THE SILVA GABRETA BIODIVERSITY MONITORING DATABASE: ASSESSING BIOLOGICAL DIVERSITY IN THE ŠUMAVA NATIONAL PARK, CZECH REPUBLIC

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ABSTRACT

The Bohemian Forest spans the borders of Bavaria, Czechia and Upper Austria, and is important for studying forest biodiversity in central European mountain ecosystems. This study focuses on assessing the patterns in biodiversity in the Šumava National Park. Species richness, Shannon diversity index, evenness and dominance were determined for 117 forest plots (large sample) and a subsample of 49 plots (small sample) using comprehensive monitoring techniques within the Silva Gabreta project, a cross-border initiative implemented together with the Bavarian Forest National Park. Data were collected for the following taxonomic groups: plants, fungi, mammals and invertebrates, using a variety of trapping methods and survey techniques. Results indicate significant differences in the number of species in the different taxonomic groups, with Lepidoptera, fungi and Bryophyta with the highest species richness and diversity, whereas groups such as Neuroptera, Curculionidae and mammals had lower values. Although most biodiversity indicators were not significantly different between the large and the small sample at the taxonomic level, species richness and Shannon diversity were higher in the small sample. This may be attributed to the trapping methods used in those plots, which are likely to have resulted in more complete captures of the species than in the plots of the large sample. The findings indicate that 49 plots are a suitable number for long-term biodiversity monitoring, provided key plots with efficient trapping setups are included. This study highlights the importance of careful plot selection and suggests that a mixed monitoring strategy, incorporating both broad taxonomic assessments and targeted approaches for specific taxa, may be the most effective for monitoring biodiversity.

Keywords: biodiversity; database; forest disturbance; forest management; monitoring; sampling design

Introduction

The Bohemian Forest is an extensive forest ecosystem, which in past decades was significantly affected by large-scale natural disturbances (wind, insect outbreaks), but spared the effects of intensive logging, thanks to which it regenerated naturally. A new generation of trees successfully growing among the trunks of trees killed by bark beetles is a guarantee of the natural renewal of this forest ecosystem. But less is known about how disturbance and post-disturbance forest management affect the biodiversity recorded in central European mountain ecosystems.

This forest extends across the borders of Bavaria, Czechia and Upper Austria, hosts a diverse array of habitats including old-growth forests, glacial lakes, peat bogs and mountain grasslands. The most valuable parts of this landscape are protected under the Natura 2000 network and form part of the Bavarian Forest National Park (BFNP) and the Šumava National Park (ŠNP). These areas, along with the Šumava Protected Landscape Area, offer significant opportunities for long-term ecological research (Heurich et al. 2011), particularly in the context of environmental changes and their effects on biodiversity.

The long-standing collaboration between BFNP and ŠNP has been formalised in the transboundary Long-Term Socio-Ecological Research (LTSER) platform, *Silva Gabreta*. This cooperation aims to improve the coordination of research activities, harmonise methodologies and establish the same method of monitoring in the region. The common Czech Republic – Bavaria Interreg project called "Silva Gabreta – monitoring of mountain ecosystems" (project No. 368) was started in January 2015 (Křenová and Seifert 2014). The results of this project enabled the implementation of the proposed monitoring activities in a three-year project. The Interreg V project No. 26 "Silva Gabreta – Monitoring of biodiversity and water regime" (henceforth called *Silva Gabreta* project) was jointly prepared and later successfully funded by the Cross-border cooperation programme Czech Republic – Bavaria Free State ETC goal 2014–2020 (Křenová and Seifert 2018). This project included a range of key habitats, including forest ecosystems, mires, and aquatic ecosystems, and also supplementary activities, such as the modelling of mesoclimatic conditions and studies on the effects of de-icing salt. The 2016–2018 forest biodiversity monitoring project was built upon previous biodiversity research efforts conducted in the Bavarian Forest, notably the BIOKLIM project initiated in 2006 (Bässler et al. 2010). BIOKLIM investigated the effects of climate change and large-scale disturbances, such as windthrows and bark beetle outbreaks, on forest ecosystems. The findings from BIOKLIM highlighted the importance of long-term data for understanding the factors that determine the biodiversity in forested landscapes.

Similarly, the *Silva Gabreta* project enhanced the level of understanding of patterns in biodiversity, ecosystem

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processes and how these may be influenced by environmental and climatic changes. The main aim of this research was to assess species richness and other biodiversity indicators, such as the Shannon diversity index, species evenness and species dominance, for 17 taxonomic groups including plants, fungi, mammals and invertebrates. The monitoring aims to describe the biodiversity in terms of 17 groups of flora and fauna along gradients in altitude and forest structure using a jointly developed design based on the BIOKLIM project (Bässler et al. 2015). A total of 157 study sites were established in BFNP (121 in the national park and 36 in the surrounding area) and 120 study sites in ŠNP (95 sites in the ŠNP and 25 sites in Šumava PLA) to optimise the transboundary monitoring network. Much of the data from Bavarian plots has been processed and published by researchers in the Bavarian Forest NP. Their publications focused on many taxonomic groups and research aims. They used various sophisticated methods, such as LiDAR data to determine bird assemblages (Bae et al. 2018) and habitat use by bats (Kortmann et al. 2018) or airborne laser scanning (ALS) and colour-infrared aerial imagery (CIR) to identify tree characteristics used by woodpeckers (Zielewska-Büttner et al. 2018). Their research interest also targeted highly debated questions about bark beetle outbreaks in Central Europe (Sommerfeld et al. 2021) or pest control connected with nature conservation (Hagge et al. 2019). They also carried out complex research on compositional diversity and biomass productivity in temperate zones (Dieler et al. 2017). There were also studies on the life in forests (Thorn et al. 2020a,b) and its connection to the underground communities of decomposers and gastropods (Kirchenbaur et al. 2017; Hagge et al. 2019, p. 20).

Several findings recorded for the Šumava NP, particularly regarding the flora and selected fauna, remain unpublished. This paper aims to present and analyse these data, focusing on the following taxonomic groups: insects (Aculeata, Carabidae, Cicadina, Collembola, Curculionidae, Gastropoda, Lepidoptera, Neuroptera, and Opiliones), fungi, bryophytes, lichens, birds, mammals, and vascular plants. In addition, 120 forest plots and a subsample of 49 plots were used to evaluate whether a smaller number of samples from plots with all types of traps would be just as efficient for reliably assessing biodiversity throughout the region. By providing detailed information on species diversity, commonness and rarity in the Šumava NP, could facilitate conservation, optimise monitoring design in the future and guide biodiversity management in this transboundary region (Ferraz et al. 2021).

Methods

Study area

Šumava National Park (ŠNP), with an area of 680.64 km², is the largest national park in Czechia (Fig. 1). It is in the Bohemian Forest, which forms part of the broader Šumava uplands, one of the oldest mountain ranges in Central Europe. The park's geomorphological features are shaped by a history of glaciation during the Quaternary period, which resulted in the creation of significant landforms such as cirques, glacial lakes, frost cliffs and boulder debris. The park is positioned along the Czech-Bavarian border and connected with the Bavarian Forest National Park in Germany, forming one of the largest transboundary protected areas in Central Europe. The altitude in ŠNP ranges from approximately 605 to 1,350 m a.s.l. However, the highest peak in the entire park, Plechý, reaches 1,378 m a.s.l. The area is dominated by a plateau that lies at around 1,000 m a. s. l., interspersed with ridges and valleys, and features unique formations such as slightly domed upland and valley raised bogs. These bogs, along with other geomorphological features provide habitats for many endemic and endangered species and a rich biodiversity.

The climate in ŠNP is characterised by a continental regime with oceanic influences, typical of the region's altitude and geographic position. The mean annual temperature of the forest plots studied is 5.73 °C, ranging from 3.71 °C to 7.53 °C, while annual precipitation averages 1078 mm, varying between 826 and 1385 mm. These climatic and altitudinal gradients support a variety of types of vegetation, including mountain spruce forests, mixed forests and wetlands. Forest cover over 85% of the park's area, with key types of vegetation ranging from ombrotrophic dome-shaped raised bogs to minerotrophic fens, often surrounded by spruce mire or birch forest on peaty soils.

ŠNP is also notable for its old-growth forest remnants, secondary grasslands and aquatic ecosystems such as glacial lakes and mountain streams. Historically, the region was part of the Iron Curtain corridor, which served as an unintended conservation area, limiting human intervention and preserving the park's natural ecosystems. Today, the park is home to a variety of rare species, including lynx, capercaillie and the freshwater pearl mussel. In addition, mires in the area, many of which were affected by past drainage and peat extraction, have been the focus of recent restoration efforts aimed at conserving these sensitive ecosystems. This diverse landscape, shaped by both natural and anthropogenic factors, provides an ideal setting for long-term monitoring of biodiversity. The park's complex ecosystems, ranging from forests and mires to high-altitude bogs, support a mosaic of habitats that are vital for species conservation at both local and regional scales.

Data collection and sampling design

A biodiversity assessment was conducted in the ŠNP in 2016 and 2017, and species were determined in 2018 and 2019. The BIOKLIM project developed and designed the monitoring of flora and fauna along an altitudinal gradient in the forest (Bässler et al. 2015). Forest biodiversity

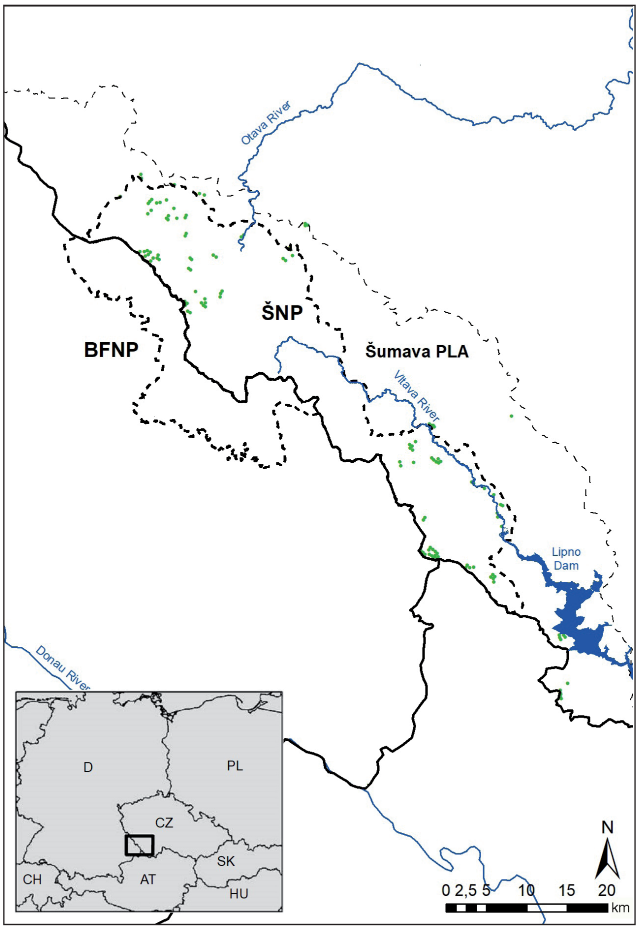

Fig. 1 Map showing the location of the study areas (green) in the Šumava National Park. Map of 120 plots (green points) where monitoring of forest biodiversity was conducted. Dashed lines are borders of the Bavarian Forest National Park (BFNP), Šumava National Park (ŠNP) and Šumava Protected Landscape Area (Šumava PLA).

was monitored at 120 study sites (95 sites in the ŠNP and 25 sites in the Šumava Protected Landscape Area) selected from the set of the biomonitoring project plots studied for long term changes in the ŠNP (Čížková et al. 2011). Twenty-five sites located in nature reservations in the Šumava Protected Landscape Area were included to extend the altitudinal gradient (Křenová and Seifert 2018). The data was collected in the western and southern parts of the ŠNP. In the western part the altitudinal gradient extended from the northern foothills of the Bohemian Forest (the lowest altitude of 605 m a. s. l. in the Otava River valley) over the high-mountain plateau to the highest area on the border with Germany (Plesná Mt., 1332 m a. s. l.). The southern part of the ŠNP ranges from the Lipno reservoir (688 m a. s. l. in the Jasánky Nature Reserve) to the main border range (Trojmezná Mt., 1340 m a. s. l.). Subset of 50 plots was selected on which more detailed monitoring was done (including the use of Malaise traps, light traps and photo traps). In addition to the 120 sites selected for forest biodiversity monitoring, another 30 sites were included, which were treeless areas on mountain plains, mire meadows, Nardus meadows and heathlands, all important Natura 2000 habitats. Data from these plots were not included in analyses presented in this paper.

The data on 15 taxonomic groups (Aculeata, Carabidae, Cicadina, Collembola, Curculionidae, Gastropoda, Lepidoptera, Neuroptera, and Opiliones, fungi, bryophytes, lichens, birds, mammals and vascular plants) were collected in circular plots of different sizes, such as 0.02 ha, 0.1 ha, and 1 ha (see Table 1, Fig. 2) (for more details, also see (Friess et al. 2018).

The description of the methods involved in the collection of data is largely based on Křenová and Seifert (2018). To monitor insects (Aculeata, Arachnida, Carabidae, Cicadina, Collembola, Curculionidae, Heteroptera, Lepidoptera-butterflies, Neuroptera, and Opiliones), four types of insect traps (Malaise, flight interception, pitfall and light traps) were used. The collected insects were identified according to the taxonomic groups. The highly informative sites were continuously monitored using Malaise traps from May to September and some insects such as moths were collected at night in these plots. Light traps were used once a month and were placed at a height of about 2 m in relatively open areas and set at nights when it was still and not raining.

Birds were recorded in all 1 ha plots using quantitative grid mapping (cf. Bibby 2000; Moning and Müller 2008) based on hearing their songs and presence. Bird song was first listened for at the edge of each plot for one minute and then continued in the centre of the plot for eight minutes. Then one minute was spent listening at the other edge to distinguish between birds in and outside the plot, which was used to correct detection errors recorded at the centre. To optimise the data, bird mapping was done five times during the season: at the end of March, in mid-April, at the beginning and end of May, and at the beginning of June (Müller 2005; Moning and Müller 2008). Mapping was done from sunrise till 11 a.m. on sunny days with little wind and no rain (Müller 2005; Moning and Müller 2008). Camera traps were installed in highly informative plots to record mammals passing through or occurring there.

All fungi (in 0.1 ha plots), as well as bryophytes and lichens (at 0.02 ha plots) were recorded along with type of substrate up to a height of 2 m. Vascular plants were recorded in a single survey of 0.02 ha plots from May to September and focused on the vascular understorey vegetation (including ferns) up to 1 m in height, which was estimated visually using percentage cover or a modified scale of Londo (1976). For analysis, coverage percentages were converted to abundance data as follows: ≤ 0.5% = 1 individual, 0.6–1% = 2 individuals, 2–5% = 3, 6–10% = 4, 11–25% = 5, 26–50% = 6, 51–75% = 7 and 76–100% = 8.

Data analysis

Data from several plots were lost or damaged due to natural events (storm, animal damage), and therefore only data from 117 forest plots (including 49 plots with complex monitoring) were used in the analyses. The raw data were thoroughly cleaned to remove typographic errors and missing values. The species names were checked for conformity with the official list of species names included in the International Code of Zoological Nomenclature for animals (International Commission on Zoological Nomenclature 1999) and the International Code of Nomenclature for algae, fungi, and plants (Turland et al. 2018) for plants. The following biodiversity indicators were calculated: (1) species richness, (2) Shannon diversity index, (3) evenness index and (4) dominance index. These indices quantitatively measure the number of species and their distribution within the area studied.

Species richness refers to the total number of different species present in each plot.

The Shannon diversity index, also known as the Shannon-Weiner index, quantifies the diversity within a specific area or community by considering both species richness and the relative abundance of each species. This index provides a more comprehensive view of species composition compared to species richness alone, as it accounts for how evenly species are distributed in the area studied. The Shannon diversity index is calculated using the following formula:

$$H = -\sum_{i=1}^{S} p_i * ln p_i \tag{1}$$

where H is the Shannon diversity index, p_i is the percentage of individuals of species i, $ln p_i$ is the natural logarithm, and S is the total species richness. The Shannon diversity index can be interpreted as follows: $H \leq 1$ – low diversity; $1 < H \leq 3$ – moderate diversity; $H \geq 3$ – high diversity.

The evenness index measures the degree of similarity in the abundance of different species within an environment. Pielou's evenness index (Pielou 1966) quantifies how evenly individuals are distributed among the species in a community. It is calculated using the formula:

$$J = H/H_{max} \tag{2}$$

where J is the evenness index, H is the Shannon diversity index, and $H_{\max}$ is the natural logarithm of the richness of the community studied ($\ln(S)$). The value of J ranges from 0 to 1, with higher values indicating greater evenness in species distribution. The evenness index can be categorised as follows: $0 < E \leq 0.5$ – weak community; $0.5 < E \leq 0.75$ – unstable community; $0.75 < E \leq 1$ – stable community.

The dominance index measures the extent to which one or a few species dominate a community. It is also referred to as Simpson's dominance index and is calculated using the formula:

$$D = \Sigma n_i(n_i - 1) / N(N - 1) \tag{3}$$

where n_i is the number of individuals of species i, N is the total number of individuals in the community. The value of the dominance index ranges between 0 and 1, with higher values indicating lower diversity and higher dominance. Dominance indices are negatively correlated with alpha diversity indices such as species richness, evenness, diversity and rarity. In general, more dominant communities are less diverse. The dominance index (DI) can be categorised as: $0 < C < 0.5$ – low dominance; $0{,}5 < C \leq 0.75$ – moderate dominance; $0.75 < C \leq 1.0$ – high dominance.

To address the dependence structure in the data, biodiversity indicators for the large sample and small sample (subset of 49 plots) were compared using a permutation test. In this method, the observed test statistic is the difference between the two groups based on the data collected and the permutation test p-value reflects the probability of observing a test statistic as extreme as, or more extreme than the observed value under the null hypothesis (Good 1994; Manly 2018). The permutation test was chosen due to its non-parametric nature, making it particularly suitable for the biodiversity data in this study, which do not follow normal distributions. Unlike traditional parametric methods, such as t-tests or ANOVA that rely on assumptions of normality and sample independence, the permutation test is robust when these assumptions are not met. This is crucial for this dataset, as the small sample is nested in the large sample, creating a dependency between groups. By generating a null distribution by resampling, the permutation test effectively accounts for this dependence. In addition, its strong performance with small sample sizes makes it ideal for comparing subsamples, as in this case. All data processing and analysis were done in R (R Development Core team 2023).

Results

The full Silva Gabreta monitoring database for the large sample includes 1982 species, including 473 species of fungi, 414 – Lepidoptera, 249 – lichens, 202 – Bryophyta, 188 – Plants, 99 – Carabidae, 90 – Cicadina, 83 – Aculeata, 70 – Aves, 48 – Gastropoda, 19 – Collembola, 14 – Curculionidae, 12 – Opiliones, 11 – mammals, and 10 species of Neuroptera. That for the small sample includes 1578 species, including 414 species of Lepidoptera, 332 – Bryophyta, 209 – lichens, 159 – Bryophyta, 120 – Plants, 75 – Aculeata, 68 – Carabidae, 63 – Cicadina, 52 – Aves, 32 – Gastropoda, 14 – Collembola, 11 – Curculionidae, 11 – Opiliones, 11 – mammals, and 7 species of Neuroptera.

Biodiversity of the different taxonomic groups

The biodiversity indices (species richness, Shannon diversity index and species evenness) of the 15 taxonomic groups are very variable. The species richness of Lepidoptera and Bryophyta was the highest (Fig. 2A). In contrast, the species richness of groups such as Neuroptera,

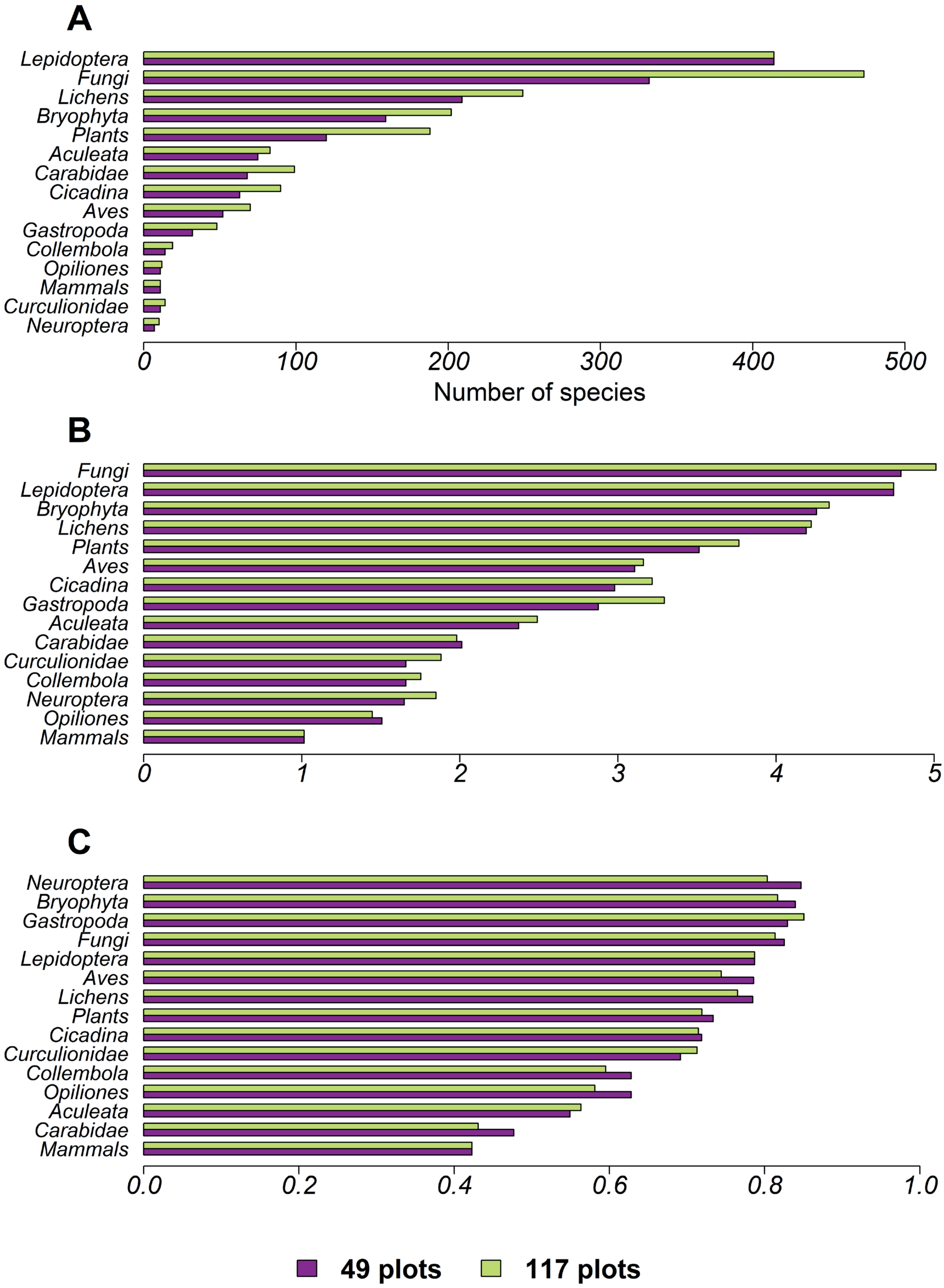

Fig. 2. Biodiversity indicators – species richness (panel A), Shannon diversity index (panel B) and species evenness (panel C) for each taxonomic group for the small sample (49 forest plots – purple) and large sample (117 forest plots – light green) monitored within the *Silva Gabreta* biodiversity monitoring project in Šumava NP. Species richness, Shannon index, evenness and dominance indices are listed in Appendix, Fig. A1–A4.

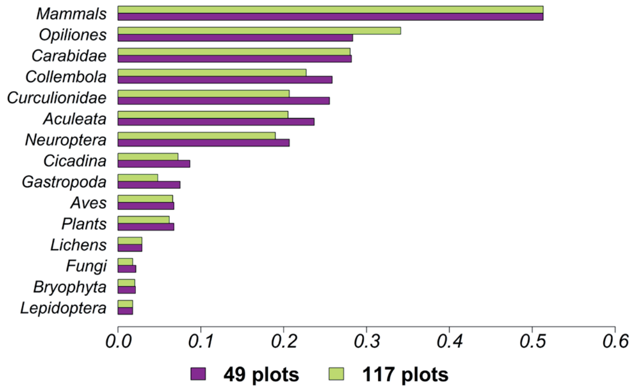

Fig. 3. Dominance indices of the taxonomic groups studied for the small sample (49 forest plots – purple) and large sample (117 forest plots – light green) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.

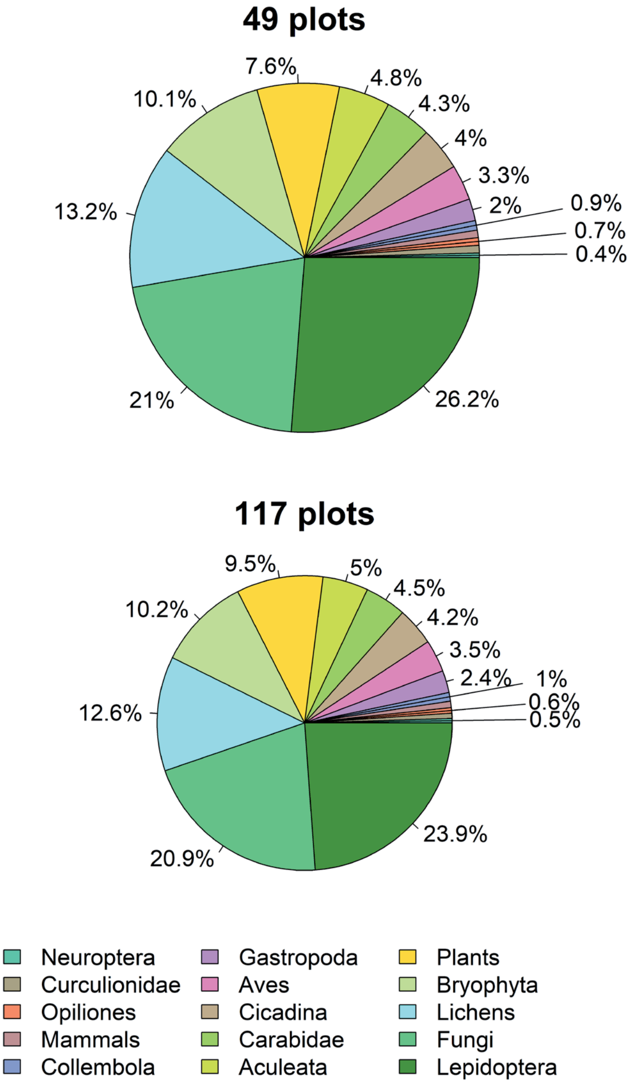

Fig. 4. Pie charts illustrating the percentage composition in terms of species richness of the different taxonomic groups studied for the small sample (49 forest plots) and large sample (117 forest plots) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.

Opiliones, and mammals was relatively low. The Shannon diversity index also varies greatly among taxonomic groups. Like species richness, Bryophyta and Lepidoptera have the highest Shannon indices, indicating a high level of diversity (a combination of both richness and evenness) in these groups (Fig. 2B). In contrast, mammals, Opiliones and Neuroptera have lower Shannon indices, indicating less diversity in these groups. The species evenness index is less variable than the other indices, but there are still notable differences among taxonomic groups. Groups such as Neuroptera, Bryophyta and Gastropoda have high levels of evenness, meaning that species within these groups tend to have more similar population sizes. In contrast, groups like Aculeata, Carabidae, and mammals have moderate levels of evenness, indicating that some species are more dominant than others in these groups (Fig. 2C).

As expected, the dominance index was very variable for the different taxonomic groups and approximately inversely mirrored the variability in the evenness index of these groups, i.e., high evenness corresponds to lower dominance of a particular group or species. Taxonomic groups have a broad range of dominance values, from 0.02 in Lepidoptera and fungi to 0.5 for mammals, which indicate significant differences in their relative abundances in the forest plots (Fig. 3). Certain taxonomic groups, such as mammals and Carabidae are consistently dominant in both the large and small samples, indicating either a competitive advantage or they are abundant in the area studied. In contrast, other groups, such as lichens, fungi, Bryophyta and Lepidoptera, have markedly low dominance, reflecting their small contribution to overall community structure (Fig. 3).

Biodiversity and sample size

For most taxonomic groups, species richness is consistently higher in the large than the small sample (Fig. 2A). This is especially so for groups like plants and fungi, with significantly more species in the large sample (Fig. 2A). However, for taxonomic groups like Neuroptera, Opiliones and mammals the difference in species richness between the two samples is minimal. The Shannon diversity index is generally greater for the large sample for most taxonomic groups (with the exceptions of Carabidae and Opiliones). For example, Gastropoda, in particular, the Shannon index for the small sample is 2.88 and 3.29 for the large sample (Fig. 2B). The differences for Carabidae and Collembola, in the two samples, however, is smaller. Evenness varies less with sample size than the other indices, with similar values recorded for the small and large samples for most groups. However, Carabidae, Opiliones and Neuroptera have a slightly higher evenness in the small sample (Fig. 2C). In contrast, mammals, Lepidoptera and Cicadina show little difference in evenness in the two samples (Fig. 2C).

The species richness structure, depicted in pie charts, illustrates the relative contribution of various taxonomic groups in the two samples. The percentages of individual taxonomic groups in terms of species richness are approximately similar in both the large and small sample (Fig. 4). In both samples, Lepidoptera and fungi dominate the structure in terms of species richness, each contributing over one-fifth of the total. Other taxonomic groups with a notable contribution include lichens, bryophytes and vascular plants, which together account for approximately 10–13% of the species richness. Taxonomic groups contributing 2–5% to the overall species richness are Aculeata, Carabidae, Cicadina, birds and Gastropoda. The remaining groups, including Collembola, mammals, Opiliones, Curculionidae and Neuroptera, each contribute less than 2% to the species richness structure (Fig. 4). Interestingly, in the small sample, the dominant taxonomic groups: Lepidoptera, fungi, and lichens, are at slightly higher percentages in the overall species richness structure than in the large sample. In contrast, groups with small percentages, such as bryophytes, plants, Aculeata, Carabidae, Cicadina, birds and Gastropoda, have slightly larger percentages in the large than in the small sample (Fig. 4). The biodiversity indicators (species richness, Shannon diversity index, species evenness and species dominance) calculated for each plot and sample size are listed in Appendix (Figs. A1–A4).

Sample size-specific biodiversity indicators

The permutation tests comparing biodiversity indicators between the full and small sample revealed that, both at the levels of the taxonomic group level and plot, most biodiversity indicators did not differ significantly (Fig. 5). Species richness and the Shannon diversity index were slightly and insignificantly higher in the large sample at the taxonomic group level, whereas evenness and dominance were marginally higher in the small sample. At the taxonomic group level, none of the four biodiversity indicators differed significantly in the two samples ($P > 0.05$) (Fig. 5, panels A, C, E, and G). At the plot level, species evenness and dominance also did not differ significantly in the small and large samples ($P > 0.05$) (Fig. 5, panels G and H). However, species richness and the Shannon diversity index were significantly higher in the small than in the large sample ($P < 0.001$ and $P < 0.01$, respectively) (Fig. 5, panels B and D).

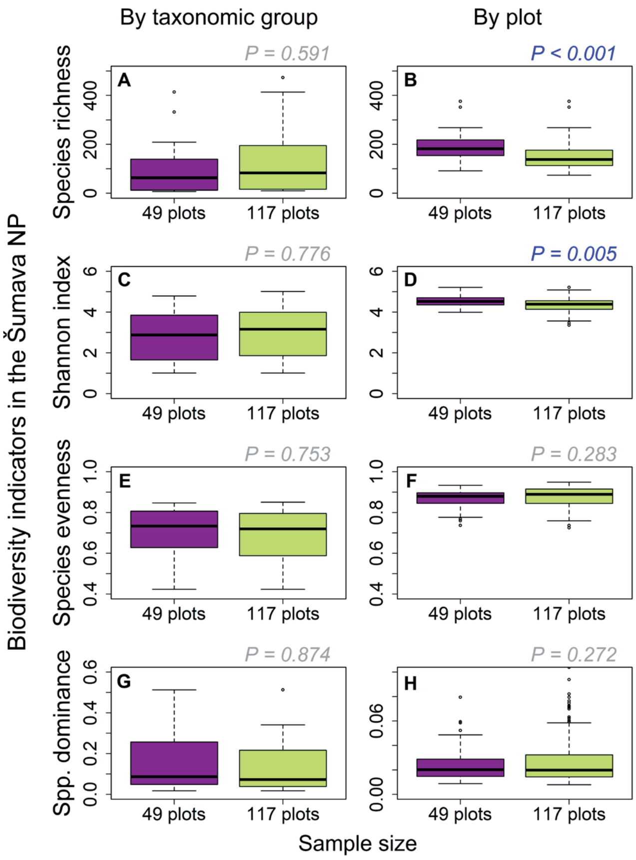

Fig. 5. Comparison of biodiversity indicators recorded for the small sample (49 forest plots – purple) and large sample (117 forest plots – light green) in the Silva Gabreta monitoring project in Šumava NP. Biodiversity indicators are quantified by taxonomic group (panels A, C, E, G) and by plot (panels B, D, F, H). Comparisons were done using permutation tests. P-values that indicate no significant difference ($P > 0.05$) are shown in light grey, while P-values indicating a significant difference ($P < 0.05$) are presented in blue.

Discussion

Biodiversity patterns across taxonomic groups

The biodiversity assessment based on the large sample from the Šumava National Park revealed substantial variability in biodiversity indicators for the taxonomic groups studied. As expected, Lepidoptera and Bryophyta had the highest species richness and Shannon diversity index, whereas smaller groups, such as Neuroptera and mammals, had lower values. These patterns are consistent with previous biodiversity studies in temperate forest ecosystems, where Lepidoptera and Bryophyta are highly diverse due to their varied ecological niches and responses to environmental factors (Shaw and Goffinet 2000; Krumbach et al. 2003).

The relatively low species richness and diversity in taxa like mammals and Neuroptera may reflect the small number of suitable habitats or fewer ecological specialisations available for these groups within the park (Hawkins et al. 2003; Rabosky and Hurlbert 2015; Engel et al. 2018; McCain et al. 2018). The dominance index results further support the variation in species distribution across taxonomic groups, with taxa such as mammals and Carabidae being dominant. This indicates that, in these groups, a few species are more abundant or have competitive advantages, potentially due to specific habitat preferences or reduced interspecific competition (Loreau 1990; Niemelä et al. 2002; Presley et al. 2019). In contrast, taxa such as Bryophyta, fungi and Lepidoptera are less dominant, reflecting a more balanced species abundance, possibly due to the greater variety of niches available for these taxa in forest ecosystems (Söderström and Herben 1997; Horton and Bruns 2001; Ober and Hayes 2010; Davison et al. 2022). Interestingly, the number of species identified in this study is less than half of what is recorded in a similar study in Germany (Friess et al. 2018). This disparity can be attributed to the significantly higher altitudinal gradient on the German side, which is likely to include a greater range of habitats and, consequently, a richer biodiversity. Thus, altitudinal variation may play a crucial role in shaping biodiversity patterns across regions, underscoring the importance of considering such factors in comparative biodiversity studies.

Sample size and monitoring efficiency

A central aim of this study was to compare biodiversity indicators based on a large and a small sample, to explore the potential for optimising future monitoring efforts. The results indicate that, at the taxonomic group level, most biodiversity indicators (species richness, Shannon diversity index, species evenness and dominance) did not differ significantly in the two samples (Fig. 5, panels A, C, E, and G). This indicates that reducing the sample size to 49 plots may not result in a significant lower biodiversity for most taxonomic groups, which has important implications for future biodiversity monitoring programmes. This finding is in accord with other studies that demonstrate the feasibility of reducing sample sizes while maintaining data precision and reliability in large-scale ecological monitoring (Archaux and Bergès 2008; Schmeller et al. 2017). However, at the plot level, species richness and Shannon diversity were significantly higher for the small sample (Fig. 5, panels B and D), which was unexpected given that the large sample included a larger number of plots. This result may be because the small sample consisted of plots that were equipped with all types of traps, which resulted in an increased capture of insect species. In contrast, some plots in the large sample lacked certain types of traps, potentially underestimating species richness and diversity in those areas. This highlights the importance of using many types of traps and different sampling methods when comparing biodiversity recorded based on different sample sizes (Work et al. 2002).

While reducing the number of plots monitored might increase efficiency, it is crucial that any downsizing does not compromise the representativeness of the data. Fewer plots could lead to underrepresentation of habitats, missing critical variations in biodiversity across environmental gradients, and under-detecting of rare or cryptic species, which are important indicators of ecosystem health. Furthermore, sampling few plots could hinder the monitoring of long-term temporal changes and ecosystem responses to disturbances, both essential for effective conservation. Ensuring the inclusion of key plots with comprehensive sampling in any subsample is therefore vital for preserving data integrity. A mixed monitoring strategy, which combines a reduction in the number of plots with intensified sampling in critical areas, could help balance resource efficiency with the need for robust conservation (Gardner 2010; Bicknell et al. 2014; Aizpurua et al. 2015).

Implications for future monitoring and management

The results of this study indicate that optimising biodiversity monitoring in Šumava NP by reducing the number of study plots is feasible, particularly when focusing on taxonomic group-level indicators. However, care should be taken to ensure that high-diversity plots are included to obtain a good estimate of the biodiversity in this park. A mixed monitoring strategy, focusing on plots with high conservation value, while incorporating broad taxonomic assessments and specialised monitoring for groups with lower species richness, such as mammals and Neuroptera, may further improve monitoring efficiency and data quality (Margules and Pressey 2000). The variation in the biodiversity of the different taxonomic groups highlights the need for adaptive and flexible monitoring methods for recording the complexity of the ecosystems in the Šumava NP.

These conclusions provide significant insights for biodiversity policy and forest management. They demonstrate that reducing the number of plots monitored can optimise efforts and reduce costs without compromising the quality of the data. This supports the development of adaptive, cost-effective monitoring programmes, while emphasising the need for targeted conservation strategies that focus on taxonomic groups with high species richness, such as Lepidoptera and Bryophyta (Lindenmayer and Likens 2011). In addition, management practices should be adjusted based on species' responses to disturbance and climate change. This study further recommends adaptive management strategies, including transboundary conservation efforts with neighbouring ecosystems like the Bavarian Forest National Park. These findings offer a strong foundation for integrating biodiversity monitoring into climate change adaptation policies and balancing conservation with sustainable forest use.

Limitations and future directions

This study has several limitations that should be addressed in future research. First, the comparison of the large and small sample did not account for temporal variability in species distributions, which could influence the patterns in biodiversity. Future studies should consider conducting longitudinal assessments to better capture temporal dynamics and trends in biodiversity (Magurran and Henderson 2010; Dornelas et al. 2013). In addition, while the small sample did not result in a significant reduction in the level of biodiversity recorded at the taxonomic group level, further research is needed to determine whether this is true for other biodiversity indicators or taxa not included in this study. Increasing the range of taxa monitored and using other biodiversity indices, such as functional diversity or phylogenetic diversity, could provide a more holistic understanding of ecosystem health (Cadotte et al. 2011; Flynn et al. 2011; Owen et al. 2019). Finally, the use of permutation tests in this study provided robust statistical comparisons; however, other statistical methods, such as multivariate analyses, could further elucidate the relationships between patterns in biodiversity and environmental variables. This could improve the understanding of the ecological factors determining the distributions of species in the Šumava NP (McCune et al. 2002; Legendre and Legendre 2012; Pilowsky et al. 2022).

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Appendix A

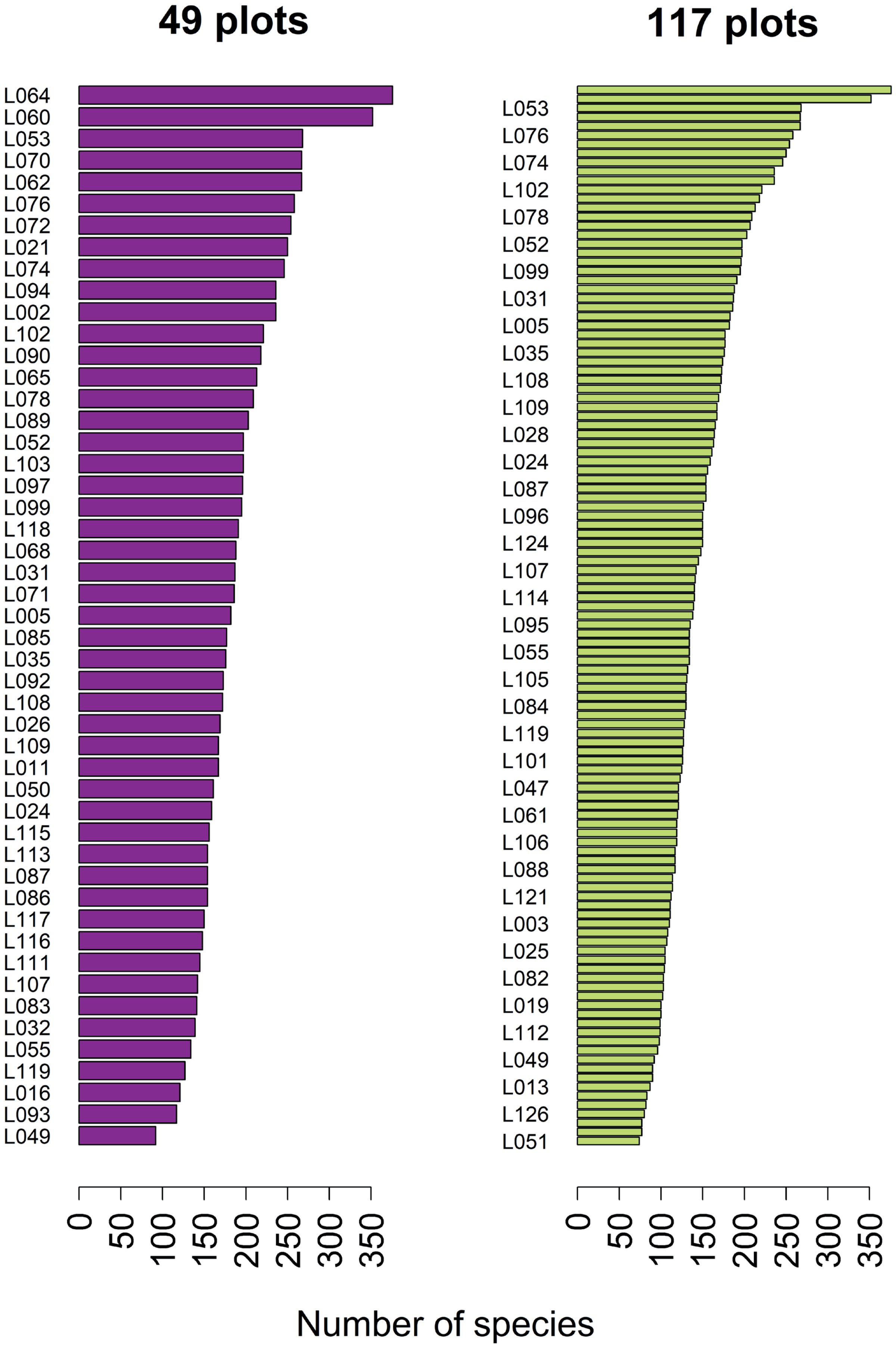

Fig. A1 Species richness of each plot for the small sample (49 forest plots – purple) and the large sample (117 forest plots – light green) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.

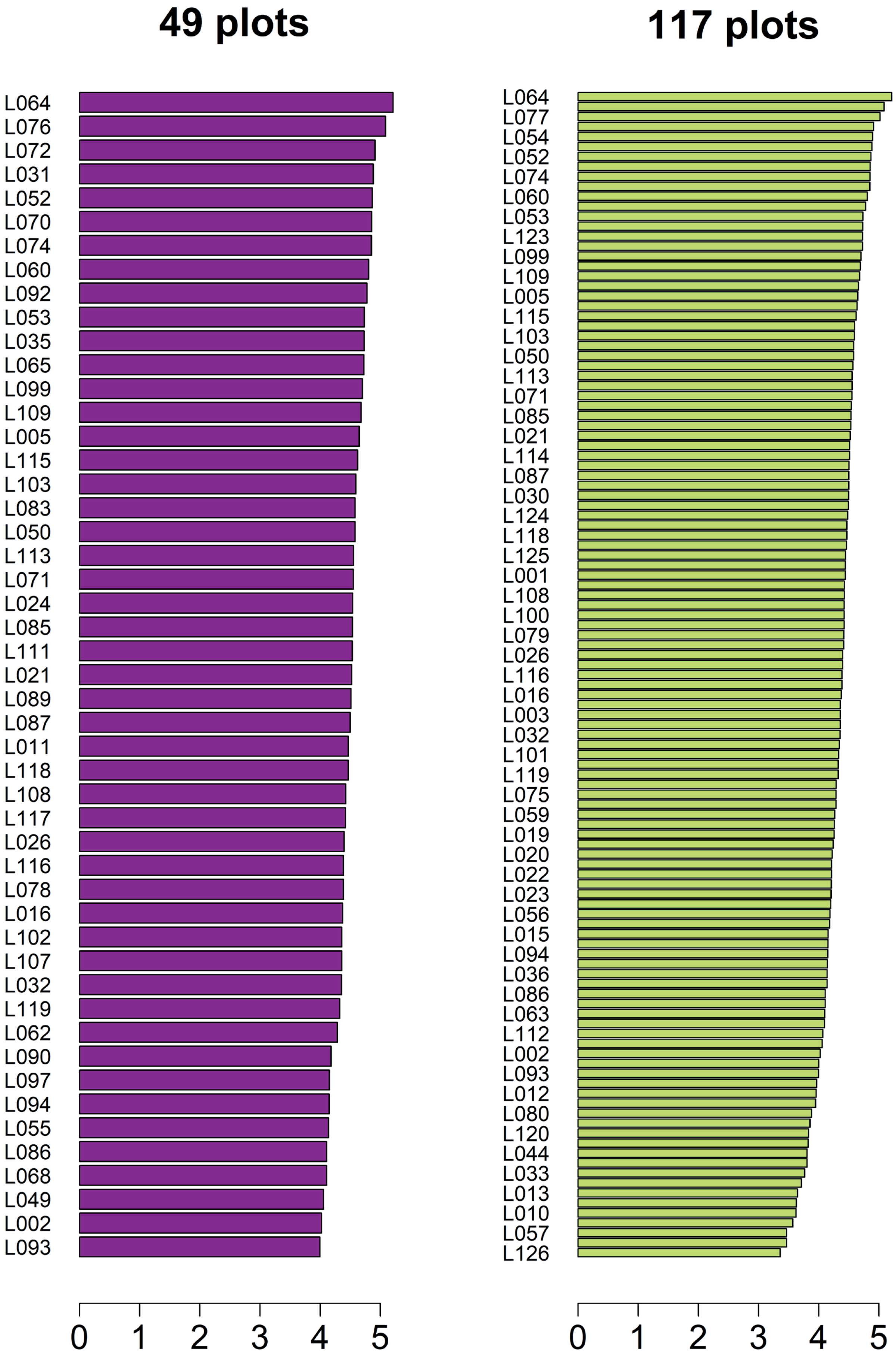

Fig. A2 Shannon diversity index of each plot for the small sample (49 forest plots – purple) and the large sample (117 forest plots – light green) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.

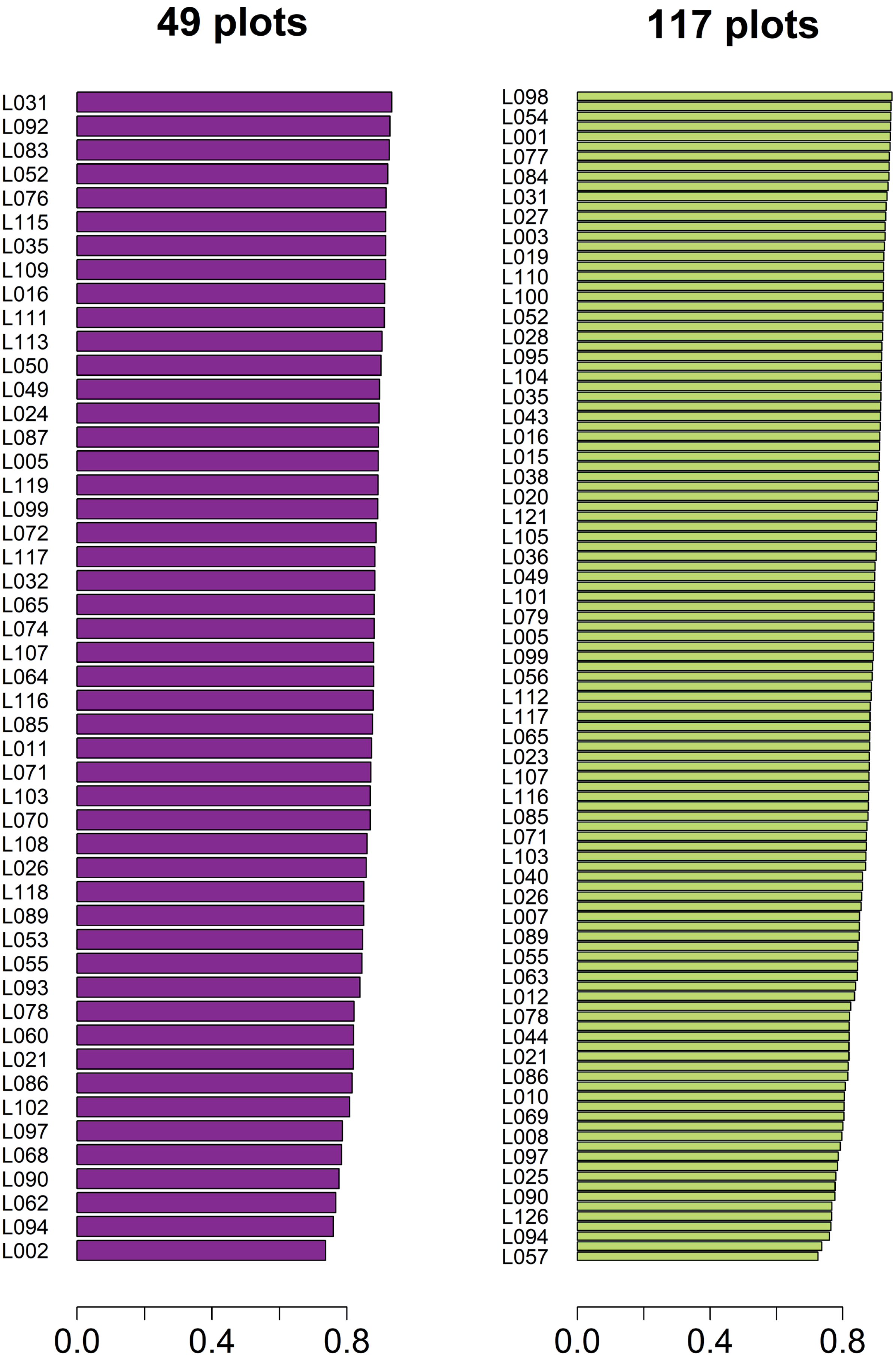

Fig. A3 Evenness index for each plot in the small sample (49 forest plots – purple) and large sample (117 forest plots – light green) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.

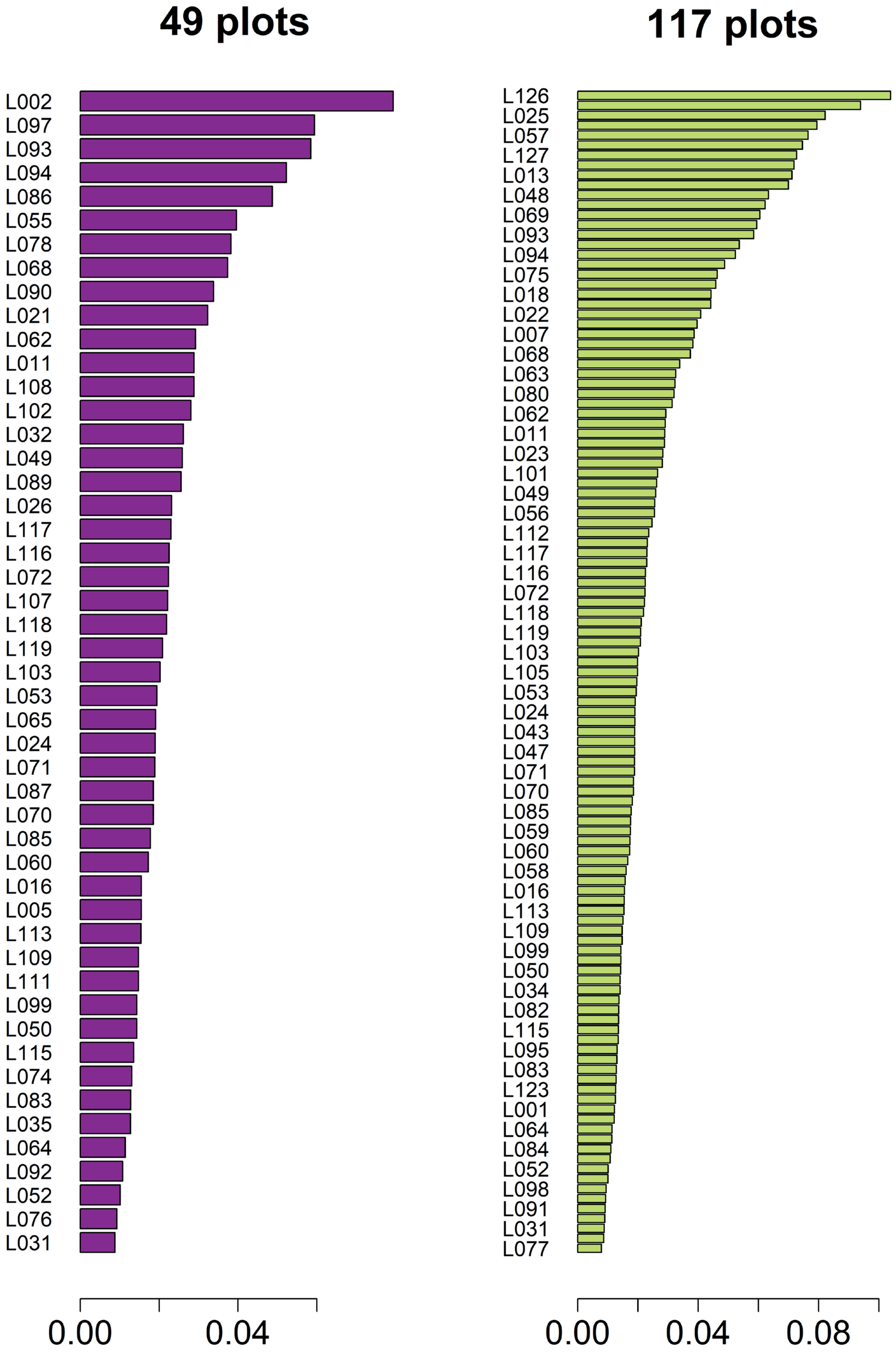

Fig. A4 Dominance index for each in the small sample (49 forest plots – purple) and large sample (117 forest plots – light green) monitored within the Silva Gabreta biodiversity monitoring project in Šumava NP.