Functional diversity of evertebrates in different types of beech forest in southern Sweden

Masters Degree project in Ecology, 30 credits

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Photos from the field work & species identification moments between 1/5-13 to 17/6-13 by Martin Larsson

Abstract

Deforestation, fragmentation and loss of biodiversity, all are elements that are common today. With this project I want to evaluate if there is a difference in functional diversity of evertebrates between beech stands of low herb and shrub type beech forest. I also want to test if there is a difference within tested areas between low herb and shrub type forests, but also if here is a difference between tested areas with the same forest type. I sampled leaf litter in beech forests in Skåne, southernmost Sweden. Litter dwelling evertebrates were identified down to family level and their functional role in the system was written down after closer inspection of each family. Their abundance was also written down in my field notes. Later on the notes were used for calculations to get the richness data, the Shannon-Weiner diversity index and the functional diversity. The species to area relation was also tested through a linear regressions analysis.

The carnivores were the most common functional group, and it was the only group that differed significantly between forest types (more common in shrub type forests). The functional diversity proved to be higher in the shrub type of forest, when compared to the herb type forest, but there was no significant difference in taxonomical diversity (analysed on the family level). There were no significant difference in the diversity between sites, within each forest type. I did not find any significance when comparing the functional levels between sites. Functional diversity did not differ between sites and there was no significant relation between functional diversity and the size of tested areas. The taxonomic diversity did not indicate any significant difference between forest types.

Therefore, I did not find any support for my hypothesis that size of the sites or presence of an additional food level in low herb type forests gave any significant responses. What I learned was that there generally is not any significant difference in community structure when it comes to the functional diversity of detrivores, herbivores, omnivores, parasites or scavengers. This may indicate that beech forests are homogeneous habitats with only small differences in functional composition across the two forest types and the different sites.

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Introduction

Southernmost Sweden has large areas of beech forests, which are used for commercial timber production, while others are protected in nature reserves or flagged as protect worthy within the EU network Natura2000 (Skånes skogar 2004 & MB 2013). Since long the habitat is fragmented and; vast forests have become mere fragments between agricultural land, cities and roads (Bernes 2011).

In Sweden we have two major types of forest-forming broad leafed trees, one is oak and the other is beech (Bernes 2011). Beech forests occur only on the Northern hemisphere of the globe (Nrm.se 2011). Beech and oak mainly occur in the nemoral growth zone where mostly broad leafed trees are found, as in comparison to the boreal zone where mostly conifers grow. In comparison to oak, beech trees have a much denser leaf foliage and generally grow in dense stands (Bernes 2011). The competition for light is high and few other trees can cope with this (Bernes 2011). Furthermore the leaves are less degradable and it takes a long time for them to actually break down, thus leading to a thick cover of leaves on the ground (Bernes 2011). Few seeds can penetrate this layer which generally leads to a less diverse flora (Bernes 2011). However where light do reach the ground, diversity can be quite rich, and the general composition of this diversity is defined by the nutrient availability in the soil (Bernes 2011). There are no known mammals or bird species that only occur in Swedish beech forests, however the evertebrate fauna can be quite rich and some of these evertebtates only occur in beech forests (Emanuelsson et al 2002).

Beech forests are very competitive (Emanuelsson et al 2002) and can reach a age of 400years (Nrm.se 2011). Many species only occur around trees that have reached a high age. Continuity is of great importance for the areas species diversity. Further, beech trees do not only pose a positive force for biodiversity as living trees, but also when they are dead. Remnants of beeches, standing or laying down, act as homes for wood-living arthropods that can either live through decomposition of the log or need it to avoid dehydration (Niklasson & Nilsson 2005).

Although we do have forests that are protected from harmful exploitation, and are managed to increase regeneration. It is still a fact that the areas that we protect are small, at least when we look at a broader scale . Only 5% of our productive grounds are covered with semi-natural forests and even these have most likely been affected by our exploits during hundreds of years, and still are. Forests are isolated by roads, plant biodiversity are restricted by increasing ground nitrogen levels from traffic-caused air pollution (Bernes 2011).

Why is it important for us to protect these areas? The answer to this may vary depending on who is asked, but the forest provide several important ecosystem services. The forest is a natural renewable resource that cleans up our excess CO2 production, stabilizes the grounds to avoid drifting of soils, they provide us with raw materials and much more. So in the end its for our own good to keep our forests in good health by keeping or strengthening their biodiversity.
Our ability to manage our forests is greatly affected by how much we know of its community structure. Particularly little is generally known about the biodiversity of forests evertebrate fauna (Carpenter et al 2012). Furthermore, some of these evertebrates can play ecologically important roles in the forest ecosystem. For example increase nutrient turnover, which is highly relevant in beech forests due to the leaf layer (Kristov et al 2006). They can also be an important food source for other animals (Kristov et al 2006).

I set out to broaden my knowledge of the forests evertebrate community through analysing the diversity of evertebrates on both the functional and taxonomical level. Functional diversity refers here to the function the organism serve in the ecosystem, as predator, degrader, omnivore etc. In this study the abundance of found families was used to calculate the functional and taxonomical diversity index (H´), the calculations were executed through using the Shannon-Weiner formula ($H´=-\Sigma p_i \ln p_i$). The taxonomical level is, in this study, family based with no regard to the functional levels. The combination of function contra family level diversity was made due to a notion I observed in an article by Janecˇek et al (2013) that they can act both mathematically and

biologically independent of each other. Thus it may strengthen my result if both show similar results with higher diversity in some areas. Furthermore they have shown to be region specific to changes in diversity that occur as a response to changes in land-use (Janecˇek et al 2013), which is of relevance to me since I tested the diversity between areas as well. The focus was on the functional diversity of evertebrates in leaf litter. The leaf litter was, in this project, defined as the top layer of dead plant material and the top moveable layer of the humus layer (Sabu et al 2009). Evertebrates found in forest leaf litter are an important focus group in many ecological studies due to the easiness to sample (Guénard & Lucky 2011) and the relevance of this group for tests of diversity (Eva Waldemarson 2013). I compared two beech forest types that were described in the county administration boards publication Skånes skogar (2004). (1) the shrub type, which is defined as a forest with a very sparse ground vegetation and only a few species of vascular plants (Skånes skogar 2004) and (2) the low-herb type, defined as a forest with a rich flora that varies between seasons with *Anemone nemorosa* dominating in spring and *Lamiastrum galeobdolon and; Stellaria nemorum* in summer (Skånes skogar 2004).

Given the varying characteristics between low herb and shrub-type forests, I expect to find differences in their litter-dwelling fauna. And due to the varying area of my sampled sites (see table 1), I also expect to find variations between sampled sites due to the specie - area effect (Ikeda et al 2008). The specie - area effect theory claim that larger areas can retain more species than smaller ones (Ikeda et al 2008). Therefore I tested the following hypotheses in my study:

$H1_1$ There will be a difference in the evertebrate diversity between the two beech forest types

$H1_2$ I expect a higher functional diversity in the areas with low herb types due to the fact that more food is present for herbivores and thus also for predators (Baini et al 2012).

H2 The functional diversity will relate to the locations area.

H0 There is no difference in either $H1_1$, $H1_2$ or H2

Material and methods

Sampling areas in Scania were chosen in order to cover a wide area, and to include both types of beech forests. I sampled both shrub and low herb types in each area.

The focus group of this study was the ground dwelling fauna, which was extracted through sieving the leaf litter through a net with a hexagonal structure (mesh size: sides. 20 mm, diameter. 30 mm). For the selection of areas I partly used the county administration boards publication (Skånes skogar 2004). To improve the spread of my sampling sites I also selected some areas in close proximity to protected sites. I checked the regulations for those areas in their database (Länsstyrelsen 2011 & 2012) and abided to the conservation plans and area regulations set up to protect those areas. Further I pre-tested my sieving tools before any sampling was performed, and my sampling method showed to have no damaging effect whatsoever. After the test, the plot was indistinguishable from the surrounding litter layer. Thus, at least in accordance to paragraph 28a in chapter 7 of Miljöbalken (eng: The Swedish Environmental Code), I did not need a permit to sample areas since the affect of my method had no effect on the area itself (MB 2013). Since the county administration boards publication was slightly out-dated I also cross checked the areas in their report (Skånes skogar 2004) with their online database over areas (Länsstyrelsen 2011 & 2012). Some areas were chosen through suggestions from interviews with people with experience from the areas.

The area size was calculated using maps, only including the areas covered with forests.

Table 1) *Size of tested areas. The size was calculated using simple polygons over maps of the areas. Roads or farmland was used as borders to restrict the area calculated.*

Area	Size (Km)
Hovdalaåns dalgång	10
Mölleröd	4
Ryssberget	96.75
Ravlunda	13.01
Söderåsen	54.95
Torups bokskogar	1.46

These areas were written down on a sheet and they were split up in polygons from which an estimated area (km^2) could be calculated (Lantmäteriverket 1996 & SOF 1994). A similar technique to this was used in an article by Carpenter et al (2012) about biodiversity of soil macrofauna in national parks.

Table 2) *Areas chosen to be sampled, their protection and N2000 code. Please note that sampling locations took place only where it was allowed, outside the protected sites border, and the coordinates are not an exact reference to where sampling actually took place.*

Area	Protection	Code	General Coordinates
Hovdalaåns dalgång	Non found	x	Lat N 56° 5′ 43″Lon E 13° 42′ 11″
Mölleröd	Natura 2000	SE 0420296	Lat N 56° 20′ 15″Lon E 13° 38′ 50″
Ryssberget	Natura 2000	SE 0420322	Lat N 56° 10′ 49″Lon E 14° 31′ 29″
Ravlunda	Natura 2000	SE 0420240	Lat N 55° 42′ 13″Lon E 14° 6′ 23″
Söderåsen	Nationalpark & Natura 2000	SE 0420154	Lat N 56° 1′ 14″Lon E 13° 7′ 52″
Torups bokskogar	Non found	x	Lat N 55° 33′ 30″Lon E 13° 12′ 17″

Description of selected areas:

General coordinates, protective status and size of the tested areas can be found in Table 1 and 2 above.

Location 1 (Hovdalaåns dalgång)

The first area was in Hovdalaåns dalgång. It was sampled during 1/5-2013, around 12:00 to 15:00. The forest was of the shrub type category, as concluded by the dominance of *Deschampsia flexuosa*. It was abundant together with- dead branches and logs of varying sizes. Re- growth of beech was also prominent.

The second forest-type was found 6/5-2013 and was categorised as a low herb type from its abundance of *Anemone nemorosa*. Samples were collected between 11:00 to 14:00.

In all other aspects it was similar to the natural state previously seen in the first site. Albeit with even more regrowth than the first one.

Location 2 (Mölleröd)

It was sampled during 13/5-2013, around 11:00 to 15:00.

The first forest was of the shrub type category, it was concluded by the lack of any plant life abundance and only a few detectable grasses that was to young to be successfully identifiable. It was abundant with dead branches and logs of varying sizes.

The second site was categorized by the high abundance of *Anemone nemorosa*. However the forest was much more densely packed with trees than the first one sampled this day.

Location 3 (Ryssberget)

This site was sampled at the 28/5-2013. Between 11:00 to 15:00.

The first area consisted of trees with varying ages and occurring re growth. It was categorised through the presence of some dried up grasses that looked similar to *Deschampsia flexuosa*, I also found *Empetrum nigrum* which made me extra sure of the categorization.

The second area was consistent with low herb type forests, younger tree stands was more prominent and the ground was quite moist. It was categorized by the greater abundance of *Anemone nemorosa*.

Location 4 (Ravlunda)

This site was sampled at the 3/6-2013. Between 11:00 to 14:00.

In the first area, even though there was some clutches of *Anemone nemorosa*, the overall area were quite poor in forest floor flora which is why it was categorized as shrub type. It was also quite abundant with dead branches and logs.

The abundance of *Anemone nemorosa* was more abundant in the second area, however the categorization as low herb type was more based on the rich forest floor flora. There was less wood on the ground than in first one but still a lot of dead branches present.

Location 5 (Söderåsen)

This site was sampled at the 12/6-2013. Between 12:00 to 15:00.

The first one consisted mostly of a steep hill and there were some pines nearby. There were some dead branches and some small logs. The main evidence for my shrub-type categorization here was the presence of *Empetrum nigrum* in the area and it was overall a very poor flora.

The second site had a very dense forest, and was very hard to categorise. There was some *Empetrum nigrum* in close proximity to the site but overall the forest floor flora was rich so finally it was marked as a low herb type in the field notes.

Location 6 (Torups bokskogar)

This site was sampled at the 17/6-2013. Between 12:00 to 14:00.

The first area was rich in different flora, this was the major reason for its classification as a low herb type forest. The beeches were well dispersed in age and there was occurring re growth.

The second site was well dispersed in age and had occurring re growth of younger beech stands. The main reason for its classification as shrub type was that the main growth consisted of

grasses like *Deschampsia flexuosa*.

Sampling and survey

I did not include areas that had recently been disturbed by human activities, since this could affect my results (Delgado et al 2013). The sites and plots were randomly selected for a good spread and good coverage of the area, a wooden frame 0.5 x 0.5 was used for the plots. Whether a site was shrub or low herb type was decided based on the most common plants in these forest types (Skånes skogar 2004), and the most common plant configurations were printed on a simple sheet with both descriptive text and detailed photographs so that I were able to successfully figure out what forest type I sampled at the moment. Percent of vegetation cover was noted to analyse if the plots followed the definition for the different beech forest types that were mentioned in Skånes skogar (2004).

The leaf litter was placed into a sieve and then sieved over a white sheet where the organisms were collected into jars. The method is similar to ”Winkler extraction” that has been used in many similar studies and it is good for achieving quantitative data (Sabu et al 2009). I received a quicker extraction through shaking the leaf litter, a method previously used for moist litter where the material was left to slowly dry and let the sampling organisms fall down in a jar beneath it (Owen 1987). Since the material already was dry enough I saw no reason to wait and therefore I followed the method of stirring that was proposed in a study by Guénard & Lucky (2011). I identified all groups I found, to determine the functional diversity of all visible (at least 2-3 mm long) organisms. This was done with three sources of identification literature (Sandhall 1991, Douwes et al 2004 & Gärdenfors et al 2004). I identified to family level to be sure of the specimens function in the system, the quantity of found organisms was also noted for the diversity calculations. The functional groups were split up by their main diet, as seen when each family was investigated online and in my identification literature (Sandhall 1991, Douwes et al 2004 & Gärdenfors et al 2004). It is a necessary simplification since trophic systems usually are to complex, a lot of interconnectivity between levels, for statistical analyses. For example some of my scavengers were also fungivores. Furthermore the volume and area of the sampled plot was written down. Identification was, if possible, done in the field. Otherwise I collected them for later identification. Some generalisations of family identifications had to be made regarding juvenile exemplars of, for example, beetle and butterfly families. Keyed organisms was released out in the wild after a successful family identification. I also documented the largest individuals through taking photographs. I designed a plastic tray, from old cd containers and their transparent cd-shaped protective layers, with the purpose to restrict their movement without the need to kill them for detailed photographs. 10 plots per beech forest type was used during the sampling. A work sheet was used out in the field to ensure that the right data was written down. After identification, all data was transferred into a calculation sheet (OpenOffice v3.3.0) where the Shannon-Weiner diversity index was calculated for every locality.

The choice of diversity index was made from previous experience where the Shannon-Weiner index was used for a similar study, and also because it was among those recommended for diversity calculations in (Hubálek 2000). The Shannon-Wiener index combines evenness and richness, but it is sensitive to sample size (StatsDirect.com 2013). Differences in H can be due to a difference in richness, evenness, or even just a difference in the sampling method (StatsDirect.com 2013). However, this problem was partly dealt with by also testing for the richness of families in the tested sites.

The data was tested in SPSS (v:20.0.0, ©IBM) with a 2-Way- ANOVA (Tukey procedure at at the plot level) to test the hypothesis about a significant difference between the functional groups between sites, with extra regard taken to the size of the tested areas (H2). Both H values and abundances were used. It should be mentioned that the Shannon formula is not ideal if it is used

together with Anova. The whole formula is according to information theory, based on an infinite population and an unbiased estimator of variance does not exist (Bevilacqua 2011). This is a serious limit to using the Shannon-Wieners diversity index in Anova contexts (Bevilacqua 2011). But no clear alternatives exist, to my knowledge, to circumvent the problem of the Shannon formula ($H' = -\Sigma p_i \ln p_i$). The size to diversity relation was tested through a linear regression analysis. And with paired t-tests to test the hypothesis about a significant difference between low herb and shrub type forests (H1), and to prove that there would be a higher diversity found in the low herb type because of a higher abundance of food ($H1_2$). Abundance data was also visually represented through graphs created in SPSS (v:20.0.0, ©IBM).

Results

Effect of forest type

The result were based on area and volume calculations for functional groups and families found in the litter layer, but only the area were used here (Table 3). Volume and area displayed similar results which is why volume was excluded here. The similarities is a result of the H´ calculations, for the Shannon-Weiner diversity index, where p_i (families found/total findings) got almost identical results when using either of the area or volume calculations.

Table 3) *The mean abundance of each functional group, the taxonomic diversity at the family level, the functional diversity, and richness at the family level. P values show significances when the shrub type forest was tested against low herb type forest (Paired t-test).*

The unit m^2 is based on normalized values for number of families found for each functional group, in all plots. The value to used for normalisation was 2.5 (0.5x0.5m x 10 plots= 2.5m^2).

Richness per 0.25m^2 is based on the mean number of families found (Mean.nbr_Family = mean number of families)in each plot (0.5x0.5m = 0.25m^2).

	Shrub	**LowHerb**	
Functional group:	**Mean.Abund / Group**		**P-value**
	Per m²		
Carnivore	11.500	9.500	0.049
Detrivore	5.000	4.500	0.541
Herbivore	5.000	3.333	0.233
Omnivore	1.667	1.667	1.00
Parasite	1.000	0.667	0.465
Scavenger	0.833	1.333	0.363
Other:	**Mean_H**	**Mean_H**	**P-value**
	Per m²		
Taxonomic diversity	2.169	2.234	0.156
Functional diversity	2.710	2.459	0.032
	Mean.nbr_Family		**P-value**
	Per 0.25m²		
Richness (Family)	1.493	1.749	0.309

For most groups there were no significant difference in diversity between the types of forest (Table 3). As can be seen from (Table 3) only the functional diversity, in general over all sites, showed any significance (P=0.032). However on the functional group level, the carnivores were more diverse (P=0.049) in shrub type forests (Table 3). The taxonomic diversity showed no significant differences between the low herb and shrub type forests, but the mean functional diversity was significantly higher (P=0,032) in the shrub type (Table 3). When the sites were tested separately no difference could be found (Table 4).

Table 4) *Results from several paired t-test runs in SPSS, separated by tested sites (Hovdala, Mölleröd, etc). The comparison is made between the shrub and low herb type forests. The value tested is the overall functional diversity.*

To clarify it, Hovdala will be used as an example: The mean diversity (H) of all functional groups in Hovdala Shrub type forest is tested against the mean diversity (H) of all functional groups in Hovdala Low herb type forest. No distinction on actual functional group was made.

The means, for each site and type,was acquired in the additional table that was generated before the actual probing values were calculated in the paired t-test run.

The unit of m^2 is based on normalized values for abundances of families found for each functional group, in all plots. The value used for normalisation was 2.5 (0.5x0.5m x 10 plots= 2.5m^2). FunctDiv (Within sites) describe the difference in functional diversity within the sites Hovdala, Mölleröd etc. N is the amount of functional groups, which normally was 6 per site. However, only 5 functional groups could be found in Torups beech forests (no parasites).

Parameter	Pair Shrub – LowHerb			
	N	Mean.H Shrub	Mean.H LowHerb	Sig. (2-tailed)
FunctDiv(Within sites):		Per m²		
Hovdala	6	1.540	1.360	0.402
Mölleröd	6	1.440	1.630	0.293
Ryssberget	6	1.870	1.570	0.115
Ravlunda	6	2.200	1.850	0.306
Söderåsen	6	1.490	1.480	0.925
Torups boksk	5	1.450	1.360	0.095

Effects between forests of the same type and the relevance of size

When the data was analysed using a two-way ANOVA with forest type and site as factors, there was no effect of neither site nor forest type. To be able to make a full run with the two-way ANOVA I had to take the results plot wise, instead of site wise (as was done for the t-tests). This lead to less resolution in the results and the H calculation got more sensitive to deviant values. There were too few samples in the parasite data to actually be able to run the test, thus it will only be visually represented through the graphs below. Only omnivores for Söderåsen showed, at first, any significant results when Söderåsen was tested against the other sites (Hovdala to Torup). A secondary run was performed, due to the resolution problem, where deviant families were replaced with more commonly observed values for said families (see text under Figure 2). No significance was observed upon this change ($P \geq 0{,}912$). The previous significance came from the fact that the omnivores were less diverse here than in the other sites. The functional groups were limited in the tested plot as well. And the high abundance of ants due to the proximity to the ant hill, affected my Shannon-Weiner index (H´) calculations by increasing the total value that p_i was divided with (H´= the calculated diversity, and p_i= the proportion of individuals of species "i"). Which lead to a much lower value.

Upon testing if there were any connection between functional diversity and size of tested sites, through a linear regression analysis with functional diversity as a dependent value and size of the areas as a independent value, no significance was observed for either forest type ($P \geq 0{,}837$). Furthermore the analysis indicated a low goodness of fit (R-Square 0.001) which further strengthen the result of no significance by indicating that the size of tested areas simply did not explain the functional diversity found there (spssakuten 2009).

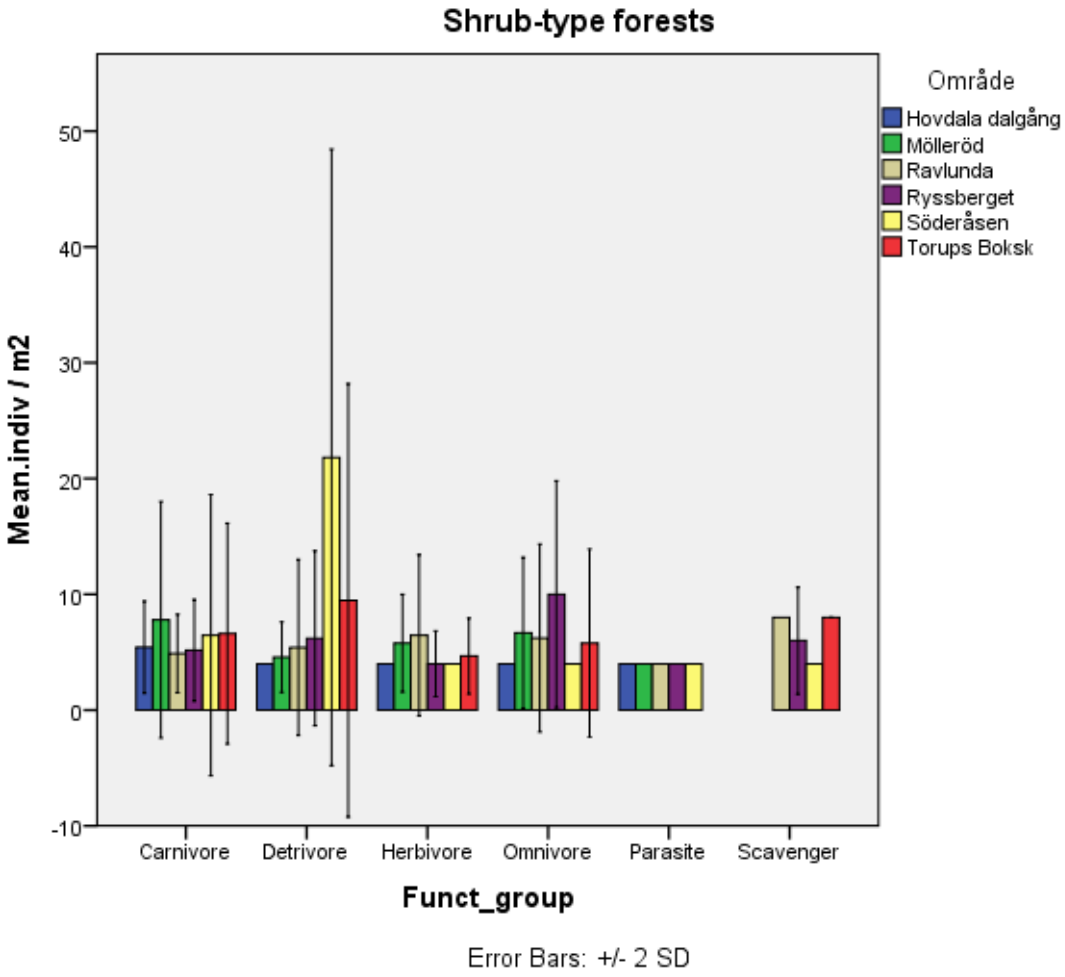

Figure 1) *Graph displaying the mean number of individuals within each functional group, per site (Shrub-type forests)*.

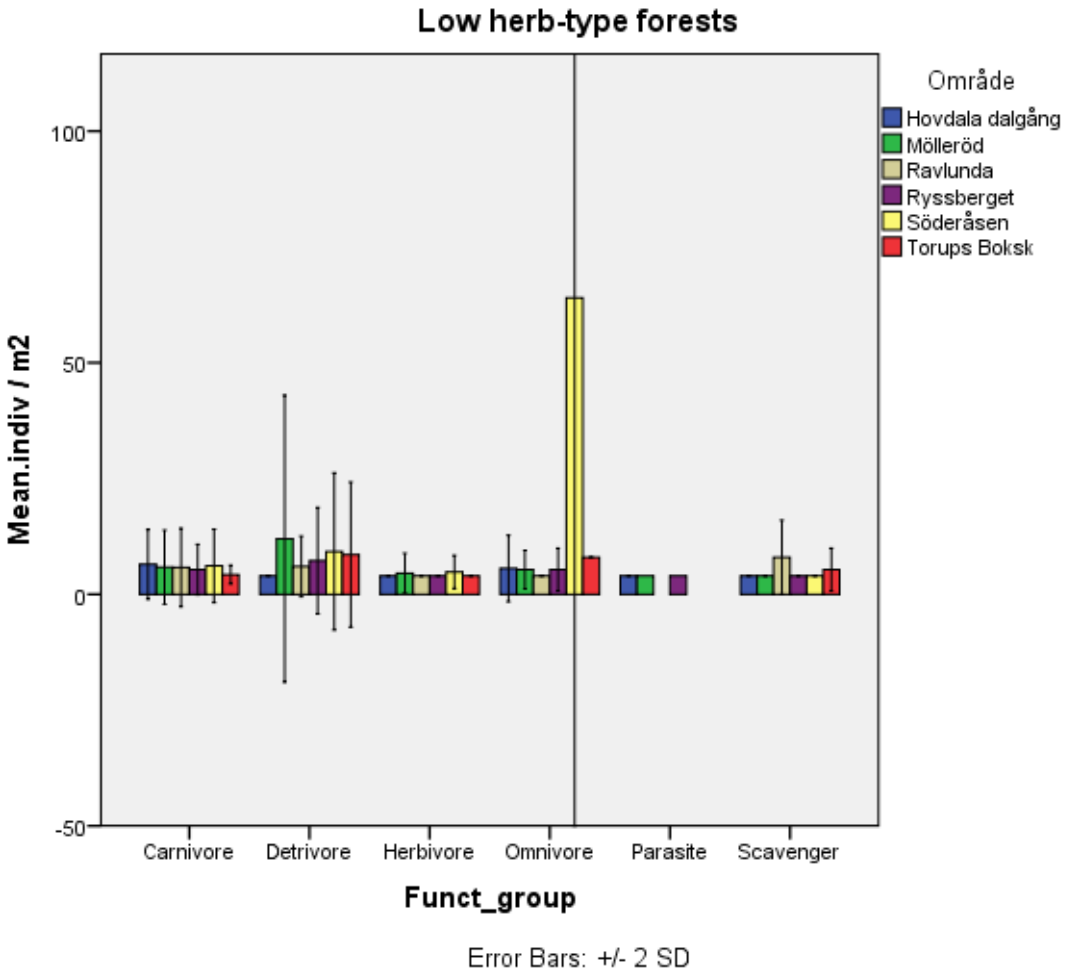

Figure 2) *Graph displaying the mean number of individuals within each functional group, per site (Low herb-type forests). (Missing SD for Söderåsen Omnivore is -171 – 299 (Cut of for better display of data), the main constituent of this bar is approximately 60 ants due to one of the plots being close to an ant hill).*

Only some minor differences is observed in the graphs, as missing groups or some that went slightly higher than average. The only interesting result is the higher abundance of detrivores shown in the shrub type forest in Söderåsen (Figure 1). The Söderåsen low herb omnivore sample may at first seem interesting (see Figure 2) but the result it is actually due to the same abnormal plot value as mentioned in the 2-way ANOVA run above.

Families found

The most common families and their mean abundance per family observed, were presented in the table below to give a general idea of what was found (table 5). The complete list can be found in appendix table A. Overall, if we do not consider the different forest types, there were 30 families of carnivores, 21 herbivore families, 11 detrivore families, 4 parasite families and 2 scavenger and omnivore families (See the complete list in appendix table A). So 70 families in total. If we do take the forest type into consideration, there were 23 carnivore families in the shrub type and 26 in the low herb type, 9 detrivore families in the shrub type and 10 in the low herb type, 13 herbivore families in the shrub type and 14 in the low herb type and 3 parasite and 2 omnivore and scavenger families in both of the forest types (See the complete list in appendix table A).

The values mentioned in the text above is presence and absence data of families, ergo it is not

connected to the taxonomical diversity values in table 3 above.

Table 5) *The mean abundances of the most common families, and their respective functional groups, found over all sites. The unit of m^2 is based on normalized values for abundances of families found for each functional group, in all plots. The value to used for normalisation was 2.5 (0.5x0.5m x 10 plots= 2.5m^2) and for each site. Families with values below 0.2 , in both the low herb and shrub type forests, were excluded for easier insertion into this report (original had 70 families). (Complete list in appendix table A)*

Parameter		Shrub	LowHerb
Family:	**Funct_Group**	**Mean.abund_Fam**	
		Per m²	
Agelenidae (Trattspindlar)	Carnivore	1.400	1.000
Archaeognatha (Hoppborstsvansar)	Detrivore	0.133	0.200
Armadilidiidae (Klotgtåsuggor)	Detrivore	0.200	0.400
Cantharidae (Flugbaggar)	Carnivore	0.133	0.267
Carabidae (Jordlöpare)	Carnivore	1.133	0.200
Cercopidae (spottstritar)	Herbivore	0.133	0.200
Clubionidae (säckspindlar)	Carnivore	0.067	0.733
Curculionidae (Vivlar)	Herbivore	0.267	0.533
Diptera larvae	Detrivore	0.667	0.467
Elateridae (Knäppare)	Herbivore	0.533	0.200
Forficulidae (hjärttvestjärtar)	Omnivore	0.667	1.200
Formicidae (myror)	Omnivore	5.267	2.867
Ixodida (Fästing)	Parasite	.000	0.333
Glomeridae (Klotdubbelfotingar)	Detrivore	.000	0.333
Gnaphisidae (plattbukespindlar)	Carnivore	0.400	0.667
Julidae (kejsardubbelfoting/mångfoting)	Detrivore	0.933	0.733
Lepidoptera larvae	Herbivore	0.667	0.867
Licronidae (spindlar)	Carnivore	1.733	1.600
Linyphiidae (spindel)	Carnivore	0.333	.000
Lithobiidae (stenkrypare/mångfoting)	Carnivore	1.067	1.000
Siphonaptera larvae (Lopplarv)	Parasite	0.067	0.267
Lumbricidae (daggmaskar)	Detrivore	1.200	1.533
Lycosidae (Vargspindlar)	Carnivore	0.467	1.000
Nabidae (fälltrovskinnbaggar)	Carnivore	0.200	0.333
Oedemeridae (blombaggar)	Herbivore	.000	0.333
Onischidae (Skogsgråsuggor)	Detrivore	0.333	0.733
Oppoliones	Carnivore	1.800	2.200
Philodromidae (snabblöpar spindlar)	Carnivore	.000	0.400
Philosciidae (Mossgråsuggor)	Detrivore	1.933	1.933
Polydesmidae (Plattdubbelfotingar)	Carnivore	0.333	0.067
Pristilomatide (Kristallsnäckor)	Herbivore	0.133	0.200
Psocoptera (Stövsländor)	Detrivore	.000	1.333
Salticidae (Hoppspindlar)	Carnivore	.000	0.400
Scarabaeidae (Skogstordyvel)	Detrivore	.000	0.267
Coleoptera (larvae)	Carnivore	0.533	0.267
Sminthuridae (Hoppstjärtar)	Detrivore	5.400	5.867
Staphylinidae (Kortvingar)	Scavenger	1.400	1.133
Theridiidae (klotspindlar)	Carnivore	4.533	3.267
Thysanoptera (tripsar)	Herbivore	0.133	0.400
Zoridae (taggfoting/spindel)	Carnivore	0.200	0.067
Miridae (Ängsskinnbagge)	Carnivore	0.133	0.200

Discussion

Shifts in soil fauna can have severe consequences for higher trophic levels, and also for the organisms living from or by them in the habitat (Delgado et al 2013). For example, a shift in predator/herbivore ratios can have severe effects on the local plantlife. Other functional groups like detrivores affect the nutrient soil turnover, which is of great importance to forests soil nutrient availability (Jacob et al 2009). Detrivores are therefore relevant to us as well, at least if we want to continue to harvest our forests for wood. (Sabu et al 2011) also mention the ground dwelling arthropod fauna as important factors for habitat predictions, especially for designing future conservation strategies.

However, even though forests are so important to us, not much is known about the community structure of soil fauna in forests (Carpenter et al 2012).

Difference in diversity between low herb and shrub type forests?

H1 was partially proven, there is a difference in functional diversity between low herb and shrub type forests ($H1_1$), however my distinction that I would find more in the low herb type because of a higher abundance of food was incorrect ($H1_2$). When it comes to functional groups alone, only the carnivores showed any significant differences between forest types. The search for similar studies was unfruitful to say the least, the only indications to what could be behind these predator values were in (Gibbl et al 2013) where it is stated that the Shannons H, for predators only, increased with the age of the forest stands. Thus, at the very least, indicating that I sampled old beech stands. The other tests with regard to taxonomical distinctions of family did not help in strengthening the validity of the results above (Janecˇek et al 2013), neither did the H based on family level or the richness data for said families. Another possibility may have been that other functional groups than herbivores had a higher effect on the presence of predators than was expected.

Differences in diversity between sites?

My results for the second hypotheses (H2) did at first indicate a difference, but only for omnivores which was less diverse than the rest. And only when deviant results were included. The same indications can be seen in the graphs (Figure 1 & 2).. However the significance is most likely due to that the deviant specimens affected the H calculations, as stated in my results. Ultimately I cannot say that there is any prof for H2.

The results for the graphs (Figure 1&2) were basically the same over all sites. All but one basically show the same or close to the same abundance values, among those the largest and third largest sites. The detrivore sample in Söderåsen shrub type forest is to be expected due to the higher amount of forest floor litter, however the result were affected by the higher degree of *Sminthuridae* (springtails) that was found there. The Söderåsen low herb site shows the largest occurrence of omnivores, but the data is in this case highly affected by the high occurrence of *Formicidae* (ants) due to the proximity to an ant hill.

Given the fact that the significance disappeared when the deviant specimen was removed from my H calculations, and that the rest did not show any significant difference. It is only logical to conclude that the null hypothesis is more likely to be correct.

The effect of area

My linear regression analysis did not show a significant species to area relation. And since the goodness of fit further strengthen that result, it is only logical to conclude that my second

hypothesis (H2) was disproved. But the analysis did not disprove other possible factors. As mentioned above some taxa, either the presence or the calculated diversity, gave indications of forests in the later stages of ecosystem recovery. Given the fact that the forests have been undisturbed for a longer period of time may, precipitate niche separation so that more families can coexist in the area even though the area is small. It is also a possibility that the areas were larger before and hasn't had the time to react to the diminished area. Or perhaps that the site is not as isolated from other forests as was expected.

Quality of sites

Quality will in this paragraph, and further down in the conclusion, mainly refer to a environment with characteristics that that can sustain higher diversity. This paragraph should mainly be seen as something extra that is worth mentioning, but not as a major part of this study.

From a purely visual interpretation of the sites I can say that they were all of high quality, at least if we go by the standards of occurring re-growth with both old and new trees in mixed stands. And with the presence of dead wooden debris consisting of both thick logs and branches of varying sizes. But these are not the only things that got noticed. Several of the taxa found (see table 5 above and table B in appendix) are used as bioindicators of different environmental aspects (Gerlach et al 2013). Isopods (Such as: *Armadilidiidae* and *Onischidae*) and Oppoliones (Harvestmen) are slow to recolonize recovered areas so their presence indicate the later stages of ecosystem recovery (Gerlach et al 2013). However their function as a bioindicator for forest continuity may be questioned since their presence also are affected by the hydrology of the leaf layer. A thicker and more dens layer is certainly more able to keep a high level of moisture than a thinner layer. In my data the isopods were found in all shrub type forest sites, while in the low herb forest sites they were found in almost all with the exception of Mölleröd. The *oppoliones* were found for all low herb sites but only half of the shrub type forest sites (Ravlunda, Söderåsen and Torup). *Collembola* (such as: *Sminthuridae*) are sensitive to pollutants so their presence indicate a non-polluted environment (Gerlach et al 2013). In my data the *collembola* were found in all low herb sites and in almost all shrub type forest sites, with the exception of Mölleröd. Centipedes, specifically chilopoda, can be used as well since their presence may indicate good environmental values for other taxa (Gerlach et al 2013), but in my data they were not common enough to say anything more of value that had not already been indicated by the above mentioned taxa.

Given the above data, some sites may at first seem to be of a lower quality with regard to the indicator species present. But this may not be the case. If we take the low herb oppoliones data into consideration it is quite clear that all of the missing sites were done much earlier in the project (1/5-6/5, 13/5 and 28/5). Oppoliones may have been more active closer to June. The same factor may be the cause of the missing isopod indicator in Mölleröd or the missing collembola indicator in the shrub type forest in Mölleröd. There are many factors that can intervene, and a clear statement about the quality of these sites cant be given until further samples have been taken at a later date.

Limitations of the study

It was colder in the beginning of the project, thus it is likely that these results may be affected by the lower activity of the evertebrates. Furthermore It is also likely that many specimens hadn't even awoken or hatched yet.

Sampling took place between 12:00 and 15:00 o´clock but some evertebrates may have been more active closer to the end. Thus the specimens found, in both low herb and shrub type forests, may have been affected by which type of forest that was found first.

There were also some differences in the presence of wood substrates in the forests tested, for

example some sites had more logs present. This of course may have lead to more plots being close to logs in these sites. Logs may act as refugees and thus positively influence the species diversity in forests (Evans et al 2003).

In some sites there were many juvenile stages in the litter layer and I did not see how it would be possible to discard those results without chopping off a functional level that were, in fact, present. Thus some juvenile stages couldn't be determined to any specific family, which resulted in that some generalisations had to be made. Like for example diptera larvae, beetle larvae and lepidoptera larvae. Therefore the family richness calculations may be a bit weakened in some sites and plots, due to fewer families being represented because of the generalisations. But the functional diversity calculations were not affected by this problem.

Not all specimens were equally mobile, for example families with flight capabilities were found in both shrub and low herb type forests. Thus the diversity results may be affected by the mobility of the families in the sampled sites.

Conclusion

In the beginning I set out with the task to learn more about our biodiversity in beech forests, and to evaluate the overall community structure. My results indicated the carnivores to be the most diverse functional group in shrub type forests. But no difference could be observed with the other functional groups. The taxonomic diversity did not show any significant differences between forest types, this may indicate that there is no difference between forest types when it comes to different taxa. Furthermore, no difference between sites could be seen with either the Shannon-Weiner index values or the graphs created with regard to abundance. This was concluded upon reviewing the data and finding deviant values with a clear effect in the bars and subsequently also the statistics, which validated a re test of the data.

The linear regression data did not indicate any connection between functional diversity and the size of tested areas, but it doesn't disprove other possible factors that I did not test for in this study.

My sampled areas seem to have been of good quality with regard to age and presence of suitable substrates, such as wooden debris. Furthermore some of the taxa I found, specifically the Isopods *Collembola and Oppoliones,* indicated forests of high age and low pollutants.

The results have been subject so several factors that could have had an effect on the data, from time of day to seasonal changes, and unexpected abundances of specimens in plots.

It would have been easier to focus on a specific group of evertebrates, but since I started so early in May I had to take in everything I could find from the beginning. Any distinctions on specific suitable specimens could not be made until much later in the project, approximately at the 3rd site, and even then I couldn't be sure that said group would be found in all of the remaining sites. I couldn't risk any change in sampling tactics.

As an extra notice, especially since it is important to take community structure into consideration when devising conservation strategies. I suggest that we do not superimpose any conservation strategies from other forests, we clearly need to know the community structure of the specific forest species configuration and forest type we aspire to protect. As for example the presence of detrivores may have affected the diversity indexes of predators more than what was expected in my study.

For future studies

I suggest that more replicates of sites are chosen, to easier be able to test the H2 without the extreme sensitivity to deviant values that occur when the plots are used directly. This would also help to get more variation in the sites as well. The plots were randomly chosen and thus had a good spread of different litter layers, branch and log occurrences and different water saturations. The sites themselves were quite different to one another, even if they shared the same type of either low herb or shrub type forest qualities, one example that can be mentioned is the density of foliage. I suggest a configuration of 6sites (or more if there is time), in each site both forest types should be sampled, 2-3 duplicates of each site, and 10 plots in each duplicate. I also suggest that the project is started later in May, possibly in June. Or any time when more equalized temperatures over time have been observed. In my case that would have been 2-3 weeks after the actual sampling started.

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Appendix

Table A) *The mean abundances of all families, and their respective functional groups, found over all sites. The unit of m^2 is based on normalized values for abundances of families found for each functional group, in all plots. The value to used for normalisation was 2.5 (0.5x0.5m x 10 plots= 2.5m^2) and for each site.*

All families

Parameter	Column 1 Funct_Group	Shrub	LowHerb	Parameter	Column 2 Funct_Group	Shrub	LowHerb
Family:		Mean abund:	Mean abund:	Family:		Mean abund:	Mean abund:
Acari (Rött kvalster)	Carnivore	,067	,133	Julidae (kejsardubbelfoting/mångfoting)	Detrivore	,933	,733
Agelenidae (Rattspindlar)	Carnivore	1,400	1,000	Lumbricidae (daggmaskar)	Detrivore	1,200	1,533
Amaurobiidae (mörkrumsspindlar)	Carnivore	,067	,067	Onischidae (Skogsgråsuggor)	Detrivore	,333	,733
Araneidae (Hjulspindlar)	Carnivore	,067	,000	Philosciidae (Mossgråsuggor)	Detrivore	1,933	1,933
Cantharidae (Flugbaggar)	Carnivore	,133	,267	Scarabaeidae (Skogstordyvel)	Detrivore	,000	,267
Carabidae (Jordlöpare)	Carnivore	1,133	,200	Sminthuridae (Hoppstjärtar)	Detrivore	5,400	5,867
Chernetidae (blindklokrypare)	Carnivore	,000	,133	Achanthosomatide (Taggbärfisar)	Herbivore	,067	,000
Clubionidae (säckspindlar)	Carnivore	,067	,733	Arion ater (Svart skogssnigel)	Herbivore	,067	,000
Coleoptera (larvae)	Carnivore	,533	,267	Attelabidae (bladrullwivlar)	Herbivore	,067	,067
Dictynidae (nätverksspindlar)	Carnivore	,000	,067	Blattellidae (Små kackerlackor)	Herbivore	,000	,067
Gnaphisidae (plattbukespindlar)	Carnivore	,400	,667	Cerambycidae (långhorningar)	Herbivore	,133	,067
Gnaphosidae (plattbukspindlar)	Carnivore	,000	,067	Cercopidae (spottstritar)	Herbivore	,133	,200
Hydrophilidae (palpbaggar/vattenbaggar)	Carnivore	,000	,067	Chrysomelidae (bladbaggar)	Herbivore	,000	,067
Licronidae (spindlar)	Carnivore	1,733	1,600	Curculionidae (Vivlar)	Herbivore	,267	,533
Linyphiidae (spindel)	Carnivore	,333	,000	Dermestidae (Ängrar)	Herbivore	,067	,000
Liocranidae (Månspindlar)	Carnivore	,000	,067	Elateridae (Knäppare)	Herbivore	,533	,200
Lithobiidae (stenkrypare/mångfoting)	Carnivore	1,067	1,000	Lepidoptera larvae	Herbivore	,667	,867
Lycosidae (Vargspindlar)	Carnivore	,467	1,000	Miridae type 2 (Ängsskinnbaggar)	Herbivore	,067	,000
Miridae type 1 (Ängsskinnbaggar)	Carnivore	,133	,200	Oedemeridae (blombaggar)	Herbivore	,000	,333
Miturgidae (Säckspindlar)	Carnivore	,067	,133	Oxychilidae (glanssnäckor)	Herbivore	,000	,133
Nabidae (fälttrovskinnbaggar)	Carnivore	,200	,333	Phlaeothripidae (tripsar/thysanoptera)	Herbivore	,000	,067
Oppiliones	Carnivore	1,800	2,200	Phytidae (barkplattbaggar)	Herbivore	,067	,000
Philodromidae (snabblöpar spindlar)	Carnivore	,000	,400	Pristilomatide (Kristallsnäckor)	Herbivore	,133	,200
Polydesmidae (Plattdubbelfotingar)	Carnivore	,333	,067	Psocoptera (Stövsländor)	Herbivore	,000	1,333
Polyzonidae (Koppardubbelfoing/mångfoting)	Carnivore	,067	,067	Silvanidae (smalplattbaggar)	Herbivore	,000	,067
Reduviidae (Rovskinnbaggar)	Carnivore	,000	,067	Tenebrionidae (svartbaggar)	Herbivore	,000	,067
Salticidae (Hoppspindlar)	Carnivore	,000	,400	Thysanoptera (tripsar)	Herbivore	,133	,400
Theridiidae (klotspindlar)	Carnivore	4,533	3,267	Forficulidae (hjärttvestjärtar)	Omnivore	,667	1,200
Thomisidae (Krabbspindlar)	Carnivore	,000	,067	Formicidae (myror)	Omnivore	5,267	2,867
Zoridae (taggfoting/spindel)	Carnivore	,200	,067	Flee larvae	Parasite	,067	,267
Aradidae (skinnbagge)	Detrivore	,133	,000	Ixodida (Fästing)	Parasite	,000	,333
Archaeognatha (Hoppborstsvansar)	Detrivore	,133	,200	Phthiraptera (Djurlöss)	Parasite	,133	,067
Armadillidiidae (Klotgråsuggor)	Detrivore	,200	,400	Strange parasite on one of the spiders	Parasite	,067	,000
Diptera larvae	Detrivore	,667	,467	Silphidae (Asbaggar)	Scavenger	,133	,067
Glomeridae (Klotdubbelfotingar)	Detrivore	,000	,333	Staphylinidae (Kortvingar)	Scavenger	1,400	1,133

Table B) *The amount of specific taxa, that can be used as bioindicators, found in each site and forest type.*

		LowHerb					Shrub				
Taxa	Plot	Mölleröd	Ryssberget	Ravlunda	Söderåsen	Torups boksk	Mölleröd	Ryssberget	Ravlunda	Söderåsen	Torups boksk
		Number of taxa found					Number of taxa found				
Collembola	1	0	0	0	12	0	0	0	4	24	0
Collembola	2	0	24	0	8	0	0	0	12	32	0
Collembola	3	56	8	4	0	0	0	0	24	48	8
Collembola	4	4	16	8	0	0	0	0	12	20	0
Collembola	5	20	4	8	28	0	0	0	16	40	0
Collembola	6	4	0	0	28	0	0	24	0	16	4
Collembola	7	12	16	0	0	0	0	4	0	16	0
Collembola	8	12	8	0	0	0	0	8	4	16	0
Collembola	9	0	16	0	4	0	0	0	0	16	0
Collembola	10	4	0	0	16	0	0	0	0	8	0
Isopods	1	0	0	8	0	16	4	4	0	0	4
Isopods	2	0	4	0	4	0	0	0	4	0	0
Isopods	3	0	4	0	4	0	0	0	4	4	16
Isopods	4	0	0	0	0	8	0	8	12	0	0
Isopods	5	0	4	16	0	4	0	4	4	0	0
Isopods	6	0	0	0	0	8	0	0	8	0	12
Isopods	7	0	4	0	0	0	0	0	4	0	4
Isopods	8	0	0	4	0	12	0	4	12	0	40
Isopods	9	0	4	8	0	4	0	4	0	0	0
Isopods	10	0	0	0	0	32	0	4	0	0	24
Oppoliones	1	0	8	4	0	0	0	0	0	4	0
Oppoliones	2	4	0	4	20	4	0	0	0	8	0
Oppoliones	3	4	0	0	4	0	0	0	4	8	4
Oppoliones	4	4	0	4	0	0	0	0	0	0	4
Oppoliones	5	0	0	20	0	0	0	0	0	4	0
Oppoliones	6	4	0	4	4	0	0	0	0	4	12
Oppoliones	7	4	4	4	0	0	0	0	4	4	20
Oppoliones	8	0	0	0	0	0	0	0	4	4	8
Oppoliones	9	0	0	0	0	0	0	0	0	4	16
Oppoliones	10	0	0	0	0	4	0	0	8	4	4