Anthropogenic disturbances in an unmanaged alpine Norway spruce forest: effects of early-stage sanitary logging on soil health and mycobiome and microbiome biodiversity

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European forest biodiversity has been profoundly shaped by centuries of anthropogenic disturbance, including silvicultural practices. Old-growth and unmanaged forests constitute low-disturbance systems that are essential for sustaining biodiversity and ecosystem functioning. The analysis of environmental DNA is useful for biomonitoring and biodiversity assessment in disturbed ecosystems. The aim of this work was to compare soil health and mycobiome and microbiome biodiversity before and after a post-Storm Vaia sanitary felling due to bark beetle (*Ips typographus* L.) infestation in an unmanaged alpine Norway spruce forest stand in Adamello Brenta Park (Trentino Alto-Adige, Italy) to investigate possible early symptoms of disturbance. The selected stand has been excluded by silvicultural treatments for about 40 years. Forest structure, including live and dead woody components, was assessed through ground-based measurements of standard dendrometric variables. Soil samples were collected in summer 2024, prior to the sanitary felling, and again in summer 2025. Physical chemical traits, C and N stable isotopes, and enzyme activities were measured in both years. Moreover, bacterial 16S and fungal ITS2 regions were analysed with a HT-NGS metabarcoding approach. Bioinformatic analyses were conducted using QIIME2 and in the R environment. Selective, early-stage sanitary logging removed approximately 20% of the stand basal area during the initial–intermediate phase of bark beetle infestation. The analysis of soil reveled a decrease in available P and an increase in Pb concentration probably related to the increased exposure of soil surface to the atmospheric conditions and the use of thinning instruments. The analysis of C and N stable isotope and C/N ratio showed also a qualitative change of soil organic matter. The changes in light exposure affected soil enzymes related to the C, N and P cycles, showing higher activity in 2025 than in 2024. Microbiome and mycobiome biodiversity will be discussed considering the microorganism functional activities.