BIOFORDIV

Taxonomic, functional and phylogenetic diversity of forest biocenoses along a gradient of naturalness

Métaprogramme BIOSEFAIR

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The BIOFORDIV project uses a multi-taxonomic and interdisciplinary approach to analyse the response of forest biodiversity to the history of silvicultural management and the naturalness gradient of ancient native fir forests. This work is highly relevant in the current climate high societal and operational expectations regarding sustainable forest management and biodiversity conservation, particularly in mountain ranges with contrasting histories of exploitation.

Work was carried out in two mountain ranges in the Pyrenees: Canigou and Burat. The forests studied were representative of three categories corresponding to a gradient of anthropisation: (i) production forests that are currently exploited, (ii) forests that were formerly exploited and have been left to evolve freely for at least 50 years, and (iii) old forests with very few traces of exploitation, dating back more than 100 years. BIOFORDIV used the study of three complementary indicator groups (forest birds, saproxylic beetles and vascular flora) to characterise biodiversity in different dimensions (taxonomic, functional and phylogenetic) and analyse its determinants.

Biological communities and environmental components were characterised using standardised inventories, coupled with the evaluation of innovative biodiversity monitoring methods, such as passive acoustics, automated data analysis and molecular tools based on environmental DNA (eDNA). Comparisons with conventional methods were used to test their complementarity, performance and operational limitations.

The results highlights the different ways in which biological communities respond to forest management history. At the multi-taxonomic level, species richness appears to be mainly determined by the specific context of each forest. In contrast, community composition, abundance, and certain aspects of diversity are strongly influenced by the degree of naturalness and maturity of the stands. Among the 241 species of saproxylic beetle recorded, species richness varied little according to management. However, the composition of assemblages was clearly structured by silvicultural history, highlighting the importance of habitat quality and continuity rather than resource quantity alone. Bird communities (24 species) showed a dominance of generalist species ; however, their richness, abundance, and phylogenetic diversity increased with the structural complexity of the stands and the density of tree microhabitats, which were identified as key elements. Vacular flora (85 species) revealed a strong differentiation between massifs and a marked influence of local conditions, while highlighting a floristic specificity associated with old forests.

Innovative approaches have proven their value. Passive acoustics, coupled with the automated identification tool BirdNET, has shown comparable performance to standardised bird point counts. eDNA analyses have detected a significant proportion of the insect species and genera identified morphologically, as well as species that complement conventional approaches. These analyses have also provided access to poorly documented fungal diversity.

Overall, BIOFORDIV highlights the importance of integrating qualitative indicators of forest structure, such as dendro-microhabitats and ecological continuity, into forest assessment and management. The project thus reinforces recommendations in favour of silvicultural practices that preserve or enhance these elements, including in production forests. The identified results and limitations have directly led to the development of the SALUD project (2025–2029), which builds on BIOFORDIV by broadening the spatial scope and the taxa studied, and by integrating a ‘One Health’ approach, thereby strengthening the scientific and operational scope of the work.

Detailed results

Response of biodiversity drivers to forest management history

Biodiversity inventories conducted in the Canigou and Burat mountain ranges revealed that biological communities responded differently to forest management history and the local environmental context. A joint analysis of saproxylic beetles, birds, and vascular flora highlights a recurring decoupling between species richness and community structure, as well as the importance of the qualitative characteristics of forest stands.

The surveyed saproxylic beetle communities comprised 241 species and a total of 4,568 individuals. Species richness did not vary significantly according to silvicultural management history, suggesting that species diversity at the stand level was relatively insensitive to recent management practices. Conversely, species diversity was strongly influenced by the specific context of each forest, likely due to biogeographical and environmental factors, as well as long-term forest history. However, the taxonomic composition and abundance of saproxylic assemblages were clearly influenced by management history, reflecting a marked response by communities to the degree of naturalness and maturity of stands.

The absence of a significant relationship between beetle abundance, dead wood quantity, and number of dendro-microhabitats suggests that these communities depended more on the quality, diversity, and spatio-temporal continuity of available resources than on their quantity.

A total of 24 species and 384 individuals were surveyed in the forest bird communities. The majority of species were common to both mountain ranges, reflecting regional homogeneity in bird assemblages. However, a few species reflected local specificities. The specific composition appeared to be relatively insensitive to forest management history, suggesting dominance by generalist species. However, species richness and abundance varied between forest areas, being positively correlated with stand structure and resource availability — particularly dendro-microhabitats — which were more prevalent in old-growth and mature forests. Phylogenetic bird diversity of birds also increased with tree microhabitat density and vegetation complexity, while no relationship was observed with the amount of dead wood or with functional diversity indices. This suggests a high level of functional redundancy, likely inherited from the earlier anthropogenic filtering of these communities.

The inventory of vascular flora identified 85 species, with a marked difference between the two massifs, only 32 taxa being common to both. Floristic richness varied greatly at the subplot level and was significantly higher in Burat than in Canigou, reflecting a predominant massif effect. Management history had no clear, generalizable influence on species richness, which was mainly explained environmental openness and local heterogeneity. However, analysis of the floristic composition highlighted an impact of management, allowing production forests to be distinguished from old forests, with ancient forests occupying an intermediate position. This suggests richer soils and increased dynamics of organic matter in the oldest stands. This underlines the potential importance of conserving old forests, as these can harbour more specific flora. In our case, this includes nitrophilic species that are typical of these forests, such as *Circaea alpina*.

Comparison of traditional inventory methods with innovative methods

For forest birds, we evaluated BirdNET's performance in automatically identifying species from audio recordings made in situ. We used Audiomoth passive acoustic recorders to collect acoustic data from bird communities at the Canigou and Burat sites. A total of 1,512 hours of recordings were analysed and filtered to retain only those of sufficient quality to be analysed by BirdNET, an algorithm for recognising bird vocalisations covering approximately 6,000 species worldwide. We then compared BirdNET's performance in characterising avian species richness to that of inventories carried out by an expert ornithologist using in situ bird point counts. Across all sites and species, BirdNET detected four fewer species than the expert. For species recognised by both methods, the concordance rate between BirdNET detections and expert observations was 67%. However, at certain sites, BirdNET detected the presence of three species that were not observed at certain bird count sites, highlighting the value of passive acoustics for estimating species richness, particularly thanks to the increased temporal coverage of the sampling.

With regard to insects, the results are based on a comparison between taxonomic identifications obtained through metabarcoding (Illumina sequencing) of the trapping solvent, and of identifications through entomological expertise of morphology. The analyses showed that 20.7% of the species and 28.7% of the genera identified morphologically were also detected by environmental DNA (eDNA), illustrating a partial but significant concordance between molecular and traditional approaches. EcoDNA samples taken from dendro-microhabitats and soil detected 31 additional species belonging to different insect orders that were not identified by other methods. Moreover, using trapping solvent and soil samples provided unparalleled insight into the fungal diversity associated with the studied habitats, revealing 206 fungal species in the solvent and 145 genera in the soil. These results highlight the strong potential of eDNA approaches for the integrative characterisation of entomological and fungal biodiversity, while demonstrating their complementarity with traditional inventory methods.

Overall, the project results showed that specific richness, at the multi-taxonomic level, was mainly determined by the local context of the mountain ranges, while community composition, abundance, and certain dimensions of diversity (functional and phylogenetic) were strongly influenced by management history and forest maturity. Site conditions and stand structure thus appeared to be major determinants of the diversity of the communities studied, sometimes more important than management history alone. Dendro-microhabitats in particular emerge as key structuring elements promoting multi-taxonomic diversity.

The BIOFORDIV project therefore supports recommendations for forest management practices that preserve or enhance dendro-microhabitats in production forests in order to maintain communities similar to those found in minimally or unexploited forests. More broadly, these results highlight the importance of integrating qualitative indicators of forest structure, naturalness, and ecological continuity to improve our understanding of the impact of silvicultural management on biodiversity and encourage their consideration by forest managers and public decision-makers.

Scientific perspectives.

Although the models developed performed satisfactorily from a statistical point of view, several methodological and contextual limitations necessitate cautious interpretation of the results and open up clear prospects for the continuation of the project. The high variability observed within the modalities, combined with the limited number of subplots and massifs studied, reduces the ability to generalize certain statistical relationships that have been identified, particularly at a

fine scale. For insects, unfavorable climatic conditions during the sampling period probably affected the activity and detectability of species, pote,tially masking or attenuating certain ecological trends. More broadly, intra- and inter-site variability remains high, highlighting the need to expand the spatial and temporal scope in order to confirm the robustness of the results. Replicating these trends on a larger geographical scale, incorporating a greater number of forest areas and plots, appears essential in order to refine the analyses and consolidate management recommendations. Continuing BIOFORDIV in this context would therefore enable these constraints to be overcome, better integrate the effects of historical dynamics and past anthropogenic pressures, and strengthen the operational scope of the results in terms of sustainable forest management and biodiversity conservation.

Overall, the lessons learned from BIOFORDIV informed the development of the SALUD project (2025–2029), which is a flagship initiative of the Biosefair metaprogramme. This project aims to deepen and broaden the results obtained by repeating the biodiversity inventories on the three taxa studied, while extending the scheme to six forest areas nationwide, from the Vosges to the Pyrenees. SALUD also aims to explore the effect of the naturalness gradient on the biodiversity of additional taxa, such as bats, small mammals, and ungulates. Finally, the project includes a new component dedicated to human health, within the “One Health” conceptual framework, with a particular focus on ticks and associated vector-borne diseases. This integrative approach, which is a direct extension of the explorations made possible by BIOFORDIV and will strengthen the scientific and operational scope of the work by linking biodiversity, forest ecosystem functioning, and public health issues.