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9 **Wood-inhabiting bryophyte communities are influenced by different**
10 **management intensities in the past**
11

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22 **Abstract:**

23 Many studies have underlined the fact that once forest continuity is broken, communities of wood-
24 inhabiting organisms may never be restored to their original status. However, only a few studies have
25 actually presented results from sites that have current old-growth structure, and where the history of
26 human interventions is known. In this study we compared the species richness, nestedness, beta
27 diversity, and composition of bryophytes from living trunks and dead logs of beech (*Fagus sylvatica*) in
28 seven forest stands in the Czech Republic with old-growth structure and various histories of past
29 human impact. Our analysis showed that these communities are nested and that their beta diversity
30 is lower than random. There was a significant proportion of shared species, and rare species were
31 present only in the most heterogeneous and the least man affected habitats. We found that bryophyte
32 communities of forests with more intensive past management were significantly impoverished in
33 terms of both species richness and composition. Beta diversity was not related to management history
34 and reflected current habitat heterogeneity. The effect of decay stage on species richness and beta
35 diversity was stronger than the site effect. Our results demonstrate that the protection of current
36 natural beech-dominated forests and improvements to their connectivity in fragmented landscapes
37 are crucial for the survival and restoration of the diversity of wood-inhabiting bryophytes.

38 **Key words:** beech; beta diversity; bryophytes; Central Europe; dead wood; management history
39

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7 Office (GINOP 2.3.3-15-2016-00019).

8 **Introduction:**

9 Beech-dominated forests are one of the major types of natural vegetation in the temperate zone
10 of Europe (Bohn et al. 2003; Box and Fujiwara 2005). Due to its broad ecological amplitude and high
11 competitiveness, beech (*Fagus sylvatica*) dominates forests at different environmental ranges
12 (Leuschner et al. 2006), and can occur in combination with a broad spectrum of other tree species, like
13 silver fir (*Abies alba*) and spruce (*Picea abies*) in harsher climatic conditions and maples (*Acer*
14 *platanoides*, *A. pseudoplatanus*), hornbeam (*Carpinus betulus*), ash (*Fraxinus excelsior*) and oaks
15 (*Quercus robur*, *Q. petraea*) in milder climate zones (Peters 1997; Standovár and Kenderes 2003).

16 Temperate broadleaved forests have generally been heavily affected by human activities. Even
17 before the introduction of forestry in the 18th and 19th centuries, beech forests had been pastured for
18 centuries and selectively cut for timber (Hahn and Fanta 2001). Large areas had been also coppiced for
19 firewood and other purposes, although beech has a relatively low ability to produce vegetative shoots
20 (Peters 1997). With increasing demand for timber in the 19th century, many of these forests were
21 cleared and replaced by coniferous plantations. Most of the recent beech forest stands are managed
22 by rotation forestry systems, mainly a shelterwood forestry system using 100-120 years as the rotation
23 period (Hahn and Fanta 2001). This type of management results in even aged monodominant stands
24 with low structural heterogeneity (Brunet et al. 2010). Modern forest management has a serious
25 negative impact on the overall diversity of forest species and thus ecological stability (Larsen 1995;
26 Gamborg and Larsen 2003; Brunet et al. 2010). Tree species and age unification along with a significant
27 reduction of senescent trees and coarse woody debris in forests negatively influence species across
28 different groups (Harmon et al. 1986; Samuelsson et al. 1994; Jonsson et al. 2005; Friedel et al. 2006;
29 Fritz et al. 2008a; Halme et al. 2013). One of the species groups most threatened by the exploitation
30 of temperate forests are epixylic bryophytes (inhabiting decaying wood). Many studies have shown
31 that the diversity of epixylic bryophytes is directly linked to the coarse woody debris of different tree
32 species, volumes and decay stages (e.g. Rambo and Muir 1998; Ódor and Standovár 2001; Ódor and
33 van Hees 2004; Táboriská et al. 2015), which is rather scarce in managed forests. Epiphytic bryophytes
34 (inhabiting the trunks of living trees) are also very sensitive to forest management. Many species are
35 associated with large, veteran trees because they can provide the necessary microhabitats and allow
36 a sufficient time for the colonization of dispersal-limited species (Fritz et al. 2008b; Madžule et al. 2011;
37 Király et al. 2013). These assemblages are also very sensitive to forest continuity and fragmentation
38 (Löbel et al. 2006; Ódor et al. 2006; Snäll et al. 2004).

39 With the greater recent emphasis on nature conservation in Europe, remnants of natural and old-
40 growth forests are often protected by law, and there has been an effort to restore beech forest sites
41 that have been disturbed in the past (e. g. Zerbe et al. 2002; Bauhus et al. 2009; Felton et al. 2010).
42 There have been many studies concluding that once the continuity of a forest is disturbed (including
43 from the point-of-view of certain substrates such as large senescent trees or decaying logs), the full
44 restoration of specialist communities may be long delayed and in some cases is not even possible
45 (Andersson and Hytteborn 1991; Similä et al. 2003; Ódor et al. 2006; Moning and Müller 2009;
46 Heilmann-Clausen et al. 2014). But few of these studies have actually presented results from sites

1 which have current old-growth structure and where the history of disturbances is known (Fritz et al.
2 2008a).

3 One way to describe and compare community structures on a gradient of management history is
4 the analysis of beta diversity (Anderson et al. 2011). According to Podani and Schmera (2011) and
5 Carvalho et al. (2013), beta diversity patterns consist of two distinct processes: species replacement
6 and species loss (or gain), the latter being closely related to nestedness. Nestedness refers to the
7 extent that species-poor assemblages are a subset of species-rich ones (Atmar and Patterson 1993)
8 and therefore it can give us valuable information about the distribution of certain species. In the case
9 of fragmented habitats it is usually related to patch size and the level of isolation (Berglund and Jonsson
10 2003; Hokkanen et al. 2009; Fahrig 2013).

11 In this paper, we explored the patterns of epiphytic and epixylic bryophyte assemblages in beech
12 dominated forest reserves of different management history in the Czech Republic. Our aim was to
13 contribute to the general knowledge of wood inhabiting (epiphytic and epixylic) bryophyte
14 communities in long-term unmanaged beech-dominated forests. To accomplish this we examined the
15 bryophyte assemblages of beech trunks and logs (for simplicity hereinafter referred to as logs) of large
16 volumes, focusing on the effect of forest history (between sites) and decay stages (within sites) on the
17 community structure (species richness, beta diversity, nestedness, species composition). Our main
18 questions were:

- 19 (i) To what extent do management history and decay stage determine the site and log-level
20 species richness of wood inhabiting bryophytes and the species composition of the
21 communities?
- 22 (ii) Are site and log-level beta diversity and nestedness values of the community different
23 from random (neutral) references?
- 24 (iii) Are beta diversity values different between and within sites, and between decay stages
25 within sites?
- 26 (iv) How is beta diversity related to the management history and species richness of sites?

27

28 **Material and Methods:**

29 *Study sites and sampling*

30 This study comprised 7 old-growth mixed forest sites with different management histories in the
31 Czech Republic. All of them are currently protected as nature reserves and excluded from logging and
32 other management activities. All sites have old-growth structure with a long-term absence of human
33 influence, characterized by the presence of old veteran trees, regeneration in naturally created gaps,
34 a fine scale mosaic of forest developmental stages and a high amount of coarse woody debris (CWD)
35 (Král et al. 2014a). None of these sites has ever been clear-cut, but different human activities in
36 different combinations were performed at every site except one virgin forest site. Based on historical
37 data we divided them into three groups according to the intensity of past management. The general
38 features of the sites along with their environmental characteristics, management history and derived
39 classification are shown in Table 1. Detailed information about the proportion of living trees and dead
40 wood of important tree species in the total volume for each locality are presented in Table 2. Most of
41 these localities are naturally dominated by beech, with the exception of Boubín, where spruce has a
42 similar dominance as beech (Table 2).

1 For the preselection of appropriate logs we used census datasets from all investigated sites. All
2 standing and downed trees of $DBH \geq 10$ cm at these seven sites had previously been mapped and the
3 DBH recorded. In the 1970`s, 1990`s and 2000`s stem-position maps were based on tripod-based
4 theodolite positioning (with sub-meter absolute positional accuracy anticipated). In the 2000`s we also
5 used Field-Map technology (<http://www.fieldmap.cz>). Tree heights were measured on a sample of ca.
6 10% of trees and fitted using Näslund's height curve (Näslund, 1936). Deadwood measurements (incl.
7 lying stem lengths, decay stage determination) were carried out according to the „Deadwood Protocol“
8 (Král et al. 2014b - supplementary material).

- 1 Tab. 1 Table of seven studied old-growth beech-dominated stands in the Czech Republic with structural and climatic variables and their affiliation to defined
 2 management history groups.

| abbreviation | BO | KO | MI | PO | SA | ZF | ZH |
|-----------------------------------------------------------------------------|---------------------------|---------------------------------------------------------------------------------------------------------|---------------------------|---------------------------|---------------------------|--------------------------------|---------------------------|
| Reserve | <u>Boubínský prales</u> | <u>Kohoutov</u> | <u>Mionší</u> | <u>Polom</u> | <u>Salajka</u> | <u>Žofínský prales</u> | <u>Žákova hora</u> |
| GPS ("mid-point" of studied area) | 48°58'43"N, 13°48'43"E | 49°55'26"N, 13°46'18"E | 49°32'11"N, 18°39'30"E | 49°47'32"N, 15°40'20"E | 49°24'07"N, 18°25'17"E | 48°39'58"N, 14°42'28"E | 49°39'20"N, 15°59'39"E |
| Elevation (m) | 925 – 1105 | 417 – 568 | 778 – 890 | 545 – 625 | 715 – 820 | 730 – 837 | 725 – 800 |
| Total size (ha) | 666.4 | 30.1 | 170 | 18 | 21.9 | 101.7 | 38.1 |
| Studied area (ha) | 46.6 ^f | 25.3 | 9.4 | 19.3 | 19 | 74.2 | 17.5 |
| Spontaneous development since | ever | 1933 | 1935 | 1925 | 1930 | 1838 | 1929 |
| Historical management: | | | | | | | |
| <i>deadwood haulage till</i> | never | 1933 | 1935 | 1936 | 1930 | 1888 | 1929 |
| <i>deadwood haulage full (f)/ partly, randomized (p)</i> | --- | f | p | f | p | p | p |
| <i>selective felling in the past (yes/no)</i> | n | n | y | y | y | y | y |
| <i>group felling in the past (yes/no)</i> | n | y | n | y | n | n | n |
| <i>planting or reforestation in the past (part of the reserve) (yes/no)</i> | n | n | n | y | n | n | y |
| <i>charcoal burning in the past (yes/no)</i> | n | y | n | n | n | n | y |
| Level of human influence in the past^a | A | C | B | C | B | B | C |
| Other common tree species besides beech | <i>Picea abies</i> | <i>Acer platanoides, Quercus petraea, Acer pseudoplatanus, Carpinus betulus, Tilia sp., Picea abies</i> | <i>Abies alba</i> | <i>Picea abies</i> | <i>Abies alba</i> | <i>Abies alba, Picea abies</i> | <i>Picea abies</i> |
| Living/dead wood ratio | 65/35 | 85/15 | 69/31 | 83/17 | 68/32 | 60/40 | 81/19 |
| DBH of dead wood^b | 80 (48, 132) | 94 (72, 125) | 81 (60, 105) | 108 (76, 140) | 81 (55, 120) | 101 (74, 129) | 91 (65, 115) |
| Bedrock | shist | rhyolite | flysh | migmatite, amphibolite | flysh | granite | migmatite, orthogneiss |
| T_{ave} (°C)^c | 4.9 | 7.8 | 5.2 | 7.4 | 6.2 | 4.3 | 6.1 |
| Precipitation (mm)^d | 1067 | 597 | 1207 | 774 | 1142 | 704 | 781 |
| References^e | Vrška et al. 2012 | Průša 1985 | Vrška et al. 2000 | Vrška et al. 2002 | Vrška 1998 | Pícha 2010, 2012 | Vrška et al. 2002 |

3

1 ^aThree levels: A = no human impact, B = only selective felling, C = combination of more activities.

2 ^bMean diameter at breast height (DBH) based on the investigated dead trees, minimum and maximum are in brackets.

3 ^cMean annual temperature (source: Czech Hydrometeorological Institute, data interpolation from 1981-2011).

4 ^dAnnual precipitation (source: Czech Hydrometeorological Institute, data interpolation from 1981-2011).

5 ^eHistorical data were published mostly in regional journals in Czech language. Whenever possible, we refer to literature in English.

6 ^fCore part which has never been managed by man 46.6 ha.

7

8 Tab. 2 Proportions of living trees and deadwood (DBH > 10 cm) in the total volume for individual tree species calculated according to tree counts, basal area
9 and volume for seven studied old-growth beech-dominated stands in the Czech Republic

| site | BO | KO* | MI | PO | SA | ZF | ZH |
|---------------------------------------------------|-------|-------|-------|-------|-------|-------|-------|
| proportion of deadwood (% of volume in total) | | | | | | | |
| <i>Fagus sylvatica</i> | 16.4 | 88.4 | 32.8 | 40.4 | 15.8 | 25.5 | 54.5 |
| <i>Abies alba</i> | 20.0 | 4.4 | 62.2 | 24.8 | 79.2 | 16.4 | 3.2 |
| <i>Picea abies</i> | 63.5 | 0.0 | 2.7 | 31.1 | 4.9 | 57.7 | 39.8 |
| other | 0.1 | 7.2 | 2.3 | 3.7 | 0.1 | 0.4 | 2.5 |
| total | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| proportion of living trees (% of volume in total) | | | | | | | |
| <i>Fagus sylvatica</i> | 45.7 | 80.8 | 78.9 | 17.0 | 68.5 | 62.0 | 73.9 |
| <i>Abies alba</i> | 4.3 | 0.1 | 5.0 | 0.6 | 21.7 | 3.4 | 0.0 |
| <i>Picea abies</i> | 49.8 | 0.7 | 0.2 | 70.7 | 8.9 | 33.4 | 13.5 |
| other | 0.2 | 18.5 | 15.9 | 11.7 | 0.9 | 1.2 | 12.6 |
| total | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |

10

11

1 Here we focused on those beech trees with maximum DBH, and selected 35 such logs at each
2 locality. For the purpose of this study we distinguished three decay stages: DS 0 – trunks of standing
3 living trees, 10 per each locality; DS 1 – dead logs in early decay stages characterized by hard wood
4 and high bark cover (corresponding to decay stage 1 and 2 sensu Heilmann-Clausen 2001), 10 per each
5 locality; DS 2 – dead logs in intermediate and late decay stages characterized by soft wood, without
6 bark (corresponding to decay stage 3, 4 and 5 sensu Heilmann-Clausen 2001), 15 per each locality
7 (except for the locality Salajka, where DS 2 was represented by only 12 logs).

8 In 2015, the presence of bryophytes was surveyed on the whole log surface from the ground to 2
9 meters high in the case of living trees and on the whole surface of dead logs above ground, excluding
10 branches. If the logs included an uprooted part it was not included in the survey. Species were
11 identified in the field or collected for microscopic identification. Voucher specimens are deposited in
12 herbarium of the first and second authors. The species *Hypnum andoi* and *H. cupressiforme* were not
13 distinguished and are here referred to together as *H. cupressiforme*. Nomenclature followed Kučera et
14 al. (2012).

15 16 *Data analysis*

17 The effect of site and decay stages on log-level species richness was tested by ANOVA with nested
18 error structure (logs of different decay stages were nested within sites, Crawley 2007). The levels of
19 the factors were compared by Tukey multiple comparisons (Zar 1999).

20 Community diversity structure was explored by the SDR simplex approach proposed by Podani and
21 Schmera (2011). This involves partitioning the relationship between a pair of sample units into three
22 additive components summing up to 1: similarity (S) as measured by the Jaccard index, species
23 replacement (R) and richness difference (D). Beta diversity (also called turnover, T) between pairs was
24 expressed as $D+R$, and nestedness (Nest) as $S+D$. These functions were calculated between site pairs
25 (using cumulative species lists of the sites) and log pairs. The R script of the studied functions is given
26 in Appendix 1. The mean of the functions were calculated as descriptive statistics, and the position of
27 the pairs were plotted in ternary plots. These measures are dependent on the proportion of the
28 presence records in the matrix (also called matrix fill) as well as on the total number of species in the
29 matrix. The difference of the statistics from randomness was tested by a Monte-Carlo simulation using
30 999 restricted permutations of the original matrix keeping the size and the presence fill of the matrix
31 as well as the sampling unit species richness fixed. For more details on the method see Podani and
32 Schmera (2011) and Halme et al. (2013).

33 The effects of sites and decay stages on the beta diversity of log pairs were then studied in more
34 detail. Within- and between-site beta diversity were compared by a Monte-Carlo simulation (using 999
35 permutations of the original beta diversity values), and beta diversity between and within decay stages
36 (analyzing only within site pairs) were also studied in a similar way. The effect of sites on within-site
37 beta diversity values and the effect of decay stages on within-site, within-decay stage beta diversity
38 values were tested by F statistics via a Monte-Carlo simulation and Tukey multiple comparisons. In
39 each analysis, site was used as an explanatory factor, but sites of the same management histories were
40 visualized by colors in the boxplots.

41 The effect of sites and decay stages on species composition was studied by Redundancy Analysis as
42 a direct ordination method (Borcard et al. 2011). The effects of these factors on species composition
43 were also tested by permutational multivariate analysis of variance (Anderson 2001) using the R
44 function “adonis”.

1 All analyses were carried out in the R 3.3.2 environment (RCore Team 2013), with the “vegan”
2 package used for multivariate analyses (Oksanen et al. 2013), and the “multcomp” package for multiple
3 comparisons (Hothorn et al. 2008).

4 5 **Results**

6 *Species richness*

7 We sampled 243 beech logs and found a total 98 bryophyte species (20 of them were liverworts
8 and 78 mosses). Boubín was the richest site (71), Žofín and the reserves with selective felling in the
9 past had intermediate site level richness (60 in average), while reserves with higher levels of past
10 human activities had the lowest values (50 in average; Fig. 1a). Log-level species richness had similar
11 patterns, and the effect of site was significant (nested ANOVA, $F = 5.68$, $p = 0.005$): based on multiple
12 comparisons the sites more influenced by human activities (KO and PO) significantly differed from
13 those less influenced (Fig. 1b). Log-level species richness significantly differed among decay stages
14 (nested ANOVA, $F = 13.63$, $p < 0.001$), with living trunks having the highest species richness, the early
15 decay stage having intermediate values, and the late decay stage the lowest (Fig. 2).

16 *Beta diversity and nestedness*

17 On the site level, the mean values of similarity and richness differences were higher, while species
18 replacement was lower than the randomized values, which indicated higher nestedness and lower beta
19 diversity than predicted by the null model (Fig. 3, Tab. 3). The data points in the ternary plot are closer
20 to the S-vertex and side representing richness agreement, and all points are in the lower part of the
21 triangle. This means that on the site level, the effect of similarity is higher than species replacement in
22 bryophyte communities, which generally indicates low beta diversity. There is a short gradient of
23 nestedness along the bottom side of the ternary plot. The high level of nestedness is also
24 demonstrated by the species list (Appendix 2).

25 On the log level we found the same patterns as on the site level (Tab. 3). In the case of log-level
26 data, matrix fill is much lower than for sites. This results in a high percentage of species replacement
27 and therefore the beta diversity is increased artificially (Podani and Schmera 2011). The resulting beta
28 diversity index is quite high (0.771), but still lower than in a random community of similar matrix fill.
29 On the other hand, nestedness is higher.

30 Log-level beta diversity was higher between sites than within sites (Fig. 4a, Monte-Carlo simulation
31 $p < 0.001$). In addition, within-site values of beta diversity were higher between decay stages than
32 within decay stages (Fig. 4b, Monte-Carlo simulation $p < 0.001$). Within-site beta diversity was
33 independent of the species richness of the sites ($F = 0.4$, $p = 0.56$, Fig. 5). The effect of site on beta
34 diversity was significant (Fig. 6, $F = 51.7$, $p < 0.001$), but this was not related to forest history. Decay
35 stage also had a significant effect on beta diversity, being higher in the case of decaying logs (DS 1 and
36 2) than for living trunks (DS 0, Fig. 7, $F = 24.23$, $p < 0.001$).

37 *Species composition*

38 In the RDA (Fig. 8), constrained axes determined by tree decay stages and seven sites explained
39 28.3 % of total variability ($F = 37.7$, $P = 0.001$). The first constrained axis (11.6 %) was related to the
40 gradient of decay stages, and the second constrained axis (5.6 %) reflected different sites. Samples
41 from localities with past human interventions were mostly associated with positive RDA2 values, which
42 are correlated with a higher ratio of beech, both live ($R^2 = 0.05$, $P = 0.001$) and dead ($R^2 = 0.27$, $P =$

1 0.001), whereas samples from natural forests with minimal human impact were associated with
 2 negative RDA2 values that are correlated with a higher presence of coniferous trees, both live ($R^2 =$
 3 0.09 , $p = 0.001$) and dead ($R^2 = 0.36$, $p = 0.001$). These results are also supported by the multiresponse
 4 permutation test, which confirmed differences in species composition between different decay stages
 5 ($R^2 = 0.10$, $P < 0.001$) and also between different sites ($R^2 = 0.15$, $P < 0.001$).

6 Tab. 3 Results of the SDR simplex approach, partitioning the relationship between a pair of sample
 7 units into three additive components summing up to 1: similarity (S) as measured by the Jaccard
 8 index, species replacement (R) and richness difference (D). Beta diversity (also called turnover, T)
 9 between pairs was expressed as $D+R$, and nestedness (Nest) as $S+D$. These functions were
 10 calculated between all site pairs (using cumulative species lists of the sites) and all log pairs. The
 11 difference of the statistics from randomness was tested by a Monte-Carlo simulation using 999
 12 restricted permutations of the original matrix keeping the size and the presence fill of the matrix as
 13 well as the sampling unit species richness fixed.

| <u>Site level</u> | Mean value | Confidence interval lower (95 %) | Confidence interval upper (95 %) | Standard error | Difference from random |
|-------------------|------------|----------------------------------|----------------------------------|----------------|------------------------|
| S | 0.409 | 0.40838 | 0.40948 | < 0.001 | Higher |
| D | 0.116 | 0.11606 | 0.11616 | < 0.001 | Higher |
| R | 0.475 | 0.47437 | 0.47555 | < 0.001 | Lower |
| Betadiversity | 0.591 | 0.5905 | 0.59162 | < 0.001 | Lower |
| Nestedness | 0.525 | 0.52445 | 0.52563 | < 0.001 | higher |
| <u>Log level</u> | Mean value | Confidence interval lower (95 %) | Confidence interval upper (95 %) | Standard error | Difference from random |
| S | 0.064 | 0.06445 | 0.06449 | < 0.001 | higher |
| D | 0.249 | 0.24866 | 0.24867 | < 0.001 | higher |
| R | 0.687 | 0.68684 | 0.68689 | < 0.001 | Lower |
| Betadiversity | 0.936 | 0.93551 | 0.93555 | < 0.001 | Lower |
| Nestedness | 0.243 | 0.24304 | 0.24316 | < 0.001 | higher |

14

15 Discussion

16 *Different management history and current species richness and composition*

17 In this paper we present data from beech-dominated forest sites with old-growth structure in terms
 18 of the availability of coarse woody debris, the presence of large and senescent trees, and spontaneous
 19 development. All of them have remained unmanaged for at least 80 years and have never been clear-
 20 cut in the past, but they have had different histories of human activities. Although all these sites
 21 currently provide sufficient good-quality substrates for wood inhabiting bryophytes, our results
 22 suggest that past human intervention negatively influenced the site and log level species richness as
 23 well as the species composition. In the past, selective felling in combination with full deadwood
 24 haulage and/or charcoal burning was focused on the largest trees - living or recently dead – which are
 25 the most important substrate for bryophytes (eg. Ódor et al. 2006; Hofmeister et al. 2015a). This effect
 26 was likely apparent long after management had ceased as a result of delay in species colonization. This
 27 is consistent with most studies dealing with the diversity of different groups of organisms bound to
 28 live trees and dead wood in forest ecosystems (e.g. Brunet et al. 2010; Nordén et al. 2014; Flensted et
 29 al. 2016).

1 Once the continuity of the forest is disturbed, restoration of wood-inhabiting communities is long-
2 lasting process (Andersson and Hytteborn 1991, Ódor et al. 2006, Heilmann-Clausen et al. 2014). One
3 of the main reasons is forest fragmentation, which is common in the European landscape (Kolb and
4 Diekmann 2004; Fritz et al. 2008a; Flensted et al. 2016). In fragmented landscapes with small patches
5 of well-preserved forests often very isolated from each other, recovery is limited by several factors
6 such as dispersal abilities, permeability of the landscape or the availability of suitable microhabitats
7 (Nordén and Appelqvist 2001; Pharo and Zartman 2007; Ódor et al. 2013). The smaller the area of
8 unmanaged stands and the greater the distance to the nearest refuge, the less likely species are to
9 survive (Hofmeister et al. 2015a).

10 One factor that complicates the interpretation of our results is the fact that in central Europe the
11 intensity of management history is very often correlated with elevation. Forests in lowlands have been
12 influenced by human activities for much longer and more intensively than more-inaccessible mountain
13 forests (Kaplan et al. 2009; Chytrý 2012). The positive relationship of the species richness of bryophytes
14 to the rising altitude has been described earlier (Bruun et al. 2006) and these two factors are so closely
15 linked that it is difficult to separate their common influence. This needs to be considered when
16 interpreting the results, however we hope that within one vegetation type this effect could be minor.

17 *The strong effect of decay stage*

18 Decay stage also had a significant effect on both species richness and species composition. The
19 highest species richness was associated with DS 0, i.e. living trees, and decreased with increasing decay
20 stage. The initial high species richness resulted from the high proportion of epiphytic species in the
21 community, which decreases rapidly during the decay process because of gradual bark loss. Late decay
22 stages are represented mostly by generalists, since epixylic specialists prefer the logs of conifers
23 because of more suitable substrate pH and water holding capacity (Táborská et al. 2015).

24 Considering the beta diversity between decay stages within sites, it was higher on logs (DS 1 and
25 DS 2) than on trunks (DS 0), in contrast to species richness. The higher beta diversity on logs likely
26 resulted from higher habitat diversity. Logs are more heterogeneous, consisting of a mosaic of
27 microhabitats like bark, soft wood, rot holes or humus, while trunks are much more uniform and
28 extreme in terms of microclimatic conditions (desiccation, direct sun shine, abrasion etc.), especially
29 in the case of beech. Generally, beta diversity between trunks is mainly driven by different tree species
30 (Mežaka et al. 2012; Ódor et al. 2013) and tree size (Fritz 2008b; Király et al. 2013), but in our case
31 these factors were excluded by the sampling design.

32 We found that within-site beta diversity was lower than between-site beta diversity. The site effect
33 was significant, but relatively small. In species composition, decay stage effect overwhelmed the
34 differences between sites. On a larger (continental) scales, regional differences for wood inhabiting
35 bryophyte communities are very strong and more important than local factors (Quian et al. 1998; Ódor
36 et al. 2006; Heilmann-Clausen et al. 2014). Also, within a region the differences among sites are
37 generally more important for species composition than within site factors like decay stage, driven
38 mainly by climatic differences (Ódor and van Hees 2004). In our study we included data not only from
39 lying logs (DS 1 and DS 2) but also from live trunks (DS 0). These two substrates have very different
40 conditions (mainly water holding capacity, surface pH) and there was also a large difference between
41 our DS 0 and DS 1-2 in terms of physical and chemical properties. This could explain why in our case
42 decay stage had a stronger effect on species composition than the site.

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1 *Nestedness and beta diversity in old-growth forests with different management histories*

2 Based on the SDR analysis we found that wood-inhabiting bryophyte communities in our studied
3 sites are nested. In other words, the species composition of species-poor plots is a subset of richer
4 plots (Patterson and Atmar 1986). This was true both on the site and log levels. The beta diversity of
5 wood-inhabiting bryophytes was lower than random both on the site and log levels. These results
6 indicate that there is a significant proportion of shared species present both in species-rich and
7 species-poor communities resulting in small differences in beta diversity; this is typical for organisms
8 with good dispersal ability (Qian 2009). While the long-distance dispersal ability of bryophytes is still
9 under discussion (Laaka-Lindberg et al. 2006; Barbe et al. 2016), on a local scale most bryophytes are
10 considered to be good colonizers due to their microscopic wind-dispersed spores and the generally
11 rich production of propagules (Frahm 2008). In addition to common species, we found a group of rare
12 species that were arranged in a nested pattern (eg. *Neckera pennata*, *Nowellia curvifolia*,
13 *Pseudoamblystegium subtile*, *Zygodon dentatus*). This group is represented by substrate specialists
14 that tend to increase in number with rising habitat heterogeneity (Brunet et al. 2010) in space and
15 time.

16 Based on our data we found that beta diversity and site level species richness are independent of
17 each other. This is consistent with Hofmeister et al. (2015b), who published similar results for
18 bryophytes in their study comparing forests with different current management intensity to nature
19 reserves. Ujházyová et al. (2016) also confirmed that the species richness and beta diversity of beech
20 forest vegetation can be driven by different environmental factors. Moreover, site- and log-level
21 species richness were related to the intensity of management in the past while beta diversity was
22 independent of it. The present lower species richness on sites with broken continuity could be
23 explained by local extinctions caused by a lack of suitable microhabitats in the past. Beta diversity, on
24 the other hand, reflects current local conditions and environmental heterogeneity of the studied
25 substrate independently of the management history.

26 *Implications for nature conservation*

27 Our study confirms that forest conservation activities should be aimed at the protection of natural
28 sites and improvements to their connectivity in fragmented landscapes. This is in line with the
29 conclusion of the review of Nordén et al. (2014) that permanent reserves are still key conservation
30 tool. Dispersal limitation in combination with random extinctions, and possibly also colonization delay,
31 are the strongest factors threatening current wood-inhabiting bryophyte populations and complicating
32 their re-establishment after disturbances (Fritz et al. 2008a). The isolation of natural and old-growth
33 forests could be reduced by retention forestry management, which introduces the inclusion of old-
34 growth attributes in managed forests (Lindenmayer et al. 2012, Fedrowitz et al. 2014). The presence
35 of large senescent trees of different species and coarse woody debris of different volumes and decay
36 stages is crucial for the survival of specialized species (Hofmeister et al. 2015a). However, nature
37 conservation expectations should be realistic with respect to the management history of the site, since
38 as our study demonstrates the quality of old-growth forests is strongly limited by past human impacts,
39 at least within the time period we focused on. We also found that beta diversity indices are good for
40 measuring environmental heterogeneity, but should not be used as indicators of the biodiversity value
41 for bryophyte communities.

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1 **Conclusions**

2 In this study we analyzed wood-inhabiting bryophytes in seven beech-dominated old-growth
3 forests with different management intensities in the past. We confirmed an impoverishment in terms
4 of both species richness and composition on sites with previous human intervention. This is consistent
5 with studies describing the influence of forest continuity disruption on different groups of specialized
6 organisms. On the other hand, we found no relationship between management history and site- and
7 log-level beta diversity. Unlike simple species richness, indices of beta diversity give us information
8 about the current habitat heterogeneity and species niche preferences. The effect of decay stage on
9 species richness, composition and beta diversity was stronger than the effect of site. We included live
10 tree trunks, considered decay stage zero, and distinguished only two decay stages for dead logs. These
11 classes differed significantly from each other from the point of view of their physical and chemical
12 properties, leading to clear differences in all studied parameters. To preserve diverse wood-inhabiting
13 bryophyte communities, protection of current old-growth forests and improvements in their mutual
14 connectivity must be provided.

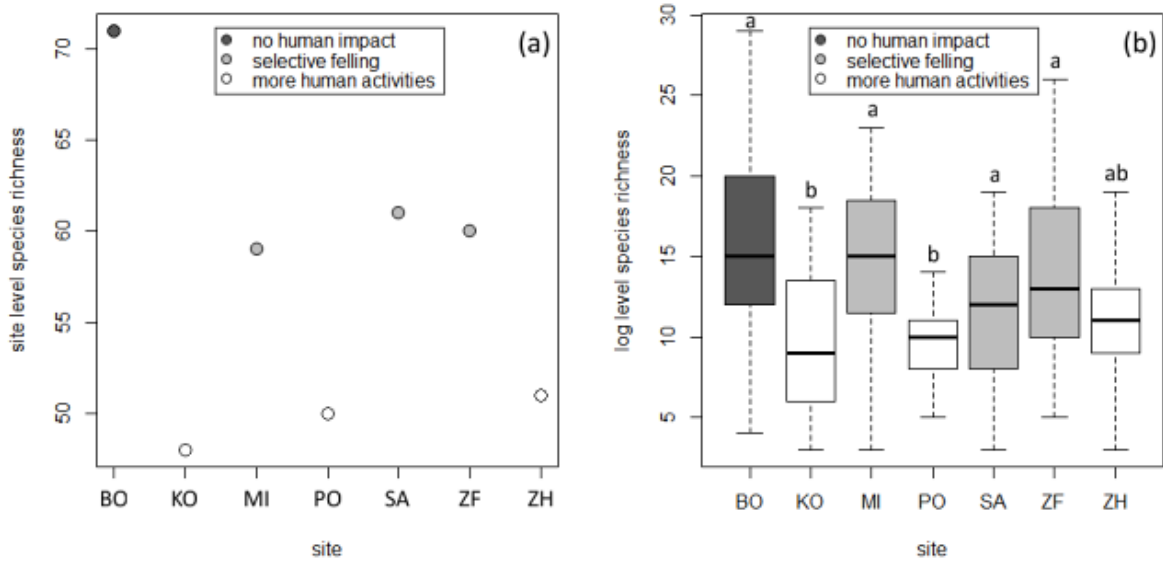
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2 **Figures:**

3 Fig. 1 Site-level (a) and log-level (b) species richness recorded on 243 logs at 7 old-growth beech-
4 dominated sites in the Czech Republic. Site name abbreviations are listed in Table 1. Each site was
5 associated to one of the three levels of human influence in the past according to Table 1 which are
6 indicated by different colors. Significant differences based on Tukey multiple comparisons are marked
7 by different letters.

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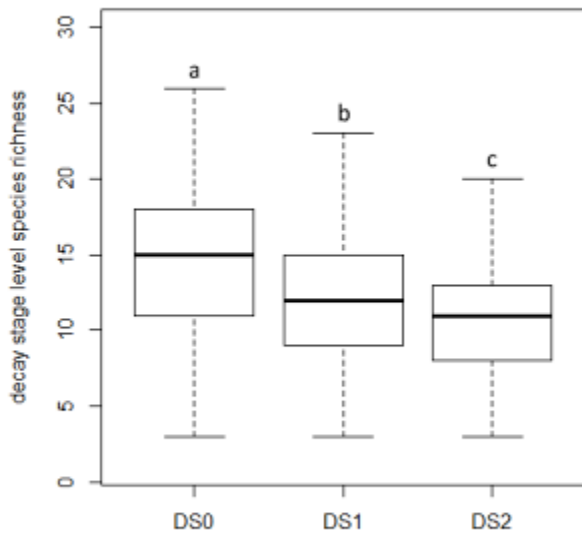


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Fig. 2 Decay stage level species richness recorded on 243 logs at 7 old-growth beech-dominated sites in the Czech Republic. For a description of the used decay stages see the “Material and Methods”. Significant differences based on Tukey multiple comparisons are marked by different letters.

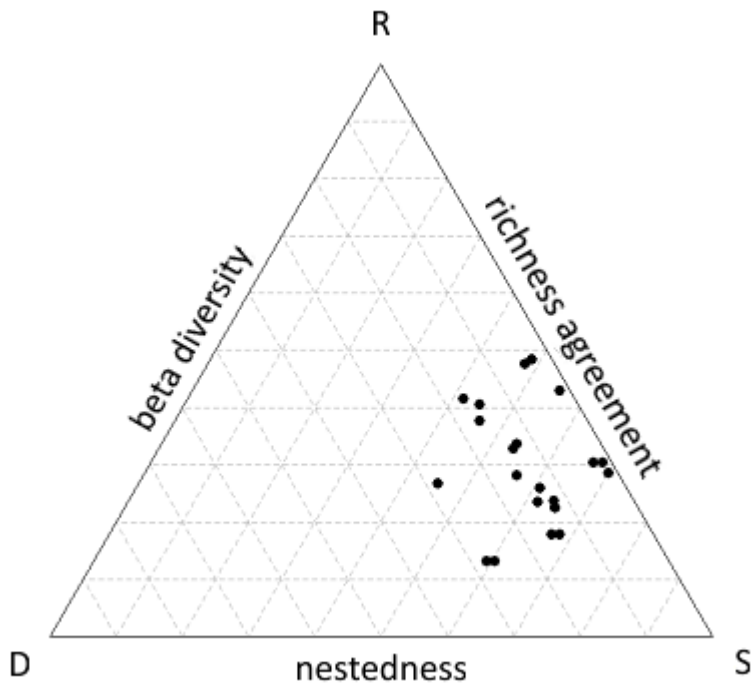


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2 Fig. 3 SDR simplex approach involves partitioning the relationship between a pair of sample units into
3 three additive components: S = similarity, R = species replacement, D = species richness difference.
4 The position of each data point within the ternary plot (the distance from each vertex and site)
5 characterizes the type of difference in community structure measured between each pair of sites. For
6 a more detailed explanation of this type of plotting see Podani and Schmera (2011) and Halme et al.
7 (2013).

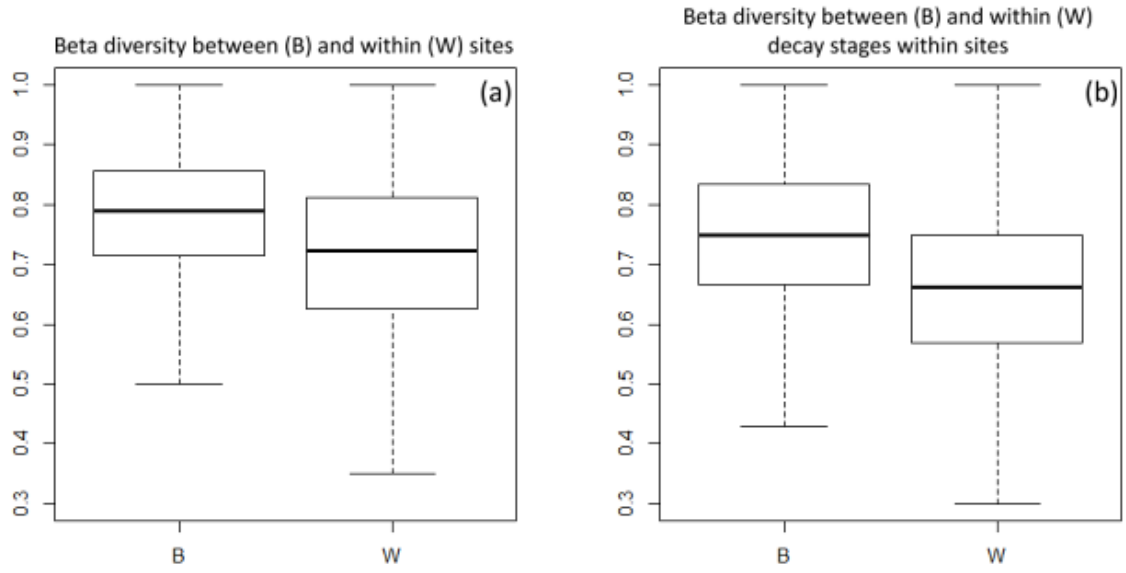
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Fig 4. Beta diversity between (B) and within (W) sites (a), and beta diversity between (B) and within (W) decay stages within site (b). The differences of median values were significant ($p < 0.001$), based on a Monte-Carlo simulation.

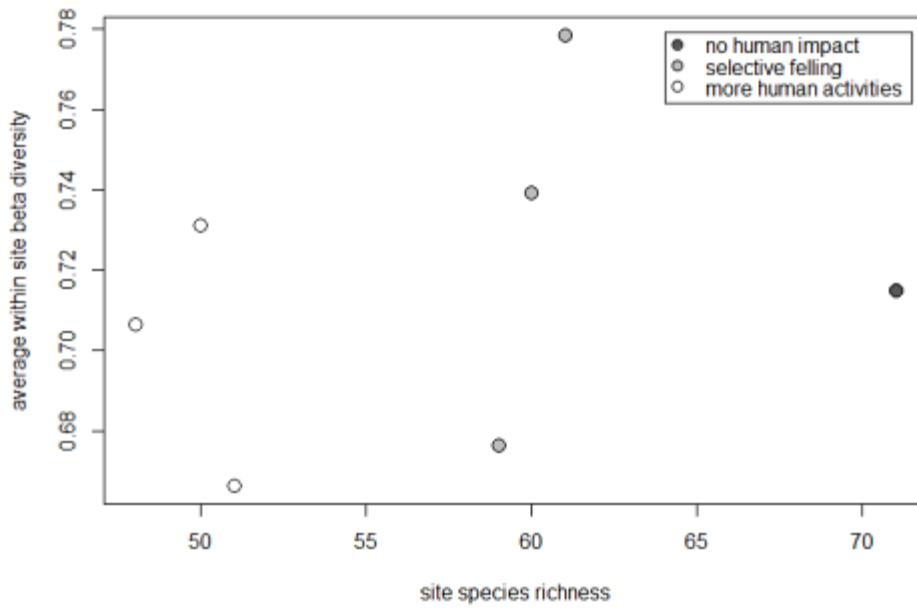


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2 Fig. 5. Relationship between bryophyte species richness in the sites and average within-site beta
3 diversity ($F = 0.4$, $p = 0.56$). Each site was associated to one of the three levels of human influence in
4 the past according to Table 1.

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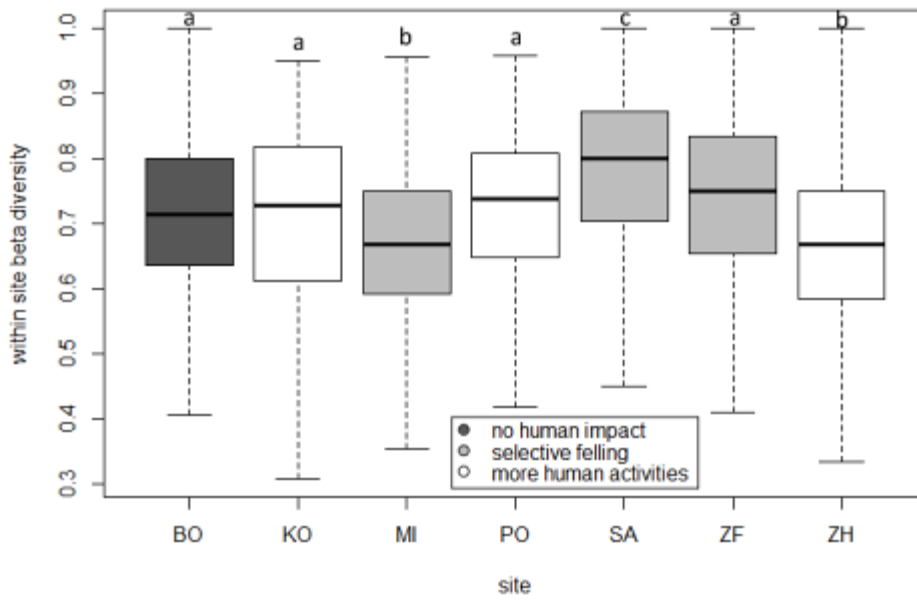
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2 Fig. 6. Boxplot of the beta diversity of sites ($F = 51.7, p < 0.001$). Significant differences based on Tukey
3 multiple comparisons are marked by different letters. Site are colored based on their human influence
4 categories (Table 1), which were not related to beta diversity.

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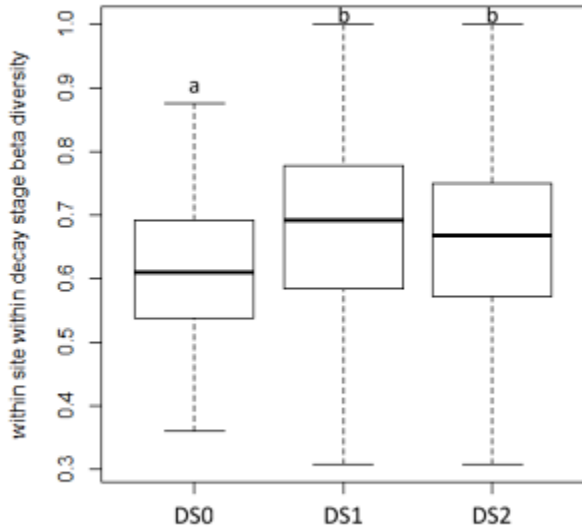


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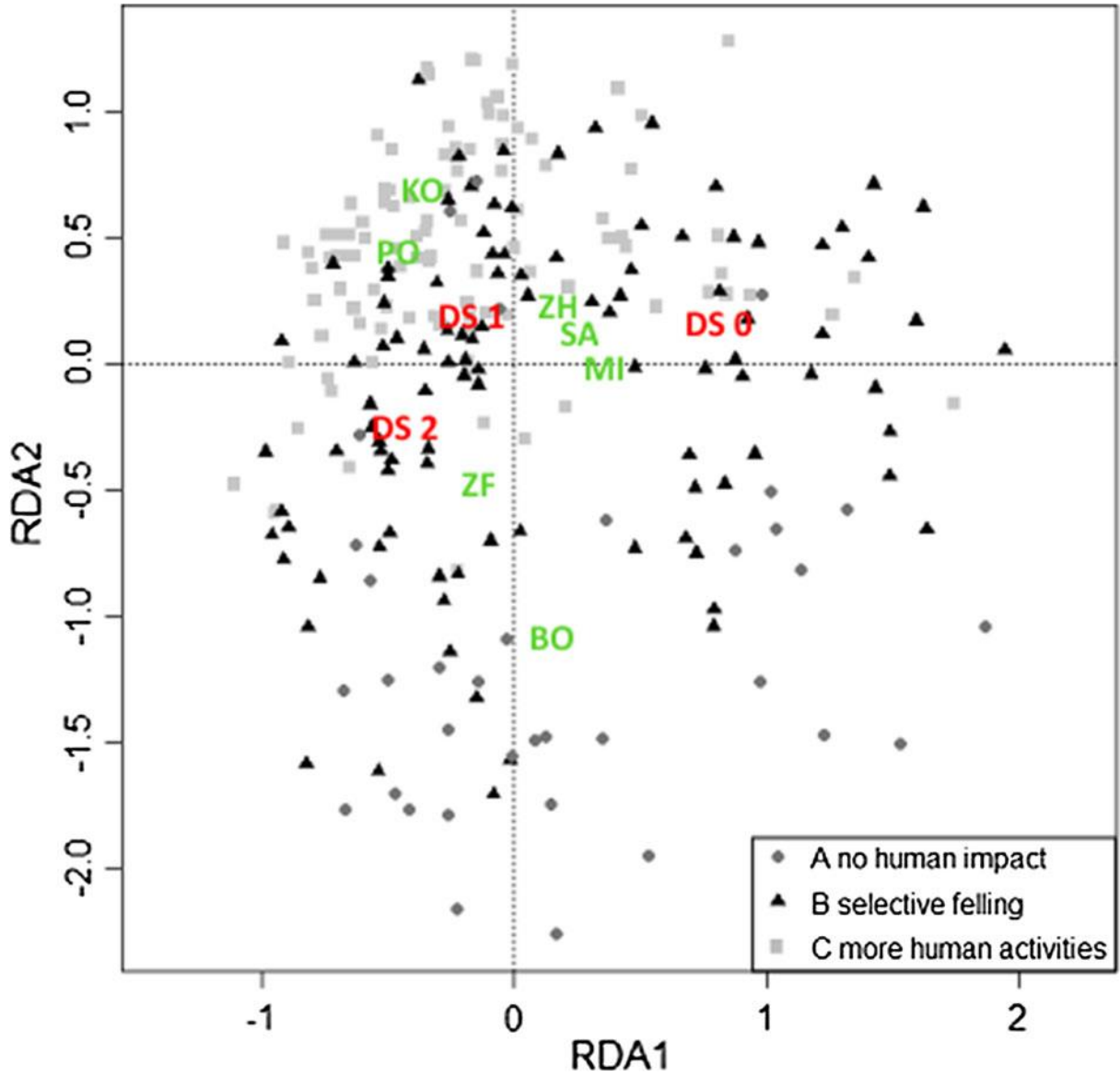
- 1 Fig. 7. Boxplot of the beta diversity of decay stages (F=24.23, p<0.001, permutation test). Beta diversity
- 2 values were calculated within sites and within decay stages.
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Fig. 8 RDA ordination of logs, marked by different human intervention categories of sites. The explanatory factors are decay stages (red) and sites (green).



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13 7
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- 15

```

1  Appendix 1.
2
3  #Analysis for SDR simplex (Podani and Schmera 2006)
4  #Made by Attila Lengyel, 6/Jan/2017., version 2.2.
5
6  #A, B and C components are calculated first for each pair of sites
7  ABCmat<-function(comm)  { #comm is the community matrix
8  comm[comm>0]<-1
9  N<-nrow(comm)
10 Amat<-Bmat<-Cmat<-matrix(NA, N,N)
11 rownames(Amat)<-rownames(Bmat)<-rownames(Cmat)<-colnames(Amat)<-
12 colnames(Bmat)<-colnames(Cmat)<-rownames(comm)
13 o<-1
14 oo<-N*(N-1)/2
15 pb<-txtProgressBar(1/oo,1,1/oo, style=3)
16 for(i in 1:(N-1)) {
17   rel1<-as.numeric(comm[i,])
18   for(j in (i+1):N) {
19     rel2<-as.numeric(comm[j,])
20     a<-sum(rel1==rel2 & rel1==1)           #shared species
21     b<-sum(rel1-rel2==1)                 #unshared species for first site
22     ci<-sum(rel1-rel2==-1)              #unshared species for second
23   site
24     Amat[i,j]<-Amat[j,i]<-a
25     Bmat[i,j]<-Bmat[j,i]<-b
26     Cmat[i,j]<-Cmat[j,i]<-ci
27     o<-o+1
28     setTxtProgressBar(pb,o/oo)
29   }
30 }
31 diag(Amat)<-rowSums(comm)
32 diag(Bmat)<-diag(Cmat)<-0
33 ABC<-structure(list(A=Amat,B=Bmat,C=Cmat))
34 return(ABC)
35 }
36
37 #simplexABC calculates SDR indices from A, B and C components
38 simplexABC<-function(A,B,C,relative=T)  { #relative=TRUE returns
39 index values to sum up to 1,
40                                     #if relative=FALSE,
41 returned values are species numbers without standardization
42 tot<-A+B+C
43 if(any(tot==0)) {print("At least two sites have no species! Unable to
44 calculate relative index values!", quote=F)
45   relative=F
46 }
47 ifelse(relative==T, sim<-A/tot, sim<-A)
48 ifelse(relative==T, repl<-2*pmin(B,C)/tot, repl<-2*pmin(B,C))
49 ifelse(relative==T, rich<-abs(B-C)/tot, rich<-abs(B-C))
50 SDR<-
51 structure(list(similarity=sim,richness.difference=rich,replacement=repl))
52 return(SDR)
53 }
54
55 #the nestedness function
56 nestABC<-function(A,B,C, strict=T, relative=T)  { #relative=TRUE
57 standardizes with total species number in the pair of plots, as in
58 simplexABC
59 tot<-A+B+C

```

```

1  if(any(tot==0)) {print("At least two sites have no species! Unable to
2  calculate relative nestedness!", quote=F)
3  relative=F
4  }
5  nn<-(A+abs(B-C))
6  nn[A<=0]<-0
7  if(strict==T) { nn[B==C]<-0 }           #'strict' nestedness
8  ifelse(relative==T, nest<-nn/tot, nest<-nn)
9  return(nest)
10 }
11
12
13 #####Example#####
14 require(vegan)
15 data(dune)
16
17 x<-ABCmat(dune)
18
19 sdr<-simplexABC(A=x$A, B=x$B, C=x$C, relative=T)           #for the three basic
20 components
21 nest<-nestABC(A=x$A, B=x$B, C=x$C, strict=F, relative=T)   #for
22 absolute nestedness
23
24 #Similarity matrix:
25 sdr$similarity
26 #Replacement matrix:
27 sdr$replacement
28 #Richness difference matrix:
29 sdr$richness.difference
30
31 sdr$similarity+sdr$replacement+sdr$richness.difference     #sums up to 1,
32 if relative=T
33
34 #simple handling as distance matrices, different ways of indexing
35 S<-as.dist(sdr[[1]])
36 D<-as.dist(sdr[[2]])
37 R<-as.dist(sdr$replacement)
38
39 #triangle plot
40 require(klaR)
41 triplot(D,R,S, label=c("D","R","S"))           #note the order of components
42 which is now according to the conventional way by Podani, Schmera et al.
43                                           #see klaR package functions
44 triplot, triline, tripoints, etc. for more graphical options
45
46

```