



Cross-taxon congruence of soil biodiversity in *Pinus nigra* plantations two years after a selective silvicultural treatment

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The Selpibioliife project (LIFE13 BIO/IT/000282) has the main objective to demonstrate the potential of a selective thinning silvicultural treatment to enhance soil and flora biodiversity under black pine stands. The monitoring has been carried out by comparing selective and traditional thinning methods to artificial and unmanaged stands. The monitoring survey was carried out in the mountain areas of Pratomagno and Amiata Val D'Orcia (Central Italy). The immense variety of soil organisms including micro- (e.g. bacteria, fungi and nematodes), meso- (e.g. mites and springtails) and macro-fauna (e.g. coleoptera) fauna and the overlying flora play a fundamental role in ecological processes, interacting with one another and with above-ground biodiversity in a complex and intricate network of biological activity. A large literature deals with co-variation of species diversity in grasslands soil whilst few are the works about forests in general and even less about plantation forests. Thus, in order to explore the ecological linkages between aboveground and belowground biota affecting the ecosystem functioning in artificial black pine forests, a cross-taxon congruence analysis has been carried out before any silvicultural operations (T0). To the best of our knowledge no other research took into account the same soil taxa as those used in SelpiBioLife project so far. Biodiversity features have been assessed both before any treatment (T0) and after 1 year (T1) and two years (T2) after thinning. The microbial (bacteria and fungi) diversity was assessed by both biochemical (microbial biomass, microbial respiration, metabolic quotient) and molecular (microbiome) approaches whereas QBS (Soil Biological Quality) index and diversity indexes were determined for mesofauna and other organisms, respectively, including flora.

In general, at T0 the distribution pattern of almost all the analysed groups showed highly supported inter-group congruence except nematoda whose were not significantly correlated with other taxa. All biological groups detained close relationships with the overall dataset of environmental predictors: the highest one was found in bacteria ($r = 0.97$; $p < 0.001$) followed by microfungi ($r = 0.87$; $p < 0.001$) and plants ($r = 0.84$; $p < 0.001$). The results highlighted a different composition and activity of microbial communities within the two areas before thinning, and revealed a significant difference between the overall biodiversity of the two areas. Moreover, microbial and mesofaunal parameters revealed to be differently affected by treatments. Nevertheless, Coleoptera showed higher richness values in Pratomagno, where the wood degrader *Nebria tibialis subcontracta* is the dominant species, compared to Amiata. A general increase of soil biodiversity occurred in the plots after thinning at T1 and T2, compared to untreated control within the two areas, but such results are still heterogeneous and poorly statistically significant. In conclusion, the cross-taxon congruence and variation partitioning remains a useful tool to predict community patterns for other unsurveyed taxonomic groups, especially when resources for biodiversity surveys and conservation planning are limited and the lack of systematic knowledge makes difficult to use a complete species inventory. Thus, more evident and significant results are expected on the next years.