changes such as temperature and moisture[6–8].

Particulate organic matter (POM) and mineral-associated organic matter (MAOM) are among the primary SOM fractions and have distinct roles in the C cycle due to differences in their composition, turnover rates, and stabilisation mechanisms[9,10]. POM is a fast-cycling fraction mainly composed of plant and animal residues that are easily decomposed, leading to the release of C into the atmosphere[11,12]. In contrast, MAOM is a slow-cycling fraction, composed of microbially processed organic compounds bound to soil minerals. This mineral association makes the organic compounds more resistant to decomposition and thus persistent in soils[7,9,13].

Bacteria and fungi drive the transformation and stabilisation of these fractions, regulating C storage and release[10,14,15]. However, these two groups differ in their roles within SOM fractions. Fungi (including both yeast and filamentous life forms) are heterotrophic organisms involved in decomposing complex organic compounds in POM, leading to faster CO_2 release[16,17], whereas bacteria contribute to the stabilisation of MAOM by producing organic compounds that bind to mineral surfaces and are retained in the soil matrix[18,19]. These

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functional differences affect C cycling, particularly in high-altitude soils, where environmental constraints shape the microbial community[8,20].

Environmental factors such as altitude, can significantly impact microbial growth and activity, thereby affecting decomposition efficiency[21,22]. Altitude has a significant influence on local weather patterns, with pronounced effects on temperature and precipitation. These climatic shifts indirectly regulate microbial and plant growth, which in turn influence soil physical, chemical, and biological processes[23,24]. Recent research, like the one on the Microbial Efficiency-Matrix Stabilisation (MEMS) framework[25,26], emphasises that microbial processing efficiency is a key driver of SOM stabilisation. However, studies quantifying the abundance of bacteria and fungi in POM and MAOM remain scarce[27]. While these microbial groups are recognised for their essential roles in SOM cycles, published data on their abundance in these fractions remain limited so far.

Due to the limited data on microbial abundance within SOM fractions, this study aims to deepen our understanding of microbial dynamics in SOM pools and their implications for C stabilisation under changing environmental conditions. To address this gap, we quantify bacterial and fungal abundances within POM and MAOM, linking them to C and nitrogen (N) composition in alpine soils at two elevations (1526 and 2500 m above sea level (a.s.l.)). We hypothesise that C and N concentrations of POM and MAOM will differ between elevations, reflecting the influence of environmental conditions on decomposition and stabilisation (H1). Additionally, we hypothesised that fungi would be more abundant in POM, as this fraction, while often structurally complex, is more accessible to decomposition due to lower mineral protection—making it a key substrate for fungal-driven breakdown of organic compounds. In contrast, bacteria are expected to dominate in MAOM because of their stronger physical interactions, such as adhesion to mineral surfaces or entrapment within soil microaggregates, and biochemical interactions, including binding of extracellular polymeric substances and formation of organo-mineral complexes[18,19] (H2). We further expect a decrease in bacterial abundance at higher elevations due to temperature and pH constraints, whereas fungal abundance may increase, as fungi are better adapted to harsh conditions and can outcompete bacteria when decomposition rates are reduced (H3).

Materials and methods

Study area and sampling

Two experimental sites at different altitudes were selected, with an average temperature difference of 5 °C. The first sampling site is a natural grassland located at 2500 m a.s.l. near Col de Seigne, Val Veny, Courmayeur, Italy (45.751 N, 6.807 E), and has a northeastern exposure with a slope angle of 20°. It is characterised by alpine vegetation, including *Agrostis rupestris*, *Poa alpina*, and *Festuca halleri* (Table S1). These plants are adapted to the alpine zone's harsh conditions, including cold temperatures, strong winds, and nutrient-poor soils (http://www.vnr.unipg.it/habitat/cerca.do?formato=stampa&idSegnalazione=103).

The second sampling site is a mown meadow, located at 1526 m a.s.l., Val Veny, Courmayeur, Italy (45.798 N, 6.918 E), with a gentle slope and a north-northeastern exposure. This site supports a more temperate montane vegetation community, including *Bromopsis inermis*, *Elymus repens*, and *Dactylis glomerata* (Table S1). These plants are suited to milder conditions with a longer growing season than the alpine zone (http://www.vnr.unipg.it/habitat/cerca.do?formato=stampa&idSegnalazione=114). Samples were collected in September 2023. Both soils originate from the same parent rock material, comprising sandstone, slate, and limestone. They are characterised as dystric and lithic leptosols with haplic podzols with a partial cover of permanent snow at the soils at 2500 m (https://maps.europe-geology.eu/).

The soil samples were collected according to the European Soil Data Centre (ESDAC) guidelines[28]. Ten replicates were collected from each site, each consisting of a composite of 3 samples taken at 0–20 cm depth. Subsequently, all samples were air-dried and sieved to 2 mm, removing both inorganic (e.g. rocks) and organic (e.g. roots) material.

Soil texture analysis

Soil texture was analysed using a combined sieve and hydrometer method, following dispersion with sodium pyrophosphate ($Na_4P_2O_7$). 100 g of previously sieved soil were placed into a 1 L graduated cylinder, followed by the addition of 100 mL of distilled water and 25 mL of 0.1 M $Na_4P_2O_7$. The mixture was shaken vigorously for a few minutes, and the cylinder was then filled to 1 L with distilled water. After shaking again, the cylinder was set on a flat surface. The density of the suspension was measured with a hydrometer after 30 s to estimate the sand and silt fractions, and again after 2 h to determine the clay fraction. At each measurement time, the suspension temperature was also recorded.

The percentage of each fraction in the suspension (sand, silt, and clay) was calculated using the formula:

$$S = \frac{R}{W} \times 100$$

where S is the percentage of material in suspension, R is the temperature-corrected hydrometer reading, and W is the exact dry mass of the soil sample. The hydrometer reading is corrected by adding or subtracting 0.36 g for each °C above or below the calibration temperature.

Finally, the proportions of sand, silt, and clay were used to classify soil texture by locating the sample within the USDA soil texture triangle.

Total element content

Approximately 1.0 g of the sieved soil was finely ground using a Retsch MM400 ball mill equipped with agate beads to minimise metal contamination for 6 min at 30 Hz. The homogeneous soil was then placed into a polyethene sample cup, with both the top and bottom sealed using polypropylene films specifically designed for

XRF measurements. The soil surface was gently compacted using a plastic cylinder to obtain a smooth and even layer. Elemental concentrations were determined using an Epsilon 4 X-ray fluorescence spectrometer (Malvern Panalytical, Netherlands) with a total acquisition time of 20 min per sample. The soil samples were analysed using the pre-calibrated Omnian method, to which certified reference materials (NIST2710a) were incorporated to refine the calibration. The certified reference materials were also used to assess the measurement quality, with a recovery rate of 66% for P, 105% for K, 102% for Ca, 69% for Mg, 120% for Fe, 95% for Mn, 94% for Zn and 99% for Cu.

Fractionation and chemical analysis

The isolation of POM and MAOM was adapted and performed according to the protocol developed by Just et al.[29], using ultrasonic dispersion (at 100 J mL^{-1}, instead of 450 J mL^{-1}) and wet sieving. Briefly, 10 g of soil were combined with 150 mL of laboratory-grade water and then sonicated. The suspension was ultrasonicated using the ultrasonic sonotrode (Bandelin Sonopuls HD 4200, Germany) with a total energy input of 100 J mL^{-1} (E). The sonication time (t) was calculated according to the following equation, where P is the output power of the sonotrode:

$$t = \frac{E\left[\frac{J}{ml}\right] \times Vol_{Suspension}\,[ml]}{P\frac{J}{s}} = 100\left[\frac{J}{ml}\right] \times \frac{\left(H_2O\,[ml] + \frac{Soil[g]}{2.5\left[\frac{J}{s}\right]}\right)}{P\frac{J}{s}}$$

Following the ultrasonic dispersion, suspensions were wet sieved at 63 µm, using 2 L of laboratory-grade water. Once the fractions were separated into two crystallisers (< 63 µm/MAOM and > 63 µm/POM), the crystallisers were placed in a drying cabinet (Drying Oven SLW 400, Pol-Eko, Poland) at 60 °C for around 7 days, until the water had fully evaporated, and a constant weight was reached. Once the fractions were dry, they were finely homogenised using a ball mill (Mixer Mill MM 400, Retsch, Germany), and part of the material was stored for subsequent molecular analysis. The finely homogenised fractions were then analysed to measure total organic C (TOC) and total N (TN) within each fraction using the Flash EA 112 Elemental Analyser (Thermo Scientific, Germany). Subsequently, soil pH was measured using a 1:2.5 soil-to-water ratio by mixing 5 g of air-dried, sieved soil (< 2 mm) with 12.5 mL of deionised water. The soil–water mixture was shaken on a reciprocal shaker at room temperature for 15 min and then centrifuged at 1000 rpm for 5 min. The pH was measured using a calibrated pH meter (XS Instruments, Carpi, Italy).

All samples were processed uniformly and fractionated under consistent laboratory conditions to ensure valid comparisons of microbial abundances between fractions and sites.

DNA extraction and qPCR amplification

Total DNA was extracted from the dried, homogenised POM and MAOM fractions obtained through the described fractionation protocol. Specifically, 0.25 g of sample was analysed using the DNeasy® PowerSoil® extraction kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions, and DNA was stored at − 20 °C until subsequent analyses. DNA concentration was quantified using the Qubit 4.0 fluorometer (Life Technologies Corporation) in combination with the Qubit™ 1X dsDNA Broad Range Assay Kits (Invitrogen, Milan, Italy) and normalised to 10 ng μL^{-1} for all samples to allow for microbial abundance quantification by qPCR. Bacterial and fungal abundances were quantified by amplifying the 16S rRNA gene and the fungal ITS2 region. Amplifications were performed using the primer pairs 341F_16S/805R_16S (5′-CCTACGGGNGGCWGCAG-3′/5′-GACTACHVGGGTATCTAATCC-3′[30]) for bacteria and ITS3_KYO2/ITS4 (5′-GATGAAGAACGYAGYRAA-3′/5′-TCCTCCGCTTATTGATATGC-3′[31]) for fungi in a total volume of 20 µL. The reaction mix contained 1 µL of total DNA, 10 µL of KAPA SYBR Fast qPCR Kit Master Mix 2X Universal, 0.8 µL of each primer, and 7.4 µL of sterile ultrapure water. Each qPCR reaction was conducted using a Biorad CFX96 thermocycler (Biorad, Hercules, California, United States) with the following cycling conditions: an initial step at 95 °C for 3 min, followed by 39 cycles of 10 s at 95 °C and 20 s at 60 °C for bacteria, or 39 cycles of 10 s at 95 °C, 20 s at 53 °C and 30 s at 72 °C for fungi. Reactions concluded with a melting curve analysis, starting from 65 °C to 95 °C with a temperature increase of 0.5 °C and a transition rate of 5 s.

Using previously described protocols, standards were obtained by amplifying ad hoc synthetic sequences of known concentration, molecular weight, and copy number (IDT, Coralville, Iowa, USA). All samples were run in triplicate, along with ten-fold serial dilutions of standards and qPCR negative controls.

Statistical analysis

All statistical analyses were conducted using R software[32]. Chemical and biological data were checked for normality using the Shapiro–Wilk test. Depending on normality, differences in pH, texture and elemental concentrations between sites were evaluated using either Student's *t*-tests (for normally distributed data) or Wilcoxon rank-sum tests (for non-normally distributed data). To compare physical and chemical measurements across SOM fractions and sampling elevations, data were analysed using ANOVA followed by Tukey's post hoc test for normally distributed data, or the Kruskal–Wallis test followed by Dunn's post hoc test for non-normally distributed data, to provide an overarching comparison across all fraction–elevation combinations. Post hoc pairwise tests with corresponding p-values are reported in Table S2. Heatmaps were generated from pairwise Pearson correlation matrices to visualise relationships between soil chemical and biological variables, and non-significant correlations were excluded from the heatmap display.

	1526 m a.s.l.	2500 m a.s.l.
Coordinates (N, E)	45.767688, 6.828024	45.797312, 6.918661
Average annual T (°C)	9.7 ± 7.6	4.0 ± 7.1
Soil pH_{water}	6.0 ± 0.2[a]	4.0 ± 0.7[b]
Texture description	Loamy sand	Sandy loam
Sand content (%)	65 ± 2.1[a]	71 ± 3.6[a]
Silt content (%)	24 ± 1.7[a]	24 ± 1.2[a]
Clay content (%)	11 ± 0.6[a]	5.4 ± 2.5[b]
Pedological and mineralogical properties	Sandstone, slate, and limestone; dystric and lithic leptosols with haplic podzols	Sandstone, slate, and limestone; dystric and lithic leptosols with haplic podzols

Table 1. Details of the location, average annual temperature, soil pH, texture and mineral characterisation at the two sites. pH, temperature and texture are presented as means ± SD (n = 10). Temperature data were collected from Dolonne and Lex Blanche weather stations located in the Aosta Valley region. Statistical significance was assessed using a t-test, with different letters indicating significant differences between sites ($p < 0.05$).

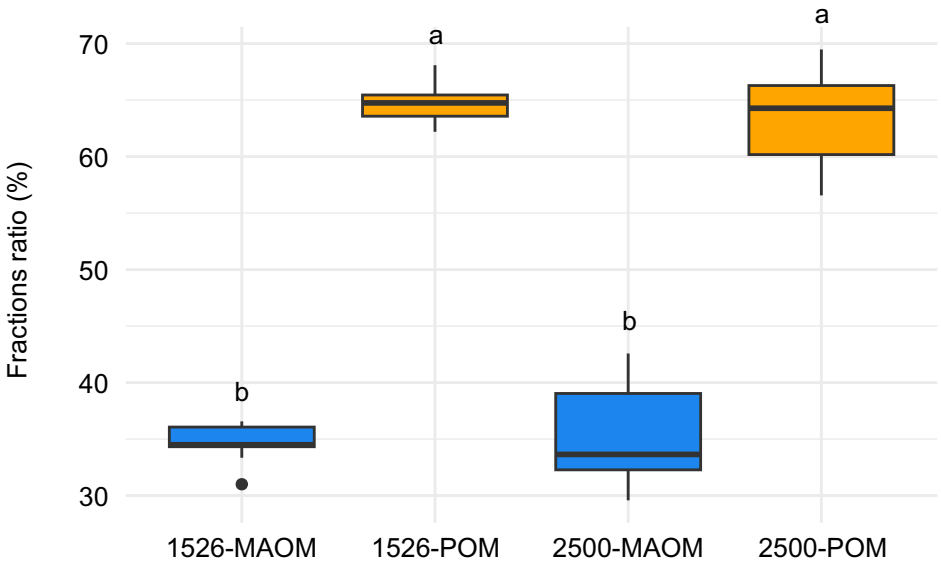

Fig. 1. The proportion of particulate organic matter (POM) and mineral-associated organic matter (MAOM) at each sampling site (n = 10). Letters indicate statistically significant differences ($p < 0.05$) assessed by Kruskal–Wallis test followed by Dunn's post hoc test. Blue corresponds to MAOM, and yellow corresponds to POM.

Results

General sites description

Soil texture and composition varied moderately between the two elevations studied (1526 and 2500 m a.s.l.). At 1526 m a.s.l., the soil was classified as loamy sand, whereas at 2500 m a.s.l., it was identified as sandy loam (Table 1). The sand content did not differ significantly between elevations, averaging 65 ± 2.1% at 1526 m and 71 ± 3.6% at 2500 m. Similarly, silt content remained constant across sites, with both elevations showing a mean value of approximately 24%. In contrast, the clay content showed a significant decrease with altitude, from 11 ± 0.6% at 1526 m to 5.4 ± 2.5% at 2500 m ($p < 0.05$).

Pedologically, both sites were characterised by substrates composed of sandstone, slate, and limestone, and soils were identified as dystric and lithic leptosols with haplic podzols, indicating similar parent materials and soil classification despite the altitudinal gradient.

Physical, chemical, and biological properties of soil organic matter fractions

The proportion of POM to MAOM was not significantly different at the two sites (Fig. 1), with the respective percentages being ~ 64% POM and 35% MAOM at 2500 m, and ~ 65% POM and 35% MAOM at 1526 m.

Significant differences can be observed within and among sampling sites when comparing the C:N ratio of the two SOM fractions (Fig. 2). MAOM C:N ratio (MAOM-2500—10.03 ± 0.55; MAOM-1526—8.20 ± 0.37) was significantly lower than POM (POM-2500—14.20 ± 3.27; POM-1526—11.12 ± 0.53) in both sites ($p < 0.05$).

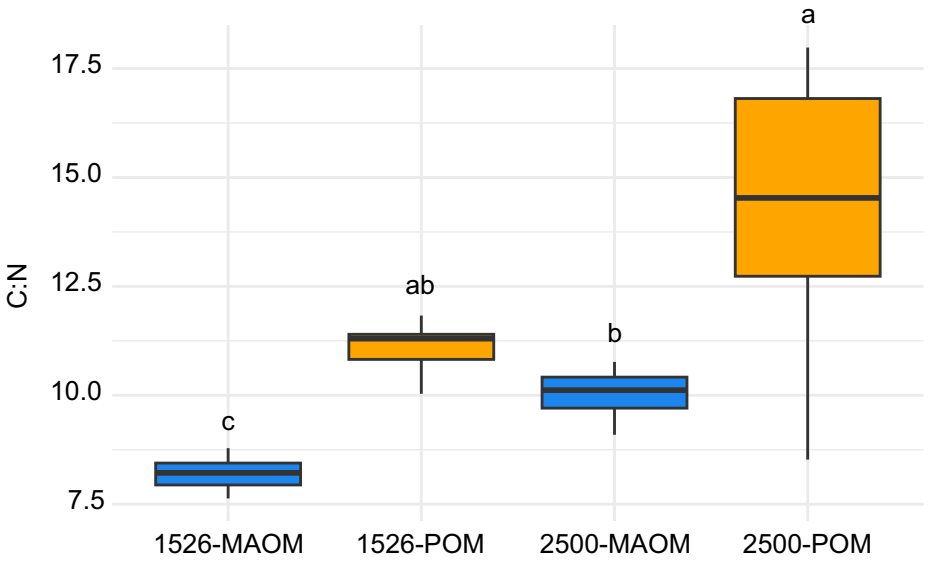

Fig. 2. Carbon to Nitrogen (C:N) ratio across fractions and sampling sites (n = 10). Letters over the boxplots indicate statistically significant differences ($p < 0.05$) assessed by Kruskal–Wallis test followed by Dunn's post hoc test. Blue corresponds to the mineral-associated organic matter (MAOM), and yellow corresponds to the particulate organic matter (POM).

Significant differences were also observed when comparing the two sites, with the C:N ratio of both MAOM and POM presenting lower values at 1526 m than at 2500 m ($p < 0.05$).

The two sites also showed significant differences in pH values (Table 1). The pH values at 1526 m ranged from 5.59 to 6.19, while at 2500 m, they were significantly more acidic, with values ranging from 3.6 to 4.14.

Abundances of bacteria and fungi, analysed through the qPCR of the 16S rRNA gene and the ITS2 region (Fig. 3), are expressed as the copy number of the target gene/region on a logarithmic scale (logCP). Bacterial abundance significantly differed between the fractions at both sites ($p < 0.05$), with higher values observed in MAOM compared to POM. Significant differences were also highlighted when comparing the two sites. Indeed, bacteria were more abundant in MAOM and POM at 1526 m than in the fractions at 2500 m. Conversely, fungal abundance showed significant differences between MAOM and POM only at 2500 m ($p < 0.05$), while when comparing the sites, no differences were detected.

Correlation analyses of biological and chemical variables in SOM fractions

Correlations between soil chemical and biological variables (C:N ratio, 16S, ITS and pH) across the two SOM fractions at the two different sites were analysed using Person's correlation, and results were visualised with heatmaps (Fig. 4). Fractions from site 2500 m (Fig. 4b) illustrate a significant correlation between fungal and bacterial abundances, but with opposite trends: indeed, in MAOM-2500, fungal and bacterial abundances are negatively correlated ($p = 0.049$), while they are positively correlated in POM-2500 ($p = 0.049$). MAOM-1526 is the only fraction in which a significant negative correlation between fungal abundance and C:N ratio ($p = 0.002$) was detected (Fig. 4a).

Discussion

According to our initial hypothesis (H1), the C and N content of POM and MAOM should differ between sites, reflecting the effects of environmental conditions (e.g., temperature and soil properties) on decomposition and stabilisation. Indeed, while the environmental parameters did not affect the MAOM-to-POM ratio (Fig. 1), we observed a higher C:N ratio in both fractions at higher elevations (Fig. 2). This suggests that although the balance between POM and MAOM remained stable across sites, decomposition dynamics were altered by environmental parameters. Previous studies[3,5,8] suggest that colder temperatures and lower pH[17,20], like those at 2500 m (Table 1), determined a slower organic matter decomposition rate, leading to more significant accumulation of plant-derived material with a higher C:N ratio[20,33–35]. Mineralogical parameters (Table 1) did not differ between sites, and soil texture varied only in clay content (Table 1). Although higher clay content generally promotes MAOM formation by providing more reactive surfaces, potentially shifting C from POM to MAOM, the modest textural differences here appear insufficient. The 2500 m site also showed lower total nutrient contents (Supplementary Table 3), which likely further constrained microbial activity and N cycling, favouring the accumulation of relatively N-poor plant residues. Also, the lower content of legumes (Supplementary Table 1) may have contributed to the increased C:N ratios observed in both fractions at 2500 m.

In the second hypothesis (H2), we expected that microbial abundances would differ between SOM fractions, with fungi (both yeast and filamentous life forms) dominating POM and bacteria dominating MAOM due to their respective functional roles in C stabilisation[18,19]. The results confirm that bacteria are more abundant in MAOM (Fig. 3a) and align with the Microbial Efficiency-Matrix Stabilisation (MEMS) framework[25,36], which

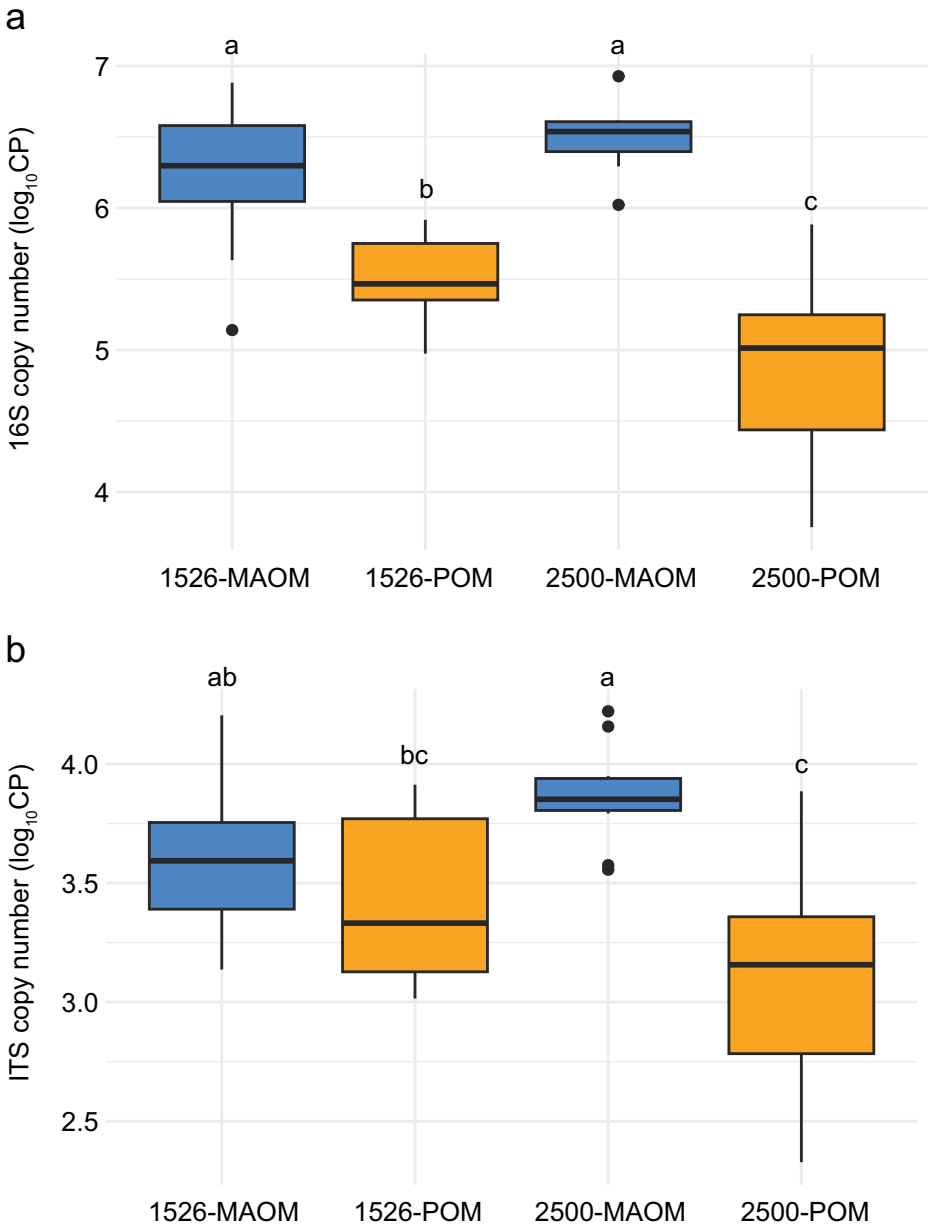

Fig. 3. Comparison of bacterial (**a**) and fungal (**b**) abundance across fractions and sampling sites, measured as the $\log_{10}$ of the 16S rRNA gene and of the ITS2 region copy number (logCP), respectively (n = 10). Letters over the boxplots indicate statistically significant differences ($p < 0.05$) assessed by one-way ANOVA followed by Tukey's post hoc test. Blue corresponds to the mineral-associated organic matter (MAOM), and yellow corresponds to the particulate organic matter (POM).

predicts that bacterial processing contributes to SOM stabilisation into MAOM[7,37]. Moreover, a lower C:N ratio in MAOM likely facilitates bacterial colonisation by providing a more readily available source of N for microbial growth[38], while the association of bacteria with mineral surfaces can serve as refuges, providing a stable microenvironment[10,39].

Contrary to our initial expectations (H2), fungal abundance was not higher in POM than in MAOM (Fig. 3b). Depending on the site, fungal abundance was either similar between the fractions or even higher in MAOM. At 2500 m, fungi were more abundant in MAOM than POM, likely due to site-specific conditions such as lower temperatures and low pH (3.95 ± 0.16), which may favour fungal colonisation in MAOM in some cases[40–42]. While POM is typically considered a more favourable habitat for fungal growth due to its high organic matter content and decomposability[16,43,44], the stability of MAOM may provide more protective microenvironments for fungal communities[19]. Moreover, the 2500 m flora includes an ectomycorrhizal host (*Salix herbacea*, Supplementary Table 1) and stress-tolerant graminoids, which favour fungal growth. Beyond *Salix*, the community is graminoid- and cushion-forb-rich (e.g., *Festuca, Nardus, Carex, Agrostis*), typical of stress-tolerant, low-input systems that favour fungal processing pathways[45,46].

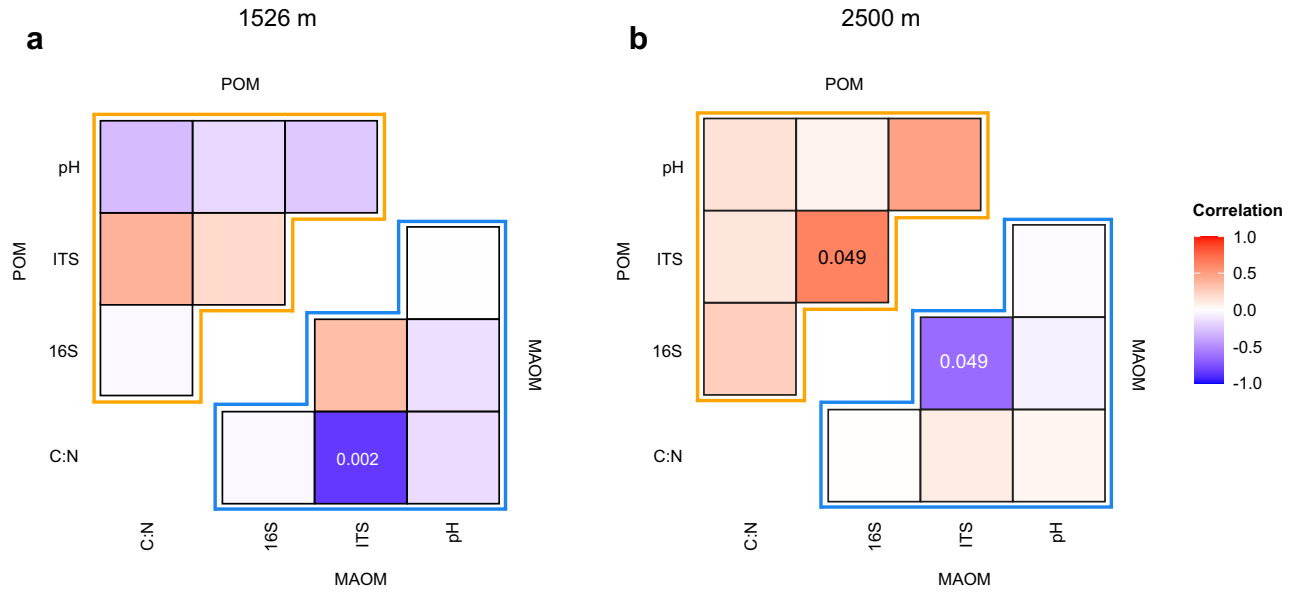

Fig. 4. Heatmap showing Pearson correlation coefficients among all biological and chemical variables for both particulate organic matter (POM) and mineral-associated organic matter (MAOM) at 2500 m a.s.l. and 1526 m a.s.l. (n = 10). Colors represent correlation values, ranging from negative (blue) to positive (red). Only statistically significant p-values ($p < 0.05$) indicating significant correlations are displayed. Sections delimited by a yellow line represent data for POM fractions, while sections outlined in blue correspond to MAOM fractions.

Fungi associated with mineral surfaces can access sorbed organic compounds and exploit microaggregates as refugia from microbial competition and predation[17,47]. In contrast, the lack of differences between POM and MAOM at 1526 m suggests that microbial contributions to SOM fractions are more evenly distributed under milder conditions[48]. Indeed, the plant communities of the 1526 m site are richer in grasses/forbs and legumes (e.g., Trifolium, Supplementary Table 1) and thus tend toward faster, bacteria-leaning C turnover[10,49].

Our third hypothesis (H3) predicted that microbial abundance would vary within the same fraction between the two elevations, with bacteria decreasing at 2500 m due to temperature constraints and fungi increasing at 2500 m as they thrive better than bacteria at lower temperatures and in more acidic conditions. The results partially confirm this hypothesis (Fig. 3). Bacterial abundance differed only between the POM fractions, being lower at 2500 m. This is consistent with higher C:N ratios, which can be connected to reduced decomposition. The low pH (3.95 ± 0.16) at 2500 m may have further inhibited bacterial growth, as bacteria generally thrive in neutral to slightly acidic soils[7,44,50].

Moreover, total nutrient concentrations were lower at the 2500 m site than at the 1500 m site (Supplementary Table 3). This difference is consistent with the reduced bacterial abundance observed in POM, whereas MAOM-associated communities appeared less affected. This is in line with the concept that nutrient scarcity disproportionately suppresses fast-growing POM-associated taxa compared with slower-growing mineral-associated taxa[51].

This supports the idea that altitude mainly affects bacterial abundance in the more labile POM, whereas MAOM, with similar organo–mineral associations at both elevations, is less responsive to elevation-driven changes. Fungal abundance also remained stable across elevations, suggesting that fungal communities are less sensitive to these constraints than bacterial communities, likely due to their greater tolerance of acidic conditions and ability to degrade more recalcitrant organic material[44,50,52].

At 2500 m, a positive correlation between fungi and bacteria in POM and a negative correlation in MAOM suggest distinct microbial interactions (Fig. 4b). The correlations were weak and close to the threshold of statistical significance ($p = 0.049$; Fig. 4b), so this interpretation should be treated with caution. Nevertheless, the patterns found are consistent with synergistic decomposition in POM and competitive dynamics in MAOM. Our findings align with conceptual models in which fungi initiate the breakdown of complex plant residues and bacteria further process these substrates, facilitating nutrient turnover[11,14]. Conversely, the negative correlation in MAOM indicates competition for limited resources, reinforcing microbial efficiency in C utilisation and promoting the transformation of organic matter into more stable forms[19,38,50]. Additionally, this competition may stimulate the production of microbial by-products, such as polysaccharides, which integrate into the mineral matrix and persist over time[39].

At 1526 m, microbial correlations appeared weaker, suggesting higher substrate availability, which supports a more stable microbial community with less competition for resources in each fraction[53–55] (Fig. 4a). The negative correlation between fungal abundance and the C:N ratio in MAOM indicates a more advanced stage of decomposition, as lower C:N ratios generally reflect microbial turnover of soil organic matter. This suggests that fungal activity contributes to this process, enhancing nutrient availability for other microbes and plants[16,56,57].

Conclusions

This study enhances our understanding of soil organic matter (SOM) dynamics by analysing microbial abundance across SOM fractions at two different elevations. Despite a similar MAOM/POM ratio across elevations, a significant increase in the C:N ratio at 2500 m suggested slower decomposition rates due to lower temperatures and reduced pH. Bacteria were more abundant in MAOM and differed significantly across the site, reflecting their role in stabilising organic matter and their sensitivity to measured site characteristics such as pH and nutrient availability. Conversely, fungal abundance was higher in MAOM only at 2500 m, and did not differ across the sites, indicating resilience to lower temperatures and more acidic soil conditions than bacteria. At 2500 m, we observed a positive correlation between fungi and bacteria in POM, which may indicate enhanced decomposition rates. In contrast, the opposite trend was exhibited in MAOM, suggesting improved C stabilisation. Weaker correlations at 1526 m suggest higher substrate availability, which can sustain a more balanced microbial community. Our results highlight the value of integrating microbial abundance data with SOM fractions to explore patterns of C distribution and microbial community structure across elevations, emphasising the importance of integrating both aspects for sustainable management practices in alpine ecosystems. The results also highlight the need for further research on the role of microbial communities in C stabilisation. In particular, the study would benefit from additional sampling time points and further sampling locations to strengthen the outcomes. Moreover, further research into the functional and taxonomic characterisation of microbial communities may provide key insights into the mechanisms behind SOM dynamics in these environments.

Data availability

The data used to support the findings of this study are available from the corresponding author upon request.

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Author contributions

I.F. and L.F. contributed equally to the present study (first authors) by conceptualizing the work, conducting the investigation, performing formal analysis, curating the data, preparing visualizations, and writing the original draft of the manuscript. R.T. and P.B. contributed to resource provision and participated in reviewing and editing the manuscript. A.A., O.G., L.Z., and L.M. contributed resources and assisted in reviewing and editing the manuscript. L.B. supervised the research, contributed to the methodology and resource acquisition, and participated in manuscript review and editing. T.M. conceptualized the work, supervised the project, contributed to the methodology and resource provision, and participated in reviewing and editing the manuscript. All authors discussed and commented on the methods and results and contributed to the final version of the paper.

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Declarations

Competing interests
The authors declare no competing interests.

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