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ORIGINAL ARTICLE

Marked differences in arthropod biomass and species richness between two types of Malaise trap

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Key words. Bartak trap, biodiversity, insect monitoring, metabarcoding, sampling method, SLAM trap, taxon richness

Abstract. Concerns about insect decline have motivated the monitoring of terrestrial arthropods, often using Malaise traps. Since the types of Malaise trap vary widely, it is essential to understand the differences in the resulting number and composition of the arthropod catch. In this study, we compared the performance of two types of Malaise trap in capturing arthropods for biodiversity monitoring and ecological studies. We placed Bartak and SLAM traps in a paired design at increasing distances from a forest edge in vineyards in southwestern Germany. We measured arthropod biomass and used metabarcoding for species identification. Bartak traps caught 7.5 times higher biomass, but only 1.5 times more species compared to the SLAM traps. There was a significant difference in species composition, whereby highly mobile flying insect species, such as those in the order Diptera, strongly dominated the Bartak traps and ground-dwelling arthropods were better represented in SLAM traps. With increasing distance to the forest edge, species richness decreased similarly in both trap types. Our study shows that differences in trapping efficiency must be taken into account when comparing results from different, and that trap types can be chosen according to the focus of each study. Nevertheless, both trap types were able to detect the biodiversity pattern in our landscape in a similar way.

INTRODUCTION

Arthropod biodiversity appears to be in a global decline (Hochkirch, 2016; Hallmann et al., 2017; Seibold et al., 2019), although the extent and causes are not yet fully understood (Müller et al., 2023). The decline is said to be mainly attributed to anthropogenic factors, of which the destruction of natural habitats, climate change, and the intensification of modern agriculture are considered the most prominent (Sánchez-Bayo & Wyckhuys, 2019). Within agricultural landscapes, the scarcity of food and nesting resources and the use of pesticides and fertilisers are major drivers of biodiversity loss (Sánchez-Bayo & Wyckhuys, 2019). However, Müller et al. (2023) show that unfavourable weather conditions, also caused by climate change, can explain the loss of insects reported in the study by Hallmann et al. (2017). Further large-scale biodiversity monitoring is therefore important for a better understanding of the dynamics of arthropod decline. Although the loss of insect diversity and biomass has been of particular concern in recent years, leading to efforts to expand terrestrial arthropod monitoring, few programs are currently in place (Welti et al., 2022; Geiger et al., 2016; Karlsson et al., 2020; Lehmann et al., 2021). Implementing large-scale biodiversity monitoring requires a thorough understanding of the use and effectiveness of monitoring methods.

Common sampling methods for arthropods include pitfall traps, vacuum sampling, sweep netting, window traps, pan traps, bait traps, light traps, and Malaise traps (Yi et al., 2012; Henderson & Southwood, 2021). Different sampling methods tend to be particularly suitable for specific functional or taxonomic groups. For example, Malaise traps capture mostly flying insects, with Diptera and Hymenoptera being by far the most abundant taxa; pitfall traps are used to study surface-dwelling arthropods, such as spiders and ground beetles; pan traps are used to study pollinating species, such as bees (Malaise, 1937; Woodcock, 2005; Skvarla et al., 2021; Krahner et al., 2024). Malaise traps are passive traps that do not use light, colour, or scents to attract organisms (Skvarla et al., 2021). Depending on their construction and size, they are divided into different types, such as Bartak, SLAM (Sea, Land, and Air Malaise), and Townes traps (Skvarla et al., 2021; Uhler et al., 2022). What they have in common is the use of a fine-mesh netting in a tent-like structure to intercept arthropods and direct them towards a trapping device (Skvarla et al., 2021). Malaise traps often capture large numbers of arthropods, making taxonomic identification time-consuming (Karls-

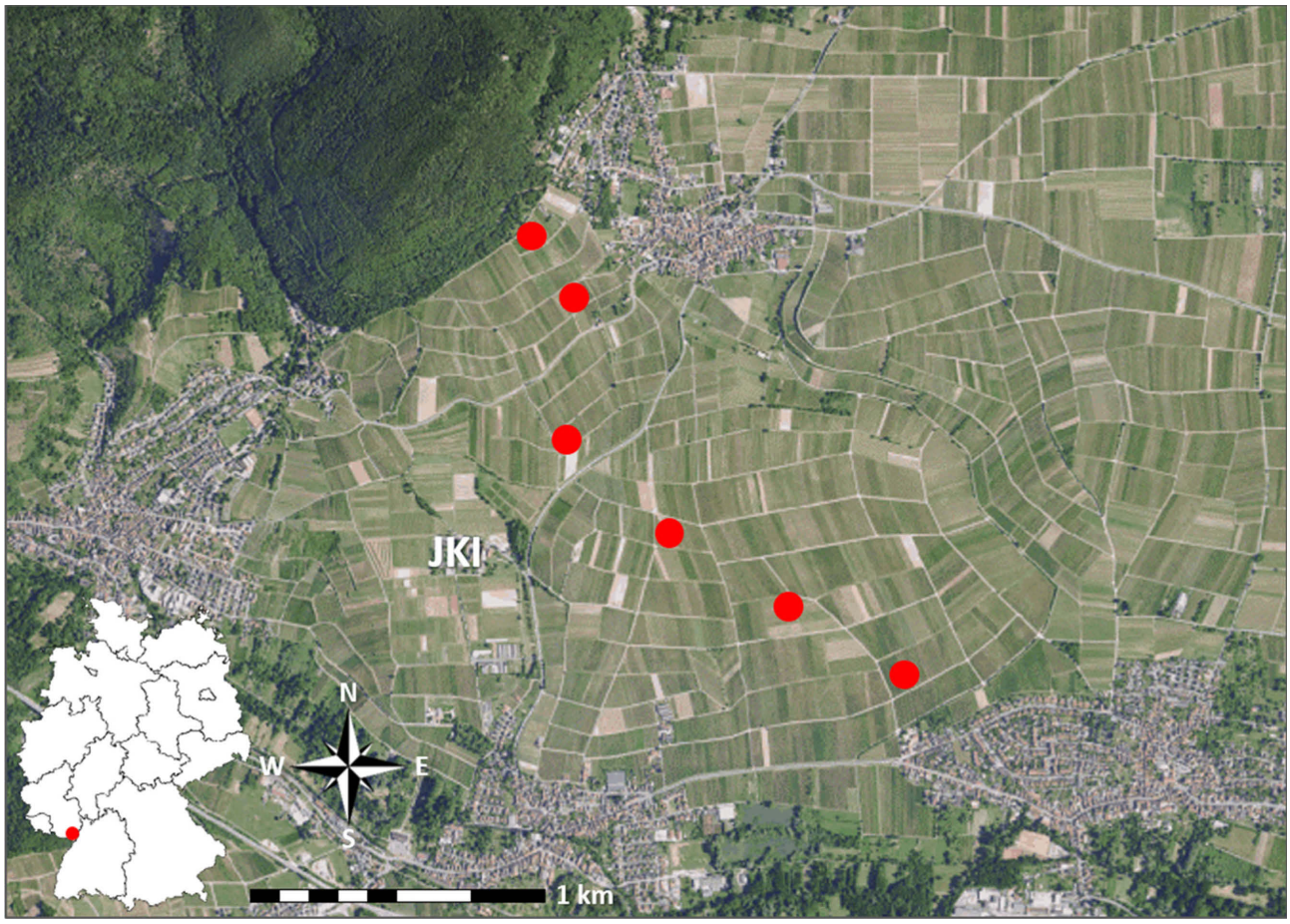

Fig. 1. Map of the study area with the location of the Julius Kühn Institute in Siebeldingen (JKI) and the nearby sampled vineyards (red dots). Basic map data by © GeoBasis-DE/LVermGeoRP (2023).

son et al., 2020). Metabarcoding allows such large bulk samples to be processed to study entire arthropod communities, even including the highly diverse orders Diptera and Hymenoptera (deWaard et al., 2019). Specimens are identified based on DNA sequences in the cytochrome c oxidase I (COI) gene. Similar sequences are then clustered into operational taxonomic units (OTU), which can be assigned barcode index numbers (BIN) containing taxonomic information based on reference sequences in the Barcode of Life Data System (BOLD; Ratnasingham & Hebert, 2013). In this way, metabarcoding provides a valuable tool for large-scale monitoring, identifying taxa in a time- and cost-effective manner (deWaard et al., 2019). Furthermore, data can be effectively stored and shared for re-analysis (Yu et al., 2012; deWaard et al., 2019). In addition to recording species diversity, trapping arthropods also allows the measurement of biomass, which underlies their important role as prey for subsequent trophic levels (Montgomery et al., 2021). Recent non-invasive techniques such as acoustic monitoring, computer vision, radar, and molecular methods for analysing environmental DNA, are desirable from a conservation perspective in order to reduce environmental impacts and maintain public support for arthropod conservation (van Klink et al., 2022; Lövei et al., 2023). However, these methods are still in a proof-of-concept stage and often do not record biodiversity as comprehensively as trapping (van Klink et al., 2022).

In this study, we compared the arthropod catch between two types of Malaise trap in vineyards in southwestern Germany in order to compare their performance for biodiversity monitoring and ecological studies. The two types differed in construction and size, with the Bartak trap being larger than the SLAM trap. We were also interested in their suitability for recording changes in insect activity along a gradient of forest distance. To do this, we placed Bartak and SLAM traps in a paired design at increasing distances from a forest edge, measured the biomass of the trapped arthropods, and used metabarcoding for species identification. We tested the following hypotheses: (H1) arthropod biomass and (H2) species richness are higher in Bartak traps compared to the smaller SLAM traps. We were further interested in examining if (H3) species composition differs between the two Malaise trap types and if (H4) the species richness pattern along a forest distance gradient is recorded differently by the two types.

MATERIAL AND METHODS

Study area and sites

We conducted our study in the German wine-growing region Palatinate, which is located in the Upper Rhine Valley east of the Palatinate Forest and characterised by a warm, temperate cli-

Fig. 2. The two used in our study: Bartak trap (left), SLAM trap (right). In contrast to the study design, the two traps were set up in adjacent inter-rows for demonstration purposes.

mate (Beck et al., 2018). The average annual temperature over the last 15 years was 11.3°C and the total annual precipitation was 690.1 mm (Agrarmeteorologie Rheinland-Pfalz, 2024). We sampled six vineyards near the Julius Kühn Institute in Siebeldingen (ranging between 49.228400°N, 8.049500°E and 49.214300°N, 8.068400°E; Table S1). The vineyards were located along a distance gradient from the Palatinate Forest, ranging from adjacent to the forest up to 2,020 m (Fig. 1).

Design and sampling

We set one pair of Malaise traps (one Bartak and one SLAM trap) in each of the six vineyards. Two pairs were placed in the vineyard closest to the forest, resulting in seven pairs of traps and 14 sampling plots. We sampled seven times from mid-April to mid-June 2022 (Table S2). Each time, the traps were set for five consecutive days. Only the last sampling period was shorter at 3 days. Both Bartak traps (Malaise trap bioform after Bartak, bioform Dr. J. Schmidl e.K., Nürnberg, Germany; Bioform, 2025; Fig. 2 left) and SLAM traps (MegaView Science Co., Ltd., Taichung, Taiwan; MegaView Science, 2025; Fig. 2 right) were set up in 2-m-wide inter-rows between vine rows, at equal distances from the vineyard border, and placed in non-adjacent inter-rows. The Bartak traps have a base area of 100 × 270 cm (370 cm net with ground contact), stand 175 cm high, and consist of olive-green mesh, topped with a collecting bottle and transparent lid. The SLAM traps have a size of 110 × 110 × 110 cm (283 cm net with ground contact) with black mesh for the horizontal surfaces and white mesh in the roof area, and a collecting bottle screwed onto the bottom of a collection container at the top of the traps. Collecting bottles were filled with 70% ethanol denatured with about 1% methyl ethyl ketone (EtOH MEK). We weighed the wet biomass of the sampled arthropods using a sieve and let the liquid drain away (adapted from Hallmann et al., 2017). In addition, the remaining water at the bottom of the sieve was removed with a paper tissue. The total biomass across the seven sampling rounds was calculated for each plot.

Metabarcoding

We transferred all samples to undiluted EtOH MEK prior to metabarcoding analysis. For each plot, we pooled the material from the seven samplings into a single bulk sample. All samples were processed by AIM – Advanced Identification Methods GmbH, where metabarcoding of a 313-base-pair mini-barcode region in the CO1-5P target region and bioinformatics was conducted following the protocol and methods of Hausmann et al. (2020) and Morinière et al. (2016; for details see Kaczmarek et al., 2023a). We filtered the results table for arthropod operational taxonomic units (OTU) with a Hit-%-ID value (Overlap of an OTU sequence with a reference sequence in the Barcode of Life Data System (BOLD)) ≥ 97%. While many OTUs are not assigned a taxonomic species name in BOLD, barcode index numbers (BIN) are considered to correspond well with Linnean species numbers (Zahiri et al., 2014). Thus, only OTUs with an assigned BIN were used in this study. We condensed BINs that occurred more than once into one entry. We used taxonomic species information from BOLD and condensed doubled species to one entry. For BINs for which no species name is specified in the database, we used the BOLD ID instead. Hereafter, we refer to BINs as species.

Data analysis

For analysing data and creating figures, we used R v.4.2.3 (R Core Team, 2023) and RStudio v.2023.03.0 (RStudio Team, 2023) with the R packages blmeco (Korner-Nievergelt, 2015), car (Fox & Weisberg, 2019), rcompanion (Mangiafico, 2024), MuMIn (Bartoń, 2020), lme4 (Bates et al., 2015), vegan (Oksanen et al., 2020), indicspecies (Cáceres & Legendre, 2009), ggplot2 (Wickham, 2016), and ggpubr (Kassambara, 2020).

To test whether species richness recorded within the most common orders (Coleoptera, Diptera, Hemiptera, Hymenoptera, and Lepidoptera) differed between Bartak and SLAM traps, we used paired t-tests (function *t.test*) for normally distributed data and Wilcoxon signed-rank tests (function *wilcox.test*) for non-normally distributed data. For the following statistical analyses of species richness and composition, the data from one SLAM trap was omitted as an outlier, because it had a much lower species richness at a similar biomass compared to other SLAM traps. To examine how Malaise trap type and distance of a trap to the forest edge affect log-transformed biomass, we used a linear mixed-effects model (function *lmer* from the *lme4* package). To examine how Malaise trap type and the distance of a trap from the forest affect the number of species recorded, we used a generalised linear mixed-effects model with negative binomial distribution and logarithmic link function (function *glmer.nb* from the *lme4* package). We included the interaction of the two explanatory variables and further the pair of sampling plots as a random factor in both models. We rescaled and centred the distance from the forest variable for a better model fit. To test the effects, we used type III ANOVA (function *Anova* from the *car* package) with a significance level of $p < 0.05$. We further investigated the effects of the two explanatory variables (trap type, distance from forest) on arthropod species based on the presence-absence data of the arthropod species recorded using a distance-based redundancy analysis (dbRDA; function *dbrda* from the *vegan* package) with Jaccard dissimilarity. To test the effects, we used a permutational test with 999 permutations (function *anova.cca* from the *vegan* package). We identified arthropod species selectively recorded in either one of the two Malaise trap types using a species indicator analysis with 9999 permutations (function *multipatt* from the *indicspecies* package). Based on the recommendations of Moran (2003), and in consideration of the multiple significant results in the species indicator analysis, we decided not to adjust the *p*-values.

Table 1. Mean number of arthropod species (BINs) and families recorded with Bartak and SLAM traps. Results of tests for differences in species richness per order between trap types are indicated with *V*-value, *z*-value, and *p*-value for Wilcoxon signed-rank tests and *t*-value, degrees of freedom, and *p*-value for paired *t*-tests.

Order	Bartak		SLAM		Statistic
	Species	Families	Species	Families	
Coleoptera	34	15	103	24	$V = 0, z = -2.28, p = 0.016$
Diptera	351	46	194	43	$t_{(6)} = 6.081, p < 0.001$
Hemiptera	54	9	63	11	$t_{(6)} = -0.155, p = 0.882$
Hymenoptera	124	15	75	16	$t_{(6)} = 7.681, p < 0.001$
Lepidoptera	54	20	44	17	$t_{(6)} = 1.849, p = 0.114$
Others	16	14	40	26	$t_{(6)} = -4.749, p = 0.003$
Total	633	119	519	137	$t_{(6)} = 2.864, p = 0.029$

RESULTS

We retrieved a list of 900 species (BINs) from metabarcoding, 586 of which were assigned a species name (for details see supplementary results). We recorded 633 species from 119 arthropod families using the Bartak traps and 519 species from 137 families using the SLAM traps, totalling 900 species from 162 families (Fig. 3, Table S3). The most species-rich orders in our study were Diptera (415 species from 51 families), Coleoptera (116 species from 25 families), Hymenoptera (162 species from 20 families), Lepidoptera (77 species from 24 families), and Hemiptera (87 species from 13 families). Bartak traps recorded significantly higher numbers of Diptera (+81% compared to SLAM traps) and Hymenoptera (+65% compared to SLAM traps), while SLAM traps recorded significantly more Coleoptera species (+203% compared to Bartak traps) and species outside the five most species-rich orders in our study (+150% compared to Bartak traps; Table 1). Overall species richness was significantly higher in the Bartak traps (+22% compared to SLAM traps). The number of Hemiptera and Lepidoptera was not significantly different between the two trap types.

On average, total biomass across the seven sampling rounds was approximately 7.5 times higher in Bartak traps (mean = 38.3 g, SD = ±21.5 g) compared to SLAM traps (mean = 5.1 g, SD = ±2.2 g; Fig. 4A, Table 2, Table S3). The mean number of arthropod species per trap was approximately 1.5 times higher in Bartak traps (221 species, SD = ±36 species) compared to SLAM traps (149 species, SD = ±57 species; Fig. 4B). Biomass decreased significantly with increasing distance from the forest, but a significant interaction between trap type and distance from the forest indicates that biomass decreased more in Bartak traps than in SLAM traps (Fig. 4C). The number of species recorded decreased significantly by about 50 species within 2,000 m distance of the forest in both Bartak and in SLAM traps (Fig. 4D).

Based on the results of the dbRDA, species composition was significantly different between Bartak and SLAM traps (Sum of squares = 0.9, $F = 3.7$, $p = 0.001$; Fig. 5). The two trap types shared 28.0% of the recorded species (18.1% of Coleoptera, 31.3% of Diptera, 34.5% of Hemiptera, 22.8% of Hymenoptera, 27.3% of Lepidoptera, and 30.2% of other species). 409 of the total 900 species were recorded at only one of the 14 sampling plots, resulting in a high turnover between traps of the same type. Each Bartak trap caught an average of 34.8% of the total species

Table 2. Effects of Malaise trap type and the distance of trap plots to the forest as well as their interaction on biomass (linear mixed-effects model) and species richness (generalised linear mixed-effects model with negative binomial distribution and log-link). Chi-square (χ^2), degrees of freedom (*df*), and the *p*-value are indicated.

Variable	Log(biomass)			Species richness		
	χ^2	*df*	*p*-value	χ^2	*df*	*p*-value
(Intercept)	640.4	1	<0.001	16180.0	1	<0.001
Trap type	228.7	1	<0.001	23.0	1	<0.001
Distance from forest	12.1	1	<0.001	4.5	1	0.034
Trap type: Distance from forest	4.0	1	0.047	3.5	1	0.063

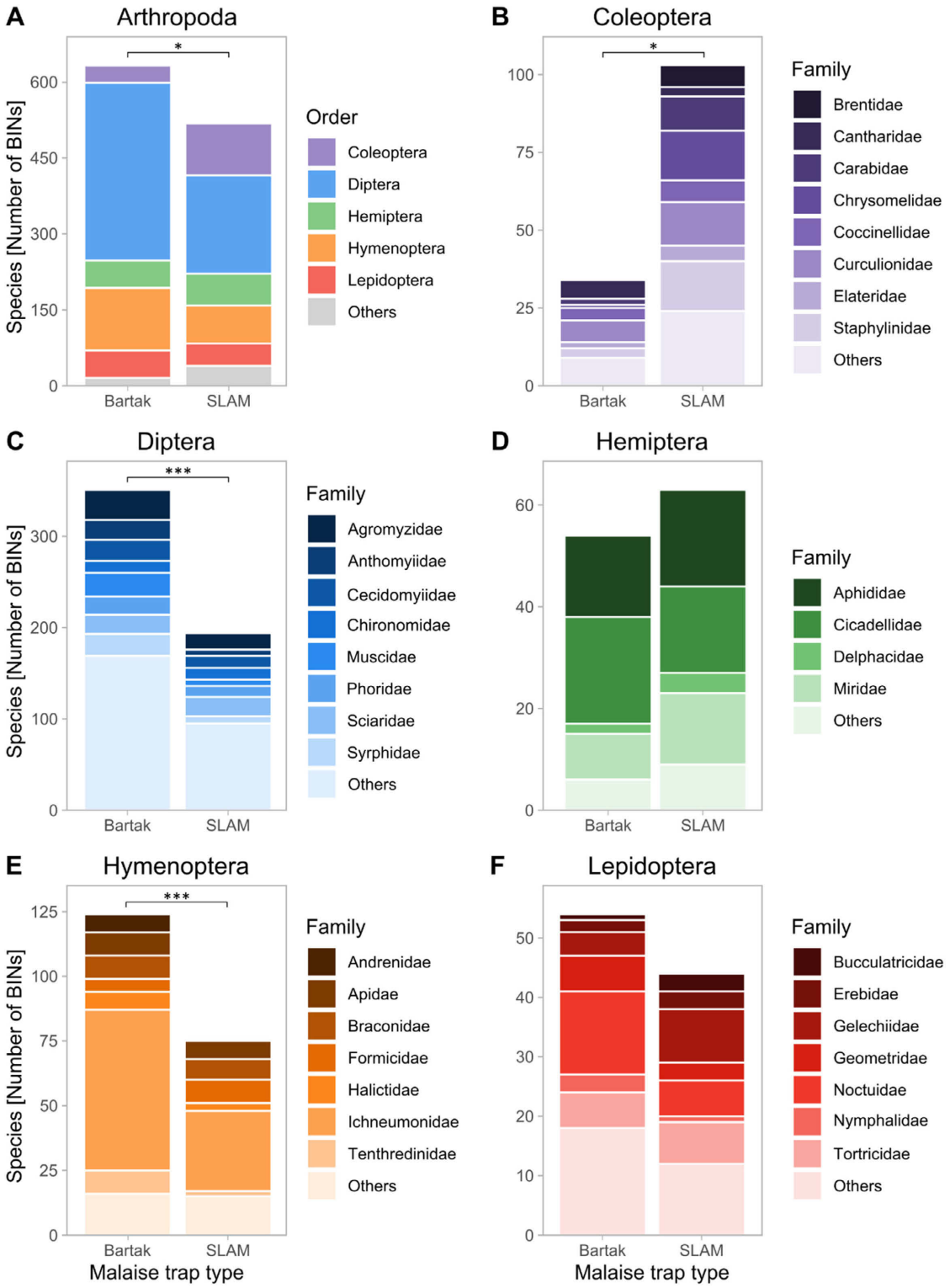

Fig. 3. Number of arthropod species (BINs) for Bartak and SLAM traps within the most common orders (A) and families of Coleoptera (B), Diptera (C), Hemiptera (D), Hymenoptera (E), and Lepidoptera (F). Significance codes based on results from paired t-tests for A and C–F and Wilcoxon signed-rank tests for B: ***$p < 0.001$, *$p < 0.05$.

recorded in Bartak traps and each SLAM trap caught an average of 28.6% of the total species recorded in SLAM traps. The distance of trapping plots to the forest edge did not affect the species composition of arthropod communities (Sum of squares = 0.3, $F = 1.3$, $p = 0.103$).

Based on the indicator species analysis, 59 species were significantly associated with the Bartak traps, of which 40 belonged to the order Diptera, twelve to Hymenoptera, three to Lepidoptera, two to Hemiptera, and one to Coleoptera and Orthoptera (Table 3). 20 species were significantly associated with the SLAM traps, of which seven

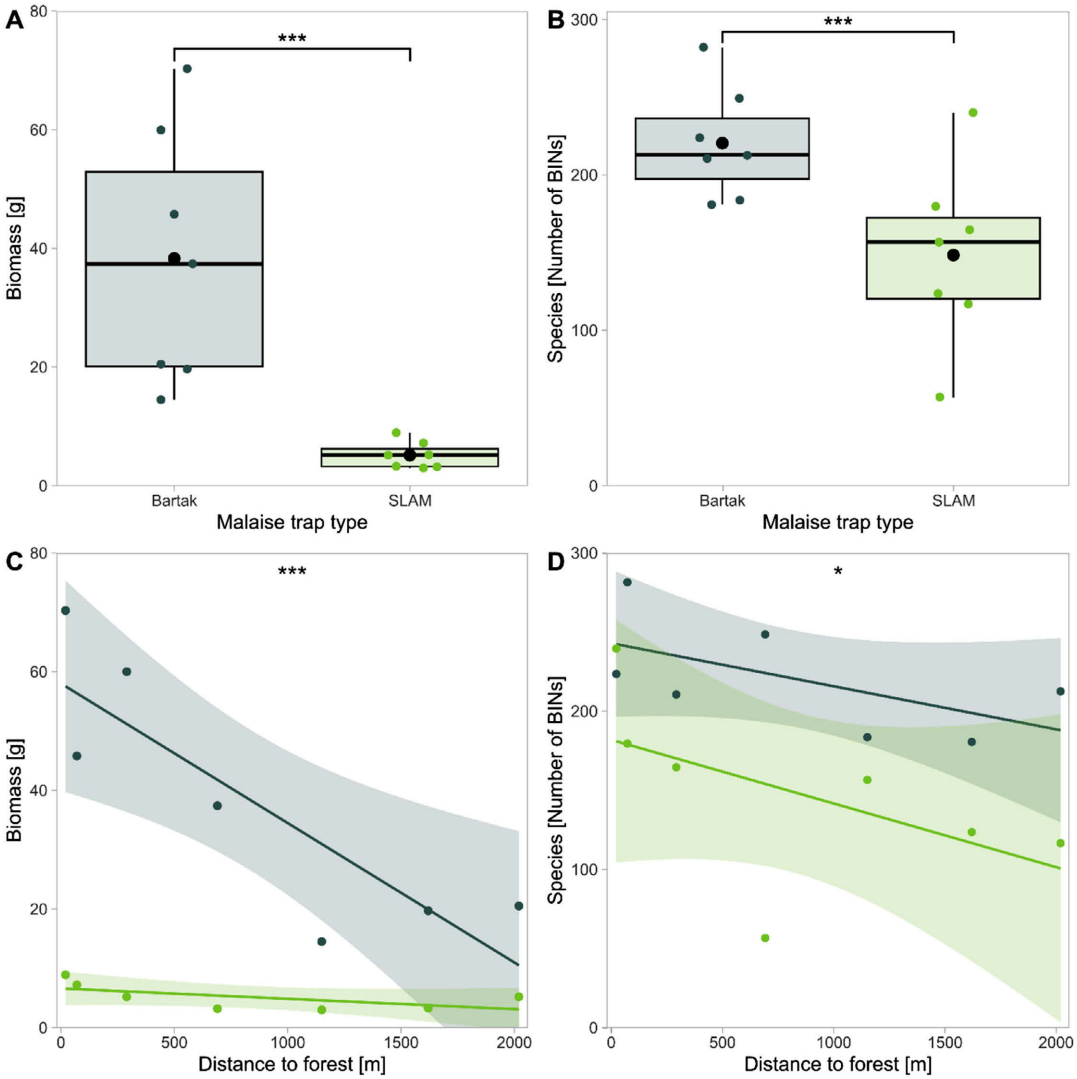

Fig. 4. Biomass in g (A) and number of species (BINs; B) as well as biomass (C) and number of species (BINs; D) for distance from the forest in m per Malaise trap type (Bartak traps (dark green) and SLAM traps (light green)). Significance code based on results from linear mixed-effects model for A and C and from generalised linear mixed-effects model with negative binomial distribution and log-link for B and D: ***$p < 0.001$, *$p < 0.05$.

belonged to the order Coleoptera, three to Hymenoptera, three to Diptera, two to Hemiptera, and one to Araneae, Dermaptera, Lepidoptera, Neuroptera, and Psocodea, respectively (Table 3).

DISCUSSION

We investigated the differences in arthropod biomass, species richness, and species composition between two Malaise traps types, and assessed the consistency with which they recorded an ecological pattern.

The Bartak traps captured 7.5 times higher arthropod biomass, but only 1.5 times more species. This confirms our first two hypotheses, where we expected a higher biomass and species richness in Bartak traps compared to SLAM traps. While Malaise traps are generally known to capture large quantities of arthropods (Skvarla et al., 2021), our study showed that there can be significant differences between types of Malaise trap. This supports previous findings that differences in trap construction influence catches (Townes, 1972; Matthews & Matthews, 1983; Hansen,

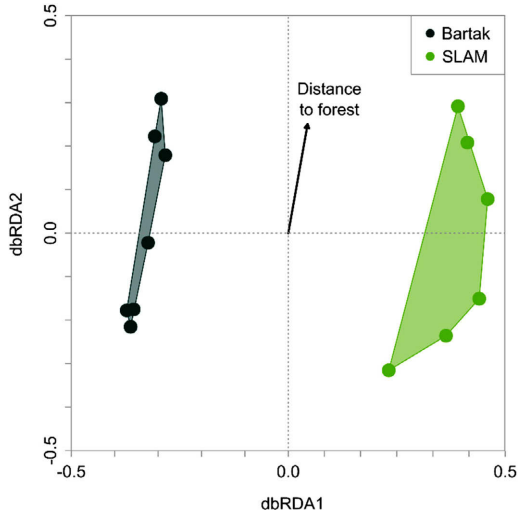

Fig. 5. Redundancy analysis triplot (dbRDA) with scaling 1 for arthropod communities based on the presence-absence data of the species (BINs) recorded with Bartak traps (dark green) and SLAM traps (light green) and the effect of the distance from the forest. The first two dbRDA axes are shown, explaining 24.81% and 8.79% of the total variation, respectively.

Table 3. Arthropod species (BINs) per order related to either Bartak or SLAM traps with IndicSpecies Stat value (Stat) and *p*-Value.

Bartak			SLAM		
Species	Stat	*p*-Value	Species	Stat	*p*-Value
Coleoptera			Araneae		
Dorcus parallelipipedus	0.691	0.031	*Dictyna uncinata*	0.707	0.021
Diptera			Coleoptera		
Delia radicum	1.000	< 0.001	*Agelastica alni*	1.000	<0.001
Megaselia pleuralis	1.000	< 0.001	BOLD:AAI8935	0.866	0.004
Phaonia subventa	1.000	< 0.001	*Clanoptilus geniculatus*	0.845	0.004
Phaonia tuguriorum	1.000	< 0.001	*Longitarsus pellucidus*	0.845	0.005
BOLD:AAA7374	1.000	< 0.001	*Tachyporus nitidulus*	0.845	0.005
BOLD:ACR1468	1.000	< 0.001	*Longitarsus ochroleucus*	0.707	0.022
Coenosia albicornis	0.866	0.004	*Olibrus corticalis*	0.707	0.022
Copromyza stercoraria	0.866	0.004	Dermaptera		
Lasiomma seminitidum	0.866	0.005	BOLD:AAG9897	0.745	0.021
Peribaea tibialis	0.866	0.004	Diptera		
Sarcophaga incisilobata	0.866	0.004	*Corynoptera perpusilla*	1.000	< 0.001
Triarthria setipennis	0.866	0.004	BOLD:AAN6431	0.745	0.022
BOLD:AAD0853	0.866	0.004	BOLD:ACP4736	0.691	0.030
BOLD:AAG2108	0.866	0.004	Hemiptera		
Fannia armata	0.845	0.005	*Laodelphax striatella*	0.745	0.020
Fannia canicularis	0.845	0.005	BOLD:AEI6714	0.707	0.022
Helina evecta	0.845	0.005	Hymenoptera		
BOLD:ABV5497	0.845	0.005	*Anthophora plumipes*	0.845	0.005
BOLD:ACR1376	0.845	0.005	*Zatypota bohemani*	0.845	0.005
Anthomyia pluvialis	0.745	0.021	*Triaspis pallipes*	0.745	0.022
Episyrphus balteatus	0.745	0.021	Lepidoptera		
Nephrotoma flavescens	0.745	0.019	*Ancylis mitterbacheriana*	0.707	0.022
Pollenia sp.	0.745	0.020	Neuroptera		
BOLD:AAD0642	0.745	0.021	*Hemerobius humulinus*	0.845	0.005
BOLD:AAM9376	0.745	0.021	Psocodea		
BOLD:ACD8702	0.745	0.023	*Valenzuela piceus*	0.845	0.005
BOLD:ACI7021	0.745	0.022			
BOLD:ACR0876	0.745	0.021			
Coenosia infantula	0.707	0.021			
Coenosia testacea	0.707	0.021			
Neurigona quadrifasciata	0.707	0.022			
Pollenia pediculata	0.707	0.023			
BOLD:AAJ0967	0.707	0.022			
BOLD:AAN5505	0.707	0.021			
BOLD:ACD2824	0.707	0.020			
Nephrotoma appendiculata	0.691	0.030			
Orfelia nemoralis	0.691	0.027			
BOLD:AAB2866	0.691	0.029			
BOLD:ACB4751	0.691	0.030			
BOLD:ACP2283	0.691	0.028			
Hemiptera					
Eupteryx atropunctata	1.000	< 0.001			
Arytaina genistae	0.707	0.021			
Hymenoptera					
Bombus ruderatus	1.000	< 0.001			
Andrena minutula	0.866	0.005			
BOLD:AAC0157	0.866	0.004			
BOLD:AAG6192	0.866	0.004			
BOLD:ACC3068	0.866	0.004			
Diplazon laetatorius	0.845	0.005			
Ethelurgus sodalis	0.745	0.022			
Pemphredon inornata	0.745	0.023			
BOLD:ACL8330	0.745	0.022			
Amblyteles armatorius	0.691	0.031			
Woldstedtius citropectoralis	0.691	0.027			
BOLD:ACR2933	0.691	0.032			
Lepidoptera					
Acronicta rumicis	0.845	0.005			
Apamea lithoxylaea	0.691	0.030			
Oligia latruncula	0.691	0.030			
Orthoptera					
BOLD:AAC5779	0.707	0.021			

1988; Uhler et al., 2022). Uhler et al. (2022) compared Bartak traps to another type of Malaise trap, the Townes trap. The shorter but taller Townes traps captured significantly higher biomass and species (Uhler et al., 2022). In our study, the increased biomass and species richness in the Bartak traps compared to the SLAM traps is likely due to the greater height of the former. As a result, taller Malaise traps appear to be more likely to intercept a greater number of flying or drifting insects, especially dipterans. However, the fact that SLAM traps capture a comparatively high number of species despite the significantly lower biomass, could be advantagious from a conservation perspective. Especially in sensitive environments, the removal of less arthropod biomass by the trap may be desirable. Such concerns should not be exaggerated, since the global fresh weight of aboveground arthropods is estimated to be >10 kg/ha (Rosenberg et al., 2023), which makes the catch of a Bartak trap seem minor (ca. 1 g per day). Nevertheless, minimising the killing of arthropods is desirable from an ethical perspective, and reducing the environmental impact is important for maintaining public support for arthropod conservation (Lövei et al., 2023). Thus, obtaining 77% of species information in only 13% of biomass can be an argument to favour SLAM over Bartak traps. If the survey focus is on taxonomic groups such as Diptera or Hymenoptera, our results indicate that Bartak traps are still preferable, while for Lepidoptera and Hemiptera SLAM traps may be a less invasive alternative. Nevertheless, when designing a study from an ethical perspective, it is important not to overlook the informative value of the data required to answer a scientific question, including suitable analysis. The choice of trap type, with its advantages and disadvantages compared to other types, depends on the specific research questions.

In addition to the differences in the captured arthropod richness and biomass, the catches of the two trap types also differed significantly in species composition. The fact that only about a third of the species were captured in both trap types shows that there are differences in species composition between the types, which was the focus of our third hypothesis. However, it is important to note that Malaise trap samples typically contain a large number of species with a single occurrence across all samples (Steinke et al., 2021). These singletons are likely to consist of transient and low abundance species (Kaczmarek et al., 2022). Consequently, the proportion of species shared, even between samples of the same trap type, remains relatively low. Malaise traps primarily capture flying insects, especially the orders Diptera and Hymenoptera (Matthews & Matthews, 1983; Skvarla et al., 2021). This selectivity towards flying insects was even stronger in Bartak traps compared to SLAM traps, likely due to their height as discussed above. In contrast, SLAM traps captured significantly more coleopterans and may perform better at capturing less mobile species in general, such as ground-dwelling arthropods. The lower height may increase the likelihood of such species reaching the collecting bottle. Accordingly, our indicator species analysis included ground-dwelling species of the orders Araneae and Psocodea for the SLAM traps.

The two types of Malaise trap also differ in other design features. The SLAM traps have white roofs, which increases capture by inducing species to move upward toward the brighter area with the collecting bottle (Montgomery et al., 2021). The white roof also alters species composition, as the colour itself may attract pollinating species (Uhler et al., 2022). However, in contrast to our study, Uhler et al. (2022) reported reduced rates of Coleoptera in a white-roofed trap compared to its black-roofed counterpart. Thus, reduced height may be more relevant for capturing Coleoptera than roof colour. Altogether, the difference in species composition between the two trap types allows researchers to make an informed choice for one or the other, depending on the focus of each study. With a focus on flying insects from the wider surrounding landscape, Bartak traps may be preferred. A more balanced range, which includes ground-active arthropods, is obtained with SLAM traps placed on the ground. However, SLAM traps can also be made more selective towards flying insects by suspending them in the air (Skvarla et al., 2021). Complementing Malaise traps with a second trap type, such as pitfall traps, is even more effective for recording ground-dwelling arthropods than the use of SLAM traps, as Malaise and pitfall traps have little overlap in taxa collected (McCravy, 2018; Skvarla et al., 2021).

Along our forest gradient, both biomass and species richness decreased with increasing distance from the forest edge. This pattern was also observed in previous studies, with similar effects on, e.g., aboveground nesting bees and birds (Kaczmarek et al., 2024; Rösch et al., 2024). The large differences in mean biomass captured by the two trap types resulted in a much larger decrease with increasing distance from the forest edge in the Bartak traps. In the SLAM traps, biomass was very low, so a possible effect of the forest gradient was probably less discernible. In addition, the Bartak traps, because they capture more flying insects, may be better at capturing transient and drifting species for which the forest may be a source habitat. Although the two trap types differ to some extent in the way they measure biomass due to their construction, as described above, species richness decreased similarly with forest distance in both trap types. This is not consistent with our final hypothesis where we expected the two trap types to differ in measuring biodiversity along a gradient of forest distance. Thus, it appears that ecological studies can derive similar patterns from both types of Malaise trap. However, Busse et al. (2022) reported opposite results between Malaise and light traps along a gradient of canopy openness. The different patterns were due to differences in the species predominantly captured by each of the two studied traps (Busse et al., 2022). Because influences of the landscape such as a forest gradient on species vary among groups of organisms (Kaczmarek et al., 2023b, 2024), and sampling methods vary in their representation of taxa, the choice of trap can potentially affect the outcome of a study. Particu-

larly in meta-analyses, specific characteristics of sampling methods need to be taken into account (Busse et al., 2022).

In conclusion, our study has shown that the choice of trap type used for biodiversity monitoring or ecological studies determines which taxonomic groups will be predominantly recorded. Many studies have compared the efficiency of Malaise traps with other trapping methods (e.g., Campbell & Hanula, 2007; Yi et al., 2012; Henderson & Southwood, 2021; Anderson et al., 2024), while few studies have compared differences between types of Malaise trap (e.g., Darling & Packer, 1988; Hansen, 1988; Uhler et al., 2022). Our study extends this knowledge to a relatively new type of Malaise trap, the SLAM trap. Our results support earlier findings that taller Malaise traps capture more flying insects, while lower traps capture more ground-dwelling arthropods. In our study, both types were able to detect the pattern of the forest gradient in a similar way. Finally, the choice of trap type depends on the specific objectives of a study. The term "Malaise trap" refers to traps with a similar trapping mechanism, but the types compared here each capture a distinct composition and quantity of species. Consequently, the type of Malaise trap must be taken into account when comparing the results of different studies.

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REFERENCES

Agrarmeteorologie Rheinland-Pfalz 2024: *Weatherstation Siebeldingen: Mean Values 2008–2023.* URL: https://www.wetter.rlp.de/Internet/AM/NotesAM.nsf/amweb/752dce127578072cc12572eb0020c16c?OpenDocument&TableRow=2.1.2,2.6#2.1. (last accessed 19 Dec. 2024).

Anderson N., Petersen S., Johnson R., Terry T., Kunzelman J., Lariviere D. & Anderson V. 2024: Pan trapping and Malaise trapping: A comparison of bee collection techniques in subalpine meadows. — *Diversity* **16**: 536, 21 pp.

Bartoń K. 2020: *MuMIn: Multi-Model Inference (R Package Version 1.43.17).* URL: https://cran.r-project.org/web/packages/MuMIn/index.html (last accessed 27 Oct. 2025).

Bates D., Mächler M., Bolker B. & Walker S. 2015: Fitting linear mixed-effects models using lme4. — *J. Stat. Softw.* **67**: 1, 48 pp.

Beck H.E., Zimmermann N.E., McVicar T.R., Vergopolan N., Berg A. & Wood E.F. 2018: Present and future Köppen-Geiger climate classification maps at 1-km resolution. — *Sci. Data* **5**: 180214, 12 pp.

Bioform 2025: *Malaise-Falle Bioform nach Bartak*. URL: https://www.bioform.de/shop.php?action=tree&wg=1&pid=706&treeid=225 (last accessed 7 Jan. 2025).

Busse A., Bässler C., Brandl R., Friess N., Hacker H., Heidrich L., Hilmers T., Merkel-Wallner G., Schmid-Egger C., Seifert L. et al. 2022: Light and Malaise traps tell different stories about the spatial variations in arthropod biomass and method-specific insect abundance. — *Insect Conserv. Divers.* **15**: 655–665.

Cáceres M.D. & Legendre P. 2009: Associations between species and groups of sites: Indices and statistical inference. — *Ecology* **90**: 3566–3574.

Campbell J.W. & Hanula J.L. 2007: Efficiency of Malaise traps and colored pan traps for collecting flower visiting insects from three forested ecosystems. — *J. Insect Conserv.* **11**: 399–408.

Darling D.C. & Packer L. 1988: Effectiveness of Malaise traps in collecting Hymenoptera: The influence of trap design, mesh size, and location. — *Can. Entomol.* **120**: 787–796.

deWaard J.R., Levesque-Beaudin V., deWaard S.L., Ivanova N.V., McKeown J.T.A., Miskie R., Naik S., Perez K.H.J., Ratnasingham S., Sobel C.N. et al. 2019: Expedited assessment of terrestrial arthropod diversity by coupling Malaise traps with DNA barcoding. — *Genome* **62**: 85–95.

Fox J. & Weisberg S. 2019: *An R Companion to Applied Regression*. SAGE Publications, Thousand Oaks, CA, 608 pp.

Geiger M.F., Morinière J., Hausmann A., Haszprunar G., Wägele W., Hebert P.D.N. & Rulik B. 2016: Testing the Global Malaise Trap Program – How well does the current barcode reference library identify flying insects in Germany? — *Biodivers. Data J.* **4**: e10671, 22 pp.

Hallmann C.A., Sorg M., Jongejans E., Siepel H., Hofland N., Schwan H., Stenmans W., Müller A., Sumser H., Hörren T. et al. 2017: More than 75 percent decline over 27 years in total flying insect biomass in protected areas. — *PLoS ONE* **12**(10): e0185809, 21 pp.

Hansen J.D. 1988: Trapping methods for rangeland insects in burned and unburned sites: A comparison. — *Gt. Basin Nat.* **48**: 383–387.

Hausmann A., Segerer A.H., Greifenstein T., Knubben J., Morinière J., Bozicevic V., Doczkal D., Günter A., Ulrich W. & Habel J.C. 2020: Toward a standardized quantitative and qualitative insect monitoring scheme. — *Ecol. Evol.* **10**: 4009–4020.

Henderson P.A. & Southwood R. 2021: *Southwood's Ecological Methods, 5th ed*. Oxford University Press, Oxford, 528 pp.

Hochkirch A. 2016: The insect crisis we can't ignore. — *Nature* **539**(7628): 141.

Kaczmarek M., Entling M.H. & Hoffmann C. 2022: Using Malaise traps and metabarcoding for biodiversity assessment in vineyards: Effects of weather and trapping effort. — *Insects* **13**: 507, 13 pp.

Kaczmarek M., Entling M.H. & Hoffmann C. 2023a: Differentiating the effects of organic management, pesticide reduction, and landscape diversification for arthropod conservation in viticulture. — *Biodiv. Conserv.* **32**: 2637–2653.

Kaczmarek M., Gillich M., Entling M.H., Hoffmann C. & Schirmel J. 2023b: Differential responses of Orthoptera in vineyards to organic farming, pesticide reduction, and landscape heterogeneity. — *J. Insect Conserv.* **27**: 729–741.

Kaczmarek M., Entling M.H. & Hoffmann C. 2024: Wild bee conservation in viticulture: Effects of semi-natural habitats, organic management, and fungicide reduction. — *Ecol. Evol.* **14**: e70378, 13 pp.

Karlsson D., Hartop E., Forshage M., Jaschhof M. & Ronquist F. 2020: The Swedish Malaise trap project: A 15 year retrospective on a countrywide insect inventory. — *Biodiv. Data J.* **8**: e47255, 35 pp.

Kassambara A. 2020: *ggpubr: 'ggplot2' Based Publication Ready Plots. R Package Version 0.4.0*. URL: https://cran.r-project.org/package=ggpubr (last accessed 27 Oct. 2025).

Korner-Nievergelt F. 2015: *Bayesian Data Analysis in Ecology Using Linear Models with R, Bugs, and Stan: Including*

Comparisons to Frequentist Statistics. Academic Press, Amsterdam, 328 pp.

Krahner A., Dietzsch A.C., Jütte T., Pistorius J. & Everaars J. 2024: Standardising bee sampling: A systematic review of pan trapping and associated floral surveys. — *Ecol. Evol.* **14**: e11157, 18 pp.

Lehmann G.U.C., Bakanov N., Behnisch M., Bourlat S.J., Brühl C.A., Eichler L., Fickel T., Geiger M.F., Gemeinholzer B., Hörren T. et al. 2021: Diversity of insects in nature protected areas (DINA): an interdisciplinary German research project. — *Biodiv. Conserv.* **30**: 2605–2614.

Lövei G., Ferrante M., Möller D., Möller G. & Vincze E. 2023: The need for a (non-destructive) method revolution in entomology. — *Biol. Conserv.* **282**: 110075, 5 pp.

Malaise R. 1937: A new insect-trap. — *Entomol. Tidskr.* **58**: 148–160.

Mangiafico S.S. 2024: *rcompanion: Functions to Support Extension Education Program Evaluation. R Package Version 2.4.35.* URL: https://cran.r-project.org/package=rcompanion (last accessed 27 Oct. 2025).

Matthews R.W. & Matthews J.R. 1983: Malaise traps: The Townes model catches more insects. — *Contrib. Am. Entomol. Inst.* **20**: 428–432.

McCravy K.W. 2018: A review of sampling and monitoring methods for beneficial arthropods in agroecosystems. — *Insects* **9**: 170, 27 pp.

MegaView Science 2025: *SLAM Trap – Standard*. URL: https://shop.bugdorm.com/product_info.php?products_id=109 (last accessed 7 Jan. 2025).

Montgomery G.A., Belitz M.W., Guralnick R.P. & Tingley M.W. 2021: Standards and best practices for monitoring and benchmarking insects. — *Front. Ecol. Evol.* **8**: 579193, 18 pp.

Moran M.D. 2003: Arguments for rejecting the sequential Bonferroni in ecological studies. — *Oikos* **100**: 403–405.

Morinière J., Cancian de Araujo B., Lam A.W., Hausmann A., Balke M., Schmidt S., Hendrich L., Doczkal D., Fartmann B., Arvidsson S. & Haszprunar G. 2016: Species identification in Malaise trap samples by DNA barcoding based on NGS technologies and a scoring matrix. — *PLoS ONE* **11**: e0155497, 14 pp.

Müller J., Hothorn T., Yuan Y., Seibold S., Mitesser O., Rothacher J., Freund J., Wild C., Wolz M. & Menzel A. 2023: Weather explains the decline and rise of insect biomass over 34 years. — *Nature* **628**: 349–354.

Oksanen J., Simpson G.L., Blanchet F.G., Kindt R., Legendre P., Minchin P.R., O'Hara R.B., Solymos P., Stevens M.H.H., Szoecs E. et al. 2020: *vegan: Community Ecology Package . R Package Version 2.5-7*. URL: https://CRAN.R-project.org/package=vegan (last accessed 27 Oct. 2025).

R Core Team 2023: *R: A Language and Environment for Statistical Computing. Version 4.2.3*. R Foundation for Statistical Computing, Vienna. URL: https://www.R-project.org/ (last accessed 27 Oct. 2025).

Ratnasingham S. & Hebert P.D.N. 2013: A DNA-based registry for all animal species: the barcode index number (BIN) system. — *PLoS ONE* **8**: e66213, 16 pp.

Rösch V., Chavez F., Krey L., Möth S., Petrović B., Richart-Cervera S., Rusch A., Tiedemann M., Tolle P., Weyandt L. et al. 2024: Semi-natural habitats are key to breeding bird diversity in intensified vineyard landscapes across Europe. — *Basic Appl. Ecol.* **81**: 66–74.

Rosenberg Y., Bar-On Y.M., Fromm A., Ostikar M., Shoshany A., Giz O. & Milo R. 2023: The global biomass and number of terrestrial arthropods. — *Sci. Adv.* **9**: eabq4049, 12 pp.

RStudio Team 2023: *RStudio: Integrated Development for R. Version 2023.03.0.* RStudio, Boston, MA. URL: http://www.rstudio.com/ (last accessed 27 Oct. 2025).

Sánchez-Bayo F. & Wyckhuys K.A. 2019: Worldwide decline of the entomofauna: A review of its drivers. — *Biol. Conserv.* **232**: 8–27.

Seibold S., Gossner M.M., Simons N.K., Blüthgen N., Müller J., Ambarli D., Ammer C., Bauhus J., Fischer M., Habel J.C. et al. 2019: Arthropod decline in grasslands and forests is associated with landscape-level drivers. — *Nature* **574**: 671–674.

Skvarla M.J., Larson J.L., Fisher J.R. & Dowling A.P.G. 2021: A review of terrestrial and canopy Malaise traps. — *Ann. Entomol. Soc. Am.* **114**: 27–47.

Steinke D., Braukmann T.W.A., Manerus L., Woodhouse A. & Elbrecht V. 2021: Effects of Malaise trap spacing on species richness and composition of terrestrial arthropod bulk samples. — *Metabarcod. Metagenom.* **5**: e59201, 8 pp.

Townes H. 1972: A light-weight Malaise trap. — *Entomol. News* **83**: 239–247.

Uhler J., Haase P., Hoffmann L., Hothorn T., Schmidl J., Stoll S., Welti E.A.R., Buse J. & Müller J. 2022: A comparison of different Malaise trap types. — *Insect Conserv. Divers.* **15**: 666–672.

van Klink R., August T., Bas Y., Bodesheim P., Bonn A., Fossøy F., Høye T.T., Jongejans E., Menz M.H.M., Miraldo A. et al. 2022: Emerging technologies revolutionise insect ecology and monitoring. — *Trends Ecol. Evol.* **37**: 872–885.

Welti E.A.R., Zajicek P., Frenzel M., Ayasse M., Bornholdt T., Buse J., Classen A., Dziock F., Engelmann R.A., Englmeier J. et al. 2022: Temperature drives variation in flying insect biomass across a German malaise trap network. — *Insect Conserv. Divers.* **15**: 168–180.

Wickham H. 2016: *ggplot2: Elegant Graphics for Data Analysis, 2nd ed*. Springer International Publishing, Cham, 260 pp.

Woodcock B.A. 2005: Pitfall trapping in ecological studies. In Leather S.R. (ed.): *Insect Sampling in Forest Ecosystems*. Blackwell Science, Hoboken, NJ, pp. 37–57.

Yi Z., Jinchao F., Dayuan X., Weiguo S. & Axmacher J.C. 2012: A comparison of terrestrial arthropod sampling methods. — *J. Resour. Ecol.* **3**: 174–182.

Yu D.W., Ji Y., Emerson B.C., Wang X., Ye C., Yang C. & Ding Z. 2012: Biodiversity soup: metabarcoding of arthropods for rapid biodiversity assessment and biomonitoring. — *Methods Ecol. Evol.* **3**: 613–623.

Zahiri R., Lafontaine J.D., Schmidt B.C., deWaard J.R., Zakharov E.V. & Herbert P.D.N. 2014. A transcontinental challenge – A test of DNA barcode performance for 1,541 species of Canadian Noctuoidea (Lepidoptera). — *PLoS ONE* **9**: e92797, 12 pp.

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Table S1. Location of the seven sites.

Study site	Coordinates
1	49.228146°N, 8.049807°E
2	49.226289°N, 8.051941°E
3	49.221704°N, 8.051420°E
4	49.219080°N, 8.056636°E
5	49.216643°N, 8.062704°E
7	49.214733°N, 8.067906°E

Table S2. Dates of the seven trapping periods.

Trapping period	Date
1	14/04/22 – 19/04/22
2	22/04/22 – 27/04/22
3	04/05/22 – 09/05/22
4	11/05/22 – 16/05/22
5	20/05/22 – 25/05/22
6	27/05/22 – 01/06/22
7	07/06/22 – 10/06/22

Supplementary results

A total of 1,211,499 paired-end sequences came from the sequencer. Across all samples, a median of 97.09% of the reads merged, with a mean of 95.73%, a minimum of 80.91%, and a maximum of 98.95%. Adapters were detected in a median of 99.9% of the forward and 93.5% of the reverse-complement reads. After quality filtering, 873,842 sequences were kept and 245,781 sequences were discarded. Out of 566,054 unique sequences in all samples, 46,574 unique non-singleton sequences were kept after dereplication. 2,643 OTUs out of a total of 4,302 OTUs were kept after de novo chimera detection, of which 2,195 found matches in the databases following OTU table cleaning. However, this DNA metabarcoding analysis included six samples that were not part of the study design presented in the article. 1,263 OTUs out of the 2,195 OTUs belonged to the presented study, of which 917 had a BOLD Hit-%-ID equal to or greater than 97% and were assigned to 900 unique BINs.

Online Supplement S1 (http://www.eje.cz/2026/006/S01.xlsx):

Table S3. Distance to the forest in m, total biomass and biomass per sampling period in g, number of total species (BINs) and number of species (BINs) of the most common orders, and presence of species (BINs) for each Bartak and SLAM trap in the seven sampling pairs.