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## ORIGINAL ARTICLE

# A comparison of two widely used methods for estimating taxonomic and functional diversities of epigeal arthropods in some temperate grasslands

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## Abstract

Suction sampling is increasingly being used to estimate abundance and diversity of epigeal arthropods, yet no study has quantified its efficiency to simultaneously assess diversity at different taxonomic and functional scales. Here, we evaluated the efficiency of this method (G-Vac) relative to the pitfall (Barber) trap, which has been used for a long time, and their possible complementarity. To do that, we compared several diversity metrics of a wide range of arthropod taxa, with a particular focus on spiders (species level), and using functional traits such as trophic diet, hunting guild, and body size. Sampling took place in some coastal grasslands of Brittany (France) using a spatially paired design of vacuuming and unfenced pitfall trapping. In total, 21159 arthropods were identified to order or family levels, including 1018 adult spiders identified to species. Suction sampling was more efficient than pitfall trapping in collecting phytophagous arthropods, web-builders, and small species living in the vegetation compared to detritivores, large-bodied arthropods, and spiders living near the soil surface. We conclude that short-term G-Vac suction is more interesting than pitfall trapping to obtain a 'snapshot' of patterns in taxonomic richness. However, for assessing functional diversity, G-Vac suction and pitfall trapping are complementary sampling methods.

## KEYWORDS

Araneae, Barber trap, body size, Brittany (France), epigeal arthropods, G-Vac, hunting guild, method efficiency, pitfall trap, spiders, suction sampling, trophic guild

## INTRODUCTION

Arthropods dominate terrestrial ecosystems in terms of animal diversity (Stork, 2018) and biomass (Bar-On et al., 2018) and play a key role in several ecosystem processes (Yang & Gratton, 2014). Due to the large variation in morphological and behavioral traits they exhibit, arthropods occupy many trophic niches and are involved in a range of ecological functions (Samways, 1993; Wong et al., 2019).

One of the main current challenges in arthropod research and conservation remains to efficiently characterize and survey their diversity with standardized methods in order to compare and monitor assemblages over space

and time (Malumbres-Olarte et al., 2017). Species richness, abundance, and trait value are fundamental parameters to describe taxonomic and functional diversities of arthropods, but the success of a monitoring scheme depends not only on the appropriate geographical and temporal scale of the study, but also the methods chosen used to inventory diversity and the way that the data are analyzed (Stork et al., 1996; Gotelli & Colwell, 2011). Often, one single sampling method does not provide a complete inventory of arthropod taxa (Yi et al., 2012), and a combination of methods is usually required to properly assess their diversity (e.g., Delabie et al., 2000; Snyder et al., 2006; Cardoso, 2009). In addition, taxonomic, spatial, and temporal

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bias are inherent to all sampling tools, and their design and calibration depend on specific biodiversity targets and/or ecological contexts (Bonar et al., 2011).

Since its invention almost 1 century ago (Barber, 1931), pitfall trapping (using the so-called Barber trap) became the device most widely used to collect ground-dwelling arthropods (Spence & Niemelä, 1994). There are many designs of pitfall trapping, depending on the target taxa. In particular, they can be underground or not, fenced or not, baited or not, and may present a multitude of sizes and collecting fluids (Owen, 1995; Brown & Matthews, 2016). Although the method is frequently used, it suffers from many biases, which have been more or less quantified (e.g., Luff, 1975; Adis, 1979; Brown & Matthews, 2016), and related to methodology choices – such as, e.g., trap perimeter (Abensperg-Traun & Steven, 1995), color (Buchholz et al., 2010), and type of collecting fluid (Schmidt et al., 2006) –, environmental factors – importantly, ambient temperature (Saska et al., 2013), but also habitat structure (Privet et al., 2020) – and species characteristics (e.g., escape behavior; Melbourne, 1999). Some methodological studies have compared pitfall trapping with other sampling methods, such as hand collection (Baars, 1979) and depletion quadrats (Mantzouki et al., 2012). These studies suggest that pitfall trapping can be useful for monitoring mobile ground-dwelling arthropods, such as carabid beetles or amphipods, and to obtain information on the size or biomass of populations, but hardly for estimating an accurate composition of species populations and assemblages. Indeed, the mobility of individuals varies according to their stage of development and sex. It is therefore relevant to use other sampling methods in addition to pitfall trapping.

Over the last 40 years, suction sampling has been used increasingly for collecting ground- and vegetation-dwelling arthropods. As with pitfall traps, there are various designs of suction samplers, but this method is more difficult to standardize as its effectiveness directly depends on the user (Southwood, 1966). The very first machine called D-Vac (Dietrick, 1961), an upgraded backpack motor, was improved by converting a leaf-blower into a modified D-vac, now commonly referred to as ‘G-Vac’ (Stewart & Wright, 1995). This sampling method has been particularly used in agroecosystems and grasslands with varying characteristics – e.g., winter wheat fields (Topping & Sunderland, 1992), alfalfa crop (Samu et al., 1997), and limestone grasslands (Bell et al., 2000) – and can replace pitfall trapping in large spatial scale studies, due to its rapid set-up and use (Pétillon et al., 2014; Lafage & Pétillon, 2016). Previous methodological studies have (1) shown that this method is reliable for assessing the abundance and diversity of some arthropod taxa such as beetles (Coleoptera), true bugs (Hemiptera: Heteroptera), planthoppers (Hemiptera: Auchenorrhyncha), and spiders (Araneae) (Brook et al., 2008), and (2) compared this method with other sampling methods more classically used in grasslands, e.g., fenced and unfenced pitfall traps (Mommertz et al., 1996) and sweep nets (Doxon et al., 2011). These studies have

shown different invertebrate assemblages, depending on the sampling method used. According to Mommertz et al. (1996), some large and heavy individuals of Carabidae (Coleoptera), Staphylinidae (Coleoptera), and Lycosidae (Araneae) are underestimated by G-Vac sampling. As reported by Doxon et al. (2011), some orders such as Diptera, Hemiptera (Homoptera), and Hymenoptera dominate vacuum samples whereas Orthoptera and Araneae dominate sweep-net samples. Like pitfall trapping, G-Vac sampling efficiency, in addition to being taxon-dependent, can be influenced by several traits, including individual morphological and behavioral characteristics (sensu Pey et al., 2014) – e.g., individuals can be too heavy, resulting in insufficient nozzle wind speed (Mommertz et al., 1996), or too mobile and escape as the sampler approaches (Bell et al., 2000) –, but also habitat properties, such as vegetation height (Henderson & Whitaker, 1977) and humidity (Sunderland et al., 1995). Despite the importance of such studies, comparisons of sampling methods have not been done at multiple taxonomic scales, or considering both taxa and trait diversity.

In this study, we evaluated the efficiency of G-Vac sampling for community analysis (taxonomic and functional diversity) relative to pitfall (Barber) trapping. In addition to analyzing capture efficiency trends for all arthropods (order or family levels), we focused on a major taxon of predatory arthropods, spiders (Araneae), because they are abundant and diversified predators in grasslands (Jocqué & Alderweireldt, 2005). Spider diversity in body size, micro-habitat preference, and foraging strategy allows for an interesting comparison of several functional traits between suction sampling and pitfall trapping. In order to assess the complement of both methods, we used a double approach, taxonomic and functional, by assessing the diversity of arthropod taxa (orders, families, and species), their habitat preference and diet, and the species diversity, hunting guild, and body size of spiders.

We tested the general hypothesis that suction sampling and pitfall trapping are basically complementary methods, and we consequently expected taxonomic and functional diversities to be similar between the two sampling methods but with different taxa and traits assessed due to the different lifestyle of arthropods living on the ground vs. in the vegetation.

From a taxonomic point of view, we expected that (1) the sampling efficiency for suction sampling and pitfall trapping would vary among arthropod orders, with some of them absent from suction sampling due to their predominantly ground-based lifestyle, and others, living in the vegetation, absent from pitfall trapping. We also expected that (2) suction sampling is more efficient for assessing spider diversity than pitfall trapping because of a lesser sampling effort over time (active vs. passive methods).

From a functional point of view, we expected (3) phytophagous arthropods to be more sampled by suction sampling, detritivorous arthropods by pitfall trapping, and no difference in abundance of predators and omnivores.

We finally expected (4) some differences between the sampling methods in terms of both body size and hunting guilds of spiders, with web-building and smaller species living mainly in vegetation more sampled by suction sampling and larger spiders actively hunting on the ground more sampled by pitfall trapping.

## MATERIALS AND METHODS

### Fieldwork

The study area was located in the north of the Ille-et-Vilaine department (NW France, 48.696097, -1.872614), where 11 mesophilic littoral grasslands were selected as spatial replicates (Figure 1). Some of the sites were clustered in small groups, whereas others were isolated by ca. 1.5 km. In each site, four pitfall traps were placed along a transect in the middle of the grassland, 10 m apart, in order to avoid any interference between them and limit the edge effect (Topping & Sunderland, 1992). Hence, the experimental design ensured that there was no intra- and inter-grassland influence when targeting mesophilic littoral grasslands only. Each pitfall was a polypropylene cup (10 cm diameter, 20 cm deep) filled to one third with a 250 g L<sup>-1</sup> salt-saturated water solution (brine) and a few drops of scentless washing-up liquid. In the vicinity of each pitfall trap (<5 m), 20 one-second (1-s) aspirations were made with the suction sampler (Brook et al., 2008). The suction sampler was a modified leaf-blower (model SH56 27, 2 cc; Stihl, Waiblingen, Germany), commonly referred as a G-Vac (Stewart & Wright, 1995).

The highest activity period for epigeal arthropods is from May to June in Brittany (e.g., for spiders: Varet et al., 2013). Interception trapping was carried out from 7 to 14 June 2017, and suction sampling just after traps were removed, i.e., on 14 June.

Arthropods were preserved in 70% ethanol and stored for identification at the ECOBIO department (University of Rennes 1, Rennes, France).

### Taxa identification and trait attribution

Arthropods were identified to order or family level (depending on the taxonomic level needed to assess trophic habits of the arthropods) and spiders down to species level. For arthropods except spiders, we used the Aberlenc (2020) identification key. Spiders were identified to species according to Roberts (1985, 1987, 1995). The nomenclature used for spiders is that of the World Spider Catalog v.22.0 (<https://wsc.nmbe.ch/>).

Some individuals (n=31) such as *Drassodes cupreus* (Blackwall) and *Drassodes lapidosus* (Walckenaer) (Gnaphosidae), were grouped together into *Drassodes* spp. complex (Bolzern & Hänggi, 2006). In addition, in order to avoid abundance overestimation, juveniles from the 'marsupia' (sacs between the legs of woodlice) of female isopods were not counted, nor were the juvenile stages of Lycosidae carried by females on their abdomen (called 'pulli').

Trophic guilds were assigned to all taxonomic units (at the order/family level) mainly following Aberlenc (2021). Hunting guilds and body size traits were assigned to spider species using the World Spider Trait Database (<https://spidertraits.sci.muni.cz/>).

### Statistical analysis

Analyses were carried out with R software (R Core Team, 2022). To assess whether suction and pitfall trap sampling efficiencies varied between taxa of arthropods, we built a Tree map for each method to correctly visualize



**FIGURE 1** (A) Location of the study sites in Brittany, France. (B) Map of selected mesophilic grasslands (red) in the study area (background map: Orthophoto GéoBretagne). (C) Photograph illustrating the sampled habitat type.

the proportion that each taxon occupied by the individuals collected by each method. In order to plot and test for potential differences in the composition of assemblages sampled by each method, we made a correspondence analysis using the package 'FactoMineR' (v.2.6). We then used the ANOSIM dissimilarity measure to test for differences between communities using the package 'vegan' (v.2.5–7).

To compare the efficiency of both methods to assess arthropod and spider diversity, according to the sampling effort (and especially the sampling time), we computed species accumulation curves (SAC) with the specaccum function of 'vegan'. Species accumulation curves are used to see whether all/most of the species living in a specific environment have been sampled or not. To do that, we kept only the arthropods identified to the family level, for the dominant orders, i.e., Coleoptera, Hemiptera, Araneae, and Isopoda. The other individuals were grouped into a category 'others'.

In order to verify whether the measures of taxonomic diversity of spiders obtained with the two methods are similar, we calculated the Shannon-Wiener index:  $H' = -\sum_i p_i \log_b p_i$ , where  $p_i$  is the proportional abundance of spider species  $i$  and  $b$  is the base of the logarithm. As the Shannon index is sensitive to the presence of rare species, we also computed the Simpson index, which is complementary to the Shannon index due to its sensitivity to the presence of frequent species:  $D = \sum p_i^2$ . Finally, in order to measure the distribution of individuals within species independently of species richness, we calculated Pielou's evenness:  $J = H' / \log(S)$ . All these indices were computed using 'vegan'.

To estimate the association of spiders to a type of sampling method, we calculated the indicator value of species for each method according to the IndVal method (Dufrene & Legendre, 1997) using the package 'indicspecies' (v.1.7.9).

In order to verify whether phytophagous arthropods were more sampled by suction sampling and detritivorous arthropods by pitfall trapping, a  $\chi^2$  test was performed on the relative abundances of phytophagous, detritivorous, predatory, and omnivorous trophic guilds. To meet the conditions of application of the test, the abundance of arthropods representing <1% of the total for each trophic guild were grouped into a category 'others' to include them in the analyses. At a lower taxonomic resolution, and on spiders only,  $\chi^2$  tests were carried out on the different hunting guilds, taking juveniles into account or not. The minority guilds of the web-building spiders were grouped together (sheet-web, space-web, and orb-web weavers). The other hunting guilds, specialists, ambush hunters, and other hunters, which were insufficiently represented, were not included in this analysis. The two remaining hunting guilds were the ground-hunting and the weaver spiders.

To test for the potential influence of sampling method on the body size of species collected, we calculated a community weighted mean (CWM), i.e., in our case the values of the assemblage traits (body size) weighted by the

abundance of species in the assemblage. We did this for the classes sheet-web, space-web, and orb-web weavers as well as ground hunters, ambush hunters, and specialists using the packages 'tidyr' (v.1.2.1) and 'dplyr' (v.1.0.10). For practical reasons, we decided to use size as a proxy for mass using values from the literature (see above 'Taxa identification and trait attribution'), by sex in order to account for sexual size dimorphism in spiders (e.g., Foellmer & Moya-Larano, 2007). Each sample (G-Vac or trap) was considered a species assemblage and consequently used as a statistical individual in analyzes. We first tested the normality of data using a Shapiro–Wilk test ( $W=0.96$ ,  $P=0.46$ ) and the homogeneity of variances with a Bartlett test ( $\chi^2=0.07$ , d.f. = 1,  $P=0.79$ ). As the application conditions were met, mean values were compared between methods using a parametric Student's  $t$  test.

## RESULTS

### Taxonomic approach (Tables S1–S3)

In total, 21159 arthropods including 1018 mature spiders and 1340 juvenile spiders were collected and identified to various taxonomic levels (from order to species). Spiders sampled by aspiration were mainly immature (only 13.7% mature spiders), whereas those sampled by pitfall trapping were mostly mature (91% mature spiders).

The arthropod communities obtained by aspiration were mainly composed of four orders and one class. The percentage of individuals of each order in the suctioned arthropod communities was 38% for Hymenoptera, 15% for Hemiptera, 12% for Araneae, and 8% for Isopoda, and the class Collembola (Entomobryomorpha) represented 7% of the total arthropods (Figure 2A). Of the arthropods caught with pitfall trapping, the communities were mainly composed of five orders: Isopoda, Hymenoptera, Araneae, Coleoptera, and Hemiptera represented 36, 20, 14, 11, and 11%, respectively (Figure 2A). Species accumulation curves reached asymptotes, indicating a sufficient sampling effort for both methods (Figure 2B and C). The same pattern was found for all trophic group.

Nevertheless, it is important to specify that even if some taxonomic units were shared by the two sampling methods, numbers of individuals in families and species within taxonomic units were actually very different. Thus, some Hemiptera families were mostly sampled with suction, such as Aphididae (89% of the total number of 2481 individuals sampled), Cicadellidae (85% of 2400), Nabidae (83% of 294) and Berytidae (79% of 14) whereas other Hemiptera families such as Tingidae (95% of 255), Cydnidae (87% of 31), Lygaeidae (57% of 161), and Pyrrhocoridae (100% of 10) were mostly sampled with pitfalls (Figure 3).

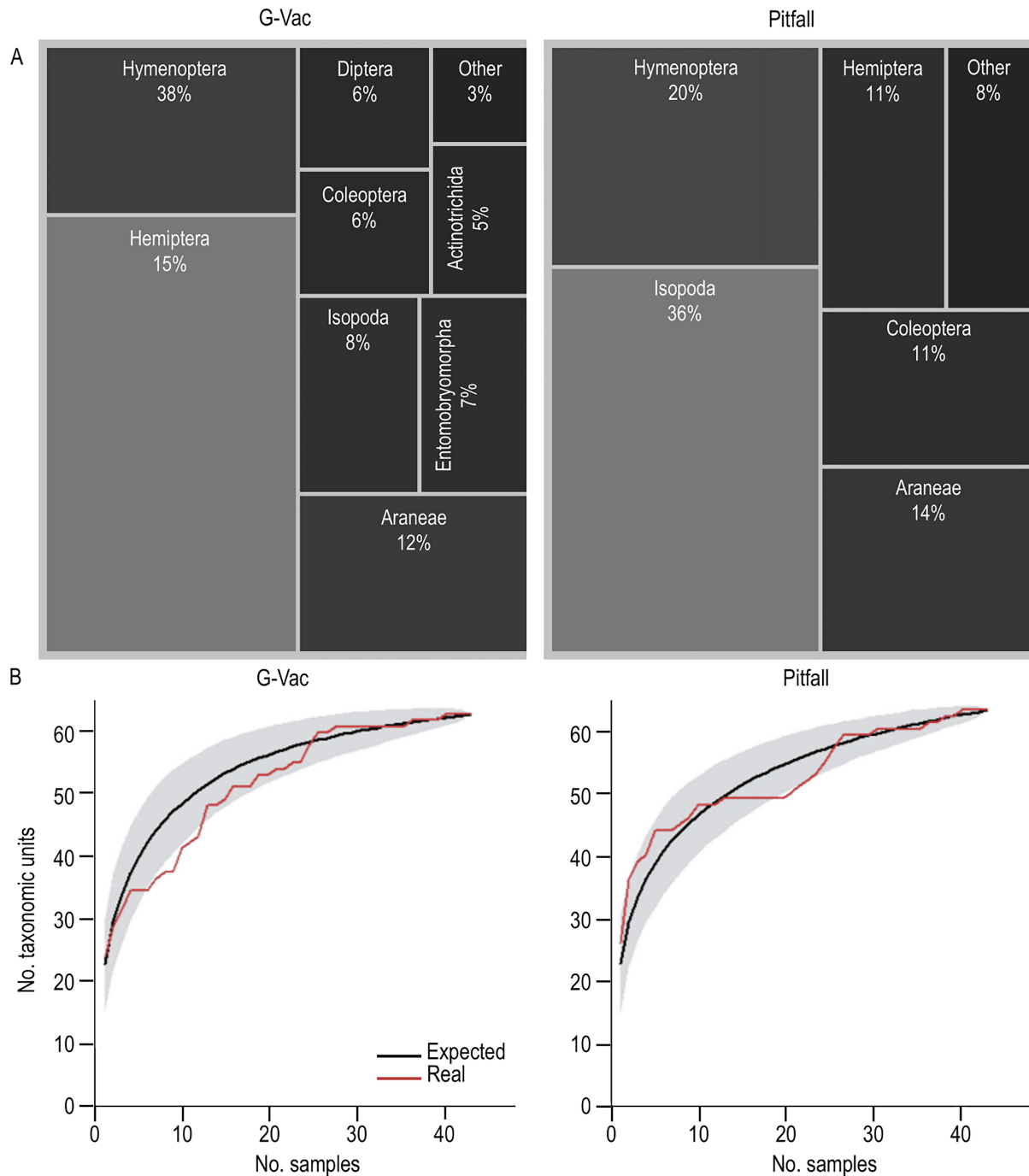
Some Coleoptera were mostly sampled with G-Vac such as Apionidae (77% of 259) and Chrysomelidae (68% of 34), and others were mostly sampled with pitfalls, such as Silphidae (100% of 21), Carabidae (87% of 207), Elateridae

(87% of 30), Phalacridae (80% of 20), Coccinellidae (78% of 76), Histeridae (75% of 57) and Staphylinidae (61% of 487) (Figure 3).

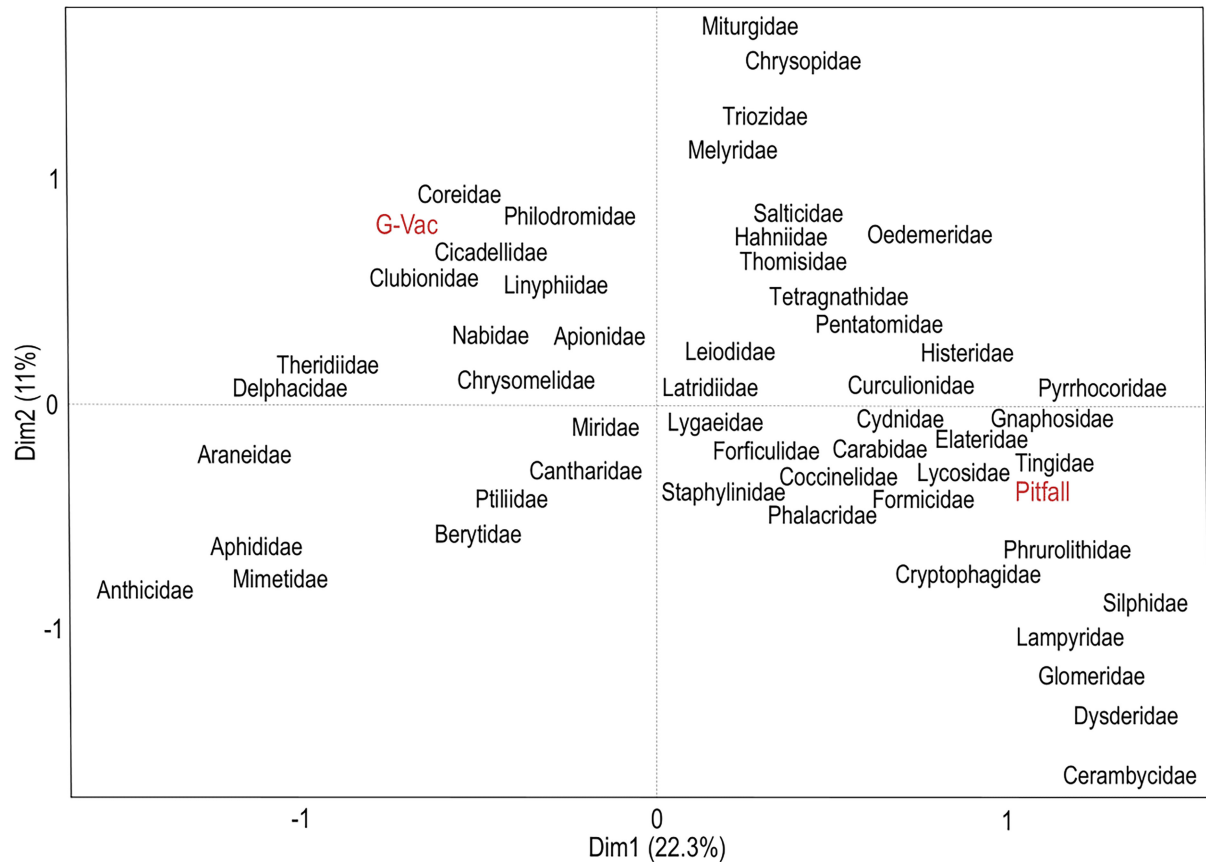
Collembola were mostly sampled with G-Vac (Entomobryomorpha: 90% of 1002; Symphypleona: 95% of 241), as were the Thysanoptera (94% of 48) and Zygentoma (78% of 37) were mostly sampled with G-Vac, whereas the isopods (77% of 4349) were mostly sampled with pitfalls.

Some Chelicerata such as Actinotrichida (72% of 856) were mostly sampled with G-Vac whereas Opiliones (88% of 158) were mostly sampled with pitfalls.

The Shannon-Wiener index was higher for spider assemblages collected by pitfall traps (G-Vac:  $H=0.70$ ; pitfall:  $H=1.69$ ). The same pattern was found for the Simpson index (G-Vac:  $1-D=0.53$ ; pitfall:  $1-D=0.76$ ) and Pielou's evenness (G-Vac:  $E=0.70$ ; pitfall: 1.51). Only one third of



**FIGURE 2** (A) Tree map of the largest arthropod taxonomic units sampled with suction (G-Vac,  $n=12100$  specimens in total) or pitfall traps ( $n=9059$ ). (B) Accumulation curves of the arthropod taxonomic units sampled with G-Vac or pitfall traps. The grey area around a curve of expected richness indicates the standard error. The real lines correspond to the observed richness.



**FIGURE 3** Correspondence analysis (CA) of arthropods families in relation to sampling methods (G-Vac or pitfall). The bi-dimensional graph represents 33.3% of the total variation, with 22.3% explained by the first dimension, and 11% by the second dimension. The arthropod families are represented in black, whereas the sampling methods are represented in red.

spider species found in the littoral meadows were shared between the two sampling methods. Each method allowed the sampling of a specific set of exclusive species (17 for the G-Vac, 29 for the pitfalls). One species in particular has been associated with aspiration sampling – *Tenuiphantes tenuis* (Blakwall) (IndVal=0.46,  $P < 0.05$ ), whereas 11 were found for the pitfalls (IndVal  $> 0.25$ ): *Ozyptila simplex* (O. Pickard-Cambridge) (IndVal=0.73), *Trachyzelotes pedestris* (C.L. Koch) (IndVal=0.55), *Alopecosa pulverulenta* (Clerck) (IndVal=0.55), *Pardosa pullata* (Clerck) (IndVal=0.50), *Pardosa cf. tenuipes* (C.L. Koch) (IndVal=0.49), *Drassyllus pusillus* (C.L. Koch) (IndVal=0.45), and *Micaria micans* (Sundevall) (IndVal=0.41, all  $P < 0.05$ ).

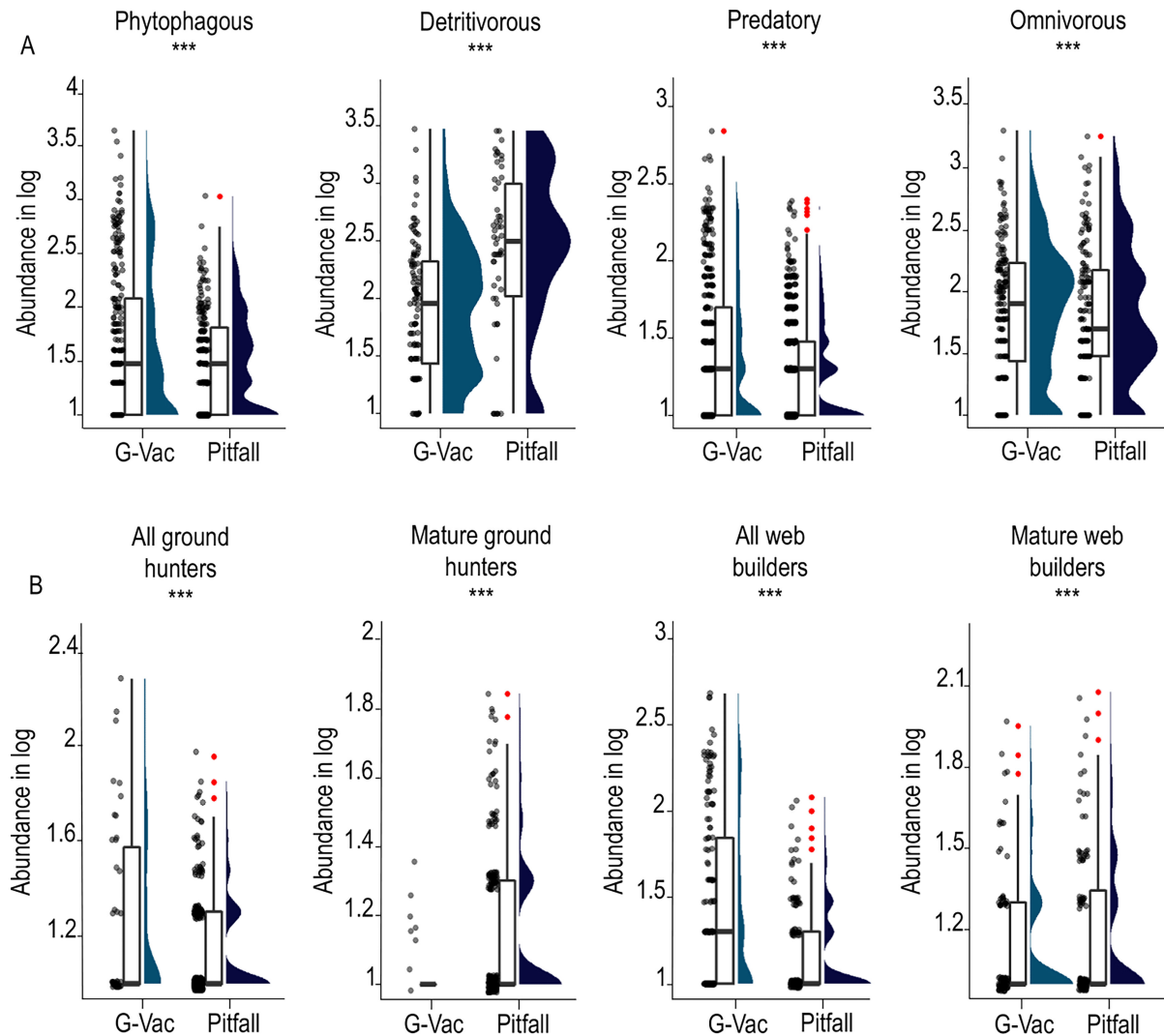
### Functional approach (Tables S1 and S2)

The two methods differed significantly concerning the composition of functional arthropod assemblages (Figure 4A). Phytophagous individuals were collected in higher numbers using G-Vac (80% of phytophagous arthropods collected) and the composition of phytophagous arthropod assemblage differed between the two methods from a taxonomic point of view ( $\chi^2 = 1386$ ,

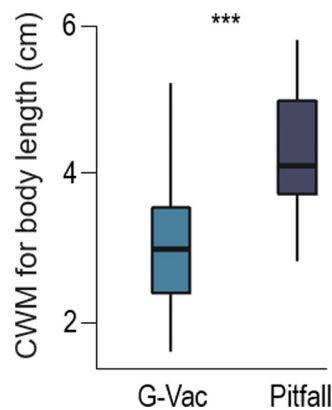
d.f. = 6,  $P < 0.0001$ ). In contrast, detritivores were collected in higher numbers using pitfalls (62%) and predators and omnivorous were collected in similar numbers using both methods (50% for both) but with differences in assemblage composition (predators:  $\chi^2 = 421$ , d.f. = 7; omnivores:  $\chi^2 = 776$ , d.f. = 4, both  $P < 0.0001$ ).

The two methods also differed significantly in the patterns of spider hunting guilds depending on whether juveniles were considered or not (Figure 4B). If juveniles are taken into account, 81% of spider individuals captured by G-Vac were web builders; taxonomically, web builders found in the G-Vac were different from the species found in the pitfalls (with juveniles:  $\chi^2 = 641$ , d.f. = 29; without juveniles:  $\chi^2 = 83$ , d.f. = 25, both  $P < 0.0001$ ). In contrast, ground hunters were collected in higher numbers using pitfalls, regardless whether juveniles were considered or not (75%), and patterns of ground hunters differed between the two methods (with juveniles:  $\chi^2 = 423$ , d.f. = 17; without juveniles:  $\chi^2 = 65$ , d.f. = 14, both  $P < 0.0001$ ).

The size (and thus body mass) of the collected spiders differed between the two sampling methods (Student's *t* test on CWM values:  $t = 5.02$ , d.f. = 20,  $P < 0.0001$ ; Figure 5). Spiders collected by G-Vac were on average smaller than spiders collected with pitfalls.



**FIGURE 4** Boxplots and violin plots of functional communities sampled with suction (G-Vac) or pitfall traps, (A) arthropod species, reflected by their trophic group: phytophagous, detritivorous, predatory, and omnivorous; (B) spiders, reflected by their hunting guild: all ground hunters, mature ground hunters (adults without juveniles), all web builders, and mature web builders (adults without juveniles). In the boxplots, the upper and lower boxes indicate the first and third quartiles, the thick line in between is the median, the whiskers indicate  $1.5\times$  the interquartile range of values in the dataset. The grey and black dots indicate individuals, outliers are represented by red dots. The violin plots show the distribution of the data and their probability density. Asterisks indicate significant differences between sampling methods ( $\chi^2$  test: \*\*\* $P < 0.001$ ).



**FIGURE 5** Boxplots of community weighted mean (CWM) spider body size (cm). Asterisks indicate significant difference between sampling methods (Student t-test: \*\*\* $P < 0.001$ ).

## DISCUSSION

We found that suction sampling and pitfall trapping are complementary sampling methods for a taxonomic and functional survey of grassland arthropods. Using these two methods, we collected different taxa with distinctive functional traits (i.e., concerning diets: phytophages, detritivores, predators, omnivores, and other), behavioral traits (i.e., spider hunting guilds: web-builders, ambush hunters, ground hunters, specialists, and other), and morphological traits (i.e., spider body size).

The capture efficiency of suction sampling significantly differed between arthropod taxa and was consistent with their preferred life-strata. For suction sampling, the catchability of individuals with a predominantly vegetation-dwelling lifestyle, mostly phytophagous species, was generally higher



than that of individuals with a ground-based lifestyle, and inversely for pitfall trapping. These results are in accordance with the literature as suction sampling has been shown to be efficient in catching arthropods in vegetation (Brook et al., 2008), although this was not formalized on a range of taxonomic levels and diversity metrics.

Our data suggest that suction sampling can be recommended to assess the densities of several families of Hemiptera mainly found in the vegetation of mesophilic grasslands, especially Aphididae, Cicadellidae, and Nabidae. In the case of Hemiptera, pitfall trapping should be used in combination with suction sampling to assess densities of families mainly found in the soil surface such as some Tingidae, Cydnidae, and Lygaeidae. Pitfall trapping can be recommended in combination with suction sampling to assess several taxa of Coleoptera, especially Carabidae, Elateridae, Coccinellidae, Histeridae, Curculionidae, Latridiidae, and Staphylinidae. For some other Coleoptera, suction sampling can be recommended, to assess densities of Apionidae and Chrysomelidae. Also for Collembola, suction sampling can be recommended to assess densities of Entomobryomorpha and Symphypleona. Some representatives of Chelicerata, such as Actinotrichida and spiders found in the vegetation, were more sampled with suction sampling, whereas pitfall trapping can better be used to sample ground-dwelling spiders and Opiliones.

Some of these results are not in accordance with the literature. For example, with regard to Hemiptera, Sanders & Entling (2011) found that aphids were not properly sampled by suction sampling, probably due to their defensive behavior of falling to the ground. Nevertheless, Tormala (1982) and Brook et al. (2008) found, like we did, that suction sampling was efficient to collect leafhoppers. For Coleoptera, suction sampling was efficient, but for a limited number of taxa. Although there are few taxonomically detailed studies for beetles, our results are in accordance with the available literature. The low efficiency of suction sampling to collect Carabidae and Staphylinidae was previously reported (e.g., Mommertz et al., 1996). However, contrary to Mommertz et al. (1996) and Sanders & Entling (2011), we have remarked here that suction sampling allowed sampling of many small individuals of Staphylinidae, whereas staphylinid individuals sampled with pitfall trapping were generally much larger. Finally, Collembola are rarely reported to be sufficiently sampled using suction, yet they were in our study similarly abundant using either trapping method. Suction sampling could therefore prove useful for sampling this group, that is known for its bioindicator qualities and its important role in soil functioning, especially in grasslands (Rusek, 1998).

Although suction sampling had a much shorter time of use compared to pitfall trapping (20×1 s vs. 1 week), it allowed us to obtain five new exclusive families of spiders (Araneidae, Clubionidae, Miturgidae, Philodromidae, and Theridiidae) whereas pitfall trapping allowed us to

obtain only one exclusive family, the Dysderidae. Suction sampling obtained 17 exclusive spider species whereas pitfall trapping captured 29 exclusive species. In addition, suction allowed the sampling of proportionally more juvenile spiders, which is in line with the observations of Bergthaler (2000).

The use of feeding traits confirmed that certain individuals' characteristics, such as diet specialization (which largely relates to the preferred life-strata), led to a high catchability of phytophagous individuals with suction sampling, in contrast to detritivorous individuals that had a high catchability with pitfall trapping. The density of predaceous and omnivorous arthropods was hardly different between the sampling methods; however, predaceous and omnivorous arthropod species composition did differ.

Using behavioral traits at a more precise taxonomic scale, such as spider hunting guilds, confirmed that individual traits other than diet specialization led to different catchabilities of species depending on the sampling method. Thus, for the same diet specialization (i.e., predatory), web-weaving spiders, very often associated with vegetation, were more easily sampled with suction whereas ground-dwelling spiders were more easily sampled with pitfalls. The higher relative abundance of weaver spiders in aspiration samples as compared to pitfall samples can be explained by the fact that this hunting guild is represented by a family that is not very mobile, Linyphiidae, thus easier to catch. Conversely, ground-dwelling spiders, which are generally mobile on the ground and do not climb along the vegetation, are overestimated by pitfall trapping (Mommertz et al., 1996, Mantzouki et al., 2012).

Finally, the use of body size has shown that suction does not allow for complete sampling of large individuals but catches rather small species with low weights, in contrast to pitfall trapping, in which larger species with higher weights are sampled (Mommertz et al., 1996). Moreover, one has to keep in mind that suction sampling cannot be used during wet weather or on grasslands with a heavy dew. Dense vegetation can also interrupt the air flow and cause a filter under which predators can hide to avoid capture (Sunderland et al., 1995). Moreover, the efficiency itself is dependent on the duration of suction and on the vegetation height (Henderson & Whitaker, 1977). Suction sampling is not well standardized – no specific G-Vac model is currently used widely, and this is a problem because its efficiency also depends on the suction power (Macleod et al., 1994), sampling time, and nozzle size. Bell et al. (2000) have shown that increasing the nozzle area decreases the number of spiders captured, but increasing the sampling time had no significant effect on the community composition. Macleod et al. (1994) and Bell et al. (2000) suggested that G-Vac sampling should rely on a 1-s sample to collect spiders. However, as suction time is dependent on habitat, it seems that a longer period of time is sometimes necessary when the vegetation is complex. That said, Brook et al. (2008) showed that 16-s suction was sufficient to collect 90% of all individuals and species of grassland beetles, with less time required for the true bugs,

spiders, and planthoppers. Samu et al. (1997) described an edge effect caused by differences in the diameter of the nozzle: the smaller the size of the nozzle, the greater the edge effect (oversampled). It is also difficult to standardize this method because as pointed out by Bell et al. (2020) suction time errors can be made inadvertently, due to lack of concentration of the user or due to difficult terrain. Finally, the continuous exposure of pitfall traps over several days may have an effect on the abundance and/or richness of local arthropods. Nevertheless, in combination with pitfall traps, we have shown that G-Vac is quite powerful to assess the diversity of arthropods in mesophilic grasslands.

## CONCLUSION

Suction sampling is thus complementary to pitfall trap for assessing both taxonomic and functional diversity of grassland arthropods. Therefore, it is necessary to combine these two methods in order to estimate trait diversity, although suction sampling seems to be better suited than pitfall trapping for taking 'snapshots' of taxonomic richness patterns. A combination of the two methods is needed to get a more accurate estimation of arthropod diversity. This study was realized in an open environment and it is important to make similar comparisons in other habitat types such as temperate and tropical forests. Such methodological studies are crucial in the characterization and study of biodiversity, and are certainly useful in the monitoring and conservation of terrestrial arthropods.

## AUTHOR CONTRIBUTIONS

**Dylan Amiar:** Data curation (lead); formal analysis (equal); investigation (equal); visualization (lead); writing – original draft (lead). **Camila Leandro:** Formal analysis (equal); supervision (supporting); visualization (supporting); writing – original draft (supporting); writing – review and editing (equal). **Cyril Courtial:** Methodology (equal). **Julien Pétilion:** Conceptualization (lead); data curation (supporting); formal analysis (supporting); methodology (equal); project administration (lead); supervision (lead); writing – original draft (supporting); writing – review and editing (equal).

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## DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**Table S1.** Numbers of individuals per taxon sampled with suction (G-Vac) or pitfall represented in two ways: abundance (no. specimens) and percentage per sampling method. A trophic guild has been associated with each taxon: phy (phytophagous), pre (predatory), omn (omnivorous), myc (mycophagous), det (detritivorous), sap (saprophagous), and hem (hematophagous). HYM, Hymenoptera; COL, Collembola; DIP, Diptera; ORT, Orthoptera.

**Table S2.** Numbers of individuals by spider family (juveniles) or spider species (mature individuals) sampled with suction (G-Vac) or pitfall represented in two ways: abundance (no. specimens) and percentage per sampling method. A hunting guild has been associated with each taxon, as well as the median body size of females and males, and daily activity.

**Table S3.** List of spider species and associated families.

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