Succession of Mite Assemblages (Acari, Mesostigmata) during Decomposition of Tree Leaves in Forest Stands Growing on Reclaimed Post-Mining Spoil Heap and Adjacent Forest Habitats

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Abstract: Mites significantly contribute, prevalently by vertical movement, to mixing of the organic layer with the mineral soil, thus they may be important in renewing soils. Our aim was to analyze the changes in abundance and species richness of mesostigmatid assemblages on decomposing leaves of *Alnus glutinosa* (L.) Gaertn., *Betula pendula* Roth, *Pinus sylvestris* L. and *Quercus robur* L. in pine and birch stands growing on a reclaimed spoil heap and adjacent forests. In December 2013, 1024 litterbags (mesh size = 1 mm) containing leaf litter of broadleaved and coniferous trees (mean initial dry weight per sample = 5.789 g) were laid out in the same number and kind in each of the two sites. Mites were extracted from litterbags which were collected every 3–6 months for 3 years. In total, 6466 mites were identified in 59 taxa. Total abundance was higher on forest habitats (5174 specimens) compared to the spoil (1292), and in birch compared to pine stands, both in forest (3345, 1829, respectively) and spoil habitats (981, 311). Throughout the experiment, mites were most abundant on oak litter samples (2063 specimens), while the remaining litter types had similar abundances (1455–1482). At the beginning of the experiment (3–6 months) mite abundance was very low, but was higher on forest habitats. The highest abundance was found after 9 months—144 specimens in pine stands on the spoil heap and 685 in birch stands on forest habitats. During the study, 49 taxa were found on forest and 29 on heap habitats. In birch stands, 37 and 22 taxa were found, whereas in pine 30 and 21, on forest and heap, respectively. The most frequent species on the heap were *Amblyseius tubae* Karg, *Asca bicornis* Canestrini et Fanzago, and *Asca aphidioides* Linneaeus, whereas in forest habitat—*Zercon peltatus* C.L. Koch, *Veigaia nemorensis* C.L. Koch, and *Trachytes aegrota* C.L. Koch. Habitat conditions, tree species and litter type significantly determined the mesostigmatid species composition, richness and abundance. By selection of dominant tree species during afforestation, it is possible to significantly affect the soil fauna composition, and thus indirectly the rate of decomposition.

Keywords: post-mining site; Gamasida; litterbags; soil mesofauna; colonization; afforestation; soil reclamation; leaf degradation; organic matter

1. Introduction

The breakdown of dead organic matter, i.e., decomposition, is the basic biogeochemical process, consisting of the physico-chemical and biological degradation of organic matter, which results in the

circulation of macro- and microelements in ecological systems [1–3]. Despite the key importance of this process for the functioning of life on the Earth, our knowledge of it is still fragmented [4], particularly with regard to the course of decomposition in disturbed ecological systems [1,4].

The soil, more precisely soil substrate, on post-mining sites (e.g., external dumps), differs significantly from forest soils, in structural, physical, chemical and biological parameters [5]. The characteristic features of soils such as structure of the soil profile, appropriate water and air conditions [6], amount of organic matter [7] and high microbiological activity are absent [5]. However, thanks to the specific conditions that arose as a result of human activity on degraded sites subjected to reclamation, these areas may be potential habitats for many species of animals [8–11], including mites [12–14]. Colonization of post-industrial areas by invertebrates, such as mites, undoubtedly supports soil-forming processes, but the scale of this process is still insufficiently recognized [14].

One of the taxonomic groups that exists in the top layer of soil and significantly contributes to circulation of organic matter in various ecological systems are mites (Acari) [15]. Their presence is observed in all soil layers; however, distinct differences in species composition of zoocenoses which they create were noticed, along with changes in depth of the soil profile [16,17]. This is conditioned on behavioural traits of soil mites such as methods of feeding or types of movements [18]. Although the soil mites are not always considered to mix the soil mechanically, their vertical movement in the soil may contribute to the mixing of the top organic layer with the mineral soil substrate [17,19].

One of the rich species groups among acarofauna is mesostigmatid mites (Mesostigmata = Gamasida) [20], among which can be distinguished parasitic [21] or free-living forms [22]. Within the order Mesostigmata, most mite species are predators, such as the suborder Gamasina [23], with the exception of a few species from the families Rhodacaridae, Ameroseiidae and Aceosejidae [19]. Predatory gamasid mites feed mainly on nematodes (Nematoda), Collembola, potworms (Enchytraeidae) and insect larvae (Insecta) [22], which contribute to the shredding of dead organic matter, thus affecting the rate of litter decomposition [3]. Vreeken-Buijs and Brussaard [24] proved that the decomposition rate was predator controlled. In general, mesostigmatid mites (predominantly as predators) do not directly affect soil processes, such as breakdown of dead organic matter, but they have real and direct influence on other soil organisms [19], e.g., fungivorous springtails [25] or herbivorous oribatid mites (Oribatida), which are the dominant mite group in the soil [22]. Due to their ecological and behavioural traits, gamasid acarofauna are located at the ends of trophic chains and are often used as a tool for bioindication or ecological monitoring of disturbed habitats [26].

Many aspects of how soil organisms influence the rate and course of ecological soil processes on industrial and post-industrial sites have been studied. However, a literature survey suggests that there are only a few papers on gamasid mite assemblages on disturbed and reclaimed mine habitats. For example, Koehler [27] and Koehler and Melecis [28] conducted their research on a rubble and debris dump. Their studies proved that specific climate conditions and successional changes of vegetation are correlated and significantly affect the structure, species composition and abundance of gamasid assemblages. Mesostigmatid mites have also been studied on a post-industrial power plant waste dump, as well as coal, zinc, lead or dolomitic dumps [29–31] or on a brown coal external spoil heap [32–34]. These investigations revealed that structure and species composition of mite assemblages is highly dependent on the habitat type and site in which they occur. For example, Madej and Skubała [30] and Piasta et al. [34] found significant differences in mite assemblages between degraded sites and surrounding forest stands. Moreover, it was found that the tree species composition of forest stands growing on reclaimed sites also significantly affected the number of mites and species composition [32].

The effects of the soil organisms that occur and their interactions on the breakdown of dead organic matter has been minimally examined. For instance, decomposition of leaves of 14 tree species was examined in relation to earthworms (Lumbricidae) [35–37] or other edaphic groups, e.g., nematodes, oribatids and predatory mites from the order Mesostigmata [37,38] in a common

garden experiment, where results have revealed that species richness and diversity of investigated soil fauna were significantly affected by the release rate and amount of micro- and macroelements, light availability in the understory or decomposition rate. Furthermore, Gergocs and Hufnagel [39] suggested that the quality of forest litter determined the density of microarthropods; however, Fujii and Takeda [3] obtained results which showed that litter quality is not a primary factor controlling the distribution of microarthropods. Also, the breakdown of litter in broadleaved and coniferous forests, as it relates to microbial activity and microarthropods, was studied by Gao et al. [40]. They revealed that addition of microorganisms to the degraded soil might accelerate the development of edaphic fauna and thus indirectly affect the leaf litter decomposition rate. Moreover, Kaneko and Salamanca [41], Riutta et al. [42], Slade and Riutta [43] and Frouz et al. [10] studied the correlation between decomposition, abundance and species composition of arthropods, and their influence and role in litter breakdown processes. Kaneko and Salamanca [41] found a positive correlation between mass loss of organic matter and microarthropod abundance in mixed litter samples, but a negative correlation in single-species litter. Results obtained by Riutta et al. [42], Slade and Riutta [43] and Frouz et al. [10] revealed positive and accelerating effects of soil macrofauna on the rate of litter decomposition, regardless of the moisture conditions [42], however, macrofauna did not significantly affect the rate of soil mineralization [10].

The decay of dead organic matter on post-industrial lands was also analyzed in a few studies (e.g., [7,44–46]), but studies linking litter decomposition and edaphic fauna, particularly on disturbed or degraded habitats, are still lacking. Only a few publications touch the problem of breakdown of dead organic matter in forest stands growing on post-industrial or degraded habitats in the context of soil organisms. The previous investigations concerned and examined the characteristics of microbial communities at initial habitats of volcanic [47] or post-mining soils [48]. For example, Frouz [8,9] and Dunger et al. [12] studied the relationships between soil organisms and breakdown processes of leaf litter on reclaimed and unreclaimed post-mining sites and they revealed that investigated soil fauna, the quality, distribution, abundance and composition of assemblages, significantly depends on site and decomposing litter features. Moreover, Frouz [8,9] have proved that macrofauna significantly affect the decomposition and removal of dead organic matter from the surface to the deeper mineral layer, but do not affect the mineralization processes.

Numerous research works which considered the soil fauna and litter decomposition lasted for one year [8,9,15,42,43]. However, some studies lasted only 30 weeks [48], others up to 2 years [12,36,41]. There are only a few studies that lasted for a longer period. For example, Fujii and Takeda [3] studied litter decomposition in relation to microarthropods for 3 years, nevertheless, their work was based on 7 collection periods at uneven time intervals (3 and 6 months). However, most of the experiments published were based on collection periods at two [15] or three [42,43] month intervals. Among the published studies, there were few that used intervals lasting less than two months or weeks [12,48]. In some publications, such as Kaneko and Salamanca [41], Frouz [8,9], Riutta et al. [42] or Fujii and Takeda [3] there were intervals of one year, which may not fully show the connections between soil fauna and ongoing processes, such as succession of organisms.

For a better understanding of predatory mite ecology and biology, the aim of our research was to analyze the rate of succession of mesostigmatid mite assemblages on the decomposing leaves of alder (*Alnus glutinosa* (L.) Gaertn.), birch (*Betula pendula* Roth), pine (*Pinus sylvestris* L.) and oak (*Quercus robur* L.) in pine and birch stands growing in different habitat conditions—on reclaimed post-mining sites and forest. All the tree species studied are widely used in reclamation of post-mining habitats and they are differentiated in their ecological features. We hypothesized that (1) habitat type (spoil heap vs. forest habitat) and stand type (birch and pine) would significantly affect the abundance and species richness of mite assemblages on decaying litter. We assumed that abundance as well as species richness would be lower on spoil heap areas compared to adjacent forest habitats, (2) in both *P. sylvestris* and *B. pendula* stands. Moreover, we hypothesized that (3) mite assemblages would differ significantly among pine and birch stands within the habitat types studied. Additionally, we assumed that (4) the

leaf litter type (alder, birch, oak, pine,) would significantly affect the assemblages of predatory mites. Along with decomposition, (5) the abundance and species richness would differ significantly among collection dates, with the highest values in the middle of the period studied.

2. Material and Methods

2.1. Site Description and Experimental Design

The study was conducted on the external spoil heap of the "Bełchatów" lignite mine (Mount Kamieńsk, Central Poland; 51.2151, 19.4345) and in the surrounding forests managed by the State Forests, representing different habitat types. Growing season length for this region is 210–220 days [49]. Average annual precipitation for this location was 665 mm and the annual air temperature was 8.65 °C during 1995–2015 (data for the nearest meteorological station, i.e., 51.4319, 19.2353, 179 m a.s.l.).

On both habitat types (spoil heap and forest, hereafter known as SH and FH, respectively), four pure stands were selected for further investigation, i.e., two silver birch (*Betula pendula* Roth) and two Scots pine (*Pinus sylvestris* L.) stands, hereafter known as Bp and Ps, respectively. The studied stands in both habitats grow in close vicinity to each other (up to 6 km). For comparison of ecological features they had to meet the following criteria: same species, similar age, identical soil granulometry, and comparable stand structure. Because of initial soil substrates on the spoil heap it was inherently hard to meet all the mentioned criteria. This is the reason that two of the birch stands are relatively close to each other (Table A1). The external spoil heap has a relative altitude of ca. 190 m above the surrounding landscape [50], and was formed during 1977–1993 [51]. The total area of the spoil heap is 1471 ha, which is the largest post-industrial area in the Centro-European Lowlands [49]. The soil substrate of the spoil heap is very differentiated from surrounding habitats. It is poor in nutrient contents and organic matter, and contains toxic Tertiary substrates elements in some places on the top [49]. The most frequent soils are Quaternary loamy, gravelly sands which sporadically comprise loam and clays. Highly acidic (pH < 4.5) Tertiary sandy strata with clay and loam inclusions also occur on the spoil heap [52].

Almost the whole reclaimed spoil heap, which was recultivated with trees, is afforested and 54% covered by young stands 26–31 years old (data for 2016) [46]. The most common herbaceous species in the herb layer were *Calamagrostis epigejos* (L.) Roth, *Dactylis glomerata* L. (abundant in birch plots, occasionally in pine plots), *Festuca rubra* L. (abundant in birch as well as in pine plots) and *Taraxacum officinale* F. H. Wigg. group (occasionally in birch, as well as in pine plots) [53]. In the herbaceous layer of research plots located on adjacent forest habitats the dominant vascular plant species were *Carex ovalis* Good. (abundant in birch plots, occasionally in pine plots), *Vaccinium myrtillus* L. (abundant in pine plots) and *Moehringia trinervia* (L.) Clairv. (occasionally in birch plots), whereas mosses were *Brachythecium rutabulum* (Hedw.) Schimp. (abundant in birch plots, occasionally in pine plots), *Polytrichastrum formosum* (Hedw.) G.L.Sm. (occasionally in birch and pine plots) and *Atrichum undulatum* (Hedw.) P.Beauv. (occasionally in birch plots) [45].

The experiment lasted for three years and was performed between 2013 and 2016. In December 2013, fiberglass litterbags containing oven-dried (dried at 65 °C) fallen leaves (mean initial dry weight = 5.789 g) of one of the four tree species (alder, birch, oak and pine), which were collected ex situ in the autumn of the same year, were laid out on the study plots. The number of research plots was 8 (2 plots per habitat type—stand type variant) (Table A1). Mesh size of the litterbags (1 mm) was chosen so that individuals of the investigated group of soil fauna moved freely through the mesh and had full access to leaf organic matter [8]. We tried to mirror the natural way in which litter is decomposed just after falling onto the forest floor. The samples were laid out in randomly chosen rows. All litter used was collected in such a way as to maintain homogeneity and equality of the research material. The samples were displayed on uncovered mineral soil substrate in stands devoid of organic layers or on the fibric soil horizon in stands where the presence of a litter layer was noted.

Overall, 1024 litterbags with leaves were laid out in an equal number to be collected at eight collection dates (128 samples: 2 habitat types × 2 stand types × 2 plots × 4 litter types × 4 samples per litter type). As a result of external factors, such as wildlife activity, eight samples were destroyed and omitted from further analysis. During our experiment, the litterbags were collected after 3, 6, 9, 12, 18, 24, 30 and 36 months after exposure on the plots. After extraction of soil invertebrates (see paragraph 2.2.), in order to determine the rate of decomposition, leaves were dried at 65 °C to obtain a constant dry mass, then the mass loss was determined in relation to the initial litter mass in every litterbag [54].

2.2. Soil Mite Investigation

Mites were extracted from litter samples using Berlese–Tullgren funnels with a 2 mm mesh size. The temperature and moisture gradient in the funnels forced soil fauna to move down, directly into containers with 75% ethyl alcohol. The extraction process of edaphic fauna lasted a minimum of 6 days, until the collected samples were completely dry. Mesostigmatid mites were separated from other soil organism groups, previously extracted from litter samples, sorted under a stereomicroscope and put into 85% lactic acid for a minimum of 3 days to ensure maximum transparency of selected specimens. Furthermore, the mite specimens were identified to genus and species level and also all developmental stages were counted using acarological keys.

Additionally, in order to determine the ecological features of species composition within the habitats and stand types studied, we used the selection of mite species into exclusive, core and common taxa after Kamczyc et al. [55]. Core species were taxa which occurred on all habitats and stand types investigated, whereas exclusive species refer to taxa which were present in only one stand type. Common species were taxa inhabiting and indicated from a minimum of two stand types. Similar divisions were made by Skubała [56], and Ulrich and Zalewski [57].

2.3. Statistical Analysis

Two-way analysis of variance (ANOVA) assuming zero inflated Poisson distributions (ZI Poisson) was conducted to determine the influence of factors studied (habitat type, stand type, litter type and collection month) on mesostigmatid mite abundance and species richness. We calculated the mean number of mite individuals and mean number of species per sample. We were able to compare 1016 observations with the factors examined. Results were considered significant when $p < 0.05$. In addition, Tukey's HSD (honestly significant difference) test was used to determine the similarity and differences between the averages obtained. Additionally, we conducted correspondence analysis (CA) for the 25 most numerous mite taxa ($n > 10$) to show site preferences, as well as the correlation of occurrences of mite taxa and environmental types (habitat type and stand type) [56,58]. Statistics were done with the software package JPM Pro 13 (https://www.jmp.com; SAS Institute Inc. Cary, NC, USA).

3. Results

3.1. Mite Abundance

In total, 6466 mite individuals were recorded. Overall, higher total abundance was recorded from stands growing in FH (5174 ind. = individuals) than from the SH (1292). Total number of mite individuals was higher in Bp in comparison with Ps stands, both in FH (3345 vs. 1829 ind., respectively) and SH (981 vs. 311). The highest total number of mites was found in litterbags with oak litter (2063 ind.), whereas for other litter types total abundance was similar (interval: 1455–1482). In Bp growing in FH, total mite abundance was 6.7 (alder), 5.1 (pine), 3.6 (birch) and 1.9 (oak) fold higher than on the SH. In Ps stands growing in FH, total mite number was 8.7 (alder), 7.3 (birch), 4.8 (oak) and 4.7 (pine) fold higher than on the SH (Table A2). In each collection date, the total mite abundance was highest in Bp stands growing in FH; only after 2 years from the beginning of the experiment, were there similar total abundances in Ps and Bp stands growing in FH (358 and 350 ind., respectively). Single specimens were found only after 3 and 30 months from the beginning of the experiment in

Ps stands on both habitats, as well as in Bp stands on the SH. After 6 months from the beginning of the study no mites were found on the SH. Altogether, the highest total number of mites was found 9 months after establishment of the experiment (1817 ind.), whereas the lowest numbers were found after 3 and 30 months (295 and 216, respectively) (Figure 1).

We found a statistically significant influence of all examined factors on mean number of mite individuals per sample (habitat type (HT)—$p < 0.0001$, stand type (ST)—$p = 0.0077$, collection month (CM)—$p < 0.0001$, litter type (LT)—$p = 0.0374$). Considering the interaction between collection month (CM) with other factors (HT, ST, LT), all interactions significantly influenced the total number of mites per sample (CM × LT—$p < 0.0001$, CM × HT—$p < 0.0001$, CM × ST—$p < 0.0001$) (Table 1). Mean mite abundance per sample was significantly higher in FH (10.13 ± 0.36 ind.) in comparison with the SH (2.53 ± 0.36). Higher mean number of mite individuals per sample was recorded from Bp stands (13.07 ± 0.50 ind. for FH and 3.85 ± 0.51 for SP) in comparison to Ps stands (7.20 ± 0.51 and 1.22 ± 0.50, respectively). Among litter types, mean mite numbers were significantly higher only for oak litter (8.07 ± 0.50 ind.), while alder (5.80 ± 0.51), pine (5.73 ± 0.51) and birch (5.73 ± 0.50) had similar mean mite abundance per sample. Overall, considering the time factor (collection month), the highest mean abundance per sample was recorded in the 9th month after the beginning of the experiment (14.12 ± 0.71 ind.), while the lowest value was found in the 30th month (1.69 ± 0.71) of the study.

3.2. Mite Species Richness

In general, higher total numbers of mite species were found in FH (49 taxa) than on the SH (29). Moreover, higher values were recorded from Bp stands (37 species) in comparison to Ps stands (30) in FH. On the other hand, on the SH, the total number of species recorded was similar between Bp and Ps stands, with 22 and 21 species, respectively. The highest number of species was found for oak litter (43 taxa), whereas the least was for alder litter (33). Pine and birch litter had the same total number of taxa (39) (Table A3). Additionally, total species richness in pooled data ranged from 7 species (3rd month) to 38 species (9th month). A similar pattern was observed for habitat types separately. Total species richness varied from 6 species (3rd month) to 31 species (9th month) in FH, whereas on the SH it varied from 3 species (3rd month) to 19 species (9th month) (Figure 2).

We did not find statistically significant influences of habitat type ($p = 0.2379$), stand type ($p = 0.8752$), or litter type ($p = 0.9633$) on mean number of species per sample. Only collection month (CM) had a significant influence ($p = 0.0281$). However, statistical analysis did not show statistically significant influences of interactions between time (CM) and the factors examined (CM × LT—$p = 0.9673$, CM × HT—$p = 0.3371$, CM × ST—$p = 0.8126$) on mean number of species per sample (Table 1). Overall, the mean number of mite taxa per sample differed between the habitats studied. Higher mean number of species per sample was recorded in FH (2.55 ± 0.06 taxa) compared to SH (0.77 ± 0.06). Moreover, higher mean number of species per sample was recorded from Bp stands (3.31 ± 0.08 taxa in FH and 0.91 ± 0.08 on SH) in comparison to Ps stands (1.77 ± 0.08 and 0.63 ± 0.08, respectively). We also noted that the highest mean number of taxa per sample was for oak litter (1.84 ± 0.08 taxa), while the lowest value was recorded in birch litter (1.51 ± 0.08). A Tukey test showed that both these types of litter were significantly different from alder (1.55 ± 0.08 taxa) and pine litter (1.71 ± 0.08). Furthermore, the highest mean number of mite taxa per sample was recorded for the 9th month (3.33 ± 0.11 taxa), while the lowest value was in the 3rd month (0.21 ± 0.11). A Tukey test revealed that only the 9th collection month was significantly different from others.
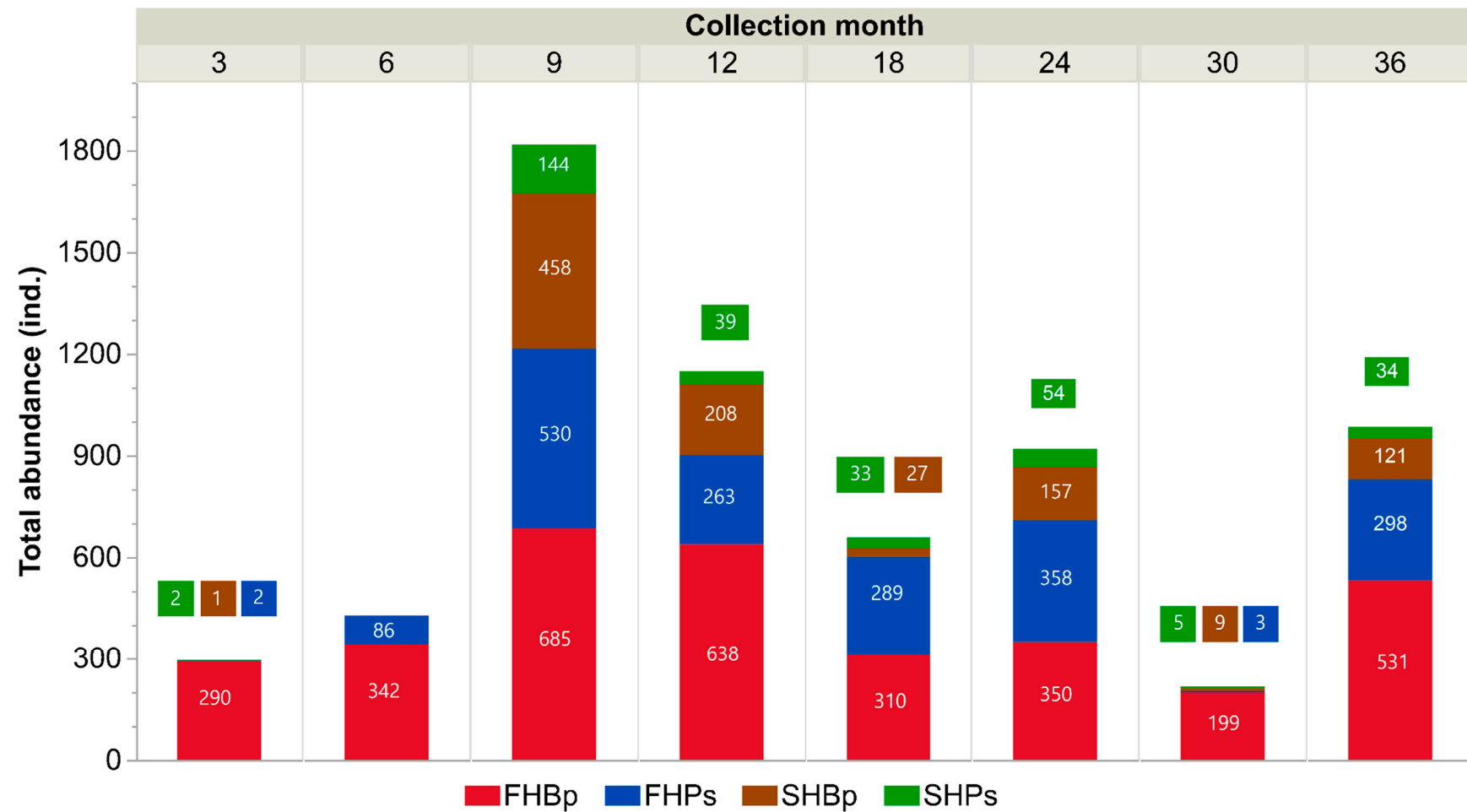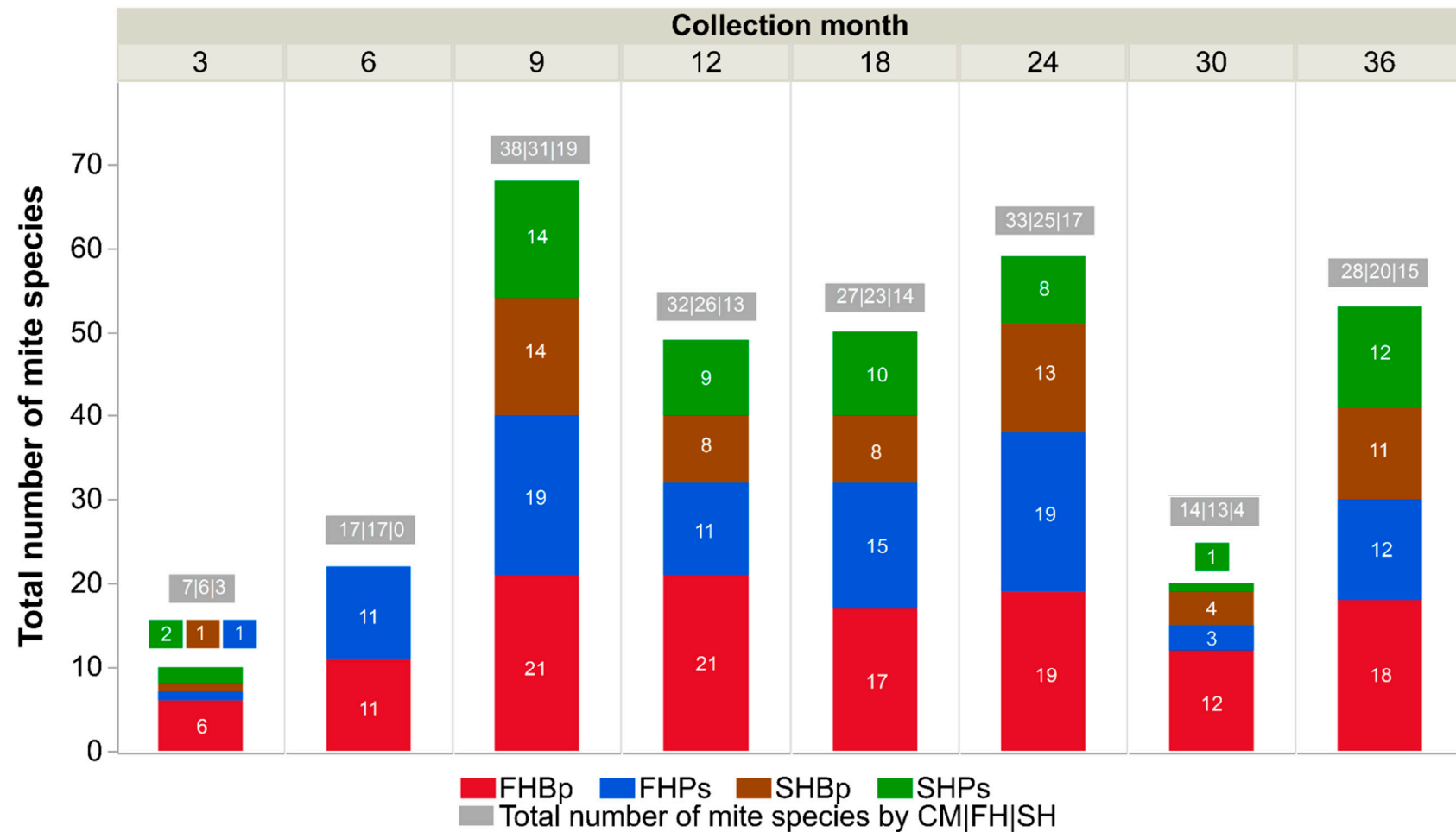
Figure 1. Number of gamasid mite individuals collected in *Betula pendula* Roth (Bp) and *Pinus sylvestris* L. (Ps) stands growing in forest habitat (FH) and spoil heap (SH) by collection month during the experiment. When total abundance was very low, we have added numbers and respective colors above the bars.

Table 1. Two-way analysis of variance (ANOVA) assuming zero inflated Poisson distributions (ZI Poisson) for mean abundance and mean species richness per sample. Abbreviations: DF—degrees of freedom, CM—collection month, LT—litter type, HT—habitat type, ST—stand type.

Fixed Factor	DF		Wald Chi-Square		Prob > Chi-Square	
	Abundance	Species Richness	Abundance	Species Richness	Abundance	Species Richness
CM	7	7	141.972	15.689	<0.0001	0.0281
LT	3	3	8.461	0.282	0.0374	0.9633
HT	1	1	22.590	1.393	<0.0001	0.2379
ST	1	1	7.111	0.025	0.0077	0.8752
CM × LT	21	21	78.628	10.756	<0.0001	0.9673
CM × HT	7	7	1365.612	7.949	<0.0001	0.3371
CM × ST	7	7	69.675	3.709	<0.0001	0.8126
LT × HT	3	3	6.848	2.115	0.0769	0.5489
LT × ST	3	3	10.256	1.578	0.0165	0.6644
HT × ST	1	1	0.797	1.159	0.3719	0.2818
CM × LT × HT	21	21	917.881	14.963	<0.0001	0.8248
CM × LT × ST	21	21	237.841	12.251	<0.0001	0.9326
CM × HT × ST	7	7	12.618	1.931	0.082	0.9635
LT × HT × ST	3	3	5.563	1.153	0.1349	0.7644
CM × LT × HT × ST	21	21	69.846	14.247	<0.0001	0.8588

Figure 2. Total number of mite species recorded in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH). Data are shown for each collection month (CM) during the experiment. When total abundance was very low, we have added numbers and respective colors above the bars.

3.3. Mite Assemblages

In general, mite communities were dominated by *Zercon peltatus* C.L. Koch (2281 ind.) and *Veigaia nemorensis* C.L. Koch (892). The mite communities on the SH, both in Bp and Ps stands, were dominated by *Amblyseius tubae* Karg (740 ind.). In Ps stands, in terms of juvenile stadia, individuals described to the genus *Pergamasus* sp. predominated (35 ind.), while in Bp stands it was *A. tubae* (24). FH was dominated by mites belonging to *Z. peltatus* (2264 ind.). However, Bp stands were characterised by higher numbers of juvenile mite instars of *V. nemorensis* (345 ind.) and *Trachytes aegrota* C.L. Koch (323) than *Z. peltatus* (219), whose juvenile forms dominated in Ps stands (492) (Table A4).

In total, 70.6% of mites collected during the experiment were adults. In general, in mature stadia the majority were female mites (85.5%), which were the dominant form in each type of habitat and stand. For juvenile stages, deutonymphs predominated (53.9% of all juvenile forms), except for the Bp stands growing on the SH, where abundance of protonymphal forms was much higher (178.3% of deutonymphs). The larval stages were predominant in FH (204 ind.), and more larvae were found in Ps stands (145) in comparison with Bp stands (59), while on the SH only single larval stages were recorded (3) (Table A4).

We found that 8 taxa were core species (*A. tubae*, *Asca aphidioides* Linneaeus, *Leptogamasus parvulus* Berlese, *Paragamasus runcatellus* Berlese, *Paragamasus* sp., *Pergamasus crassipes* Linneaeus, *Pergamasus* sp., *Z. peltatus*), which occurred in both Bp and Ps stands and on SH and FH. In total, 32 species were described as exclusive taxa, occurring only in one type of habitat (habitat type × stand type). The highest number of exclusive species were found in Bp stands growing in FH (14 taxa), whereas the least occurred in those on the SH (3). Six common taxa were described on the SH for both types of stands, while there were 10 in the FH. The number of common mite species found in Bp stands occurring on both habitats was 7 taxa, while in the Ps stands there were 4 taxa. Among the most abundant 6 species (dominance >1%) (see Table A4), half were core species (*A. tubae*, *A. aphidioides*, *Z. peltatus*). The other 3 taxa (*Olodiscus minima* Kramer, *T. aegrota*, *V. nemorensis*) were characterized as common species (Figure 3).

As a part of previous research (2011–2013) (for more details see Piasta et al. [34]), soil samples were taken to the depth of 5 cm (steel core—40 cm^2) on the same plots included in this study, to investigate gamasid mite assemblages. The comparison of the data showed that 56.9% of total mite species identified previously in the soil samples also inhabited litterbags in our study. Comparing the SH with FH, the percentage of taxa that occurred in the top layer of soil on the plots and that also colonized the litterbags was similar, 63.0% and 58.8%, respectively. Similar SH and FH comparisons for Ps stands were 62.5% and 67.7%, and for Bp stands, 70.0% and 50.0%, respectively. Moreover, it was found that *P. crassipes* was the only species that commonly occurred in the soil on all research plots, regardless of HT and ST, and also inhabited decomposing litter.

The correspondence analysis (CA) revealed that there were differences in the site (HT and ST) preferences of indicated species (Figure 4). Axis 1 and 2 explained 62.6% and 21.4% of variance, respectively. Based on the CA diagram, it can be noted that only two species, *Veigaia cervus* Kramer and *Pergamasus septentrionalis* Oudemans, were not characterized by evident preferences for type of habitat. However, *V. cervus* prefers Ps stands, while *P. septentrionalis* prefers Bp stands. The taxa which preferred FH and Ps stands were *Z. peltatus*, *Trichouropoda ovalis* C.L. Koch, *Paragamasus* sp., *L. parvulus*, *Paracercon radiatus* Berlese and *Prozercon kochi* Sellnick. At the same time, the last three species evidently preferred Ps stands in comparison to Bp stands growing in FH. On the other hand, species that preferred Bp stands in FH were: *Paragamasus jugincola* Athias-Henriot, *V. nemorensis*, *T. aegrota*, *O. minima*, *Epicriopsis horridus* Kramer, *Iphidiozercon gibbus* Berlese, *Veigaia planicola* Berlese and *P. runcatellus*. On the SH, there were taxa that strongly preferred Bp stands, i.e., *Amblyseius* sp., *A. tubae* and *Asca bicornis* Canestrini et Fanzago, while Ps stands were the preferred habitat of *P. crassipes*, *Hypoaspis praesternalis* Willmann and *Arctoseius insularis* Willmann. Despite their numerous occurrence on the SH area, *Pergamasus* sp., *Paragamasus conus* Karg and *A. aphidioides* were characterized by high preferences towards the FH (Figure 4).

Our results revealed that the colonization rate of litterbags varied. Comparing the habitat and stand types in terms of succession of the most abundant species among stand types (Dominance > 1%), it can be noted that the colonization of decaying litter occurred faster in FH compared to the SH. Only in FH were species recorded that were present throughout the whole duration of the experiment. These species were *Z. peltatus* in Ps stands, and *V. nemorensis*, *T. aegrota* and *Z. peltatus* in Bp stands. Among the dominant taxa for a given stand and habitat type, only *Z. peltatus* (Ps stands in FH) and *A. tubae* (Bp stands on the SH) were dominant throughout the entire duration of the experiment. In Ps stands growing on SH it was noted that a different mite species prevailed at each collection month, omitting a single specimen of *A. insularis* in the 3rd collection month. Moreover, in Bp stands growing in FH *Z. peltatus* dominated only in the 3rd, 6th and 24th, 30th collection months, while in the middle months (12th,18th) and in the last month (30th), the dominant species was *V. nemorensis*. Abundance and species richness of mite assemblages in the culmination month (9th month), differed in each stand type within habitat types. Bp stands were dominated by *T. aegrota* and *A. tubae*, while Ps stands by *Z. peltatus* and *A. bicornis*, in FH and SH, respectively. The critical point in the succession of mite assemblages was the 30th month of the study, when only in the Bp stands in FH were all of the six most abundant species in the stand type recorded (Table A5).
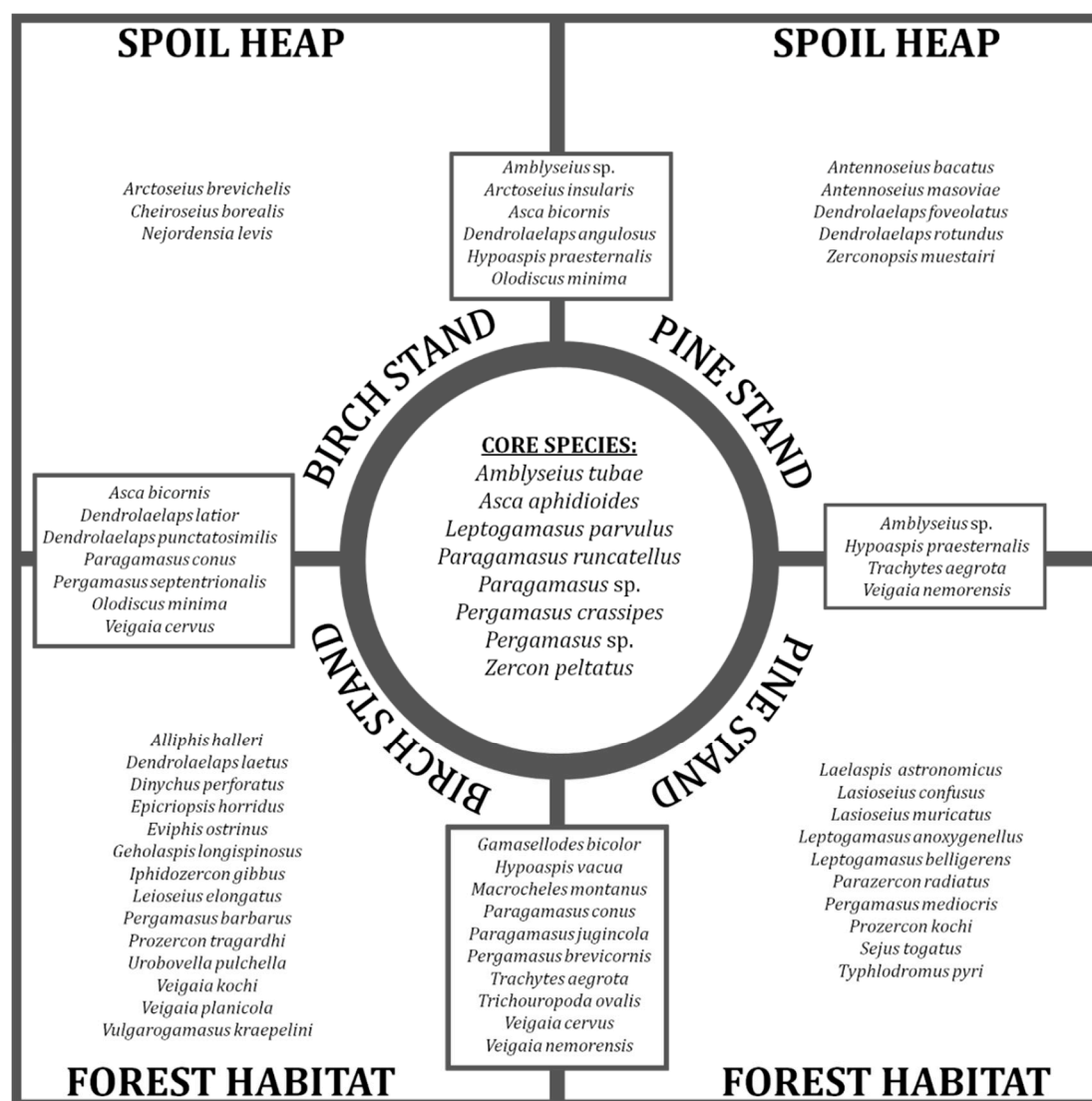
Figure 3. Core, exclusive and common (in frames) mite species in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH).
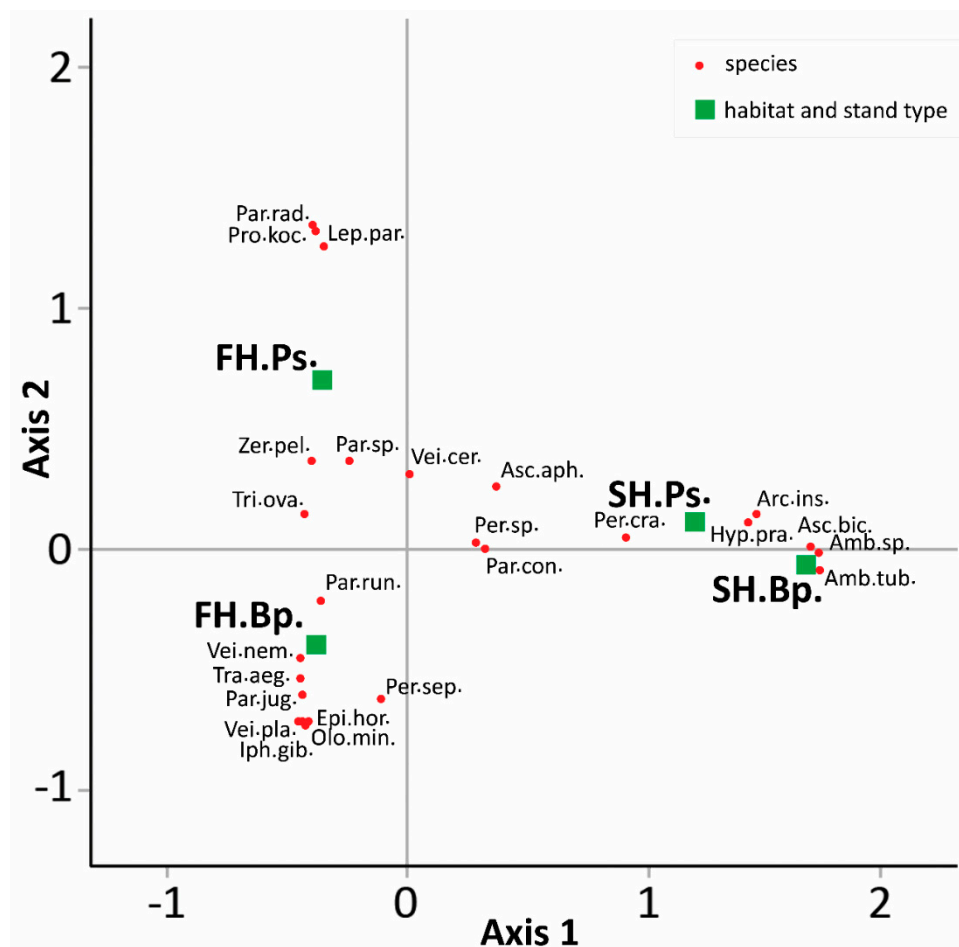
Figure 4. Correspondence analysis (CA) ordination diagram for the 25 most numerous mite taxa (*n* > 10). Habitat types are separated along Axis 1, while stands types are separated along Axis 2. Abbreviations: FH.Bp.—forest habitat-birch stand, FH.Ps.—forest habitat-pine stand, SH.Bp.—spoil heap-birch stand, SH.Ps.—spoil heap-pine stand, Amb.sp.—*Amblyseius* sp., Amb.tub.—*Amblyseius tubae* Karg, Arc.ins.—*Arctoseius insularis* Willmann, Asc.aph.—*Asca aphidioides* Linneaeus, Asc.bic.—*Asca bicornis* Canestrini et Fanzago, Epi.hor.—*Epicriopsis horridus* Kramer, Hyp.pra.—*Hypoaspis praesternalis* Willmann, Iph.gib.—*Iphidiozercon gibbus* Berlese, Lep.par.—*Leptogamasus parvulus* Berlese, Par.con.—*Paragamasus conus* Karg, Par.jug.—*Paragamasus jugincola* Athias-Henriot, Par.rad.—*Parazercon radiatus* Berlese, Per.run.—*Pergamasus runcatellus* Berlese, Par.sp.—*Paragamasus* sp., Per.cra.—*Pergamasus crassipes* Linneaeus, Per.sep.—*Pergamasus septentrionalis* Oudemans, Per.sp.—*Pergamasus* sp., Pro.koc.—*Prozercon kochi* Sellnick, Tra.aeg.—*Trachytes aegrota* C.L. Koch, Tri.ova.—*Trichouropoda ovalis* C.L. Koch, Olo.min.—*Olodiscus minima* Kramer, Vei.cer.—*Veigaia cervus* Kramer, Vei.nem.—*Veigaia nemorensis* C.L. Koch, Vei.pla.—*Veigaia planicola* Berlese, Zer.pel.—*Zercon peltatus* C.L. Koch.

4. Discussion

We found a statistically significant influence of collection month on abundance and species richness of gamasid assemblages, whereas habitat type, stand type and litter type had a significant influence only on mesostigmatid abundance. Also, we revealed significant changes in species composition of gamasid community structure involved with the decomposition process during the period studied. Lower total abundance and number of taxa were recorded from the SH (20% of total abundance, 29 taxa) in comparison to the adjacent FH (80%, 49 taxa). Similar results were obtained in research investigating orbibatid mite assemblages by Murvanidze et al. [14] and Skubała [56], which also proved the negative influence of sand-manganese and coal mine dumps, respectively, on

abundance and species richness compared with surrounding forests. Skubała [56] indicated 3 times higher mean abundance in adjacent forests in comparison to the highest recorded values on dump sites studied, whereas Murvanidze et al. [14] found that 40% of taxa (35 of 89 species) occurred only in adjacent forests compared with degraded sites. This may be explained by the fact that colonization rate is limited and impeded on newly formed soils [13]. Soil biological activity on degraded lands is relatively low [33,59] due to disturbed structure of the soil profile, and lack of appropriate water and air conditions [6] or amount of organic matter [7], whereas on undisturbed habitats, such as forest habitats, the upper layer of soils may be well covered by a litter layer [60] or vegetation which can be important buffers in ecologically stressful situations, for example droughts [19].

Likewise, we recorded a significant influence of stand type growing on both investigated habitats on mite assemblages, and proved the higher abundance and species richness in Bp stands in comparison to Ps stands. Our results are in line with previous investigations. For example, Mueller et al. [37] revealed that type of tree (evergreen or deciduous) and tree species significantly affected abundance and diversity soil invertebrate assemblages; however, they did not record significant differences in taxa richness for gamasid mite assemblages which potentially could have been affected by the factors examined. Also Skorupski [38] found significant differences between the stand types studied. He reported the highest species number in silver birch stands, whereas the lowest (half that in birch stands) occurred in coniferous stands of Douglas fir (*Pseudotsuga menziesii* (Mirb.) Franco). On the other hand, Gonzalez et al. [61] compared lodgepole pine (*Pinus contorta* Dougl. ex Loud.) and aspen (*Populus tremuloides* Michx.) stands. Their investigation showed that there was no significant influence of forest type on microarthropod density. Nevertheless, they revealed higher relative density of macroarthropods and earthworms per square meter in broadleaved stands than in coniferous stands. Also Pastwik et al. [32] reported that deciduous stands create better microclimate conditions for mite assemblages in comparison with coniferous stands; however, they revealed the highest total abundance from Scots pine stands (31% of total mite numbers). Differences between arthropod groupings occurring in varied habitats and stands could be related to site features and variables in the microenvironment, e.g., litter carbon concentration, nitrogen content [62], soil and litter temperature or moisture [42] which depend on tree species that dominate a given stand [35,36,38].

We also recorded that the number of species was not influenced by litter type. Those results are in contrast to investigations of Frouz [9] and Fujii and Takeda [3], who proved the significant influence of characteristics and type of litter on macrofauna and various groups of microarthropods, respectively. Moreover, the removal of litter layer was also found to reduce mite community richness and abundance [63]. Surprisingly, we found impacts of litter type on mite abundance which is in line with the cited authors [3,9]. However, in our study total mite abundance on decomposing pine needles was similar to birch and alder leaves. This is in contrast to Gonzalez et al. [61] who revealed two times higher mite density (three times higher for gamasid mites) from broadleaf litter in comparison with pine needles. Furthermore, Kaneko and Salamanca [41] also reported 2.5 times higher gamasid abundance, or even three times higher in the second year of investigation, from oak litter compared to pine needles. They also revealed that litter structure might affect litter microclimate, and they also showed significant differences in microarthropod assemblages depending on litter type and whether the litter was single- or mixed-species. Likewise, the fact that in our experiment the oak litter was significantly different from other leaf types might be explained by its different lignin content [64] or a different decomposition rate, which depends on lignin content, as well as micro- and macroelements [36,54]. According to Osler et al. [65] decomposition rate is strongly correlated with microarthropod assemblages, however, only after 20% litter mass loss of the initial weight. Thus, the rate of decomposition can strongly differentiate the abundance and species richness of mite communities. Research conducted by Horodecki and Jagodziński [46] revealed that the decomposition rate of oak litter is the slowest among the examined litter types. Thus, a statistically significant, higher colonization rate of oak litter in comparison with other litter types studied, revealed in our study, might result from slower degradation rate of oak leaves compared to other leaf litter. Thus, as we

assume, this may be associated with longer periods of habitation by soil organisms, which take a direct part in decomposition and are also part of the foodweb for predatory gamasid mites [3,19].

Altogether, the data obtained showed that with the passage of time (CM factor), and thus along with the ongoing decomposition, the abundance and species richness of mite assemblages changed significantly. However, we did not record the highest values for abundance and species richness in the middle of the period studied. The highest values were recorded in the 9th month after leaf litter samples were placed on the plots, and declines were recorded in the 30th collection month. This is opposite to the results obtained by Gonzalez et al. [61], who reported the initial increase, then the highest values in the middle of the two-year study period and the final decline in density of the soil fauna examined. Nonetheless, in research conducted by Osler et al. [65] the highest values of mite individuals and species per sample were found in the initial phases of the succession investigated, which coincides with results of this study. Furthermore, Berg et al. [16] obtained results similar to ours. They reported that, along with progressive litter decay, more precisely pine needles, there was an initial rapid increase in the density of predatory mites per square meter, and then a decrease in the number of specimens of predatory mites. However, as in our research, Berg et al. [16] noted a rapid drop in abundance of the mite group studied in one collection month, which they supposed was caused by the occurrence of drought in the study area. This violent collapse is in line with our results (see 30th collection month) where a rapid drop in recorded abundance of gamasid specimens also occurred. However, it was not affected by severe changes in decomposition rate of the litter type samples studied [54], but it might be a result of high average temperature (18.6 °C) and low precipitation (monthly precipitation sum = 67.5 mm) (data for the nearest meteorological station, i.e., 51.4319, 19.2353, 179 m a.s.l.) in June 2016, and thus it might be a differences in soil moisture and aeration conditions [19,65]. In general, we also assumed that our results might be explained by the diversified rates of litter degradation [46], and thereby changes in the complexity of microenvironments within the decomposing leaves, which, as reported by Schmidt [66], affect the distribution of mites. In our results, it might also be explained by decreasing mass of litter used in litterbag samples [54]. Furthermore, the abundance and species richness of gamasid mites might also depend on the presence/absence of their prey, e.g., springtails, oribatids or nematodes [19]. The density of oribatid mites, as was reported by Maraun and Scheu [67], increases with the litter thickness. Also, Erdmann et al. [68] reported slower changes in oribatid assemblages which, as they supposed, may be caused by slow changes in structure of assemblages of bacteria and fungi, or the colonization rate of macrofauna. Vreeken-Buijs and Brussaard [24] proved that the decomposition rate was predator controlled. Moreover, they found that litterbags were colonized by bacterivorous nematodes and nematophagous mites in the first phase of decomposition, whereas only in the later phases were they colonized by predatory mites and fungivorous or omnivorous springtails and mites. This is in line with our results where, during the first phase of decomposition in FH (3rd, 6th and 9th collection month), we recorded an increase in abundance and numerous occurrences of *Zercon peltatus* C.L. Koch specimens, a predatory mite species belonging to the nematophagous Zerconidae family. Afterwards, in the following collection months, the number of individuals of other predatory mite taxa increased and *Z. peltatus* individuals declined, probably due to decreasing abundance of nematodes in litterbags. The diversified degree of settling or compaction of samples or different rates of colonization might be a result of biological characteristics and species ecology of mite taxa which create communities [20,29,33]. As was reported by Maraun and Scheu [67], we cannot say that single oribatid mite species prefer one type of stand, litter or tree species. However Bonari et al. [69] revealed that there was strong relationship of oribatid mites assemblages and examined vascular plants. Skorupski [38] found that *Veigaia cervus* Kramer was most numerous in mature Scots pine stands, which is similar to the results of Berg et al. [16], who also recorded a greater number of *V. cervus* in pine stands, over 19 times higher in comparison with abundance of *Veigaia nemorensis* C.L. Koch, which is in line with our results in terms of site preferences of these taxa. However, *Pergamasus septentrionalis* Oudemans was recorded more frequently by Skorupski [38] in coniferous stands than in broadleaved stands of common oak, which is the opposite of our CA analysis

results for this species. Moreover, in this study we reported that, in terms of total abundance, the most dominant three species in Ps and Bp stands on the SH were *Amblyseius tubae* Karg, *Asca bicornis* Canestrini et Fanzago and *Asca aphidioides* Linneaeus, whereas in FH the dominant species were *Z. peltatus* and *V. nemorensis* (in both stand types), *Trachytes aegrota* C.L. Koch in Bp stands and *Leptogamasus parvulus* Berlese in Ps stands. *Z. peltatus*, *T. aegrota* and *V. nemorensis*, are species often reported from the top soil layer on forest sites. *L. parvulus* was reported from beech forests, especially from the moss and litter layer [70], whereas *A. bicornis* was classified as a pioneer mite species [22,31], often found on degraded habitats [29,34] or was classified among those species that preferred reclaimed sites [27,34]. Also, *A. aphidioides*, as revealed by Skorupski et al. [33], is a pioneer species which was reported from derelict, as well as grassy, reclaimed areas or post-coal mining sites. Furthermore, the high abundance of *A. tubae* on the SH might also be a result of the ecological characteristics and site preferences of this species. Specimens of this species occurred in herb and shrub layers in mountain rocks, as well as in the dry moss layer and lichens. Moreover, *A. tubae* individuals were reported from grass roots and humus [70]. Madej [29] reported mite individuals of *Amblyseius* sp. as pioneer organisms that were plentiful inhabitants on degraded or initial lands. Piasta et al. [34], also revealed higher abundance of mite individuals of the genus *Amblyseius* sp. on the spoil heap (in soil samples) in comparison with adjacent forests, which is in line with our results.

5. Conclusions

In conclusion, our research revealed that habitat conditions, dominant tree species of stand and litter type, significantly determine the composition and abundance, but not the species richness, of mesostigmatid mite species. On the post-mining site, the rate of colonization by mites was slower than on adjacent forest habitat, whereas species richness was also lower, notwithstanding the fact that there was no significant influence of the time factor on mean number of taxa. Nevertheless, by selecting the tree species of stands during afforestation, it is possible to significantly affect the composition of soil gamasid mites, and thus indirectly the rate of decomposition on disturbed habitats. Moreover, our research revealed that adding admixture tree species, like common oak, within pure stands of Scots pine and silver birch (which are the most commonly used tree species in reclamation of post-mining areas), will certainly accelerate soil formation processes, due to the influence of increased biological activity of the soil mesofauna occurring in the litter of admixture species, and thus reduce the reclamation time of degraded soils, which can be reflected as biological, economic and management benefits.

Appendix

Table A1. Basic characteristics of sample plots (measurements were taken in 2011 and 2012). Abbreviations: Bp—*Betula pendula* Roth, Ps—*Pinus sylvestris* L., SH—spoil heap, FH—forest habitat, CL—clay loam, S—sand, SL—sandy loam, BA—basal area at breast height, DBH—diameter at breast height, H—tree height, SE—standard error, FPMD—fresh protomoder, FPM—fresh protomor, FMD—fresh moder, FMM—fresh modermor, FM—fresh mor.

Plot No.	Coordinates	Plot Area (m²)	Stand Type	Habitat Type	Soil Texture	Humus Type	pH H$_2$O (O Layer)	Stand Age (years)	Average DBH (cm) * ± SE	Average H (m) * ± SE	BA (m² ha^{-1}) *,**	Stocking Density (ind. ha^{-1}) *,***
6	51.2207, 19.4339	604.5	Bp		CL	FPMD	6.10	22	8.87 (0.30)	9.21 (0.21)	8.54 (98.31)	1274 (74.76)
7	51.2208, 19.4339	604.5		SH	CL	FPMD	6.12	22	8.96 (0.34)	9.09 (0.22)	7.4 (95.55)	1075 (69.15)
15	51.2105, 19.4384	900.0	Ps		S	FPM	5.01	18	5.49 (0.07)	4.86 (0.04)	12.76 (99.83)	5022 (99.12)
16	51.2117, 19.4265	810.0			S	FPM	4.93	17	6.81 (0.11)	6.05 (0.05)	20.61 (99.96)	5123 (99.28)
105	51.2744, 19.4324	646.5	Bp		SL	FMD	5.55	20	10.40 (0.21)	13.66 (0.11)	15.79 (99.95)	1779 (92.00)
106	51.2747, 19.4326	450.0		FH	CL	FMD	5.57	20	10.10 (0.20)	13.44 (0.12)	18.32 (99.99)	2200 (95.19)
107	51.1738, 19.4323	750.0	Ps		S	FMM	4.68	21	8.02 (0.15)	8.90 (0.08)	23.41 (100.00)	4200 (99.68)
108	51.1746, 19.4321	750.0			S	FM	4.37	21	8.46 (0.16)	9.16 (0.08)	21.22 (99.81)	3467 (99.24)

* including only main tree species in the stand; ** in the brackets, the share of BA of the main tree species in the stand in total BA is given; *** in the brackets, the share of stocking density of the main tree species in the stand in total stocking density is given.

Table A2. Total abundance of mite individuals in four types of litter in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH).

Habitat Type	Stand Type	Litter Type				Total
		Birch	**Oak**	**Alder**	**Pine**	
FH	Bp	760	942	860	783	3345
	Ps	436	525	442	426	1829
SH	Bp	210	487	129	155	981
	Ps	60	109	51	91	311
Total		1466	2063	1482	1455	-

Table A3. Total number of mite species recorded in four types of litter in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH).

Habitat Type	Stand Type	Litter Type				Total
		Birch	**Oak**	**Alder**	**Pine**	
FH	Bp	22	23	25	26	37
	Ps	21	22	19	19	30
SH	Bp	15	19	8	16	22
	Ps	12	15	10	13	21
Total		39	43	33	39	-

Table A4. Checklist of mite species with number of individuals in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH). The "-" signs were given to make the data table more transparent and should not be equated with the lack of results. Abbreviations: F—females, M—males, D—deutonymphs, P—protonymphs, L—larvae.

No.	Species	Family	Total No. of Specimens	FH										SH									
				Bp					Ps					Bp					Ps				
				F	M	D	P	L	F	M	D	P	L	F	M	D	P	L	F	M	D	P	L
1	*Alliphis halleri* (G. et R. Canestrini, 1881)	Eviphidae	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2	*Amblyseius* sp.	Phytoseiidae	35	-	-	-	-	-	2	-	-	-	-	27	2	-	-	-	3	-	-	1	-
3	*Amblyseius tubae* Karg, 1970	Phytoseiidae	775	26	-	-	-	-	8	-	-	-	1	596	58	-	24	1	58	2	-	1	-
4	*Antennoseius bacatus* Athias-Henriot, 1961	Ascidae	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-
5	*Antennoseius masoviae* Sellnick, 1943	Ascidae	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
6	*Arctoseius brevichelis* Karg, 1969	Ascidae	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
7	*Arctoseius insularis* (Willmann, 1952)	Ascidae	45	-	-	-	-	-	-	-	-	-	-	8	-	-	-	-	32	5	-	-	-
8	*Asca aphidioides* (Linneaeus, 1758)	Ascidae	307	88	-	-	-	-	100	-	-	4	-	69	-	1	4	-	36	2	1	2	-
9	*Asca bicornis* (Canestrini et Fanzago, 1887)	Ascidae	150	1	-	-	-	-	-	-	-	-	-	75	19	-	2	-	44	8	-	1	-
10	*Cheiroseius borealis* (Berlese, 1904)	Ascidae	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
11	*Dendrolaelaps angulosus* (Willmann, 1936)	Digamasellidae	8	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	4	-	-
12	*Dendrolaelaps foveolatus* (Leitner, 1949)	Digamasellidae	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5	-	-
13	*Dendrolaelaps laetus* Shcherbak, 1980	Digamasellidae	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
14	*Dendrolaelaps latior* (Leitner, 1949)	Digamasellidae	2	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
15	*Dendrolaelaps punctatosimilis* Hirschmann, 1960	Digamasellidae	7	2	-	2	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-
16	*Dendrolaelaps rotundus* Hirschmann, 1960	Digamasellidae	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	-	-
17	*Dinychus perforatus* Kramer, 1882	Uropodiade	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
18	*Epicriopsis horridus* Kramer, 1876	Ameroseiidae	13	10	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	*Eviphis ostrinus* (C.L. Koch, 1836)	Eviphidae	4	3	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
20	*Gamasellodes bicolor* (Berlese, 1918)	Ascidae	4	1	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21	*Geholaspis longispinosus* (Kramer, 1876)	Macrochelidae	8	6	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	*Hypoaspis praesternalis* Willmann, 1949	Laelapidae	15	-	-	-	-	-	1	-	-	-	-	6	-	-	-	-	6	2	-	-	-
23	*Hypoaspis vacua* (Michael, 1891)	Laelapidae	6	2	-	-	-	-	2	1	1	-	-	-	-	-	-	-	-	-	-	-	-
24	*Iphidozercon gibbus* (Berlese, 1903)	Ascidae	18	15	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
25	*Laelaspis astronomicus* (C.L. Koch, 1839)	Laelapidae	3	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
26	*Lasioseius confusus* Evans, 1958	Ascidae	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
27	*Lasioseius muricatus* (C.L. Koch, 1839)	Ascidae	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
28	*Leioseius elongatus* Evans, 1958	Ascidae	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
29	*Leptogamasus anoxygenenellus* (Micherdziński, 1969)	Parasitidae	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
30	*Leptogamasus belligerens* Witaliński, 1973	Parasitidae	6	-	-	-	-	-	3	3	-	-	-	-	-	-	-	-	-	-	-	-	-
31	*Leptogamasus parvulus* (Berlese, 1903)	Parasitidae	112	1	1	-	-	-	44	62	1	-	-	1	1	-	-	-	1	-	-	-	-
32	*Macrocheles montanus* (Willmann, 1951)	Macrochelidae	9	5	-	2	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
33	*Nejordensia levis* (Oudemans et Voigts, 1904)	Ascidae	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
52	*Olodiscus minima* Kramer, 1882	Uropodidae	287	215	1	64	3	-	-	-	-	-	-	1	-	-	-	-	3	-	-	-	-
34	*Paragamasus conus* (Karg, 1971)	Parasitidae	12	3	2	-	-	-	3	-	-	-	-	-	4	-	-	-	-	-	-	-	-
35	*Paragamasus jugincola* Athias-Henriot, 1967	Parasitidae	72	39	27	-	-	-	1	5	-	-	-	-	-	-	-	-	-	-	-	-	-
36	*Paragamasus runcatellus* (Berlese, 1903)	Parasitidae	90	51	15	-	-	-	14	7	-	-	-	1	1	-	-	-	1	-	-	-	-

Table A4. *Cont.*

No.	Species	Family	Total No. of Specimens	FH										SH									
				Bp					Ps					Bp					Ps				
				F	M	D	P	L	F	M	D	P	L	F	M	D	P	L	F	M	D	P	L
37	*Paragamasus* sp.	Parasitidae	71	-	-	17	7	5	-	-	21	15	-	-	-	-	3	1	-	-	-	2	-
38	*Parazercon radiatus* Berlese, 1910	Zerconidae	16	-	-	-	-	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
39	*Pergamasus barbarus* (Berlese, 1904)	Parasitidae	5	-	-	4	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
40	*Pergamasus brevicornis* (Berlese, 1903)	Parasitidae	5	1	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-
41	*Pergamasus crassipes* (Linneaeus, 1758)	Parasitidae	62	9	4	-	-	-	2	4	-	-	-	9	4	-	-	-	10	19	1	-	-
42	*Pergamasus mediocris* Berlese, 1904	Parasitidae	4	-	-	-	-	-	2	1	1	-	-	-	-	-	-	-	-	-	-	-	-
43	*Pergamasus septentrionalis* (Oudemans, 1902)	Parasitidae	52	39	3	-	2	-	-	-	-	-	-	7	1	-	-	-	-	-	-	-	-
44	*Pergamasus* sp.	Parasitidae	138	-	-	20	35	2	-	-	19	11	-	-	-	8	8	-	-	-	17	18	-
45	*Prozercon kochi* Sellnick, 1943	Zerconidae	39	-	-	-	-	-	20	10	7	2	-	-	-	-	-	-	-	-	-	-	-
46	*Prozercon tragardhi* (Halbert, 1923)	Zerconidae	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
47	*Sejus togatus* C.L. Koch, 1836	Sejoidea	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
48	*Trachytes aegrota* (C.L. Koch, 1841)	Trachytidae	710	350	-	123	173	27	15	-	10	8	-	-	-	-	-	-	-	-	1	1	2
49	*Trichouropoda ovalis* (C.L. Koch, 1839)	Trematuridae	14	1	1	6	-	-	2	-	4	-	-	-	-	-	-	-	-	-	-	-	-
50	*Typhlodromus pyri* Scheuten, 1857	Phytoseiidae	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
51	*Urobovella pulchella* (Berlese, 1904)	Urodinychidae	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53	*Veigaia cervus* (Kramer, 1876)	Veigaiaiidae	114	37	-	3	2	-	26	-	20	5	-	14	-	5	2	-	-	-	-	-	-
54	*Veigaia kochi* (Trägarth, 1901)	Veigaiaiidae	2	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
55	*Veigaia nemorensis* (C.L. Koch, 1839)	Veigaiaiidae	892	432	-	223	122	-	50	-	39	25	-	-	-	-	-	-	-	-	-	1	-
56	*Veigaia planicola* (Berlese, 1892)	Veigaiaiidae	41	27	-	9	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
57	*Vulgarogamasus kraepelini* (Berlese, 1904)	Parasitidae	2	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
58	*Zercon peltatus* C.L. Koch, 1836	Zerconidae	2281	509	321	126	68	25	671	52	250	98	-	144	4	-	3	-	5	1	3	1	-
59	*Zerconopsis muestairi* (Schweizer, 1949)	Ascidae	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
				F	M	D	P	L	F	M	D	P	L	F	M	D	P	L	F	M	D	P	L
In total			6466	1881	382	602	421	59	995	147	373	169	145	826	90	23	41	1	201	45	35	28	2
				3345					1829					981					311				

Table A5. Succession and appearance of the most abundant mites species (Dominance >1%) in *Betula pendula* (Bp) and *Pinus sylvestris* (Ps) stands growing in forest habitat (FH) and spoil heap (SH). Shaded cells show the most abundant species within the collection months in each stand type.

Habitat Type	Stand Type	Species Rank	Taxon	Collection Month (Date)								Total
				3	6	9	12	18	24	30	36	
				(10.03.2014)	(09.06.2014)	(10.09.2014)	(10.12.2014)	(10.06.2015)	(09.12.2015)	(09.06.2016)	(13-14.12.2016)	
FH	Bp	1	Z. peltatus	280	141	163	111	68	104	109	73	1049
		2	V. nemorensis	5	10	145	234	106	55	44	178	777
		3	T. aegrota	1	139	225	128	32	42	3	103	673
		4	O. minima		34	51	31	40	61	19	47	283
		5	A. aphidioides	1	5	9			21	9	43	88
		6	P. jugincola				4	1	22	1	38	66
		6	P. runcatellus			13	38	5	2	1	7	66
		7	Pergamasus sp.		2	21	1	26		6	1	57
		8	P. septentrionalis			11	29	4				44
		9	V. cervus			3	23	6	2	3	5	42
		10	V. planicola				8		18		15	41
	Ps	1	Z. peltatus	2	68	339	228	158	202	1	217	1215
		2	V. nemorensis			25	6	21	47		15	114
		3	L. parvulus		2	9	16	4	46		30	107
		4	A. aphidioides		2	72	1	15	3		11	104
		5	V. cervus			19	3	22	2		5	51
		6	P. kochi			2	1	10	16		10	39
		7	Paragamasus sp.		2	5		27	1		1	36
		8	T. aegrota			26		4	3		0	33
		9	Pergamasus sp.		3	10		14	2		1	30
		10	P. runcatellus			4	2	8	5		2	21
SH	Bp	1	A. tubae			295	153	15	116	6	94	679
		2	A. bicornis			42	36	1	14		3	96
		3	A. aphidioides			73	1					74
		4	Amblyseius sp.			9	8	1	2	1	8	29
		5	V. cervus			13	2	1	5			21
		6	Pergamasus sp.			13		1	1		1	16
		7	P. crassipes			1	4	3	2		3	13
	Ps	1	A. tubae			19	3	1	35		3	61
		2	A. bicornis			41	4		6		2	53
		3	A. aphidioides			24	1	14	1		1	41
		4	A. insularis	1		2	20	2	6		6	37
		5	Pergamasus sp.			29		4			2	35
		6	P. crassipes			17	6	2	2		3	30
		7	Z. peltatus			3		2		5		10
		8	D. foveolatus						1		7	8
		9	H. praesternalis			1	1	4			2	8
		10	Amblyseius sp.			1		1			2	4
		11	D. angulosus				2				2	4
		12	D. rotundus						1		3	4
		13	T. aegrota	1		1		2				4

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