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The Effects of Wild Boar Rooting on Epigeic Arthropods in Oak Forests

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Abstract: The distribution of wild boar (*Sus scrofa* L.) on almost all continents brings with it a number of negative impacts, the intensity of which depend on the local population density. One of these impacts is the rooting of the soil surface as part of their foraging behavior, which represents an ecologically valuable disturbance to the forest ecosystem. In this study, conducted in 2022 and 2023, we placed 50 pitfall traps across 10 plots at 10 model sites to compare epigeic arthropod communities in areas affected by wild boar rooting with those unaffected by rooting activity. Our findings demonstrate the presence or absence of rooting is a highly significant factor in shaping arthropod epigeic community assemblies. Rooted plots predominantly hosted species from the taxons Araneae, Carabidae, Elateridae, and Diplopoda, whereas plots without rooting were significantly associated with the taxons Tenebrionidae, Opiliones, Gryllidae, and Geotrupidae. Diptera, and Staphylinidae were not affected by wild boar rooting activity. Throughout the study, a decreasing trend in species diversity was observed. Wild boar rooting notably impacted the composition of epigeic assemblages.

Keywords: game damage; diversity; Carabidae; post-disturbance regeneration; predators; epigeic species

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Citation: Špoula, J.; Stočes, D.; Drimaj, J.; Mikulka, O. The Effects of Wild Boar Rooting on Epigeic Arthropods in Oak Forests. *Forests* **2024**, *15*, 1169. https://doi.org/10.3390/f15071169

Academic Editor: Todd Fredericksen

Received: 22 May 2024
Revised: 27 June 2024
Accepted: 28 June 2024
Published: 5 July 2024

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1. Introduction

The wild boar (*Sus scrofa* L.), originally native to Eurasia and North Africa [1], has expanded its range to all continents except Antarctica (e.g., [2,3]). The increased population of wild boar has several negative economic impacts, particularly the damage of agricultural crops [4,5] and the rooting out of tree seedlings [6,7], which have increasingly become a significant concern [8]. Such activities do not only reverse the succession of plant communities [9], resulting in microhabitats of pioneer and invasive species [10,11]; they also impact arthropod communities through predation and habitat alteration [12,13]. Herrero et al. [14] analyzed stomachs of wild boars and found insects from at least seven orders: Coleoptera, Diptera, Orthoptera, Hymenoptera, Lepidoptera, Trichoptera, and Anoplura. Endangered insect species can benefit from the creation of new microhabitats [11,15]. For example, Cabon et al. [16] found grasshopper diversity, total richness, and richness of endangered and specialist species were positively related to wild boar rooting, as was sand lizard abundance.

Carabidae, commonly known as ground beetles, globally encompass more than 40,000 described species [17] and are frequently used as bioindicators due to their sensitivity to environmental changes [18–20]. These beetles are crucial for biological control in agriculture, preying on a diverse array of soil-dwelling pests including caterpillars, wireworms, ant larvae, ticks, springtails, aphids, and slugs [21].

While the impacts of wild boar rooting on epigeic invertebrates have been previously explored in Mediterranean forests, e.g., [22,23], the specific effects on arthropod communities in temperate oak forests remain understudied. Therefore, our study aimed to (i) to assess the effects of wild boar rooting on arthropods; (ii) describe the general successional pathway influenced by rooting; and (iii) evaluate the specific effects on ground beetle assemblages.

2. Materials and Methods

2.1. Study Sites

The study was conducted in the Hodonínská Dúbrava National Nature Reserve (48.8810° N, 17.1058° E) (Figure 1), which was designated to protect Aceri tatarici-Quercion and Carpinion forests, as well as several rare and endangered butterfly species (*Lopinga achine* Sco., *Callimorpha quadripunctaria* Poda), and beetles (*Cerambyx cerdo* L. and *Lucanus cervus* L.) [24]. The average annual (1961–2023) temperature ranges from 9.1 to 10 °C and annual precipitation from 401 to 550 mm [25].

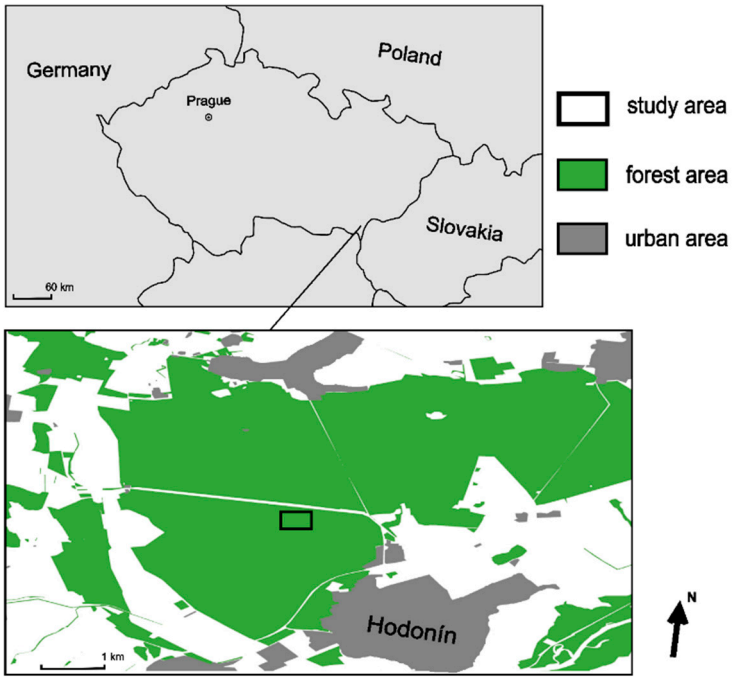

Figure 1. Study site.

The study area was not fenced and was accessible to wild boar throughout the year. Wild boar population densities in the area were around 60 ind/1000 ha in 2022 and 35 ind/1000 ha in 2023 (according to hunting records). Wild boar rooted the soil surface mainly in winter and early spring. During the growing season, rooting was concentrated in nearby fields, thus damage to the soil surface in the study area was rare. Repeated damage to the soil surface in areas affected by wild boar rooting was not recorded. In addition to wild boar, roe deer (*Capreolus capreolus* L.) and brown hare (*Lepus europaeus* Pall.) were present in study area, but their impact was also not recorded.

2.2. Pitfall Traps

Invertebrates were sampled using pitfall traps, a common method for sampling epigeal invertebrates [26]. In 2022 and 2023, 50 pitfall traps were distributed across 10 plots at 10 model sites to compare epigeic communities in areas affected by wild boar rooting (5 sites, 25 traps) and areas without rooting (5 sites, 25 traps). The rooted areas (model sites) were selected so that the traps were located in the center of an area of at least 50 × 30 m and that the rooted soil surface accounted for more than 90% of this area. Areas without

rooting (model sites) were characterized by equally sized areas with a maximum proportion of rooted surface of 5%. Both rooted and unrooted areas were selected to ensure similar environmental conditions. Each trap consisted of a 4 L glass jar buried in the ground to the top of the jar, ensuring insects would easily fall into the jar. The traps were positioned in transects, spaced 10 m apart and at least 15 m from the edge of the habitat zones to minimize edge effects. The traps were slightly elevated above ground level to allow for the dig-in effect [27,28]. The traps were placed 5 m apart and filled with 2 L of 4% formaldehyde solution and jar surfactant (Procter & Gamble, Cincinnati, OH, USA). The top of the jar was covered with a metal canopy to prevent dilution of the solution. Samples were collected monthly during the growing season from July 2022 to September 2023 and retained in a 75% ethanol solution for long-term preservation. In the laboratory, the numbers of arthropods were counted and identified to family level.

2.3. Data Analysis Statistical Approach for Epigeic Community Assemblages

Both rooted and unrooted plots were included in ordination analyses as factors representing the treatment. Partial canonical correspondence analysis (pCCA) to identify the effect of disturbance on the spatial distribution of assemblages included higher taxa data (i.e., individual abundances of taxa). Year and month served as covariables to control for any systematic or successional changes in taxon composition that might occur in monitored habitats irrespective of model parameters. Species were sampled sequentially from 2022 to 2023, so the significance of the canonical axes was assessed using a restricted Monte Carlo permutation test specifically designed for time series data, with 999 permutations. Each permutation was constrained by cyclic shifts that preserved the temporal autocorrelation of individuals. Individual abundances were log-transformed using the formula log(y + 1), to stabilize and reduce the dominance of highly abundant taxa. Rare occurrences were arbitrarily downweighted using an analysis setup wizard of ordination options. A forward selection procedure was used to identify the parameter characteristics explaining variability in the species data (i.e., rooting). Ordination analyses were performed using CANOCO (Version 5, Wageningen, The Netherlands) [29]. To assess the specific influence of rooting and year on the occurrence of individual arthropod taxons, a two-way ANOVA was performed for each taxon separately. The model included rooting (rooted vs. unrooted) and year (2022 vs. 2023) as fixed factors. This analysis was implemented in R (Version 4.4.1, Vienna, Austria) using the *aov* function, which allowed us to evaluate the main effects of each factor as well as their interaction. Before conducting ANOVA, we assessed the normality of abundance data for each taxon using the Shapiro–Wilk test and checked for homogeneity of variances across treatment groups using Levene's test. These tests ensured that the assumptions of ANOVA were met for all taxa analyzed.

To evaluate the impact of rooting on the abundance of individuals in the taxa, we created a box plot and conducted pairwise comparisons between rooted and unrooted conditions for the years 2022 and 2023, using the tukey_hsd test for significance. Additionally, to illustrate the changes in abundance between these years, we generated a line plot with the rooting effect using the *ggpubr* library with depicted error bars with the *mean_se* function [30].

Partial detrended canonical correspondence analysis (pDCCA) was performed to statistically describe the application of the Shannon–Wiener diversity index to epigeic assemblages, elucidating the directional trends of affected sites in the 2022 to 2023 study period. The pDCCA included the year as a continuous explanatory variable, with trap ID (representing traps at each site) and month serving as covariables. This approach aimed to mitigate the impact of local conditions and seasonal variation on individual composition, thereby avoiding the conflation of temporal and spatial variation. Randomization was constrained to the temporal records within each plot only. Individual abundances were log-transformed, with less weight given to rarer taxons. Significance of the canonical axes was assessed using a restricted Monte Carlo permutation test with 999 permutations.

Based on abundance data, we used an accumulation curve and rarefaction of taxa richness, and calculation was based on Chao and Jost [31].

2.4. Evaluation of Carabid Assemblage

The effect of rooting specifically on carabid assemblages was also tested. The carabid species dataset was first tested for normality using the *shapiro.test* test, then for homogeneity of variance using the *leveneTest*, both from the R (version 4.4.0) library *car.* Finally, the non-parametric *wilcox.test* from the R library *vegan* was used to compare numbers of captured individuals in rooted and unrooted areas.

To show the effect of rooting on body size (large: *Carabus* sp. or small body: other carabids) and habitat preferences (open vs. closed habitats; described in Hůrka 1996) of carabid assemblage, we used a Bayesian generalized linear model (i.e., BGLM) through the application of the *brm* function of the *brms* library [32]. Two models included interaction of fixed effects (rooting, body size, and habitat preferences) and random effects (month of collection and traps) treated as nested random effects. The a priori distribution of the model parameters were set to Gaussian distributions. We set the computation to four chains with 3000 iterations for each in the Markov chain Monte Carlo (MCMC). The robustness of the MCMC simulations was verified using the R-hat statistic, with results below the threshold value of 1.0 indicating good model convergence. Cross-validation showing the prediction accuracy of fitted BGLM were done using the loo() function of the loo package.

3. Results

3.1. Wild Boar Disturbance Shapes Epigeic Assemblages

Between 2022 and 2023, we recorded a total of 39,562 arthropod individuals from 10 taxons across 10 sites (Table 1). Using forward selection in partial canonical correspondence analysis (pCCA: R^2 = 25.9, test on all axes: *pseudo-F* = 4.7, p = 0.041), we found a significant marginal effect of rooting on assemblages, as detailed in Table 2.

Table 1. Average numbers (±SD) of captured individuals in pitfall traps.

	2022		2023	
Taxon	**Rooted**	**Unrooted**	**Rooted**	**Unrooted**
Araneae	24 ± 15	11 ± 7	26 ± 16	13 ± 8
Carabidae	30 ± 17	14 ± 8	32 ± 17	16 ± 9
Diplopoda	20 ± 18	11 ± 7	23 ± 18	14 ± 9
Diptera	20 ± 23	12 ± 5	22 ± 17	15 ± 9
Elateridae	29 ± 10	14 ± 10	26 ± 14	13 ± 8
Geotrupidae	20 ± 15	11 ± 7	27 ± 17	13 ± 8
Gryllidae	21 ± 15	13 ± 7	25 ± 16	15 ± 9
Opiliones	20 ± 16	13 ± 7	24 ± 18	13 ± 7
Staphylinidae	18 ± 13	9 ± 6	23 ± 14	10 ± 7
Tenebrionidae	34 ± 22	10 ± 8	31 ± 23	11 ± 8
Average	22 ± 16	12 ± 7	26 ± 17	14 ± 8

Table 2. Summary table calculated by forward selection of the partial canonical correspondence analysis (pCCA), with the study year and month set as covariables. The explained variation indicates how much of the variability was explained by the pCCA axes (shown in Figure 2). The conditional effects of the model parameters were tested by Monte Carlo with 999 permutations and p values (p) were corrected by false discovery rate p (adj).

Model Parameters	**Explained Variation (%)**	***Pseudo-F***	***p***	***p* (adj)**
Unrooted areas	1.0	4.6	0.046	0.046
Rooted areas	1.0	4.6	0.044	0.046

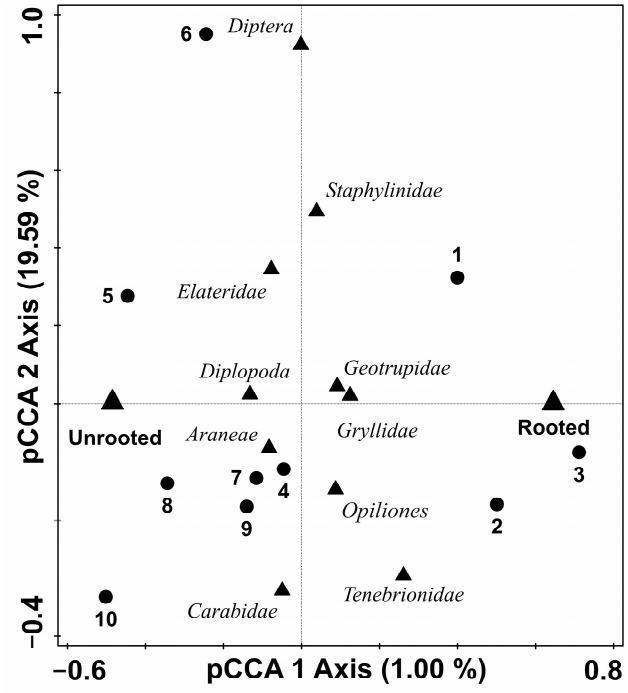

Figure 2. pCCA analysis: association of arthropods and environmental disturbance across 10 plots, observed from 2022 to 2023. Large filled triangles symbolize the disturbance, small filled triangles represent the arthropods, and filled circles represent plots.

The analysis revealed that both presence and absence of wild boar rooting (rooted vs. unrooted) were influential factors in shaping the structure of these assemblages (Figure 2). Rooting explained approximately 1% of the data variation in assemblage structure, while other unknown factors or a combination of factors explained almost 20% of the variation. Specifically, rooted areas hosted predominantly Araneae, Carabidae, Elateridae, and Diplopoda taxons, while plots without rooting significantly influenced the assemblages of the Tenebrionidae, Opiliones, Gryllidae, and Geotrupidae taxons. Diptera and Staphylinidae were present in both rooted and unrooted plots. However, the response of each individual taxon to rooting was not directly tested through pCCA. The pCCA results indicate that while rooting has a significant effect, it is not the most influential factor in determining arthropod community structure.

3.2. General Regeneration Path

The general impact of rooting on the abundance of individuals in taxons was evaluated through pairwise comparisons between rooted and unrooted areas. Our findings showed that the number of individuals caught in pitfall traps was generally higher in rooted areas compared to unrooted areas. However, this increase may be due to either higher density or greater movement activity of the taxa, and it is not possible to determine which factor was more influential in this particular case. In the first year examined, there were extremely high occurrences in rooted areas, which increased steadily during the second year (Figure 3). This shift in abundance was significantly caused by rooting (two-way ANOVA: SS = 2.40, $F = 15.54$, $p < 0.01$). Additionally, we compared the average abundance of epigeic assemblages in rooted and unrooted areas between these years (Figure 3). The results depicted in the box plot (Figure 3) show a higher abundance in rooted areas compared to unrooted areas. While the interaction between year and rooting was not significant (SS = 0.15, $F = 1.01$, $p = 0.31$), both factors individually contributed to the observed patterns in certain taxa, such as Geotrupidae, where both rooting and year were significant factors (see Table 3).

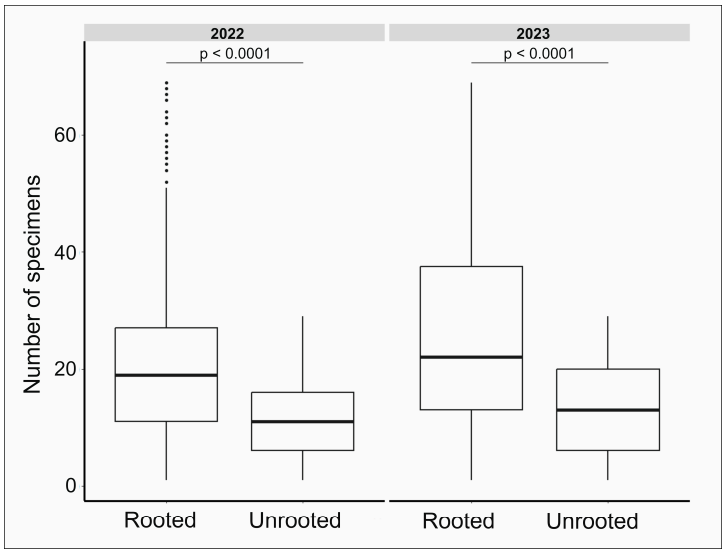

Figure 3. General impact of rooting on epigeic assemblages between years 2022 and 2023.

Table 3. Two-way ANOVA performed on captured specimens of taxa. We focused on the interaction of rooting: year.

Taxon	N	Factor of Variation	SS	df	MS	F	*p*-Value
Araneae	7441	Rooting	7.85	1	7.853	84.445	0.01
		Year	0.21	1	0.206	2.217	0.137
		Rooting:Year	0.05	1	0.05	0.542	0.462
		Residuals	34.78	374	0.093		
Carabidae	5435	Rooting	5.774	1	5.774	52.902	0.01
		Year	0.083	1	0.083	0.764	0.383
		Rooting:Year	0.016	1	0.016	0.145	0.703
		Residuals	24.341	223	0.109		
Diplopoda	4484	Rooting	2.36	1	2.364	11.922	0.01
		Year	0.19	1	0.187	0.943	0.332
		Rooting:Year	0.05	1	0.046	0.231	0.631
		Residuals	46.8	236	0.198		
Diptera	1330	Rooting	0.464	1	0.464	2.938	0.09
		Year	0.058	1	0.058	0.367	0.5469
		Rooting:Year	0.004	1	0.004	0.023	0.8795
		Residuals	10.736	68	0.158		
Elateridae	1938	Rooting	1.44	1	1.44	8.94	0.01
		Year	0.099	1	0.099	0.613	0.436
		Rooting:Year	0.027	1	0.027	0.169	0.682
		Residuals	14.494	90	0.161		
Geotrupidae	6874	Rooting	6.3	1	6.3	33.853	0.01
		Year	1.17	1	1.17	6.286	0.01
		Rooting:Year	0.22	1	0.222	1.194	0.275
		Residuals	69.6	374	0.186		
Gryllidae	4718	Rooting	3.182	1	3.182	30.337	0.01
		Year	0.1	1	0.1	0.95	0.331
		Rooting:Year	0.092	1	0.092	0.882	0.349
		Residuals	25.805	246	0.105		
Opiliones	4823	Rooting	1.29	1	1.28	8.223	0.01
		Year	0.1	1	0.166	1.064	0.303
		Rooting:Year	0.23	1	0.229	1.46	0.228
		Residuals	41.96	268	0.157		

Table 3. *Cont.*

Taxon	N	Factor of Variation	SS	df	MS	F	*p*-Value
Staphylinidae	1722	Rooting	4.058	1	4.058	25.246	0.01
		Year	0.136	1	0.136	0.844	0.36
		Rooting:Year	0.05	1	0.05	0.313	0.577
		Residuals	17.84	111	0.161		
Tenebrionidae	797	Rooting	2.34	1	2.4	15.538	0.01
		Year	0.008	1	0.008	0.053	0.818
		Rooting:Year	0.069	1	0.069	0.445	0.508
		Residuals	6.64	43	0.154		

The partial detrended canonical correspondence analysis (pDCCA) results illustrate changes in the Shannon–Wiener index of diversity of epigeic assemblages over the study period (R^2 = 13.4, test on all axes: *pseudo-F* = 24.1, p = 0.001), as shown in Figure 4. This directional trend reflects the initial disturbance caused by wild boar rooting and the subsequent regeneration process. Early successional species initially dominated rooted areas, but as time progressed, these areas underwent changes in species composition and diversity, leading to a more heterogeneous community structure. Throughout the study period, we observed a minor decreasing trend in species diversity, as measured by the Shannon–Wiener index (Figure 4). This trend suggests that while the initial disturbance promoted a burst of colonization and diversity, over time, competitive exclusion and habitat stabilization may lead to a decrease in species diversity. These dynamic changes highlight the general regeneration path influenced by wild boar rooting, where the ecosystem gradually transitions from a disturbed state to a more stable and diverse community.

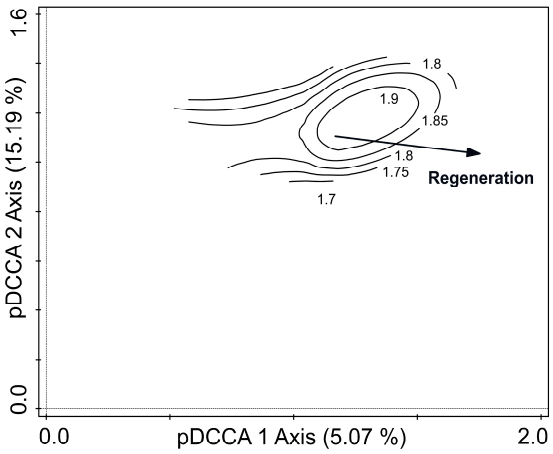

Figure 4. pDCCA analysis: application of the Shannon–Wiener diversity index to epigeic assemblages used to elucidate the directional trends of affected sites over the 2022 to 2023 study period.

To illustrate the impact of rooting disturbance on each of the 10 groups of epigeic taxa (Table 1) and reflect the changes in assemblage composition over the two-year study period (Table 3), we present the results of the two-way ANOVA (Table 3). This analysis shows that (i) initially, all taxa except Diptera were actively using rooting areas; (ii) over time, the effect of rooting did not significantly interact with the year; and (iii) earth-burying Geotrupidae species exhibited a random shift in abundance over time.

Total taxa richness achieved the highest values in the rooted areas and the lowest in unrooted areas in both years (Figure 5).

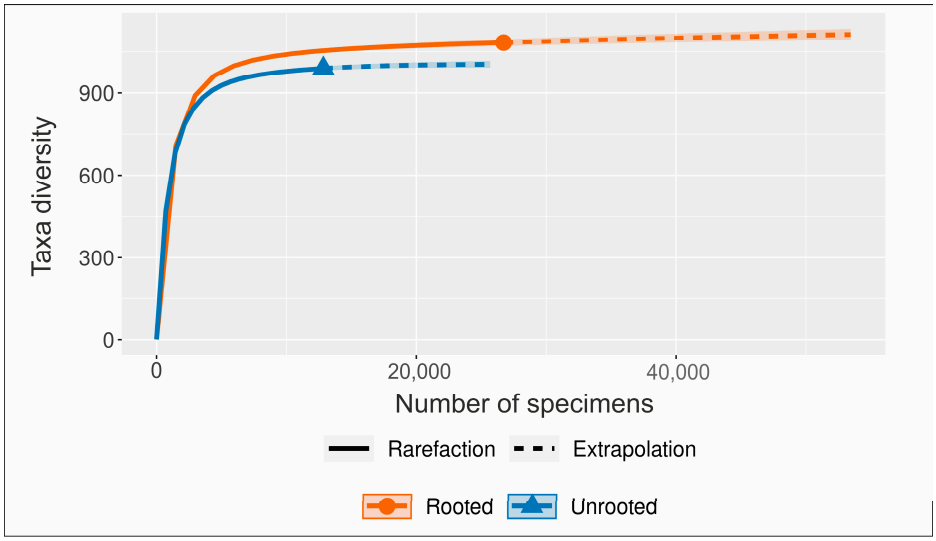

Figure 5. Sample-size-based rarefaction and extrapolation curve of epigeic assemblages in rooted and unrooted areas using taxa richness.

3.3. Effect of Rooting on Carabid Assemblages

In 2022 and 2023, we recorded 5482 individuals from 13 species of ground-dwelling beetle (Coleoptera: Carabidae) (Table 4). The dataset was not normally distributed (Shapiro–Wilk test: $W = 0.48812$, $p < 0.001$) and the assumption of homogeneity of variances was not met for the two groups being compared (Levene's test: $F = 4.25$, $p = 0.046$). Therefore, an unpaired two-sample Wilcoxon test ($W = 237.5$, $p = 0.048$) was used, which indicated that the variance of individuals across the different levels of disturbance was not the same. At the same time, a BGLM revealed the negative effect of rooting on the distribution of large *Carabus* sp. (CI: −1.11–−0.03) (Table 5), which was confirmed with a reliability of 94.9 %. Additionally, we tested the habitat preferences of species (open vs. closed habitats). For species that prefer open habitats (i.e., *Badister lacertosus*, *Nebria brevicolis*, *Poecilus cupreus*, *Calathus fuscipes*, *Harpalus rubripes*, *Licinus depressus*), the results showed that their distribution was not significantly affected by rooting (92.3% reliability), because confidence intervals of rooting: habitat preferences included zero (Table 6).

Table 4. Carabid species captured in pitfall traps.

Species	Rooted	Unrooted	Sum
Badister lacertosus (Sturm, 1815)	1		1
Calathus fuscipes (Goeze, 1777)	2		2
Carabus granulatus (Linnaeus, 1758)		1	1
Carabus hortensis (Linnaeus, 1758)	6	5	11
Carabus violaceus (Linnaeus, 1758)	1	7	8
Harpalus rubripes (Duftschmid, 1812)		1	1
Harpalus rufipes (DeGeer, 1774)	3853	1582	5435
Leistus ferrugineus (Linnaeus, 1758)	1		1
Licinus depressus (Paykull, 1790)		1	1
Nebria brevicolis (Fabricius, 1792)	2	2	4
Poecilus cupreus (Linnaeus, 1758)	1		1
Pterostichus niger (Schaller, 1783)	5	10	15
Pterostichus oblongopunctatus (Fabricius, 1789)	1		1
TOTAL	3873	1610	5482

Table 5. Credible intervals of dependent variable number of occurrences of carabid species with population- and group-level effects of body size (large vs. small species).

Population-Level Effects:					
	Estimate	Estimated Error	l-95% CI	u-95% CI	Rhat
Intercept	1.08	0.18	0.74	1.50	1.01
Rooting	0.67	0.20	0.28	1.05	1.00
Body	−0.11	0.21	−0.51	0.29	1.00
Rooting:Large body	−0.57	0.28	−1.11	−0.03	1.00
Group-level effects:					
sd (Intercept)	0.40	0.05	0.32	0.52	1.00
Month	0.21	0.20	0.01	0.77	1.00
Trap	0.07	0.06	0.00	0.21	1.00

Table 6. Credible intervals of dependent variable number of occurrences of carabid species with population- and group-level effects of habitat preferences.

Population-Level Effects:					
	Estimate	Estimated Error	l-95% CI	u-95% CI	Rhat
Intercept	1.08	0.19	0.69	1.46	1.00
Rooting	0.24	0.19	−0.13	0.63	1.00
Habitat preferences	−0.12	0.25	−0.62	0.36	1.00
Rooting:Habitat preferences	0.15	0.40	−0.61	0.95	1.00
Group-level effects:					
sd (Intercept)	0.46	0.07	0.34	0.61	1.00
Month	0.20	0.21	0.01	0.80	1.00
Trap	0.15	0.10	0.01	0.39	1.00

4. Discussion

In this study, we investigated the effects of wild boar rooting on arthropods. Wild boar are generally known to significantly alter ecosystem structures through their distinctive rooting and digging behaviors [7]. Typically, insect presence correlates positively with abundance and diversity of vegetation, which can be altered by wild boar activity [33]. Our findings suggest that the disturbances caused by wild boar rooting expose soil and its arthropod inhabitants, potentially increasing the vulnerability of these organisms to predators. While rooting was found to significantly influence arthropod community structure, explaining approximately 1% of the variation, it was evident that other unknown factors or a combination of factors played a more substantial role, explaining nearly 20% of the variation. Changes in soil management strategies and vegetation cover have been shown to influence the activity and abundance of such predators [34]. Further research is needed to identify these factors and understand their interactions with rooting disturbances. Additionally, the study observed distinct regeneration paths influenced by wild boar rooting. Initially, rooted areas showed a significant increase in the abundance of certain taxa, such as Araneae, Carabidae, Elateridae, and Diplopoda. Over time, these areas exhibited changes in species composition and diversity, indicating a regenerational pathway. The regeneration path suggests a shift towards a more heterogeneous environment, which can support a wider range of taxa. This finding implies that wild boar rooting creates dynamic habitats that undergo successional changes, ultimately contributing to increased biodiversity in the long term. Contrary to prior research which indicated that carabid assemblages were more abundant in vegetated and undisturbed areas [34,35], our results demonstrated that insect predators were more present and active in rooted areas, which is not consistent with the results of previous studies, where rooting disturbance negatively affected soil food webs [36]. However, it is important to note that these studies (i.e., [34,35]) were carried out in agricultural cropland, not forests. In our forested study sites, rooting

led to increased diversity, overall richness, and richness of endangered and specialist insect species. The same pattern was found in urban grasslands, where wild boar rooting has tended to increase the diversity of endangered or specialist species [16], an effect similar to that observed with prescribed burning in xeric grasslands [37].

Our findings may be influenced to some extent by the spatial distribution of wild boar rooting, which is not random in the environment. The wild boar's sensitive sense of smell [38] and its feeding preferences result in winter rooting being localized to areas with underground seed reservoirs of small mammals [39], terrain depressions with higher humidity [40] and specific biota such as sites rich in tubers, roots, and other plant organs (e.g., [37]). Although the study areas were selected so as not to noticeably differ in any environmental characteristics, there were inevitably some differences due to wild boar preferences. Thus, further research should focus on phytocenological and soil environmental characteristics that affect not only animal soil disturbances but also the presence and densities of invertebrate taxa.

Notably, *Harpalus rufipes* Deg., a common granivorous species that typically prefers vegetated areas [41], was the most abundant ground beetle recorded. The low species diversity and dominance of *Harpalus rufipes* in our study are attributed to the simplified nature of the environment, which is influenced both by the habitat conditions and by rooting activities that destroy the larvae of large carabid species [5]. Additionally, *Licinus depressus* Pay., a xerophilous ground beetle that inhibits dry, sandy or gravelly soils in grasslands, overgrown dunes, and dry forests [42], was documented for the first time in the Hodonín district. Two endangered species listed on the Red List of Threatened Species in the Czech Republic [43], *Cucujus cinnaberinus* Scopoli and *Selatosomus cruciatus* L., were found predominantly in unrooted areas. This distribution indicates that these specific threatened species may prefer more undisturbed habitats, suggesting a higher abundance of threatened species in such environments. This preference underscores their narrow ecological niches and reluctance to exploit newly created environments for foraging and shelter [44]. Wild boar rooting has been shown to negatively affect soil decomposition rates over the long term, potentially leading to a sustained decrease in the larvae of endangered or specialist insect species in forested areas [37].

The impact of wild boar rooting was found to be an environmental factor that had a positive effect on the majority of invertebrates studied, but a negative effect on a few specific taxa. This natural disturbance alters the biodiversity of ecosystems depending on the time and range of its occurrence. Both of these parameters are human-influenced through active hunting management (especially hunting pressure; [45]) and by offering artificial feed during non-growing seasons [46], thereby actively interfering with the population abundance, density, and distribution of wild boar in the forest environment (especially in winter). It is important that forest managers, conservationists, and public administrators are aware of the potential consequences for the biodiversity of forest ecosystems and work with hunters to accommodate wild boar pressure on soil disturbance. Our findings indicate that wild boar rooting has a negative effect on large carabid species as *Carabus hortensis*, *C. violaceus*, and *C. granulatus*, which are generally sensitive to environmental changes. Conversely, rooted sites can be regarded as the nascent stages of emerging microbiotopes [15] which, in general, enhance species diversity, particularly that of plant communities. In the context of the forest environment overall, the combination of rooted and unrooted areas creates a heterogeneous environment that generally supports an increase in biodiversity, not only of invertebrates. However, it is important that wild boar populations do not disproportionately disturb the environment, permitting rooted areas to become predominant, and consequently threaten protected species and the overall balance of the ecosystem.

5. Conclusions

Our results indicate that wild boar rooting significantly influences the activity and regeneration of epigeic arthropods. Rooting was identified as a significant factor in shaping the assembly structure, predominantly hosting taxons such as Araneae, Carabidae,

Elateridae, and Diplopoda. However, it explained only about 1% of the data variation in assemblage structure. Conversely, unrooted plots were more associated with taxons like Tenebrionidae, Opiliones, Gryllidae, and Geotrupidae. Diptera were found in both rooted and unrooted areas. The substantial portion of variation (almost 20%) attributed to other unknown factors highlights the complexity of the ecosystem and suggests that additional environmental variables or interactions need to be investigated to fully understand the determinants of arthropod community structure.

We also found that carabid assemblages are influenced by rooting, particularly regarding body size, with large species being significantly affected by rooting. These findings suggest that wild boar rooting in forests increases diversity by creating new environmental conditions favorable for various insect taxons. However, larvae of large carabid species that rely on undisturbed soil conditions for survival may be negatively affected. This study provides valuable insights into the ecological disturbances caused by wild boar rooting, highlighting its role in supporting a broader range of species that thrive in post-disturbance environments while potentially restricting those dependent on stable soil conditions.

Author Contributions: Conceptualization, J.Š.; methodology, J.Š.; software, D.S. and J.Š.; validation, J.Š.; formal analysis, D.S. and J.Š.; investigation, J.D., J.Š. and O.M.; resources, J.D.; data curation, J.Š.; writing—original draft preparation, J.Š.; writing—review and editing, D.S., J.D. and O.M; visualization, D.S. and J.Š.; supervision, J.D.; project administration, J.D.; funding acquisition, J.D. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the Internal Grant Agency of the Faculty of Forestry and Wood Technology, Mendel University in Brno, grant number IGA-LDF-22-TP-006: "Wild boar as an important factor in the development of forest ecosystems" and the Ministry of Agriculture of the Czech Republic, grant number MZE-RO0123.

Data Availability Statement: Data are available in [Zenodo] at [10.5281/zenodo.12572865].

Acknowledgments: The authors would like to thank the Internal Grant Agency (IGA) of the Faculty of Forestry and Wood Technology, Mendel University in Brno for funding the research and Martin Mullett (United Kingdom) for the English correction.

Conflicts of Interest: The authors declare that they have no known competing financial interests or personal relationships that could have influenced the work reported in this paper.

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