Partial recovery and uneven ecological responses of beetles following mire rewetting in central Sweden

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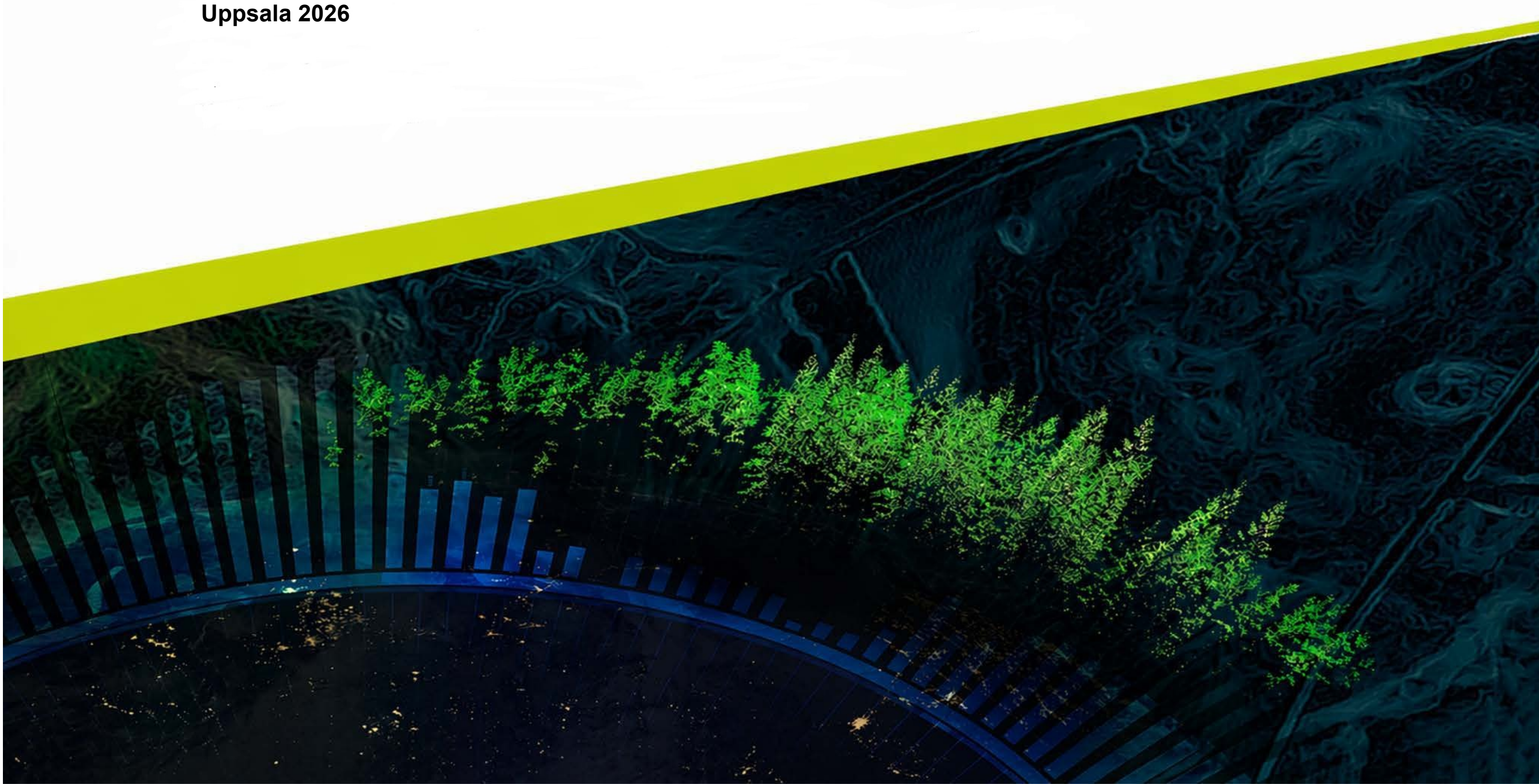

Partial recovery and uneven ecological responses of beetles following mire rewetting in central Sweden

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Abstract

Mires support specialised biodiversity and important ecosystem functions, but many have been degraded by drainage for forestry, agriculture and peat extraction. Rewetting is widely used to reverse mire degradation by restoring water levels, yet its ecological effects remain incompletely understood, particularly for diverse insect groups. Because insects are species-rich, ecologically complex and often sensitive to environmental change, they may provide useful indicators of rewetting outcomes.

In this study, I evaluated rewetting effects on beetle assemblages across 18 mires in central Sweden, including ditched, rewetted and unditched sites. Beetles were sampled using pitfall and window traps and identified to species level, enabling ecological comparisons among mire types. Environmental variables were also included to assess their contribution to the observed ecological patterns. Rewetted mires showed partial and uneven ecological responses, with some patterns closer to unditched mires and others closer to ditched mires. Wetland species richness in rewetted mires was closer to unditched conditions, whereas generalist abundances remained more similar to ditched mires. In contrast, terrestrial species and feeding guilds showed little or no response to rewetting. Environmental variables provided limited explanatory power for the observed patterns. Overall, beetles appear useful for detecting ecological responses to rewetting, although the results suggest partial rather than complete recovery.

Keywords: Mire restoration, rewetting, central Sweden, insect ecology, community ecology, Coleoptera

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Introduction

In Europe, most mires have been heavily degraded during history, through drainage for agriculture, forestry and peat extraction, with major consequences for mire ecosystem functioning and biodiversity (Andersen et al., 2017, Rydin & Jeglum, 2013). Ongoing climate changes may further alter mire ecosystems, and without restoration, degradation is likely to continue. Once mires reach certain thresholds, their function is often difficult to restore and restoration becomes economically unfeasible (Elo et al. 2024, Grootjans et al. 2012, Albert-Saiz et al. 2025, Meyer et al. 2015). To reverse mire degradation, rewetting has become the most common approach (Andersen et al. 2017). This typically involves raising and stabilizing the water table by blocking drainage ditches or constructing dams, to reduce water runoff and keep steady water levels (Andersen et al. 2017). Rewetting success has often been evaluated using abiotic factors, particularly hydrological conditions, or changes in vegetation (Wieder et al. 2006). Consequently, it is being asked how well changes in abiotic factors and vegetation can explain restoration success (Taddeo et al. 2018). Although such measures may reflect important aspects of recovery, they do not necessarily capture the response of biodiversity as a whole (McAlpine et al. 2016). Since ecological responses can vary depending on the organism groups studied (Strobl et al., 2019), targeted studies of different organism groups may improve evaluations of rewetting success (Lehmitz et al., 2020)

Insects are the most diverse animal group on Earth and are being increasingly recognized as useful indicators for evaluating peatland condition (Batzer et al., 2016; Danks & Spitzer, 2006). Most studies so far have focused on aquatic insects when evaluating the status of wetlands overall, although terrestrial insects are far more abundant and diverse in these systems, potentially making them more ecologically informative (Batzer & Wu, 2020, Krogerus, 1960). However, their high diversity also makes assessments based on multiple insect groups challenging (Batzer & Wu, 2020). Beetles (Coleoptera) have emerged as a promising alternative for evaluating rewetting effects and are among the most species-rich orders in mire systems (Alekseev et al. 2024, Krogerus, 1960, Danks & Spitzer, 2006). Still, relatively little is known about how insects respond to rewetting and what these responses reveal about restoration success, highlighting the need for further research (Hammerich et al. 2022). Many studies of beetles responses to rewetting have focused on single families, wetland-specific species or mire-specific species, often overlooking effects on beetles as a broader taxonomic group at community level (Fernandez, 2019, Hoffmann et al. 2016, Tichit et al. 2026, Watts et al. 2008). Evaluating beetles at the community level could therefore provide broader insight into how rewetting affects beetle assemblages, including the extent to which rewetted mires converge towards the community composition of unditched mires (Alekseev et al. 2024, Noreika et al. 2015, Watts & Mason, 2015).

This study examined beetle responses across mire types using community composition, habitat preference, feeding guild structure, taxon-specific associations, and environmental variables. I hypothesised that rewetted mires would show partial recovery towards unditched conditions. More specifically, I expected that (1) community composition and feeding guild structure in rewetted mires would be more similar to unditched than to ditched mires, (2) rewetted mires would support higher richness and abundance of wetland species and lower richness and abundance of terrestrial and generalist species than ditched mires. In addition, I addressed two research questions: (3) whether specific beetle taxa showed significant associations with particular mire types, and (4) whether environmental variables, including moisture, Ellenberg pH and openness, were associated with variation in ecological patterns and taxa linked to particular mire types.

Methods

Selection and classification of mires

The study area was located in the southern parts of Dalarna and northern parts of Västmanland, central Sweden, in a relatively mire-rich landscape dominated by coniferous forests. Three different types of mires were selected for the study, with five rewetted, five unditched and eight ditched localities per type. Rewetted mires included localities restored through ditch blocking using peat, timber dams, or constructions made of felled timber. All were restored in 2021, except one locality, which was restored in 2019 (Lindh et al. 2024, Karin Eklöf, SLU, pers. comm., 2025, Magnus Persson, County Administrative Board of Västmanlands län, pers. comm., 2025). Information on the duration of ditching prior to restoration was not available for the studied localities. For each rewetted and ditched mire, an unditched control mire located as close as possible was selected. Ditched mires were defined as drained mires that had not undergone restoration, while unditched mires represented near-natural conditions without ditching. Unditched and ditched mires were identified by Peter Hambäck using topographic maps, satellite imagery, historical flight images, soil moisture index and ditch map layers available in SCALGO Live (SCALGO, 2026).

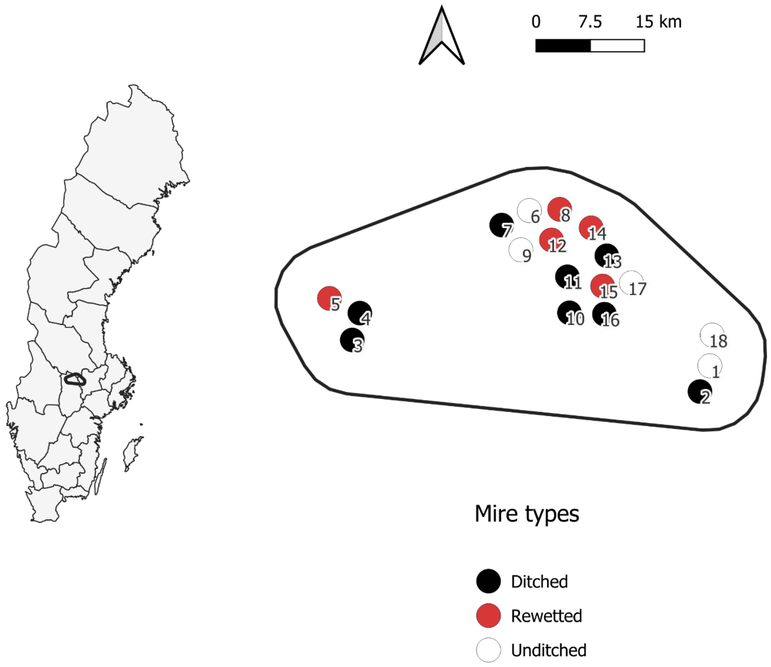


Figure 1. Overview of the study area. Exact coordinates for each locality are provided in figure A1.

Beetle sampling

Beetles were sampled using IBL window traps and three pitfall-trap designs: a linear, trough-shaped pitfall trap, a rectangular container trap, and a standard cup pitfall trap (Figure 2). Several trap-types were used because trap design may affect catch size, species richness, and species composition (Boetzl et al., 2018). One window trap and one pitfall trap of each type were placed at each locality. All traps were filled with a 50:50 mixture of propylene glycol and water. Pitfall traps were placed approximately 10 meters apart in a straight row and the window traps were placed nearby. In rewetted or ditched mires, all traps were placed at a distance of 10 meters from the ditches and in unditched mires traps were placed at mire-edges with vegetation matching that of the other treatments (see figure A9 for vegetation data from each locality). Traps were deployed between 29 and 31 May 2025 and emptied during three sampling periods- 9-12 June, 19-20 June and 6-8 July, and were removed during the last period. All traps were active for 37-41 days.

Figure 2. Trapping methods used for beetle sampling, from left: IBL-window trap and three different types of pitfall traps.

Beetle identification

Beetles were stored in propylene glycol during transportation and during the following sorting processes. A preliminary sorting process, in which all beetle specimens were separated, was carried out during July. Sorting beetles into relevant taxonomic entities was done during September. The sorting processes were performed in a laboratory and all beetles were determined to species level, with a few exceptions. Most of the specimens were identified by the author, except for Ptiliidae, identified by Mikael Sörensson and most Atheta specimens as well as single specimens of other Aleocharinae and Staphylinidae*,* identified or verified by Torbjörn Ramqvist and Gunnar Sjödin. Additional identifications were validated by Mats Jonsell, with whom uncertain cases across all beetle groups were also discussed. Species identifications were primarily based on Coleonet (Lompe, 2002), relevant volumes of *Danmarks Fauna* (vols. 14, 16, 22, 26, 29, 31, 34, 50, 55, 56, 62, 73, 74), Palm (1948–1972) for Staphylinidae, Lindroth (1942) for Carabidae, Höjer (2011) for *Epuraea*, and Persson (2016) for Ciidae.

Ecological classification of beetles

All beetle species were classified into habitat preference and feeding guild, using data from Artfakta (2026). At Artfakta, habitat preferences were assigned to three different categories: wetland species, terrestrial species or generalist species based on the available information. Further, beetles were also defined into feeding guilds, covering parts of, or their whole life cycles (depending on available data), consisting of 1). Herbivores, 2). Fungivores, 3). Carnivores, 4). Saprotrophs/saprophages/detritivores, 5). Parasitoids, 6). Omnivores and 7). Filter-feeders. A species could thus be assigned into several guilds.

Vegetation sampling

Between 9 and 12 June, classification and species determination of vascular plants were performed. An area of 10 x 10 m, adjacent to the window- and flight interception traps were surveyed for 10 minutes for each locality. The observer walked a zigzag-pattern of five transects spaced with 2 meters distance in the surveyed area. The abundance of each species was visually estimated from its proportional areal cover and classified into three semi-quantitative categories: rare, scattered, and abundant. No fixed percentage thresholds were applied. Species identification was performed in the field by using *Nordiska floran* (Mossberg, 1997) and *Svensk flora: fanerogamer och kärlkryptogamer*, Krok, Almquist, Jonsell & Jonsell, 2013. Vegetation data were subsequently used to calculate Ellenberg indicator values for pH and moisture as vegetation may integrate environmental conditions over time rather than reflect only the current state of pH and moisture at each mire (Dengler et al., 2023).

Environmental variables

Environmental variables including water depth measured in the field, Ellenberg pH and moisture values calculated from the vascular plant survey, and indices of moisture, openness, and overgrowth were calculated in QGIS.

Water depth was measured in the field during the first sampling period with a 40 cm long white plastic pipe, inserted into the peat, placed nearby the traps at each locality. Water depth was initially measured as distance to the water table, but was later inverted so that higher water tables corresponded to wetter conditions.

Ellenberg indicator values for pH and moisture were derived from the vascular plant survey using species-specific values from Tyler et al. (2021), which are calibrated for Swedish conditions. Locality-level values for moisture and pH were calculated as abundance-weighted means based on species-specific indicator scores and semi-quantitative abundance classes.

Raster data for the moisture index were obtained from Naturvårdsverkets Metadatakatalog för Geodata (layer: Markfuktighetsindex, Nationella marktäckedata; 10 m resolution). The moisture index was calculated with zonal statistics in QGIS as mean values for each locality, both at the locality level and within a 500 m buffer representing the surrounding matrix.

Openness and overgrowth were calculated as mean values within locality polygons. Eighty randomly placed points with a minimum distance of 20 m between points were generated within each locality using the function "random points in polygons." Sampling boxes of 10 × 10 m were centred on each point. For each sampling box, openness was classified as 0 = open, 1 = tendencies towards closed conditions, and 2 = closed environment. Openness values were transformed to a 0–1 scale, ranging from 0 = late succession and 0.5 = early succession to 1 = open. Overgrowth was recorded separately as 0 = no distinct overgrowth signal and 1 = a distinct overgrowth signal.

Maps and spatial calculations were produced in QGIS Desktop version 3.36.1. Systematic point displacement was applied to visually separate nearby localities. ESRI World Imagery served as a visual basemap. All spatial data were processed in SWEREF 99 TM (EPSG:3006). Locality boundaries were defined using hand-drawn polygons based on hydrological data.

Data analysis

Data handling and organisation were carried out in Google Sheets. All statistical analyses were performed in R version 4.4.0 in RStudio. Community analyses (PCoA, NMDS, PERMANOVA and PERMDISP) were conducted using the R package *vegan* (Oksanen et al., 2022).

Community composition and ecological traits

Differences in species richness of wetland, terrestrial, and generalist species among mire types were analysed using linear models (ANOVA), whereas differences in abundance were analysed using generalized linear models (GLM) with a Poisson error distribution. The package `*DHARMa*`in R was used for meeting test assumptions (Hartig, 2022). To test for an overall effect, models with and without mire type were compared using a likelihood ratio test (χ^2). Pairwise differences among mire types were then examined using Tukey-adjusted estimated marginal means (R package *emmeans*). Main analyses were conducted on pooled data across trap types to capture overall differences among mire types, whereas figures were presented separately for pitfall and window traps to assess consistency across methods.

Feeding-guild composition across mire types was visualised using PCoA based on Bray–Curtis dissimilarities for both species richness and abundance. Differences among mire types were then analysed at the community level using locality-level guild proportions. Overall differences were tested using PERMANOVA, and homogeneity of multivariate dispersion was assessed using PERMDISP. In addition, guild-specific differences were analysed using quasibinomial GLM and p-values were adjusted for multiple testing using FDR correction. Pairwise differences in guild proportions were examined using estimated marginal means (R package *emmeans*). Main analyses were conducted on pooled data across trap types and repeated separately by trap type as a sensitivity analysis.

Overall beetle community composition was visualised using PCoA and analysed separately for pooled data, window trap data, and pitfall trap data. Community dissimilarities were calculated using Bray–Curtis and Jaccard indices. Differences among mire types were tested using PERMANOVA at both global and pairwise levels, and homogeneity of multivariate dispersion was assessed using PERMDISP. Pairwise differences in centroid distances were evaluated using permutation tests. Bray–Curtis-based analyses were also repeated on untransformed abundance data as a sensitivity analysis.

Taxon-specific associations with mire types

Two complementary approaches were used to assess taxon–mire type associations. Indicator species analysis was used to identify taxa characteristic of specific mire types based on both frequency and specificity, whereas GLMs were used to test whether taxon abundances differed among mire types.

Indicator taxa for each mire type were identified across all taxonomic levels using the multipatt function in the R package *indicspecies*, with permutation-based testing (De Cáceres & Legendre, 2009). Taxa were analysed at the superfamily, family, subfamily, genus, and species levels. A prevalence filter with a minimum-occurrence threshold of 2 localities per mire type was used for all taxonomic levels.

GLMs were fitted across all taxonomic levels to test for overall differences in taxon abundance among mire types. Taxa were retained if they occurred in at least two localities within at least one mire type. Poisson models were fitted initially, and negative binomial models were used when overdispersion was detected (using *MASS::glm.nb*).

Additional diagnostic checks were performed for taxa identified as significant in the GLM analyses, including assessment of zero frequencies, leave-one-out analysis (LOO), and tests of spatial autocorrelation. P-values were adjusted for multiple testing using FDR correction.

Environmental analyses

These analyses were conducted in an exploratory framework to assess potential associations between environmental variables and beetle assemblages.

Differences in environmental variables among mire types were analysed using univariate linear models. Model fit was evaluated using residual diagnostics, and p-values were adjusted using FDR correction. Pairwise Spearman correlations among environmental variables were examined prior to analysis. Because openness and overgrowth were strongly correlated, they were not included in the same analyses. Water depth, Ellenberg pH, and openness were retained for further analyses.

Spearman rank correlations were used to assess locality-level associations between feeding guilds or habitat preferences and the retained environmental variables. P-values were adjusted for multiple testing using FDR correction.

Environmental associations in beetle community composition were analysed for Carabidae and Staphylinidae at family, subfamily, and genus levels. These groups were selected because they were species-rich in the dataset and are mostly ground-dwelling species (Boháč, 1999, Koivula, 2011). Non-metric multidimensional scaling (NMDS; metaMDS in the R package *vegan)* was used to visualise compositional differences among localities, and environmental vectors were fitted to the ordinations (envfit in *vegan)*. At family level, multivariate GLMs (R package mvabund::manyglm) with negative binomial error distribution were used to fit a full model including mire type and the retained environmental variables. At subfamily and genus levels, where the data were sparser and multivariate GLMs failed to converge, distance-based methods were used instead, including PERMANOVA and PERMDISP based on Bray–Curtis dissimilarities (R package vegan::vegdist).

P-values were adjusted for multiple testing using FDR correction. Analyses were repeated by trap type as a sensitivity analysis, except for Carabidae in window traps, where data were unavailable.

An exploratory taxon-level analysis was conducted for genus- and species-level taxa identified as significant in the GLM analyses. These levels were retained to allow a more detailed examination of taxon–environment relationships while maintaining analytical consistency and interpretability. To avoid highly sparse responses, taxa were required to occur in at least six localities in total and in at least three localities with non-zero abundance. Locality-level abundances were modelled against the retained environmental variables using generalized linear models. Poisson models were fitted first and evaluated using DHARMa residual diagnostics, and negative binomial models were used when needed. Environmental variables were standardized before analysis to allow comparison of response strength across taxa and gradients. Standardized slopes were then compared across taxon–environment relationships, and a subset was selected for illustrative presentation based on these comparisons and data coverage.

Results

In total, 344 beetle species and 3,683 individuals were recorded. Pitfall traps captured 227 species and 2,185 individuals, whereas window traps captured 241 species and 1,498 individuals. Across mire types, ditched sites had the highest number of species and individuals (237 species, 1,668 individuals) followed by rewetted (216 species and 1,229 individuals) and unditched mires (161 species, 783 individuals). A complete species list is provided in Appendix Table A8.

Beetle responses across mire types

Habitat preference

Wetland species showed the clearest response to rewetting, compared with a partial response for generalist species and no response for terrestrial species.

Wetland species
Wetland species richness differed significantly among mire types ($F(2,15) = 10.11$, $p = 0.0017$) (Figure 3). Ditched and rewetted mires ($p = 0.0032$) and ditched and unditched mires ($p = 0.0286$) differed significantly, but rewetted and unditched mires did not ($p = 0.5930$). In contrast, no overall effect of mire type on wetland abundance was detected ($\chi^2(2) = 3.34$, $p = 0.18$), although unditched and rewetted mires had higher mean abundances than ditched mires.

Generalist species
Generalist species richness differed marginally non-significant across mire-types ($F2,15=3.01$, $p=0.08$) (Figure 3). In contrast, an overall effect of mire type on generalist abundance was found ($\chi^2(2) = 8.89$, $p = 0.01$). Generalist abundances differed significantly between Ditched-Unditched mires ($p=0.0147$) and Rewetted-Unditched mires (0.0134), but not between Ditched-Rewetted mires ($p=0.9413$) (Figure 4).

Terrestrial species
Terrestrial species richness differed marginally non-significant across mire types ($F2,15)=2.88$, $p=0.08$) (Figure 3). The same was true for abundance, where no overall effect of mire type on terrestrial species was detected ($\chi^2(2) = 3.19$, $p = 0.20$).

The results remained qualitatively unchanged after performing a sensitivity analysis and overall patterns were consistent across trap datasets.

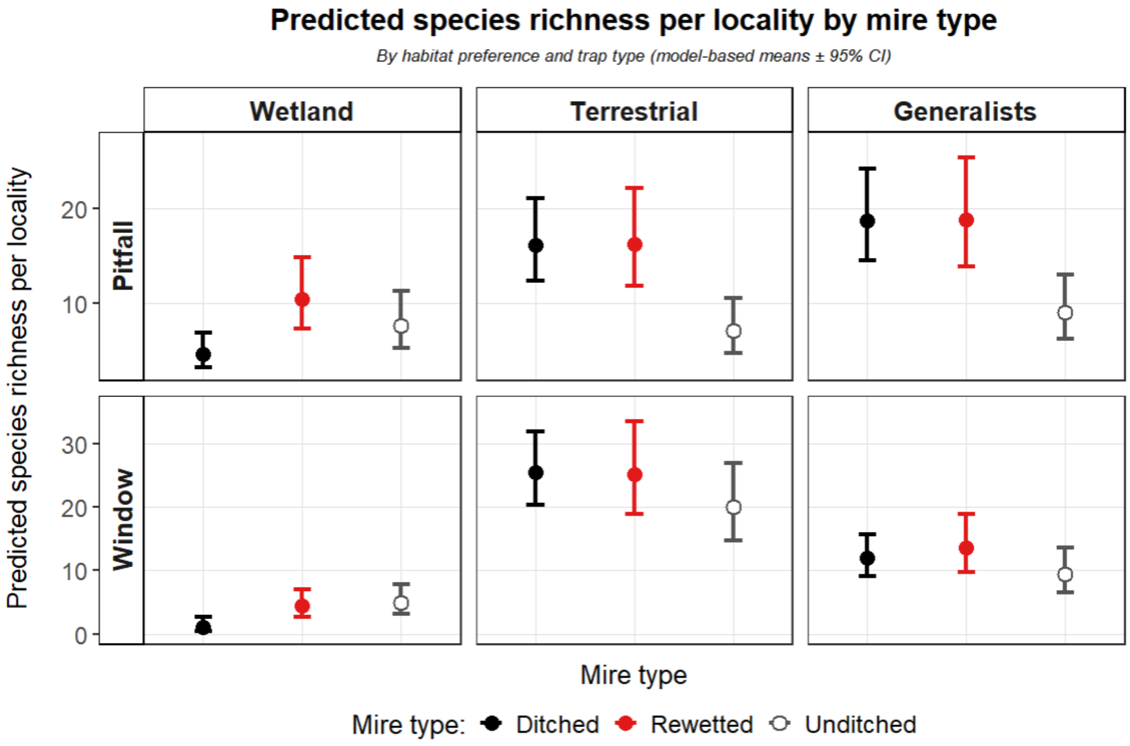


Figure 3. Differences in species richness of wetland, terrestrial and generalist beetles divided between trap types across mire types.

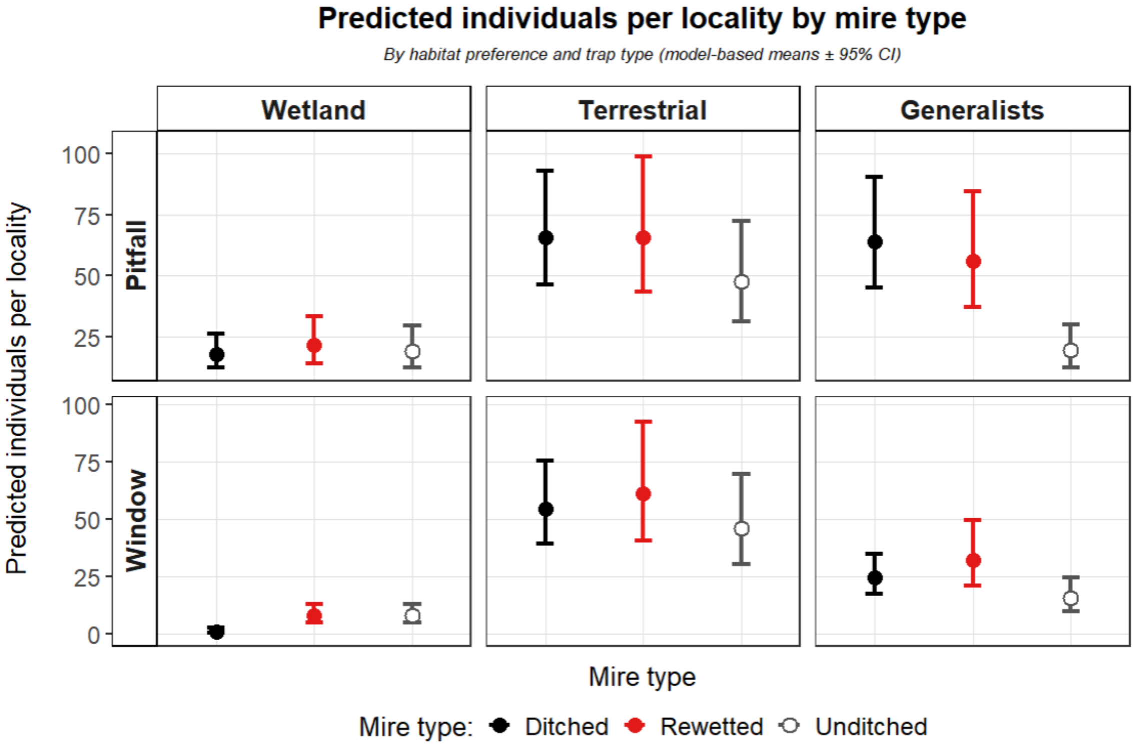


Figure 4. Differences in abundances of wetland, terrestrial and generalist beetles divided into trap types across mire types.

Feeding guild composition

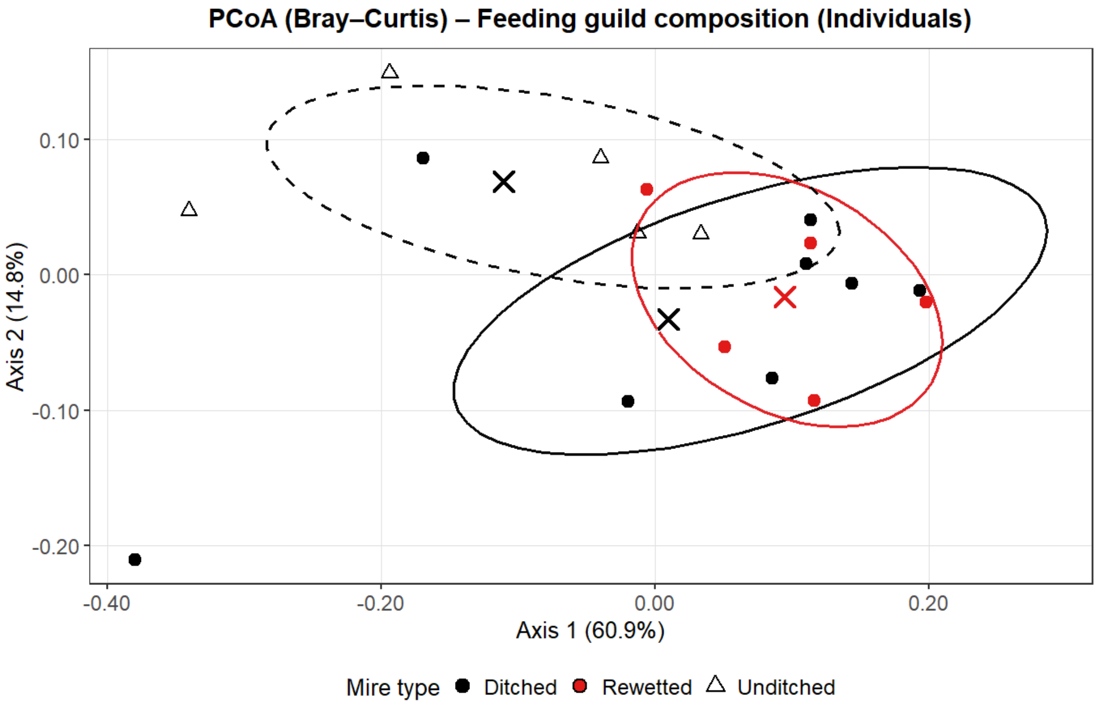


Figure 5. Principal coordinates analysis (PCoA) ordination based on Bray-Curtis dissimilarity of feeding guild composition calculated from abundances per locality. Dots represent localities, crosses represent mire types, centroids represent group means and ellipses represent 68% confidence intervals around centroids.

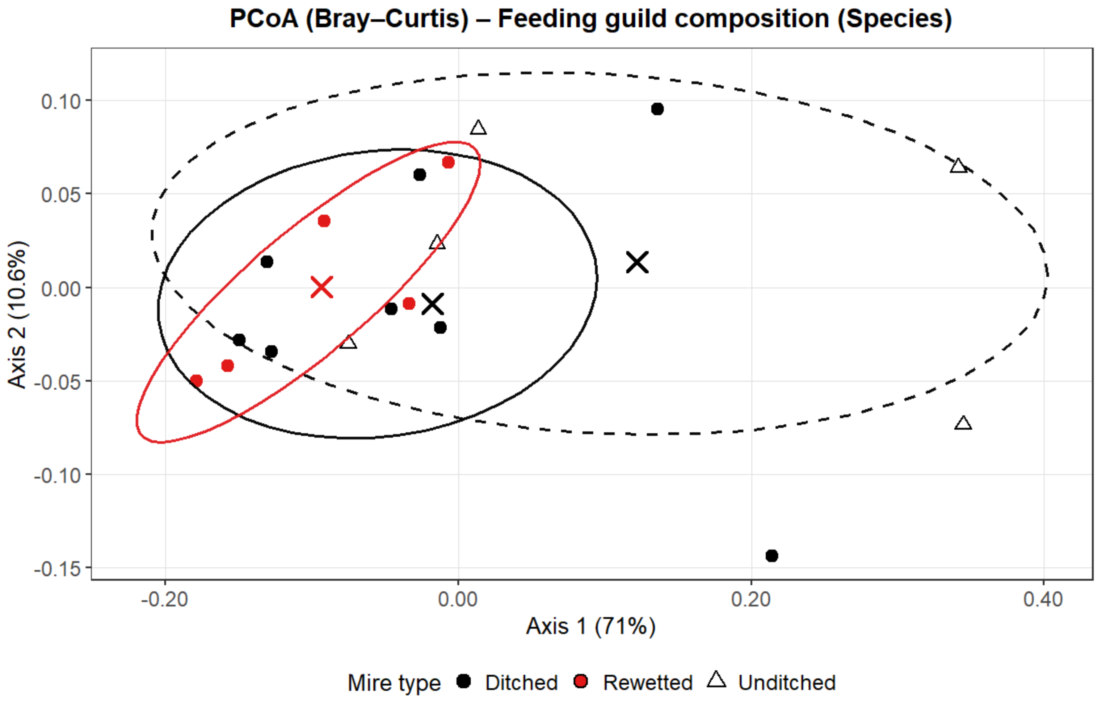


Figure 6. Principal coordinates analysis (PCoA) ordination based on Bray-Curtis dissimilarity, of feeding guild composition calculated from species richness per locality.

Feeding-guild responses were generally weak, although some differences among mire types were found for pitfall-trap abundances and for individual guilds.

Feeding-guild composition did not differ significantly among mire types in the pooled dataset. For species richness, differences were not significant (Bray–Curtis: F(2,15) = 2.48, $R^2 = 0.25$, $p = 0.05$, 999 permutations), and a similar pattern was found for abundances (F(2,15) = 2.05, $R^2 = 0.22$, $p = 0.07$). PERMDISP showed no evidence of differences in multivariate dispersion for either species richness (F(2,15) = 2.82, $p = 0.07$) or abundances (F(2,15) = 0.97, $p = 0.42$).

Sensitivity analyses showed similar patterns across trap subsets, with most analyses remaining non-significant. However, feeding-guild composition based on abundances differed significantly among mire types in the pitfall-trap dataset.

Guild-specific proportion models revealed significant differences among mire types for proportions of species in filter-feeders (F(2,15) = 15.49, FDR-adjusted $p < 0.01$) and herbivores (F(2,15) = 12.23, FDR-adjusted $p < 0.01$). For abundance proportions, only filter-feeders differed significantly (F(2,15) = 11.49, FDR-adjusted $p < 0.01$).

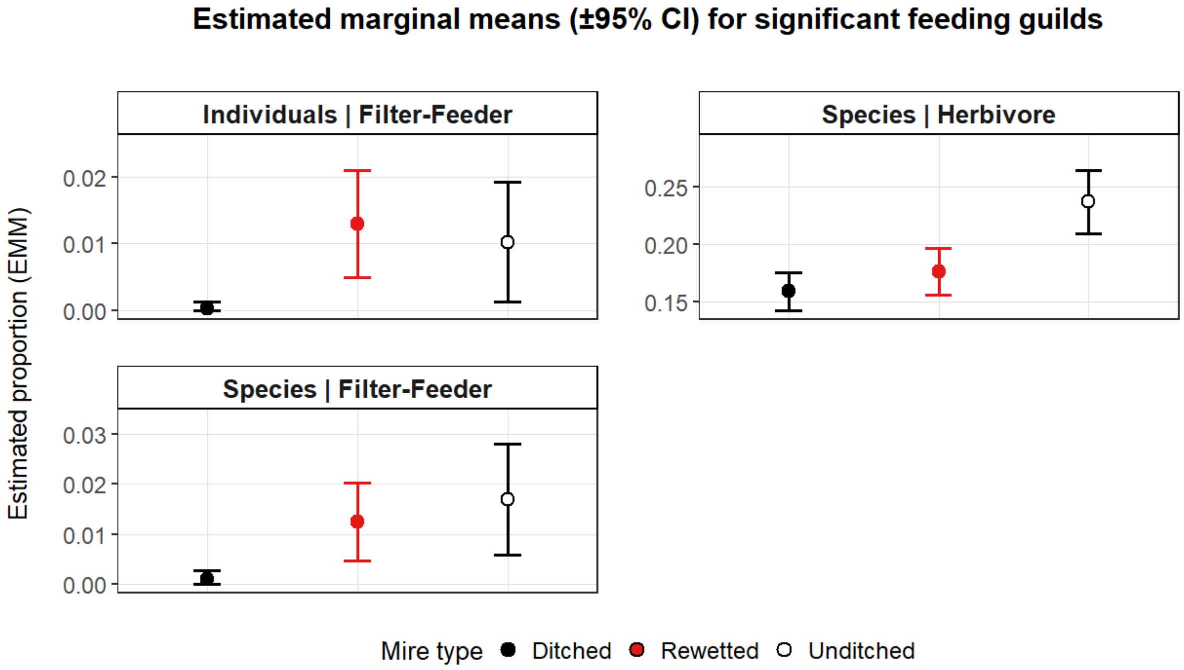


Figure 7. Estimated marginal means (EMMEANS) for significant (FDR-adjusted) feeding guilds across mire-types for 1). species proportions and 2). abundance proportions. Values are derived from Quasibinomial-GLMs weighted by total counts.

Community composition

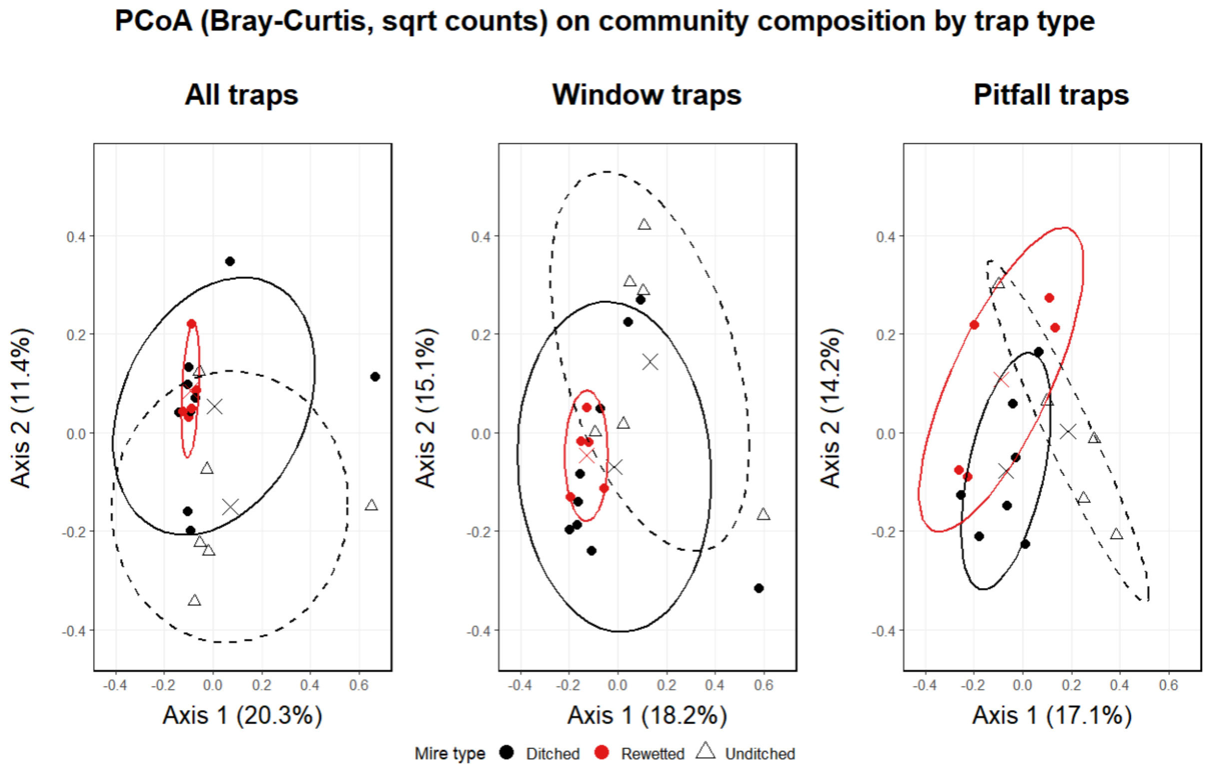


Figure 8. PCoA on Jaccards index for overall beetle community composition divided by trap type and mire type.

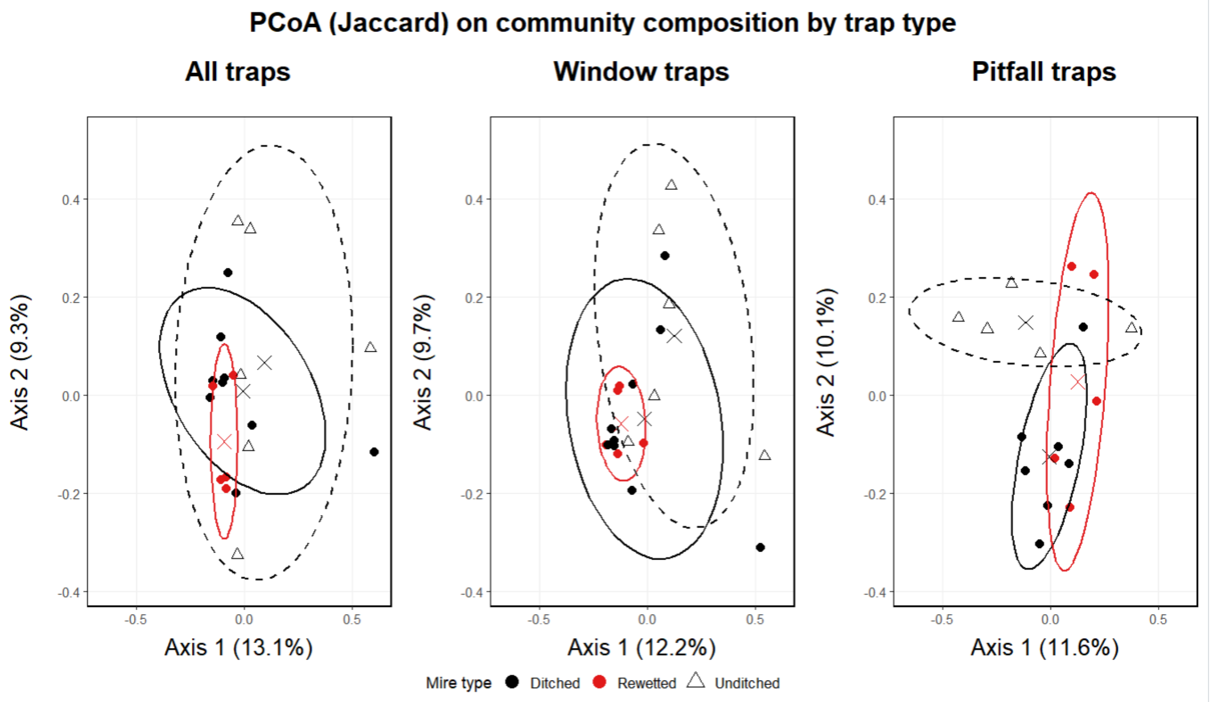


Figure 9. PCoA on Bray-Curtis (sqrt counts) for overall beetle community composition divided by trap type and mire type.

Community responses showed clear separation between ditched and unditched mires, whereas comparisons with rewetted mires were weaker and less consistent.

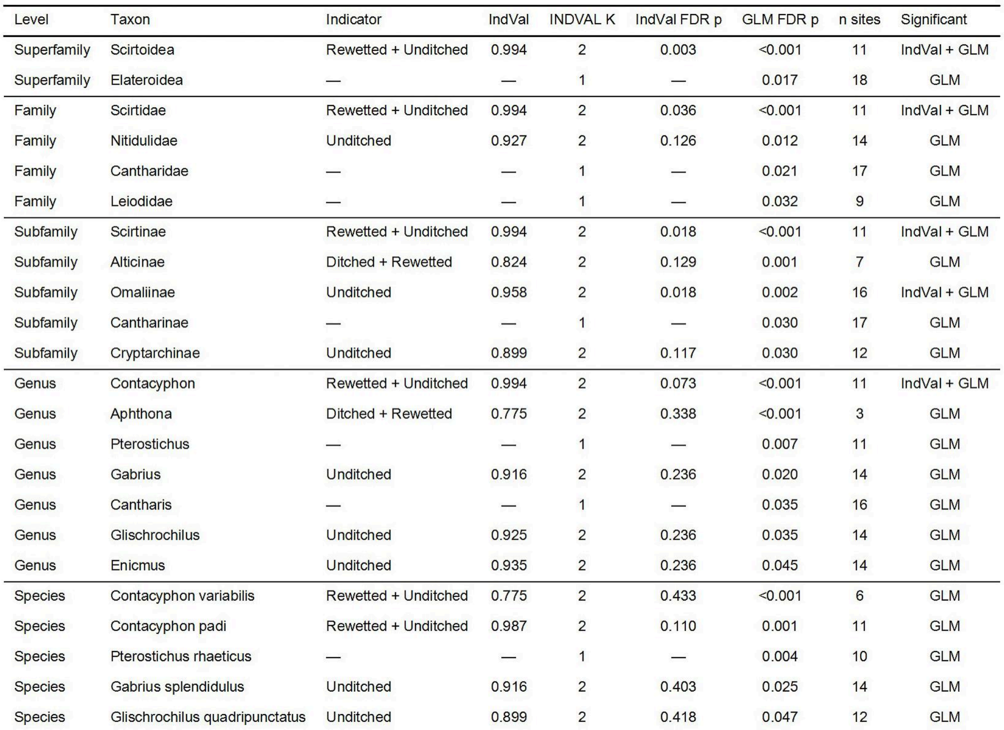
Global PERMANOVA results were significant for the pooled dataset and for both dissimilarity measures, except for pitfall traps under raw Bray–Curtis abundances. In that case, the global PERMANOVA did not show clear compositional differences among mire types ($F = 1.58$, $R^2 = 0.18$, $p = 0.05$), and PERMDISP indicated heterogeneous dispersion among mire types ($F = 4.72$, $p = 0.02$). In contrast, when square-root transformed abundances were used, the pitfall-trap dataset showed significant compositional differences among mire types (PERMANOVA: $F = 1.50$, $R^2 = 0.176$, $p = 0.01$) with no evidence of heterogeneous dispersion (PERMDISP: $F = 0.53$, $p = 0.62$) (Table A2).

Pairwise PERMANOVA tests showed that ditched and unditched mires differed consistently, with significant differences for the pooled and window-trap datasets, and a weaker but still apparent signal for the pitfall-trap dataset. Pairwise PERMANOVAS involving rewetted mires were generally non-significant and less consistent than comparisons between ditched and unditched mires (Table A3).

Pairwise comparisons using group centroids were not significant. Descriptively, centroid distances suggested a general pattern where ditched and rewetted mires tended to be most similar, whereas rewetted and unditched mires were most dissimilar. Differences between ditched and unditched were intermediate in magnitude. (Table A4).

Taxon-specific associations with mire types

GLMs identified several taxa across taxonomic levels with significant abundance differences among mire types, whereas fewer taxa were identified as significant indicators in the IndVal analysis. Contacyphon was supported by both approaches, showing significant abundance differences in the GLMs and an IndVal association with rewetted and unditched mires. Most significant IndVal taxa were associated with rewetted and unditched mires, fewer were associated only with unditched mires, and only two were associated with ditched mires.



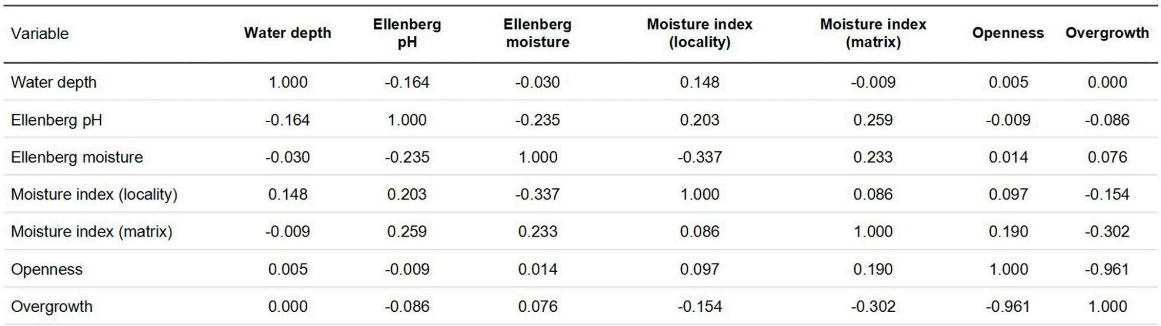
Level	Taxon	Indicator	IndVal	INDVAL K	IndVal FDR p	GLM FDR p	n sites	Significant
Superfamily	Scirtoidea	Rewetted + Unditched	0.994	2	0.003	<0.001	11	IndVal + GLM
Superfamily	Elateroidea	—	—	1	—	0.017	18	GLM
Family	Scirtidae	Rewetted + Unditched	0.994	2	0.036	<0.001	11	IndVal + GLM
Family	Nitidulidae	Unditched	0.927	2	0.126	0.012	14	GLM
Family	Cantharidae	—	—	1	—	0.021	17	GLM
Family	Leiodidae	—	—	1	—	0.032	9	GLM
Subfamily	Scirtinae	Rewetted + Unditched	0.994	2	0.018	<0.001	11	IndVal + GLM
Subfamily	Alticinae	Ditched + Rewetted	0.824	2	0.129	0.001	7	GLM
Subfamily	Omaliinae	Unditched	0.958	2	0.018	0.002	16	IndVal + GLM
Subfamily	Cantharinae	—	—	1	—	0.030	17	GLM
Subfamily	Cryptarchinae	Unditched	0.899	2	0.117	0.030	12	GLM
Genus	Contacyphon	Rewetted + Unditched	0.994	2	0.073	<0.001	11	IndVal + GLM
Genus	Aphthona	Ditched + Rewetted	0.775	2	0.338	<0.001	3	GLM
Genus	Pterostichus	—	—	1	—	0.007	11	GLM
Genus	Gabrius	Unditched	0.916	2	0.236	0.020	14	GLM
Genus	Cantharis	—	—	1	—	0.035	16	GLM
Genus	Glischrochilus	Unditched	0.925	2	0.236	0.035	14	GLM
Genus	Enicmus	Unditched	0.935	2	0.236	0.045	14	GLM
Species	Contacyphon variabilis	Rewetted + Unditched	0.775	2	0.433	<0.001	6	GLM
Species	Contacyphon padi	Rewetted + Unditched	0.987	2	0.110	0.001	11	GLM
Species	Pterostichus rhaeticus	—	—	1	—	0.004	10	GLM
Species	Gabrius splendidulus	Unditched	0.916	2	0.403	0.025	14	GLM
Species	Glischrochilus quadripunctatus	Unditched	0.899	2	0.418	0.047	12	GLM

Table 1. Taxa showing significant associations with mire types based on generalized linear models (GLMs) and indicator species analysis (IndVal) across all taxonomic levels. IndVal k indicates the minimum occurrence threshold, defined as the number of localities required for inclusion in the analysis. FDR-adjusted p-values are reported separately for the indicator species analysis and GLMs. n sites indicate the number of localities in which each taxon was recorded. Significant indicates whether support was found from IndVal, GLMs, or both methods. Spatial autocorrelation analyses did not detect any significant Moran’s I values after FDR correction. Full GLM outputs are provided in Table A5.

Environmental associations

Environmental variables showed no consistent differences among mire types and provided limited explanatory power overall for the observed ecological patterns.

Variation in environmental variables among mire types



Variable	Water depth	Ellenberg pH	Ellenberg moisture	Moisture index (locality)	Moisture index (matrix)	Openness	Overgrowth
Water depth	1.000	-0.164	-0.030	0.148	-0.009	0.005	0.000
Ellenberg pH	-0.164	1.000	-0.235	0.203	0.259	-0.009	-0.086
Ellenberg moisture	-0.030	-0.235	1.000	-0.337	0.233	0.014	0.076
Moisture index (locality)	0.148	0.203	-0.337	1.000	0.086	0.097	-0.154
Moisture index (matrix)	-0.009	0.259	0.233	0.086	1.000	0.190	-0.302
Openness	0.005	-0.009	0.014	0.097	0.190	1.000	-0.961
Overgrowth	0.000	-0.086	0.076	-0.154	-0.302	-0.961	1.000

Table 2. Correlation chart among environmental variables.

Univariate linear models showed no significant differences in environmental variables among mire types (Figure A6). Among environmental variables, only openness and overgrowth were significantly correlated, with a strong negative correlation (Spearman's $\rho = -0.96$, $p < 0.001$, $n = 18$). Descriptively, mean environmental values varied among mire types, but the direction of these differences was not consistent across variables (Table A7).

Environmental responses of feeding guild and habitat preference

For feeding guilds, no correlations with environmental variables remained significant after FDR correction for either species richness or abundance-based proportions.

For habitat preference, only the abundance proportion of wetland species showed a significant association after FDR correction, increasing with water depth (Spearman's $\rho = 0.77$, $p < 0.001$, FDR-adjusted $p < 0.01$, $n = 18$). No other habitat-preference correlations remained significant after FDR correction.

Environmental responses for community composition

At the locality level, NMDS with fitted environmental vectors (envfit) detected one significant association. For Carabidae at subfamily level, community composition was significantly associated with Ellenberg pH ($r^2 = 0.51$, $p = 0.02$). No other envfit associations were significant after correction for multiple testing.

At family level, manyglm did not detect any significant effects of mire type, water depth, Ellenberg pH or openness on community composition.

At finer taxonomic resolution, PERMANOVA did not detect any significant effects, and the corresponding PERMDISP analyses were also non-significant. Together, these results provided no clear evidence of differences in community composition among mire types or along the tested environmental gradients at subfamily or genus level.

Trap-specific sensitivity analyses did not materially alter the main results, and no additional significant effects were detected.

Illustrative genus and species responses across environmental gradients

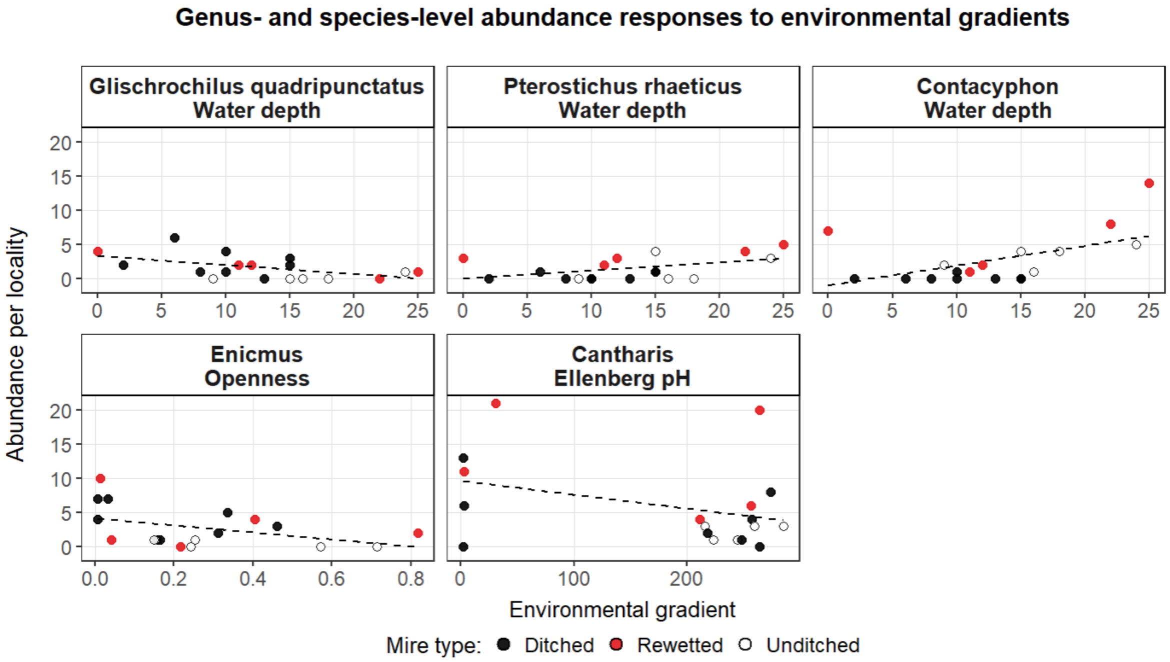


Figure 10. Plots based on generalized linear models (Poisson or negative binomial, depending on dispersion) of locality-level abundance for illustrative genus- and species-level taxa retained from the exploratory analysis, shown in relation to selected environmental gradients.

Contacyphon and *Pterostichus rhaeticus* tended to increase in abundance with increasing water depth, whereas *Glischrochilus quadripunctatus* and *Enicmus* tended to show negative responses to water depth and openness, respectively. *Cantharis* likewise showed a negative response along the Ellenberg pH gradient.

Discussion

This study shows that beetle responses to mire rewetting were partial and uneven across ecological dimensions, suggesting an incomplete recovery.

The clearest sign of recovery was found in wetland species richness, which was higher in rewetted and unditched mires than in ditched mires. In contrast, wetland species abundance, feeding guild structure, and overall community composition provided weaker or mixed evidence for convergence towards unditched conditions. Community composition showed a similar pattern, with the clearest separation between ditched and unditched mires, while the position of rewetted mires was less clearly resolved.

Thus, the hypotheses were only partly supported, with evidence of recovery strongest for wetland species and weaker or less consistent for community composition and feeding guild structure. In relation to the research questions, some taxa were associated with specific mire types, whereas environmental variables explained little of the observed variation.

Wetland species showed the clearest sign of recovery

Species richness in this group was significantly higher in rewetted and unditched mires than in ditched mires, consistent with the expectation that rewetting would benefit wetland-associated beetles. However, their abundance did not differ significantly among mire types. This indicates partial recovery: rewetted mires supported more wetland species, but not higher wetland beetle abundances.

Previous studies report similar patterns, showing that rewetting can shift beetle and insect communities towards conditions resembling unditched mires across different mire systems, while full convergence is often not reached even after 10–13 years (Noreika et al. 2015, Noreika et al. 2016, Mainda et al. 2025, Watts & Mason, 2015, Punttila et al. 2016). In other cases, rewetting effects have remained weak or absent even after 18–20 years, and responses appear to vary both within and among species groups (Fernandez, 2019, Strobl et al. 2019, Tichit et al. 2026). The present results fit this broader pattern of partial and uneven recovery.

For wetland species, this partial recovery was reflected in the stronger response of species richness than abundance. This mismatch between richness and abundance suggests that wetland species were able, at least to some extent, to colonize rewetted mires, while population sizes were still lagging behind and had not yet recovered to the same extent. Such a pattern is consistent with time-lagged responses following restoration, where species occurrence may recover earlier than population size (Watts et al. 2020)**.** Similar patterns have also been reported after peatland restoration in bogs (Krieger et al. 2019). In addition, dispersal ability varies considerably among beetle species, implying that slow-dispersing species may still colonize the studied mires in the future (Martay et al. 2014, Watts & Mason, 2015, Lakovic et al. 2015).

However, time-lagged responses may not only reflect dispersal limitation, but also incomplete recovery of habitat conditions. This partial convergence indicates that rewetted mires may not yet have regained the habitat quality of unditched mires. One possible explanation is that rewetted localities may still be affected by peat degradation, eutrophication, and lowered water tables resulting from previous ditching (Hoffmann et al. 2016, Watts et al. 2020). Such legacy effects may homogenize vegetation and abiotic conditions, with negative consequences for mire-inhabiting insects (Krieger et al. 2019, Petersen, 1954, Sushko 2017, Van Duinen et al. 2003). Clearer effects may therefore emerge over longer monitoring periods than those covered here, since vegetation structure can take decades to recover, even if the largest changes often occur during the first 10–15 years after rewetting (Allan et al., 2024).

This interpretation remains tentative, since most localities, regardless of mire type, showed signs of overgrowth, while the measured environmental variables did not differ significantly among mire types. Although the measured variables captured central aspects of mire restoration, additional unmeasured environmental variables or habitat features may also have contributed to the observed patterns. Moreover, responses are unlikely to be uniform among wetland species, as they differ in their degree of specialization and dependence on particular microhabitats (Strobl et al. 2019, Främbs 1994, Sushko, 2019, Mainda et al. 2025, Celik & Vres, 2018). This is consistent with the finding that Carabidae was associated with pH, suggesting that responses to rewetting may depend on specific local habitat conditions rather than mire type alone.

Incomplete convergence and uneven responses across ecological metrics

The uneven recovery was also reflected in the response of generalist species. Generalist abundances were significantly higher in ditched and rewetted mires than in unditched mires, whereas terrestrial species showed no clear response to mire type. This only partly matched the expectation that non-wetland species would be more common in ditched mires. This is broadly consistent with Noreika et al. (2015), who also found high generalist abundances in ditched and rewetted mires.This may indicate that rewetted mires still retained habitat conditions favourable to generalists, rather than resembling unditched mires completely (Hoffmann et al. 2016, Watts et al. 2020). Although mire conditions would generally be expected to limit strong colonization by generalist species (Gallé et al. 2019), the high abundance of generalists in ditched and rewetted mires may not necessarily reflect strong habitat affinity. It may partly reflect spillover from the surrounding forest landscape, where mobile generalist beetles can move across habitat boundaries and be sampled near mire edges (Tscharntke et al. 2012). This is particularly relevant for window traps, which may capture flying beetles with weak affinity to the immediate trap surroundings (Sverdrup-Thygeson & Birkemoe 2009). However, because similar patterns were found in both pitfall and window traps, the response likely also reflects conditions within the mires. Overall, this suggests that habitat-preference responses did not shift consistently towards unditched conditions. This incomplete shift was also reflected at the community level.

Community composition provided weaker evidence of convergence towards unditched mires. If rewetting had shifted beetle assemblages strongly away from ditched conditions, rewetted mires would be expected to resemble unditched mires more closely than ditched mires (Noreika et al., 2015; Watts & Mason, 2015). However, this pattern was not clearly supported. The clearest compositional difference was found between ditched and unditched mires, which differed significantly in both presence–absence and abundance-based analyses. No significant differences involving rewetted mires were detected otherwise, suggesting that rewetted sites had not yet become clearly differentiated from the other mire types. This is broadly in line with the general pattern reported by Noreika et al. (2015), in which ditched and unditched mires differed in species composition, while rewetted mires appeared to fall between these conditions. Descriptively, this pattern may reflect a combination of partial recovery towards unditched conditions and the development of assemblages that remain partly distinct from both ditched and unditched mires (Noreika et al., 2015; Mainda et al., 2025; Hoffmann et al., 2016). Thus, full faunal convergence following rewetting may not always be expected in wetland systems (Hoffmann et al., 2018). However, these results should be interpreted with some caution, since mire biodiversity is highly complex and heterogeneous, and community-level metrics may not capture all relevant ecological variation (Hammerich et al., 2022).

The compositional pattern was also consistent with the habitat-preference results, where wetland species richness shifted towards unditched mires, while generalist abundances remained closer to ditched mires following rewetting. Combined, these results suggest that rewetted localities showed mixed responses rather than clear convergence towards unditched conditions. In contrast, other ecological metrics responded more weakly. In particular, feeding guild results were generally weak, although abundance-based composition in pitfall traps differed significantly among mire types. Taken together, this pattern indicates uneven support for the expected recovery pattern, with clearer responses in habitat preference than in community composition or feeding guild structure. Rewetted mires therefore only showed partial convergence towards unditched conditions across ecological metrics. Previous studies have similarly shown that ecological metrics can vary substantially in their responses and may provide uneven pictures of recovery (Watts & Mason, 2015, Noreika et al. 2020, Taillefer & Wheeler, 2012). Although broad ecological metrics showed uneven recovery, taxon-level responses may reveal restoration patterns that are less visible at the community level.

Among taxon-specific results, Contacyphon provided the clearest example of this- showing abundance differences among mire types, an association with rewetted and unditched mires in the IndVal analysis, and an increase in abundance with increasing water depth. It also contributed to the observed pattern for filter-feeders. This indicates that some taxa showed clear associations with particular mire types. However, taxon-specific associations were clearer for some taxa than for others, suggesting that only part of the beetle fauna may be informative for detecting restoration responses.

Environmental variables provided limited explanatory power

The environmental variables provided limited explanatory power, suggesting that the measured gradients did not capture the main drivers of beetle responses across mire types. This provided only limited support for the expectation that moisture, Ellenberg pH and openness would explain ecological differences among mire types. A likely explanation is that the measured variables did not differ significantly among mire types, particularly water depth. Previous studies have shown that variation in water depth can drive changes in pH, vegetation, and habitat structure when certain thresholds are reached (Albert-Saiz et al. 2025). In the present study, such thresholds may not have been reached, or differences may have been too small or variable to generate clear ecological responses. In addition, the high heterogeneity and structural variation among mires overall makes it hard to make general assumptions and comparisons, since they respond differently to rewetting (Hammerich et al. 2022, Elo et al. 2024). Thus, a more comprehensive approach may be needed to better explain ecological variation across mire types.

Methodological constraints

Several methodological constraints should be considered when interpreting the results. The sampling design used in this study may have reduced how well the trap catches represented beetle assemblages within each mire type. Because sampling was restricted to limited areas within each mire, catches may have been influenced by microhabitat conditions and exact trap placement (Fernandez, 2019, Sverdrup-Thygeson & Birkemoe, 2009). In addition, window traps may have caught insects from the surrounding landscape, rather than the studied mires (Sverdrup-Thygeson & Birkemoe, 2009). Since sampling was further restricted to a limited number of trap types and part of the season, the sampled beetle assemblages may not have fully represented variation within each mire type (Knapp et al. 2020, Jonsell, 1995). The unbalanced number of localities among mire types should also be kept in mind when interpreting differences in abundance and community composition.

This issue of representativeness is also relevant at the level of mire classification. The classification of unditched and ditched mires used in this study may not have fully captured habitat conditions at each locality. Because classification was based only on spatial data sources not all aspects of mire condition may have been captured and it is possible that more subtle legacy effects from previous land use history affected mire conditions and thereby mire type classification (Tichit et al. 2026). The classification should therefore be interpreted with some caution. Similarly, variation among rewetted sites may have influenced the strength and consistency of restoration responses. Different rewetting methods were used among rewetted localities, which may have contributed to variation in hydrological responses among sites. The lack of significant differences in water depth among mire types suggests that the hydrological effects of rewetting may have been weaker or more variable than expected. Similar patterns have been reported previously, as rewetting does not always result in clear changes in water levels (Holden et al., 2011).

Finally, some ecological classifications and environmental variables were based on broad categories or proxies. The classification of beetles into feeding guilds and habitat-preference categories in this study, based on data from Artfakta, may have been too coarse to represent ecological variation among species and should therefore be interpreted with caution. In addition, most of the sampled environmental variables were derived from proxies and should be interpreted cautiously, since this may have reduced the ability to detect strong environmental relationships. For these reasons, taking field measurements of environmental variables would be valuable for future studies, as also emphasized by Wamelink et al. (2002).

Conclusions

This study examined how beetle assemblages responded to mire rewetting in central Sweden using community-level, trait-based, and taxon-specific metrics. Rewetted mires showed mixed responses, with some patterns resembling unditched mires, particularly wetland species richness, and others resembling ditched mires, particularly generalist abundance. Moreover, the results differed between ecological measurements, indicating that rewetted mires recover unevenly and partially following rewetting. Thus, rewetting may restore some key habitat conditions for beetles, but did not lead to full convergence in this study. The findings suggest that finer taxonomic information can complement broad community metrics when assessing rewetting effects and provide a more detailed understanding of ecological responses. Future studies should test whether the partial and uneven recovery observed here persists over longer timescales, and whether improved species-level ecological information can strengthen the use of beetles in restoration assessment.

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Popular science summary

Mires are unique ecosystems characterised by wet, acidic, and nutrient-poor conditions. They provide valuable ecosystem services and play an important role in climate regulation by storing both water and carbon. Historically, many mires have been heavily degraded, mainly through ditching for agriculture, forestry, and peat extraction, with negative consequences for biodiversity and ecosystem functioning. Rewetting is increasingly used to restore drained mires by raising water levels and helping them recover towards the conditions found in natural mires.

To examine how rewetting affects these ecosystems, this study used beetles as ecological indicators. Beetles are highly diverse and often respond quickly to environmental change, which makes them useful for detecting restoration effects. The study explored whether rewetting helps beetle communities in drained mires become more similar to those in natural mires.

The results suggested partial recovery after rewetting, but the response was uneven and incomplete. Environmental conditions explained only a limited part of the observed differences between mire types. Overall, the findings suggest that beetles can be useful for detecting ecological responses to rewetting, while also showing that recovery towards natural conditions may be only partial.

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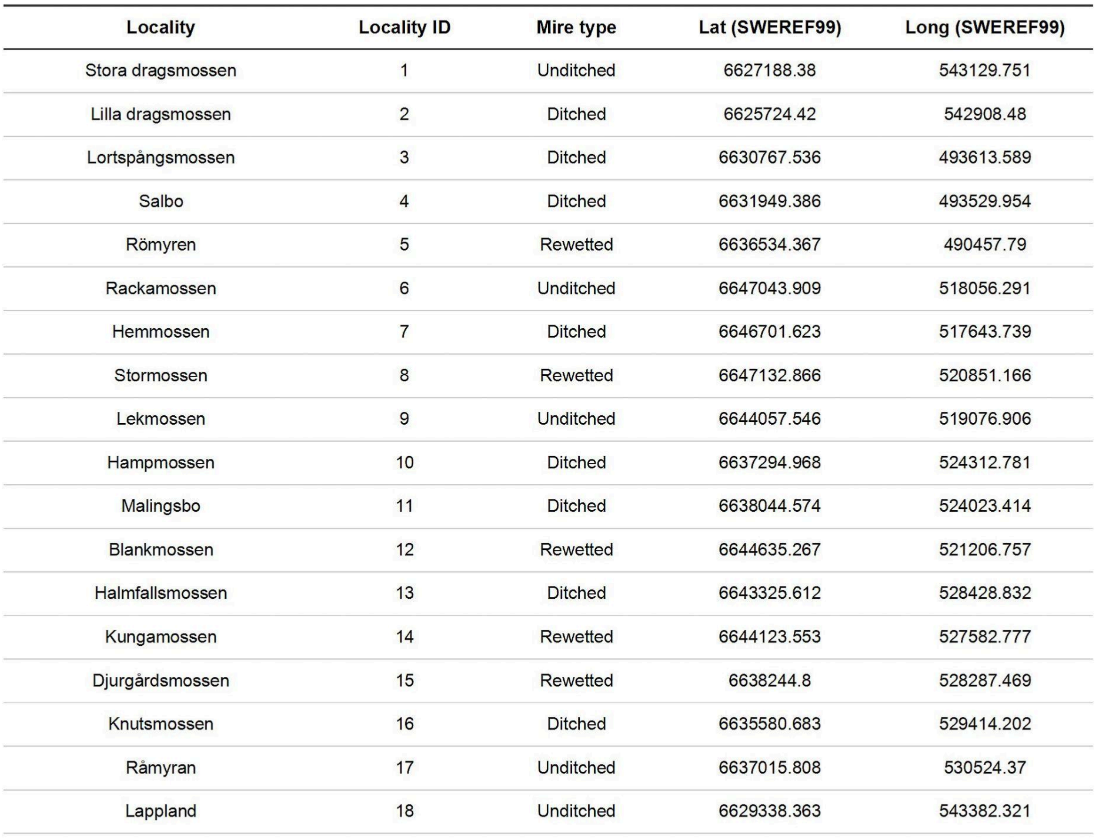
Appendix

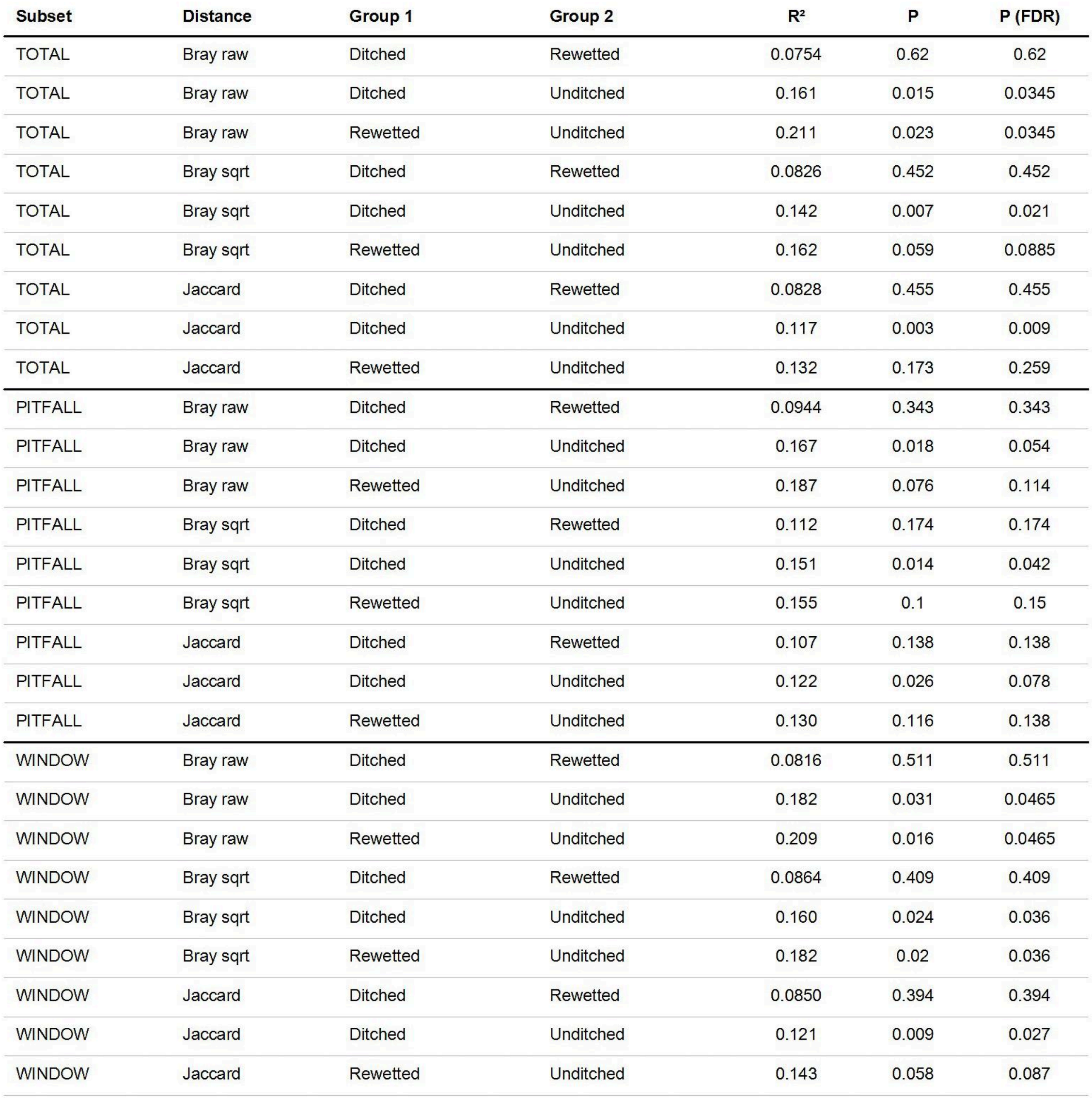


Locality	Locality ID	Mire type	Lat (SWEREF99)	Long (SWEREF99)
Stora dragsmossen	1	Unditched	6627188.38	543129.751
Lilla dragsmossen	2	Ditched	6625724.42	542908.48
Lortspångsmossen	3	Ditched	6630767.536	493613.589
Salbo	4	Ditched	6631949.386	493529.954
Römyren	5	Rewetted	6636534.367	490457.79
Rackamossen	6	Unditched	6647043.909	518056.291
Hemmossen	7	Ditched	6646701.623	517643.739
Stormossen	8	Rewetted	6647132.866	520851.166
Lekmossen	9	Unditched	6644057.546	519076.906
Hampmossen	10	Ditched	6637294.968	524312.781
Malingsbo	11	Ditched	6638044.574	524023.414
Blankmossen	12	Rewetted	6644635.267	521206.757
Halmfallsmossen	13	Ditched	6643325.612	528428.832
Kungamossen	14	Rewetted	6644123.553	527582.777
Djurgårdsmossen	15	Rewetted	6638244.8	528287.469
Knutsmossen	16	Ditched	6635580.683	529414.202
Råmyran	17	Unditched	6637015.808	530524.37
Lappland	18	Unditched	6629338.363	543382.321

Table A1. Localities, locality names, mire type and coordinates for each mire.

Dataset	Test	Distance	F (df1,df2)	R²	P
ALL TRAPS	PERMANOVA	Bray raw	1.635 (2,15)	0.179	0.021
	PERMANOVA	Bray sqrt	1.450 (2,15)	0.162	0.013
	PERMANOVA	Jaccard	1.224 (2,15)	0.140	0.037
	PERMDISP	Bray raw	2.511 (2,15)	—	0.090
	PERMDISP	Bray sqrt	0.530 (2,15)	—	0.658
	PERMDISP	Jaccard	1.038 (2,15)	—	0.388
PITFALL TRAPS	PERMANOVA	Bray raw	1.577 (2,14)	0.183	0.055
	PERMANOVA	Bray sqrt	1.503 (2,14)	0.176	0.014
	PERMANOVA	Jaccard	1.269 (2,14)	0.153	0.023
	PERMDISP	Bray raw	4.716 (2,14)	—	0.025
	PERMDISP	Bray sqrt	0.528 (2,14)	—	0.623
	PERMDISP	Jaccard	0.622 (2,14)	—	0.566
WINDOW TRAPS	PERMANOVA	Bray raw	1.818 (2,15)	0.195	0.018
	PERMANOVA	Bray sqrt	1.638 (2,15)	0.179	0.017
	PERMANOVA	Jaccard	1.291 (2,15)	0.146	0.011
	PERMDISP	Bray raw	3.398 (2,15)	—	0.070
	PERMDISP	Bray sqrt	2.945 (2,15)	—	0.076
	PERMDISP	Jaccard	2.807 (2,15)	—	0.093

Table A2. PERMANOVA and PERMDISP results for total beetle community composition across trap types (all traps, pitfall traps, and window traps), using Bray–Curtis dissimilarities (raw and square-root transformed abundances) and Jaccard dissimilarity (presence–absence).



Subset	Distance	Group 1	Group 2	R²	P	P (FDR)
TOTAL	Bray raw	Ditched	Rewetted	0.0754	0.62	0.62
TOTAL	Bray raw	Ditched	Unditched	0.161	0.015	0.0345
TOTAL	Bray raw	Rewetted	Unditched	0.211	0.023	0.0345
TOTAL	Bray sqrt	Ditched	Rewetted	0.0826	0.452	0.452
TOTAL	Bray sqrt	Ditched	Unditched	0.142	0.007	0.021
TOTAL	Bray sqrt	Rewetted	Unditched	0.162	0.059	0.0885
TOTAL	Jaccard	Ditched	Rewetted	0.0828	0.455	0.455
TOTAL	Jaccard	Ditched	Unditched	0.117	0.003	0.009
TOTAL	Jaccard	Rewetted	Unditched	0.132	0.173	0.259
PITFALL	Bray raw	Ditched	Rewetted	0.0944	0.343	0.343
PITFALL	Bray raw	Ditched	Unditched	0.167	0.018	0.054
PITFALL	Bray raw	Rewetted	Unditched	0.187	0.076	0.114
PITFALL	Bray sqrt	Ditched	Rewetted	0.112	0.174	0.174
PITFALL	Bray sqrt	Ditched	Unditched	0.151	0.014	0.042
PITFALL	Bray sqrt	Rewetted	Unditched	0.155	0.1	0.15
PITFALL	Jaccard	Ditched	Rewetted	0.107	0.138	0.138
PITFALL	Jaccard	Ditched	Unditched	0.122	0.026	0.078
PITFALL	Jaccard	Rewetted	Unditched	0.130	0.116	0.138
WINDOW	Bray raw	Ditched	Rewetted	0.0816	0.511	0.511
WINDOW	Bray raw	Ditched	Unditched	0.182	0.031	0.0465
WINDOW	Bray raw	Rewetted	Unditched	0.209	0.016	0.0465
WINDOW	Bray sqrt	Ditched	Rewetted	0.0864	0.409	0.409
WINDOW	Bray sqrt	Ditched	Unditched	0.160	0.024	0.036
WINDOW	Bray sqrt	Rewetted	Unditched	0.182	0.02	0.036
WINDOW	Jaccard	Ditched	Rewetted	0.0850	0.394	0.394
WINDOW	Jaccard	Ditched	Unditched	0.121	0.009	0.027
WINDOW	Jaccard	Rewetted	Unditched	0.143	0.058	0.087

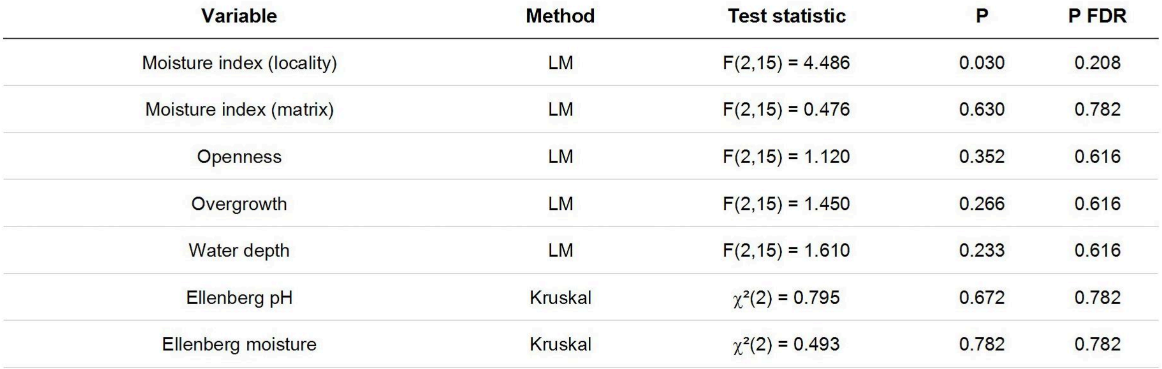
Table A3. Pairwise PERMANOVAS between mire types divided by trap type for total beetle community composition, for Bray Raw, Bray sqrt and Jaccards index.

Subset	Distance	D–R	D–U	R–U	∆ (UD-UR)	Perm p	Bootstrap CI
TOTAL	Bray raw	0.245	0.357	0.379	-0.022	0.731	-0.171–0.113
TOTAL	Bray sqrt	0.247	0.343	0.347	-0.004	0.447	-0.103–0.077
TOTAL	Jaccard	0.303	0.375	0.384	-0.009	0.316	-0.109–0.062
PITFALL	Bray raw	0.270	0.330	0.369	-0.039	0.105	-0.235–0.101
PITFALL	Bray sqrt	0.295	0.346	0.363	-0.017	0.075	-0.135–0.061
PITFALL	Jaccard	0.356	0.387	0.406	-0.019	0.063	-0.121–0.048
WINDOW	Bray raw	0.268	0.431	0.410	0.021	0.303	-0.115–0.146
WINDOW	Bray sqrt	0.268	0.395	0.385	0.011	0.315	-0.090–0.102
WINDOW	Jaccard	0.321	0.400	0.409	-0.010	0.325	-0.103–0.055

Table A4. Pairwise centroid differences for total beetle community composition between mire types across trap types.

Level	Taxon	Model	Disp.	AIC	ZI	LOO median p	n sites
Superfamily	*Elateroidea*	Negbin	4.6292	134.716	—	0.0029	—
Superfamily	*Scirtoidea*	Negbin	1.8292	63.081	—	0.0858	11.0
Family	*Cantharidae*	Negbin	3.6175	105.474	—	0.0009	17.0
Family	*Leiodidae*	Poisson	1.1285	46.504	—	0.2389	9.0
Family	*Nitidulidae*	Poisson	1.3179	66.495	—	0.1623	14.0
Family	*Scirtidae*	Negbin	1.8292	63.081	—	0.0858	11.0
Subfamily	*Alticinae*	Negbin	2.1462	53.973	0.88	0.0252	7.0
Subfamily	*Cantharinae*	Negbin	3.7635	105.852	—	0.506	17.0
Subfamily	*Cryptarchinae*	Poisson	1.3189	58.768	—	0.0013	12.0
Subfamily	*Omaliinae*	Poisson	1.4076	76.383	—	0.0197	16.0
Subfamily	*Scirtinae*	Negbin	1.8292	63.081	—	0.0858	11.0
Genera	*Aphthona*	Poisson	1.4667	36.344	0.83	0.4977	—
Genera	*Cantharis*	Negbin	3.7461	101.939	—	0.0005	16.0
Genera	*Contacyphon*	Negbin	1.8292	63.081	—	0.0858	11.0
Genera	*Enicmus*	Negbin	2.177	76.346	—	0.1529	14.0
Genera	*Gabrius*	Negbin	2.114	84.953	—	0.0985	14.0
Genera	*Glischrochilus*	Poisson	1.1826	63.323	—	0.2426	14.0
Genera	*Pterostichus*	Poisson	1.4862	63.548	—	0.0232	11.0
Species	*Contacyphon padi*	Poisson	0.9086	45.227	—	0.5654	11.0
Species	*Contacyphon variabilis*	Poisson	1.125	45.743	—	0.0055	6.0
Species	*Gabrius splendidulus*	Negbin	2.114	84.953	—	0.0985	14.0
Species	*Glischrochilus quadripunctatus*	Poisson	1.3189	58.768	—	0.506	12.0
Species	*Pterostichus rhaeticus*	Poisson	1.1591	53.99	—	0.0636	10.0

Table A5. Supplemental GLM-values for significant taxa for each mire type across all taxonomic levels. *Disp.* indicates the dispersion parameter, *AIC* the model fit (Akaike Information Criterion), *ZI* indicates zero-inflation where applicable, *LOO median p* represents the median p-value from leave-one-out analyses used to assess robustness, and *n sites* indicates the number of localities in which each taxon was recorded.



Variable	Method	Test statistic	P	P FDR
Moisture index (locality)	LM	F(2,15) = 4.486	0.030	0.208
Moisture index (matrix)	LM	F(2,15) = 0.476	0.630	0.782
Openness	LM	F(2,15) = 1.120	0.352	0.616
Overgrowth	LM	F(2,15) = 1.450	0.266	0.616
Water depth	LM	F(2,15) = 1.610	0.233	0.616
Ellenberg pH	Kruskal	$\chi^2(2) = 0.795$	0.672	0.782
Ellenberg moisture	Kruskal	$\chi^2(2) = 0.493$	0.782	0.782

Table A6. Full data for univariate tests of environmental variables in relation to mire types.

Locality	Mire type	Water depth (cm)	Ellenberg pH locality	Ellenberg moisture locality	Moisture index locality	Moisture index matrix	Openness locality	Overgrowth locality
Stora dragsmossen	Unditched	9	2,85	6,85	156.987	123.467	0.243	0.829
Lilla dragsmossen	Ditched	19	2,48	6,07	145.645	104.842	0.007	1.000
Lortspångsmossen	Ditched	14	3	6,58	170.396	117.007	0.335	0.767
Salbo	Ditched	17	2	5,96	156.121	105.031	0.311	0.844
Römyren	Rewetted	27	2,11	6,06	180.91	123.494	0.818	0.233
Rackamossen	Unditched	18	2,16	6,24	147.439	97.71	0.715	0.523
Hemmossen	Ditched	17	2,74	6	167.529	80.041	0.461	0.738
Stormossen	Rewetted	15	2,64	6,04	175.327	112.267	0.405	0.635
Lekmossen	Unditched	11	2,44	6,5	170.612	87.975	0.572	0.521
Hamppmossen	Ditched	12	2,57	6,39	153.702	99.044	0.157	0.900
Malingsbo	Ditched	12	2,18	6,43	158.267	91.028	0.166	0.984
Blankmossen	Rewetted	5	3	6,8	168.583	84.589	0.217	0.826
Halmfallsmossen	Ditched	25	2	6,12	155.317	63.156	0.034	1.000
Kungamossen	Rewetted	16	3,10	6,39	177.711	81.62	0.043	1.000
Djurgårdsmossen	Rewetted	2	2,56	5,88	167.755	106.03	0.014	1.000
Knutsmossen	Ditched	21	2,64	5,86	165.949	109.252	0.007	1.000
Råmyran	Unditched	12	2,59	5,56	173.289	95.932	0.150	0.940
Lappland	Unditched	3	2,23	6,36	138.864	123.20	0.253	0.853

Table A7. Values for environmental variables across localities.

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Abdera affinis	Generalist	Fungivore	1	0	0	0	0	0	1
Abdera flexuosa	Generalist	Fungivore	0	0	1	0	0	1	0
Acidota crenata	Generalist	Carnivore	16	4	26	0,63	0,63	0,326	0,043
Aconthocinus griseus	Generalist	Saprotroph/saprophage/detrivor	0	0	1	0	0	1	0
Acrossus rufipes	Terrestrial	Saprotroph/saprophage/detrivor	0	0	3	0	0	0,333	0,667
Acrotona sp.	NA	NA	1	0	0	1	0	1	0
Acrotrichis cognata	Generalist	Fungivore	2	0	0	1	0	0,5	0,5
Acrotrichis dispar	Generalist	Fungivore	2	0	0	1	0	0	1
Acrotrichis grandicollis	Generalist	Fungivore	0	0	1	0	1	0	0
Acrotrichis insularis	Generalist	Fungivore	1	0	1	0,5	0	1	0
Acrotrichis intermedia	Generalist	Fungivore	4	4	26	0,412	0,118	0,618	0,265
Acrotrichis rugolosa	Generalist	Fungivore	2	0	0	0,5	0	0,5	0,5
Acrotrichis silvatica	Generalist	Fungivore	1	0	0	1	0	1	0
Agabus sp.	Wetland	Carnivore	1	1	0	1	0,5	0	0,5
Agathidium seminulum	Generalist	Fungivore	2	0	0	0,5	0	0,5	0,5
Agoliinus piceus	Terrestrial	Saprotroph/saprophage/detrivor	0	0	1	0	1	0	0
Agonum ericeti	Wetland	Carnivore	11	26	17	0,926	0,352	0,444	0,204
Agriotes lineatus	Terrestrial	Herbivore	0	1	0	1	0	0	1
Aleochara bipustulata	Generalist	Carnivore	0	1	0	1	1	0	0
Aleochara brevipennis	Wetland	Carnivore ; parasitoid	1	0	0	1	0	1	0
Aleochara lanuginosa	Terrestrial	Carnivore ; parasitoid	0	0	1	0	0	0	1
Aleochara moerens	Terrestrial	Carnivore ; parasitoid	1	0	0	1	0	0	1
Aleocharinae ssp.	Generalist	Carnivore	10	1	3	0,357	0,143	0,714	0,143
Altica longicollis	Terrestrial	Herbivore	2	0	0	1	0,5	0,5	0
Alticinae sp.	NA	NA	0	3	0	0,667	0	0,333	0,667
Amara lunicollis	Terrestrial	Herbivore	4	4	31	1	0,205	0,641	0,154
Amischa bifoveolata	Generalist	Carnivore	0	0	1	0	0	0	1
Amischa sp.	Terrestrial	Carnivore	0	1	0	0	0	1	0
Ampedus balteatus	Terrestrial	Herbivore ; carnivore ; saprotroph/saprophage/detrivor	17	12	30	0,017	0,237	0,559	0,203
Ampedus nigrinus	Generalist	Carnivore ; saprotroph/saprophage/detrivor	15	5	25	0	0,622	0,222	0,156
Ampedus tristis	Terrestrial	Carnivore ; saprotroph/saprophage/detrivor	0	2	1	0,333	0,333	0,667	0
Amphicyllis globus	Generalist	Fungivore	1	0	0	1	0	1	0
Anacaena lutescens	Wetland	Carnivore ; saprotroph/saprophage/detrivor	1	0	0	1	0	1	0
Anaspis bohemica	Terrestrial	Herbivore ; carnivore ; saprotroph/saprophage/detrivor	2	7	5	0	0,143	0,5	0,357
Anastrangalia sanguinolenta	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor	0	0	1	0	0	0	1
Anidorus nigrinus	Terrestrial	Saprotroph/saprophage/detrivor ; fungivore	0	1	0	0	0	1	0
Anisandrus dispar	Terrestrial	Fungivore	4	3	10	0,059	0,118	0,765	0,118
Anisotoma axillaris	Generalist	Fungivore	1	0	2	0,333	0	0,667	0,333
Anisotoma glabra	Generalist	Fungivore	1	0	0	0	1	0	0
Anomognathus cuspidatus	Terrestrial	Carnivore	6	3	12	0,19	0	1	0
Anoplotrupes stercorosus	Terrestrial	Saprotroph/saprophage/detrivor	12	0	5	1	0	0,059	0,941
Anostirus castaneus	Terrestrial	Herbivore ; carnivore	1	0	0	1	1	0	0
Anotylus tetracarinatus	Terrestrial	Saprotroph/saprophage/detrivor	0	0	1	0	1	0	0
Anthicus ater	Wetland	Omnivore	0	0	1	1	0	1	0
Anthribus nebulosus	Wetland	Carnivore	1	0	0	0	1	0	0
Aphthona erichsoni	Wetland	Herbivore	0	3	0	1	0,667	0	0,333
Aphthona lutescens	Wetland	Herbivore	0	9	0	0,333	0,222	0,778	0
Aphthona sp.	Wetland	Herbivore	0	1	0	1	0	1	0
Apocatops nigrita	Generalist	Saprotroph/saprophage/detrivor	0	0	1	1	0	0	1
Aspidiphorus orbiculatus	Generalist	Fungivore	3	0	6	0,222	0	0,778	0,222
Atheta castanoptera	Terrestrial	Carnivore	0	0	1	1	0	1	0
Atheta crassicornis	Generalist	Carnivore	1	0	0	1	0	1	0
Atheta crassicornis/paracrassicornis	Generalist	Carnivore	4	1	5	1	0,1	0,3	0,6
Atheta crassicornis/pararassicornis	Generalist	Carnivore	0	0	2	1	0	0,5	0,5
Atheta euryptera	Terrestrial	Carnivore	0	0	2	0	0,5	0,5	0
Atheta fungi	Generalist	Carnivore	0	1	2	0	0,333	0,333	0,333
Atheta gagatina	Terrestrial	Carnivore	1	1	1	1	0	0,333	0,667
Atheta harwoodi	Terrestrial	Carnivore	2	0	2	0,25	0	0,25	0,75
Atheta hypnorum	Generalist	Carnivore	2	0	0	1	1	0	0
Atheta hypnorum?	Generalist	Carnivore	0	0	2	0,5	0	0,5	0,5
Atheta laevana	Terrestrial	Carnivore	0	0	1	0	1	0	0
Atheta nigritula	Terrestrial	Carnivore	0	0	1	0	0	1	0
Atheta paracrassicornis	Terrestrial	Carnivore	0	0	2	1	0	0,5	0,5

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Atheta scapularis	Generalist	Carnivore	2	1	6	0,778	0,222	0,667	0,111
Atheta sp.	Generalist	Carnivore	8	5	2	0,867	0,067	0,8	0,133
Atheta strandiella	Wetland	Carnivore	1	0	0	1	0	1	0
Atheta trinotata	Terrestrial	Carnivore	0	1	0	1	0	1	0
Atheta vaga	Terrestrial	Carnivore	8	0	6	0,429	0	0,857	0,143
Atheta vaga/harwoodi	Terrestrial	Carnivore	1	0	0	0	0	1	0
Athous subfuscus	Terrestrial	Herbivore ; carnivore	9	5	19	0,273	0,182	0,485	0,333
Atomaria bella	Terrestrial	Fungivore	2	0	5	0,286	0	1	0
Atomaria impressa	Generalist	Fungivore	0	0	1	1	0	0	1
Atomaria wollastoni	Generalist	Fungivore	1	0	1	1	0	1	0
Atrecus affinis	Terrestrial	Carnivore	0	1	2	0	0	1	0
Atrecus longiceps	Terrestrial	Carnivore	1	0	0	0	0	1	0
Baeocrara variolosa	Generalist	Fungivore	0	1	0	0	1	0	0
Bagous frit	Wetland	Herbivore	0	3	0	1	0,333	0,667	0
Bibloplectus sp.	Terrestrial	Carnivore	0	0	1	0	0	0	1
Bibloporus minutus	Terrestrial	Carnivore	2	1	2	0	0	0,8	0,2
Bisnius puella	Terrestrial	Carnivore	0	0	1	1	0	1	0
Bitoma crenata	Terrestrial	Carnivore	0	0	1	0	0	0	1
Bolitobius cingulatus	Generalist	Carnivore	1	0	8	1	0,556	0,444	0
Bolitophagus reticulatus	Terrestrial	Fungivore	2	0	1	0	0	1	0
Brachygluta fossulata	Generalist	Carnivore	1	0	2	1	0	0,667	0,333
Brachysomus echinatus	Terrestrial	Herbivore	1	0	0	1	0	0	1
Bradycellus ruficollis	Terrestrial	Herbivore	1	0	0	1	0	1	0
Bryaxis bulbifer	Generalist	Carnivore	1	2	2	0,2	0	0,8	0,2
Byrrhus sp.	Terrestrial	Herbivore	0	0	2	1	1	0	0
Calathus micropterus	Terrestrial	Carnivore	1	0	0	1	0	1	0
Calodera aethiops	Wetland	Carnivore	1	0	1	0,5	0	1	0
Cantharis figurata	Terrestrial	Carnivore; omnivore	7	1	1	0,556	0	0,333	0,667
Cantharis obscura	Terrestrial	Carnivore; omnivore	1	0	0	1	0	1	0
Cantharis paludosa	Terrestrial	Carnivore	54	10	32	0,896	0,698	0,26	0,042
Carabus coriaceus	Terrestrial	Carnivore	0	0	3	1	0	0	1
Carabus glabratus	Terrestrial	Carnivore	0	1	0	1	0	0	1
Carabus violaceus	Terrestrial	Carnivore	8	4	11	1	0,13	0,391	0,478
Carcinops pumilio	Terrestrial	Carnivore	0	1	0	0	0	1	0
Cardiophorus ruficollis	Terrestrial	Herbivore ; carnivore	1	1	0	0	0,5	0,5	0

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Cartodere constricta	Terrestrial	Fungivore	1	0	1	0	0	0,5	0,5
Cartodere nodifer	Terrestrial	Fungivore	0	0	1	0	0	0	1
Cerylon ferrugineum	Generalist	Fungivore	2	0	3	0,2	0	0,8	0,2
Cerylon histeroides	Generalist	Fungivore	4	1	4	0,111	0	0,444	0,556
Chaetocnema sahlbergii	Wetland	Herbivore	0	4	0	1	0,5	0,5	0
Cimberis attelaboides	Terrestrial	Herbivore	1	0	0	1	0	1	0
Cis boleti	Terrestrial	Fungivore	4	5	2	0	0,273	0,636	0,091
Cis comptus	Terrestrial	Fungivore	3	8	1	0	0	0,333	0,667
Cis micans	Terrestrial	Fungivore	2	1	3	0	0	0,833	0,167
Cis sp.	Terrestrial	Fungivore	0	0	1	1	0	1	0
Coccinella hieroglyphica	Wetland	Carnivore ; omnivore	0	1	1	0,5	0,5	0	0,5
Coccinella septempunctata	Terrestrial	Carnivore ; omnivore	1	0	0	1	0	1	0
Contacyphon coarctatus	Wetland	Herbivore ; filter-feeder	3	1	0	0,25	0,5	0,25	0,25
Contacyphon padi	Wetland	Herbivore ; filter-feeder	13	11	1	0,16	0,64	0,36	0
Contacyphon variabilis	Wetland	Herbivore ; filter-feeder	16	4	0	0,25	0,7	0,25	0,05
Corticaria crenicollis	Terrestrial	Fungivore	0	0	2	0	1	0	0
Corticaria ferruginea	Terrestrial	Fungivore	0	0	1	0	0	0	1
Corticaria impressa	Generalist	Fungivore	1	0	0	0	0	1	0
Corticaria rubripes	Terrestrial	Fungivore	0	0	1	0	0	1	0
Corticaria serrata	Terrestrial	Fungivore	0	0	1	0	0	1	0
Corticarina minuta	Generalist	Herbivore; fungivore	0	2	0	1	0,5	0,5	0
Corticarina sp.	Terrestrial	Fungivore	1	0	0	0	0	1	0
Cortinicara gibbosa	Generalist	Herbivore; fungivore	1	1	0	0	0,5	0	0,5
Cryptophagus denticulatus	Terrestrial	Herbivore ; fungivore	0	1	0	0	0	1	0
Cryptophagus setulosus	Generalist	Fungivore	1	1	3	1	0	0,8	0,2
Crypturgus cinereus	Generalist	Herbivore	5	1	1	0,143	0	1	0
Crypturgus hispidulus	Generalist	Herbivore	4	1	1	0	0	0,833	0,167
Crypturgus pusillus	Generalist	Herbivore	1	2	0	0,333	0	1	0
Crypturgus subscribosus	Generalist	Herbivore	2	0	0	0	0	0	1
Cychrus caraboides	Terrestrial	Carnivore	0	0	1	1	0	1	0
Dacne bipustulata	Terrestrial	Fungivore	1	0	1	0	0	0	1
Dadobia immersa	Terrestrial	Carnivore	0	0	2	0	0	0,5	0,5
Dalopius marginatus	Terrestrial	Herbivore ; carnivore ; saprotroph/saprophage/detrivor	18	7	27	0,019	0,442	0,308	0,25
Dasytes niger	Terrestrial	Herbivore ; carnivore	4	3	8	0	0,067	0,267	0,667

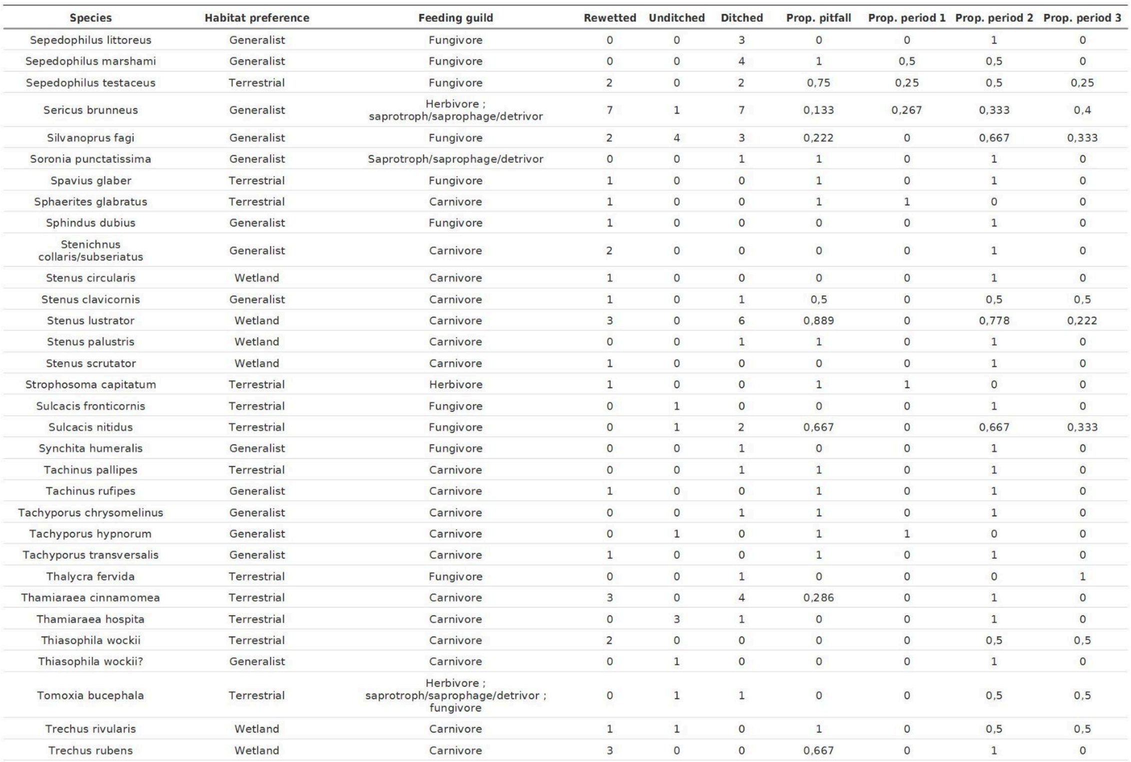
Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Dasytes plumbeus	Terrestrial	Herbivore ; carnivore	1	1	1	0	0	0	1
Deinopsis erosa	Wetland	Carnivore	1	0	0	1	0	1	0
Deliphrum tectum	Terrestrial	Carnivore	0	0	1	1	0	1	0
Dendrophagus crenatus	Generalist	Fungivore	1	0	1	0,5	0	1	0
Denticollis borealis	Generalist	Herbivore ; carnivore	0	1	1	0	0,5	0,5	0
Deporaus betulae	Terrestrial	Herbivore	1	0	0	0	0	1	0
Dermestes murinus	Generalist	Saprotroph/saprophage/detrivor	1	1	1	0,667	0	0,667	0,333
Dictyoptera aurora	Generalist	Herbivore ; carnivore	0	0	1	0	0	1	0
Dinaraea aequata	Generalist	Carnivore	1	0	0	1	1	0	0
Dinaraea linearis	Terrestrial	Carnivore	0	0	1	0	0	1	0
Dorcatoma dresdensis	Terrestrial	Fungivore	0	0	1	0	0	1	0
Dorcatoma robusta	Terrestrial	Fungivore	1	0	0	0	0	1	0
Dorcatoma sp.	Terrestrial	Fungivore	0	1	0	0	1	0	0
Dorytomus tortix	Terrestrial	Herbivore	0	0	1	0	0	1	0
Dropephylla linearis	Terrestrial	Carnivore	0	0	1	0	0	0	1
Drusilla canaliculata	Generalist	Carnivore	9	15	26	0,9	0,26	0,68	0,06
Dryocoetes autographus	Terrestrial	Herbivore	24	10	33	0	0,134	0,731	0,134
Dyschirius globulosus	Wetland	Carnivore	1	0	0	1	0	1	0
Elateroides dermestoides	Terrestrial	Fungivore	2	0	0	0	0	1	0
Enicmus rugosus	Terrestrial	Fungivore	17	2	30	0,102	0,041	0,49	0,469
Epuraea marseuli	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	0	1	4	0,8	0,2	0,4	0,4
Epuraea pygmaea	Generalist	Saprotroph/saprophage/detrivor ; fungivore	94	17	67	0,944	0,062	0,719	0,219
Epuraea rufomarginata	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	1	0	1	0	0,5	0,5	0
Epuraea unicolor/biguttata	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	1	0	1	1	0	1	0
Epuraea variegata	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	0	1	0	0	0	1	0
Euconnus claviger	Generalist	Carnivore	0	2	4	0,167	0	0,667	0,333
Euplectus mutator	Terrestrial	Carnivore	2	1	1	0	0	0,25	0,75
Euplectus nanus	Terrestrial	Carnivore	0	1	2	0	0	0,333	0,667
Eurosomides minor	Terrestrial	Carnivore	0	1	0	0	0	1	0

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Exochomus quadripustulatus	Terrestrial	Carnivore	0	2	0	0	1	0	0
Gabrius splendidulus	Terrestrial	Carnivore	31	5	31	0,06	0,03	0,851	0,119
Glischrochilus hortensis	Terrestrial	Fungivore	2	1	4	0,857	0	0,571	0,429
Glischrochilus quadripunctatus	Generalist	Carnivore; fungivore	9	1	19	0,379	0,31	0,655	0,034
Globicornis emarginata	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor	0	2	2	0	0,25	0,75	0
Gnathoncus buysonni	Terrestrial	Carnivore	0	0	2	1	0	1	0
Gnathoncus buyssoni	Terrestrial	Carnivore	1	0	2	0	0,333	0,667	0
Gyrophaena boleti	Terrestrial	Fungivore	2	0	0	0	0	1	0
Habrocerus capillaricornis	Terrestrial	Fungivore	0	0	1	1	0	1	0
Hadrobregmus pertinax	Terrestrial	Saprotroph/saprophage/detrivor	0	1	2	0	0	0,333	0,667
Haploglossa villosula	Terrestrial	Carnivore	1	0	3	0	0	1	0
Harpalus laevipes	Terrestrial	Omnivore	0	1	1	1	0	0	1
Harpalus solitaris	Terrestrial	Herbivore	0	0	1	1	0	1	0
Hydrobius fuscipes	Wetland	Carnivore ; saprotroph/saprophage/detrivor	2	0	0	0,5	0,5	0	0,5
Hylastes brunneus	Terrestrial	Herbivore	2	0	2	0,5	0	1	0
Hylastes cunicularis	Terrestrial	Herbivore	1	0	11	0,75	0,667	0,25	0,083
Hylastes opacus	Terrestrial	Herbivore	1	0	0	1	0	1	0
Hylobius abietis	Generalist	Herbivore	24	15	105	0,958	0,715	0,215	0,069
Hylobius pinastri	Terrestrial	Herbivore	1	1	1	0,333	0,333	0,667	0
Hylota ochracea	Terrestrial	Carnivore	1	1	2	0	0,25	0,75	0
Ilybius subaeneus	Wetland	Carnivore	3	2	0	1	0,6	0,2	0,2
Ilyobates nigricollis	Wetland	Carnivore	1	0	0	1	0	1	0
Ischnosoma bergrothi	Wetland	Carnivore	5	4	6	0,933	0,133	0,533	0,333
Ischnosoma longicorne	Wetland	Carnivore	2	0	0	1	0,5	0,5	0
Ischnosoma splendidum	Generalist	Carnivore	1	4	2	1	0,429	0,429	0,143
Lampyris noctiluca	Terrestrial	Carnivore	0	0	4	0,5	0	0,5	0,5
Lathrobium brunnipes	Generalist	Carnivore	0	0	2	1	0,5	0,5	0
Lathrobium longulum	Generalist	Carnivore	0	1	0	0	0	1	0
Lathrobium rufipenne	Wetland	Carnivore	0	1	2	0,667	0,333	0,333	0,333
Lathrobium sp.	Generalist	Carnivore	1	0	0	1	1	0	0
Leistus terminatus	Generalist	Carnivore	0	0	2	1	0	1	0
Leptusa pulchella	Terrestrial	Carnivore	2	0	4	0,667	0	1	0
Limnobaris dolorosa	Wetland	Herbivore	0	1	0	1	1	0	0

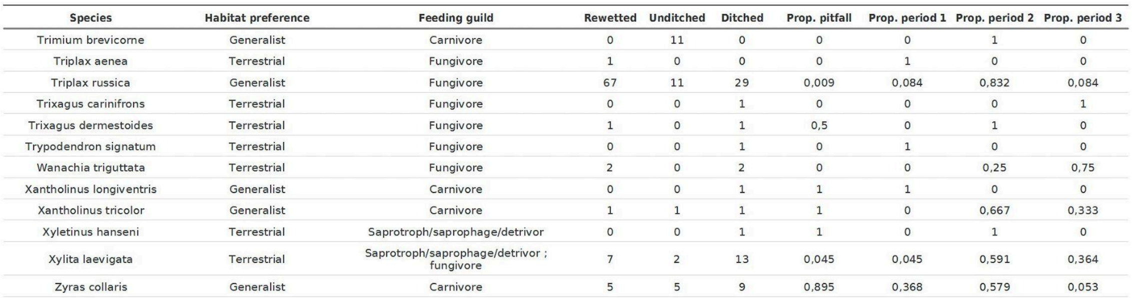
Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Litargus connexus	Terrestrial	Fungivore	1	1	0	0	0	1	0
Lochmaea caprea	Generalist	Herbivore	6	1	14	1	0,381	0,381	0,238
Lochmaea suturalis	Wetland	Herbivore	7	5	30	1	0,524	0,286	0,19
Lordithon lunulatus	Terrestrial	Carnivore	10	4	14	0	0,107	0,75	0,143
Loricera pilicornis	Wetland	Carnivore	1	1	0	1	0,5	0,5	0
Lythraria salicariae	Wetland	Herbivore	1	4	0	0,8	0	0,8	0,2
Magdalis ruficornis	Terrestrial	Herbivore	1	0	0	1	0	1	0
Malthodes fuscus	Terrestrial	Carnivore	0	0	1	1	0	1	0
Megasternum concinnum	Terrestrial	Carnivore ; saprotroph/saprophage/detrivor	2	1	0	0,667	0	1	0
Melandryidae	Terrestrial	Saprotroph/saprophage/detrivor ; fungivore	0	0	1	0	0	0	1
Melanotus sp.	Generalist	Carnivore	5	1	11	0,059	0	0,647	0,353
Meotica exilis	Generalist	Carnivore	1	0	0	0	0	1	0
Meotica pallens	Wetland	Carnivore	1	0	0	0	0	1	0
Micrelus ericae	Generalist	Herbivore	0	0	1	1	0	0	1
Monochamus sutor	Generalist	Saprotroph/saprophage/detrivor	0	0	1	0	0	0	1
Mordella holomelaena	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	1	1	0	0,5	0,5	0,5	0
Mycetina cruciata	Terrestrial	Fungivore	1	0	1	0	0	0,5	0,5
Mycetochara flavipes	Terrestrial	Saprotroph/saprophage/detrivor	1	2	3	0	0	0,167	0,833
Mycetochara obscura	Terrestrial	Saprotroph/saprophage/detrivor	0	0	1	0	0	0	1
Mycetophagus decempunctatus	Terrestrial	Fungivore	0	0	1	0	0	0	1
Mycetoporus lepidus	Generalist	Carnivore	3	0	1	0,75	0,25	0,75	0
Myllaena dubia/intermedia	Wetland	Carnivore	0	1	0	0	1	0	0
Myllaena intermedia	Wetland	Carnivore	4	3	0	0,286	0,429	0,286	0,286
Myrrha octodecimguttata	Terrestrial	Carnivore ; omnivore	0	0	1	0	0	1	0
Neocrepidodera brevicollis	Terrestrial	Herbivore	1	2	1	0,75	0,25	0	0,75
Neuraphes elongatulus	Generalist	Carnivore	0	1	1	0	0,5	0,5	0
Nicrophorus vespilloides	Terrestrial	Saprotroph/saprophage/detrivor	14	6	31	0,902	0,02	0,216	0,765
Notiophilus biggutatus	Terrestrial	Carnivore	1	0	0	1	0	0	1
Notiophilus germinyi	Terrestrial	Carnivore	4	0	2	1	0,333	0,5	0,167
Nudobius lentus	Terrestrial	Carnivore	2	0	4	0	0,167	0,833	0
Ochthephilum fracticorne	Wetland	Carnivore	1	0	2	1	0,667	0,333	0
Ocypus brunnipes	Generalist	Carnivore	8	5	17	1	0,667	0,167	0,167
Ocypus fuscatus	Generalist	Carnivore	9	10	19	0,868	0,053	0,684	0,263
Oiceoptoma thoracicum	Terrestrial	Saprotroph/saprophage/detrivor	8	3	6	0,412	0,059	0,471	0,471
Omalium caesum	Generalist	Carnivore ; saprotroph/saprophage/detrivor	7	0	6	1	0,077	0,462	0,462
Ontholestes murinus	Terrestrial	Carnivore	1	0	0	0	1	0	0
Orchesia fasciata	Terrestrial	Saprotroph/saprophage/detrivor ; fungivore	1	0	1	0	0	0,5	0,5
Orchesia minor	Generalist	Saprotroph/saprophage/detrivor ; fungivore	0	0	1	0	0	1	0
Orthocis alni	Terrestrial	Fungivore	0	1	2	0	0	0,333	0,667
Orthotomicus laricis	Generalist	Herbivore	0	0	1	0	0	0	1
Otiorhynchus carinapunctatus	Terrestrial	Herbivore	8	1	16	1	0,08	0,6	0,32
Otiorhynchus nodusus	Terrestrial	Herbivore	1	0	0	1	0	1	0
Oxymirus cursor	Terrestrial	Herbivore	0	0	1	0	1	0	0
Oxypoda brevicornis	Generalist	Carnivore	1	0	0	1	0	1	0
Paederus riparius	Wetland	Carnivore	0	2	0	0	0	1	0
Paraphotistus impressus	Terrestrial	Herbivore	12	12	17	0,268	0,293	0,439	0,268
Patrobus atrorufus	Wetland	Carnivore	0	1	0	1	0	1	0
Pella cognata	Generalist	Carnivore	8	0	27	0,943	0,371	0,429	0,2
Pella lugens	Terrestrial	Carnivore	0	0	1	1	0	1	0
Philhygra debilis/debiloides	Wetland	Carnivore	0	0	1	0	0	0	1
Philhygra melanocera	Generalist	Carnivore	0	1	0	1	0	1	0
Philonthus addendus	Terrestrial	Carnivore	4	0	2	0,833	0	0	1
Philonthus corvinus	Wetland	Carnivore	1	0	0	1	0	1	0
Philonthus nigrita	Wetland	Carnivore	2	3	1	0,667	0,167	0,333	0,5
Philonthus parvicornis	Terrestrial	Carnivore	1	0	0	1	0	0	1
Philonthus politus	Terrestrial	Carnivore	0	0	1	0	0	0	1
Philonthus succicola	Terrestrial	Carnivore	5	0	2	1	0	0,571	0,429
Philonthus varians	Generalist	Carnivore	0	1	0	0	0	1	0
Phloeopora concolor	Terrestrial	Carnivore	0	1	1	0	0	0,5	0,5
Phloeopora corticalis	Terrestrial	Carnivore	1	0	0	0	0	1	0
Phloeopora testacea	Terrestrial	Carnivore	0	0	1	1	0	1	0
Phloeostiba lapponica	Terrestrial	Carnivore	0	0	1	0	0	1	0
Phosphuga atrata	Generalist	Carnivore	1	1	2	1	0,25	0,5	0,25
Pissodes pini	Generalist	Herbivore	0	3	0	0	0	0,667	0,333
Pityogenes bidentatus	Generalist	Herbivore	2	0	1	0,333	0,333	0,667	0

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Pityogenes chalcographus	Generalist	Herbivore	0	7	3	0	0,2	0,6	0,2
Pityogenes quadridens	Generalist	Herbivore	1	0	0	1	0	1	0
Pityogenes sp.	Generalist	Herbivore ; saprotroph/saprophage/detrivor	1	0	0	0	0	1	0
Pityophthorus glabratus	Terrestrial	Herbivore	0	1	0	0	0	1	0
Placusa atrata	Terrestrial	Fungivore	1	0	1	0	0	0	1
Placusa complanata	Terrestrial	Fungivore	0	0	1	0	0	1	0
Placusa complanata/depressa	Terrestrial	Fungivore	2	0	2	0	0	0,75	0,25
Placusa cribata?	Terrestrial	Fungivore	1	0	0	0	0	1	0
Placusa sp.	Terrestrial	Fungivore	0	0	1	0	0	0	1
Placusa tachyporides	Terrestrial	Fungivore	0	0	1	0	0	1	0
Plataraea brunnea	Terrestrial	Carnivore	0	0	1	1	0	1	0
Plateumaris discolor	Wetland	Herbivore	5	12	1	0,5	0,333	0,5	0,167
Platycerus caprea	Terrestrial	Saprotroph/saprophage/detrivor	1	0	0	0	0	1	0
Platydracus fulvipes	Generalist	Carnivore	16	5	36	0,93	0,193	0,439	0,368
Platydracus latebricola	Generalist	Carnivore	1	0	18	0,947	0	0,947	0,053
Platysoma angustatum	Terrestrial	Carnivore	0	0	2	0,5	0	1	0
Platysoma lineare	Terrestrial	Carnivore	0	0	1	1	1	0	0
Plegadaerus vulneratus	Terrestrial	Carnivore	1	0	1	0	0	1	0
Plegaderus vulneratus	Generalist	Carnivore	0	0	1	1	0	1	0
Pocadius ferrugineus	Terrestrial	Fungivore	0	0	1	1	0	1	0
Podistra schoenherri	Terrestrial	Carnivore; omnivore	4	2	2	0,5	0,125	0	0,875
Poecilus cupreus	Terrestrial	Carnivore	2	2	1	1	0,2	0,8	0
Pogonocherus decoratus	Terrestrial	Saprotroph/saprophage/detrivor	0	0	1	1	1	0	0
Prosternon tesellatum	Terrestrial	Herbivore	0	1	0	1	0	1	0
Protaetia cuprea	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor	203	262	264	0,801	0,075	0,636	0,288
Pselaphus heisei	Generalist	Carnivore	8	2	9	0,895	0,053	0,684	0,263
Ptenidium nitidum	Generalist	Fungivore	1	0	0	0	0	1	0
Pterostichus diligens	Wetland	Carnivore	34	20	55	0,972	0,523	0,358	0,119
Pterostichus niger	Terrestrial	Carnivore	0	1	0	1	0	1	0
Pterostichus nigrita/rhaeticus	Wetland	Carnivore	2	1	0	1	0,333	0,333	0,333
Pterostichus oblongopunctatus	Terrestrial	Carnivore	0	0	2	1	0,5	0,5	0
Pterostichus rhaeticus	Wetland	Carnivore	17	7	3	1	0,407	0,556	0,037

Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Pyrochroa coccinea	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor	0	1	0	0	0	1	0
Pytho depressus	Terrestrial	Saprotroph/saprophage/detrivor	0	1	4	0	1	0	0
Quedius cinctus	Generalist	Carnivore	0	0	1	1	1	0	0
Quedius fuliginosus	Generalist	Carnivore	4	0	0	1	0,25	0	0,75
Quedius fuliginosus/curtipennis	Generalist	Carnivore	3	1	0	1	0,75	0,25	0
Quedius mesomelinus	Terrestrial	Carnivore	16	4	21	0,098	0,341	0,39	0,268
Quedius molochinus	Generalist	Carnivore	1	1	4	1	0,333	0	0,667
Quedius subunicolor	Wetland	Carnivore	0	2	0	1	0,5	0,5	0
Rhagium inquisitor	Generalist	Saprotroph/saprophage/detrivor	0	1	3	0,5	0,75	0	0,25
Rhagium mordax	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor	1	0	1	0	0	0,5	0,5
Rhagonycha lignosa	Generalist	Carnivore; omnivore	0	0	1	0	0	0	1
Rhagonycha testacea	Generalist	Carnivore	2	2	3	0,571	0,143	0,571	0,286
Rhizophagus bipustulatus	Terrestrial	Carnivore; fungivore	0	1	0	0	0	1	0
Rhizophagus dispar	Terrestrial	Carnivore; fungivore	0	0	1	0	0	1	0
Rhizophagus fenestralis	Terrestrial	Carnivore; fungivore	1	0	0	0	1	0	0
Rhizophagus ferrugineus	Terrestrial	Carnivore; fungivore	0	0	2	0	0	1	0
Rhyncolus ater	Generalist	Saprotroph/saprophage/detrivor	0	1	3	1	0	0,75	0,25
Rhyncolus sculpturatus	Generalist	Saprotroph/saprophage/detrivor	4	2	16	0,045	0	0,591	0,409
Rugilus erichsoni	Generalist	Carnivore	0	0	1	1	0	1	0
Rugilus rufipes	Generalist	Carnivore	9	0	8	0,941	0,118	0,529	0,353
Salpingus ruficollis	Terrestrial	Fungivore	0	1	1	0	0	0,5	0,5
Scaphidium inopinatum	Terrestrial	Fungivore	0	2	0	0	0	0	1
Scaphisoma agaricinum	Terrestrial	Fungivore	3	4	10	0,294	0,059	0,588	0,353
Scaphisoma agaricinum/inopinatum	Terrestrial	Fungivore	14	23	26	0,159	0,048	0,571	0,381
Scaphisoma boleti	Terrestrial	Fungivore	0	0	1	0	0	0	1
Scaphisoma inopinatum	Terrestrial	Fungivore	1	0	0	0	0	0	1
Schistoglossa curtipennis	Generalist	Carnivore	0	1	0	1	0	1	0
Sciodrepoides fumatus	Terrestrial	Saprotroph/saprophage/detrivor	1	0	0	1	0	0	1
Sciodrepoides watsoni	Generalist	Saprotroph/saprophage/detrivor	5	1	2	0,625	0,125	0,125	0,75
Selatosomus aeneus	Terrestrial	Herbivore	0	0	1	1	0	1	0
Sepedophilus bipunctatus	Terrestrial	Fungivore	1	0	0	0	0	1	0
Sepedophilus immaculatus	Generalist	Fungivore	2	1	0	1	0	0,667	0,333



Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Sepedophilus littoreus	Generalist	Fungivore	0	0	3	0	0	1	0
Sepedophilus marshami	Generalist	Fungivore	0	0	4	1	0,5	0,5	0
Sepedophilus testaceus	Terrestrial	Fungivore	2	0	2	0,75	0,25	0,5	0,25
Sericus brunneus	Generalist	Herbivore ; saprotroph/saprophage/detrivor	7	1	7	0,133	0,267	0,333	0,4
Silvanoprus fagi	Generalist	Fungivore	2	4	3	0,222	0	0,667	0,333
Soronia punctatissima	Generalist	Saprotroph/saprophage/detrivor	0	0	1	1	0	1	0
Spavius glaber	Terrestrial	Fungivore	1	0	0	1	0	1	0
Sphaerites glabratus	Terrestrial	Carnivore	1	0	0	1	1	0	0
Sphindus dubius	Generalist	Fungivore	1	0	0	0	0	1	0
Stenichnus collaris/subseriatus	Generalist	Carnivore	2	0	0	0	0	1	0
Stenus circularis	Wetland	Carnivore	1	0	0	0	0	1	0
Stenus clavicornis	Generalist	Carnivore	1	0	1	0,5	0	0,5	0,5
Stenus lustrator	Wetland	Carnivore	3	0	6	0,889	0	0,778	0,222
Stenus palustris	Wetland	Carnivore	0	0	1	1	0	1	0
Stenus scrutator	Wetland	Carnivore	1	0	0	0	0	1	0
Strophosoma capitatum	Terrestrial	Herbivore	1	0	0	1	1	0	0
Sulcacis fronticornis	Terrestrial	Fungivore	0	1	0	0	0	1	0
Sulcacis nitidus	Terrestrial	Fungivore	0	1	2	0,667	0	0,667	0,333
Synchita humeralis	Generalist	Fungivore	0	0	1	0	0	1	0
Tachinus pallipes	Terrestrial	Carnivore	0	0	1	1	0	1	0
Tachinus rufipes	Generalist	Carnivore	1	0	0	1	0	1	0
Tachyporus chrysomelinus	Generalist	Carnivore	0	0	1	1	0	1	0
Tachyporus hypnorum	Generalist	Carnivore	0	1	0	1	1	0	0
Tachyporus transversalis	Generalist	Carnivore	1	0	0	1	0	1	0
Thalycra fervida	Terrestrial	Fungivore	0	0	1	0	0	0	1
Thamiaraea cinnamomea	Terrestrial	Carnivore	3	0	4	0,286	0	1	0
Thamiaraea hospita	Terrestrial	Carnivore	0	3	1	0	0	1	0
Thiasophila wockii	Terrestrial	Carnivore	2	0	0	0	0	0,5	0,5
Thiasophila wockii?	Generalist	Carnivore	0	1	0	0	0	1	0
Tomoxia bucephala	Terrestrial	Herbivore ; saprotroph/saprophage/detrivor ; fungivore	0	1	1	0	0	0,5	0,5
Trechus rivularis	Wetland	Carnivore	1	1	0	1	0	0,5	0,5
Trechus rubens	Wetland	Carnivore	3	0	0	0,667	0	1	0



Species	Habitat preference	Feeding guild	Rewetted	Unditched	Ditched	Prop. pitfall	Prop. period 1	Prop. period 2	Prop. period 3
Trimium brevicorne	Generalist	Carnivore	0	11	0	0	0	1	0
Triplax aenea	Terrestrial	Fungivore	1	0	0	0	1	0	0
Triplax russica	Generalist	Fungivore	67	11	29	0,009	0,084	0,832	0,084
Trixagus carinifrons	Terrestrial	Fungivore	0	0	1	0	0	0	1
Trixagus dermestoides	Terrestrial	Fungivore	1	0	1	0,5	0	1	0
Trypodendron signatum	Terrestrial	Fungivore	0	0	1	0	1	0	0
Wanachia triguttata	Terrestrial	Fungivore	2	0	2	0	0	0,25	0,75
Xantholinus longiventris	Generalist	Carnivore	0	0	1	1	1	0	0
Xantholinus tricolor	Generalist	Carnivore	1	1	1	1	0	0,667	0,333
Xyletinus hanseni	Terrestrial	Saprotroph/saprophage/detrivor	0	0	1	1	0	1	0
Xylita laevigata	Terrestrial	Saprotroph/saprophage/detrivor ; fungivore	7	2	13	0,045	0,045	0,591	0,364
Zyras collaris	Generalist	Carnivore	5	5	9	0,895	0,368	0,579	0,053

Table A8. All identified beetle species with habitat preference, feeding guild, abundances per mire type, proportion caught in pitfall traps (and window traps the other way around) as well as the proportional abundances for each species caught during each trap period (see methods for exact dates).

Locality	Mire type	Species	Abundance score
Halmfallsmossen	Ditched	Andromeda polifolia	3
Halmfallsmossen	Ditched	Calluna vulgaris	1
Halmfallsmossen	Ditched	Drosera rotoundifolia	3
Halmfallsmossen	Ditched	Empetrum nigrum	3
Halmfallsmossen	Ditched	Eriphorum vaginatum	3
Halmfallsmossen	Ditched	Pinus sylvestris	2
Halmfallsmossen	Ditched	Rhododendron tomentosum	3
Halmfallsmossen	Ditched	Rubus chamaemorus	1
Halmfallsmossen	Ditched	Vaccinium oxycoocos	1
Halmfallsmossen	Ditched	Vaccinium uliginosum	2
Halmfallsmossen	Ditched	Vaccinium vitis-idaea	3
Hampmossen	Ditched	Andromeda polifolia	3
Hampmossen	Ditched	Betula nana	2
Hampmossen	Ditched	Betula pubescens	3
Hampmossen	Ditched	Calluna vulgaris	1
Hampmossen	Ditched	Eriphorum vaginatum	3
Hampmossen	Ditched	Picea abies	3
Hampmossen	Ditched	Pinus sylvestris	2
Hampmossen	Ditched	Trichophorum cespitosum	1
Hampmossen	Ditched	Vaccinium oxycoocos	2
Hampmossen	Ditched	Vaccinium uliginosum	3
Hemmossen	Ditched	Betula nana	3
Hemmossen	Ditched	Betula pubescens	3
Hemmossen	Ditched	Carex nigra	3
Hemmossen	Ditched	Empetrum nigrum	3
Hemmossen	Ditched	Eriphorum vaginatum	1
Hemmossen	Ditched	Picea abies	3
Hemmossen	Ditched	Pinus sylvestris	2
Hemmossen	Ditched	Rubus chamaemorus	1
Hemmossen	Ditched	Vaccinium myrtillus	3
Hemmossen	Ditched	Vaccinium oxycoocos	1
Hemmossen	Ditched	Vaccinium uliginosum	1
Hemmossen	Ditched	Vaccinium vitis-idaea	3
Knutsmossen	Ditched	Andromeda polifolia	3

Locality	Mire type	Species	Abundance score
Knutsmossen	Ditched	Betula nana	3
Knutsmossen	Ditched	Calluna vulgaris	3
Knutsmossen	Ditched	Eriphorum vaginatum	3
Knutsmossen	Ditched	Picea abies	3
Knutsmossen	Ditched	Pinus sylvestris	3
Knutsmossen	Ditched	Vaccinium myrtillus	1
Knutsmossen	Ditched	Vaccinium oxycoocos	3
Knutsmossen	Ditched	Vaccinium uliginosum	3
Knutsmossen	Ditched	Vaccinium vitis-idaea	3
Lilla dragsmossen	Ditched	Betula nana	3
Lilla dragsmossen	Ditched	Calluna vulgaris	1
Lilla dragsmossen	Ditched	Empetrum nigrum	3
Lilla dragsmossen	Ditched	Eriphorum vaginatum	3
Lilla dragsmossen	Ditched	Picea abies	3
Lilla dragsmossen	Ditched	Pinus sylvestris	3
Lilla dragsmossen	Ditched	Rhododendron tomentosum	1
Lilla dragsmossen	Ditched	Rubus chamaemorus	3
Lilla dragsmossen	Ditched	Vaccinium myrtillus	3
Lilla dragsmossen	Ditched	Vaccinium oxycoocos	3
Lilla dragsmossen	Ditched	Vaccinium uliginosum	1
Lilla dragsmossen	Ditched	Vaccinium vitis-idaea	2
Lortspångsmossen	Ditched	Betula nana	2
Lortspångsmossen	Ditched	Betula pubescens	3
Lortspångsmossen	Ditched	Calluna vulgaris	1
Lortspångsmossen	Ditched	Empetrum nigrum	3
Lortspångsmossen	Ditched	Eriphorum vaginatum	2
Lortspångsmossen	Ditched	Lysimachia europaea	3
Lortspångsmossen	Ditched	Phragmites australis	3
Lortspångsmossen	Ditched	Pinus sylvestris	3
Lortspångsmossen	Ditched	Vaccinium oxycoocos	3
Lortspångsmossen	Ditched	Vaccinium uliginosum	1
Malingsbo	Ditched	Andromeda polifolia	2
Malingsbo	Ditched	Betula nana	3
Malingsbo	Ditched	Calluna vulgaris	2

Locality	Mire type	Species	Abundance score
Malingsbo	Ditched	Carex pausiflora	3
Malingsbo	Ditched	Drosera rotoundifolia	3
Malingsbo	Ditched	Eriphorum vaginatum	3
Malingsbo	Ditched	Pinus sylvestris	3
Malingsbo	Ditched	Rubus chamaemorus	3
Malingsbo	Ditched	Trichophorum cespitosum	1
Malingsbo	Ditched	Vaccinium oxycoocos	2
Malingsbo	Ditched	Vaccinium uliginosum	3
Salbo	Ditched	Andromeda polifolia	3
Salbo	Ditched	Betula nana	2
Salbo	Ditched	Calluna vulgaris	1
Salbo	Ditched	Drosera rotoundifolia	3
Salbo	Ditched	Empetrum nigrum	1
Salbo	Ditched	Eriphorum vaginatum	3
Salbo	Ditched	Pinus sylvestris	1
Salbo	Ditched	Rubus chamaemorus	3
Salbo	Ditched	Vaccinium myrtillus	2
Salbo	Ditched	Vaccinium oxycoocos	1
Salbo	Ditched	Vaccinium uliginosum	1
Salbo	Ditched	Vaccinium vitis-idaea	3
Blankmossen	Rewetted	Andromeda polifolia	3
Blankmossen	Rewetted	Betula nana	2
Blankmossen	Rewetted	Betula pubescens	3
Blankmossen	Rewetted	Calluna vulgaris	2
Blankmossen	Rewetted	Carex canescens	3
Blankmossen	Rewetted	Carex lasiocarpa	3
Blankmossen	Rewetted	Carex nigra	3
Blankmossen	Rewetted	Eriphorum vaginatum	3
Blankmossen	Rewetted	Myrica gale	1
Blankmossen	Rewetted	Picea abies	3
Blankmossen	Rewetted	Pinus sylvestris	2
Blankmossen	Rewetted	Vaccinium oxycoocos	2
Djurgårdsmossen	Rewetted	Betula nana	2
Djurgårdsmossen	Rewetted	Calluna vulgaris	3

Locality	Mire type	Species	Abundance score
Djurgårdsmossen	Rewetted	Picea abies	3
Djurgårdsmossen	Rewetted	Pinus sylvestris	3
Djurgårdsmossen	Rewetted	Rhododendron tomentosum	3
Djurgårdsmossen	Rewetted	Rubus chamaemorus	3
Djurgårdsmossen	Rewetted	Vaccinium myrtillus	2
Djurgårdsmossen	Rewetted	Vaccinium oxycoocos	3
Djurgårdsmossen	Rewetted	Vaccinium vitis-idaea	3
Kungamossen	Rewetted	Betula nana	3
Kungamossen	Rewetted	Betula pubescens	3
Kungamossen	Rewetted	Calluna vulgaris	3
Kungamossen	Rewetted	Dactylorhiza maculata	3
Kungamossen	Rewetted	Equisetum fluviatile	3
Kungamossen	Rewetted	Eriphorum vaginatum	3
Kungamossen	Rewetted	Frangula alnus	3
Kungamossen	Rewetted	Melampyrum sylvaticum	3
Kungamossen	Rewetted	Phragmites australis	1
Kungamossen	Rewetted	Picea abies	2
Kungamossen	Rewetted	Pinus sylvestris	3
Kungamossen	Rewetted	Rhododendron tomentosum	3
Kungamossen	Rewetted	Rubus chamaemorus	1
Kungamossen	Rewetted	Vaccinium oxycoocos	2
Kungamossen	Rewetted	Vaccinium uliginosum	2
Kungamossen	Rewetted	Vaccinium vitis-idaea	3
Römyren	Rewetted	Andromeda polifolia	3
Römyren	Rewetted	Betula nana	3
Römyren	Rewetted	Calluna vulgaris	1
Römyren	Rewetted	Empetrum nigrum	1
Römyren	Rewetted	Eriphorum vaginatum	3
Römyren	Rewetted	Pinus sylvestris	1
Römyren	Rewetted	Rubus chamaemorus	2
Römyren	Rewetted	Vaccinium oxycoocos	1
Römyren	Rewetted	Vaccinium uliginosum	1
Römyren	Rewetted	Vaccinium vitis-idaea	2
Stormossen	Rewetted	Andromeda polifolia	3

Locality	Mire type	Species	Abundance score
Rackamossen	Unditched	Empetrum nigrum	1
Rackamossen	Unditched	Eriphorum vaginatum	3
Rackamossen	Unditched	Pinus sylvestris	1
Rackamossen	Unditched	Rubus chamaemorus	2
Rackamossen	Unditched	Vaccinium myrtillus	2
Rackamossen	Unditched	Vaccinium oxycoocos	3
Rackamossen	Unditched	Vaccinium vitis-idaea	3
Råmyran	Unditched	Betula pubescens	3
Råmyran	Unditched	Calluna vulgaris	3
Råmyran	Unditched	Empetrum nigrum	3
Råmyran	Unditched	Eriphorum vaginatum	3
Råmyran	Unditched	Maianthemum fluviatile	3
Råmyran	Unditched	Melampyrum sylvaticum	3
Råmyran	Unditched	Picea abies	3
Råmyran	Unditched	Pinus sylvestris	3
Råmyran	Unditched	Rubus chamaemorus	3
Råmyran	Unditched	Vaccinium myrtillus	3
Råmyran	Unditched	Vaccinium oxycoocos	2
Råmyran	Unditched	Vaccinium uliginosum	2
Råmyran	Unditched	Vaccinium vitis-idaea	3
Stora dragsmossen	Unditched	Andromeda polifolia	3
Stora dragsmossen	Unditched	Betula nana	3
Stora dragsmossen	Unditched	Betula pubescens	3
Stora dragsmossen	Unditched	Calluna vulgaris	2
Stora dragsmossen	Unditched	Carex lasiocarpa	3
Stora dragsmossen	Unditched	Drosera rotoundifolia	3
Stora dragsmossen	Unditched	Eriphorum vaginatum	3
Stora dragsmossen	Unditched	Myrica gale	1
Stora dragsmossen	Unditched	Pinus sylvestris	3
Stora dragsmossen	Unditched	Vaccinium oxycoocos	3

Table A9. Species and corresponding abundances form the vegetation survey, for each locality.

Publicering och arkivering

Godkända självständiga arbeten (examensarbeten) vid SLU kan publiceras elektroniskt. Som student äger du upphovsrätten till ditt arbete och behöver i sådana fall godkänna publiceringen. I samband med att du godkänner publicering kommer SLU även att behandla dina personuppgifter (namn) för att göra arbetet sökbart på internet. Du kan närsomhelst återkalla ditt godkännande genom att kontakta biblioteket.

Även om du väljer att inte publicera arbetet eller återkallar ditt godkännande så kommer det arkiveras digitalt enligt arkivlagstiftningen.

Du hittar länkar till SLU:s publiceringsavtal och SLU:s behandling av personuppgifter och dina rättigheter på den här sidan:

- https://libanswers.slu.se/sv/faq/228316

☑ JA, jag, Simon Carrington har läst och godkänner avtalet för publicering samt den personuppgiftsbehandling som sker i samband med detta

☐ NEJ, jag/vi ger inte min/vår tillåtelse till att publicera fulltexten av föreliggande arbete. Arbetet laddas dock upp för arkivering och metadata och sammanfattning blir synliga och sökbara.