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Comparing pitfall trapping and suction sampling data collection for ground-dwelling spiders in artificial forest gaps

László Bali, Dániel Andrési, Katalin Tuba & Csaba Szinetár



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Abstract. This study focuses on the comparison of two frequent ground-dwelling spider collecting methods, pitfall trapping and D-Vac suction sampling, in relation to artificial gap openings of a forest stand in West-Hungary. With pitfall traps, we collected 928 specimens, representing 34 species. With suction sampling, we collected 1254 specimens, belonging to 41 species. Examining the distribution of the communities, both sampling methods showed higher spider densities in forest gaps than in the forest stand. On average, the pitfall trapping accessed larger-sized spider species. The hunting and nocturnal spiders were also represented in the pitfall samples, while the D-Vac method detected more web builders. The ordination analysis showed that the two methods accessed different communities. Thus, we suggest their combined use.

Keywords: Araneae, Carpathian Basin, D-Vac, gap, pitfall trapping, turkey oak

Zusammenfassung. Vergleich von Bodenfallen und Saugfängen bodenlebender Spinnen auf künstlichen Waldlichtungen. Es werden zwei häufig angewendete Sammelmethode verglichen, Bodenfallen und D-Vac Saugfänge, und zwar auf künstlichen Lichtungen in einem Waldbestand in Westungarn. Mit Bodenfallen wurden 928 Individuen aus 34 Arten gefangen. Mithilfe der Saugfänge wurden 1254 Individuen aus 41 Arten gesammelt. Bei beiden Methoden sind die Individuenzahlen auf den Lichtungen größer als im Wald. Mit Bodenfallen wurden im Durchschnitt größere Spinnenarten gefangen. Laufjäger nachtaktive Arten waren in den Bodenfallen stärker vertreten, während mit dem Saugfängen mehr netzbauende Arten gefangen wurden. Eine Ordination zeigt, dass beide Methoden unterschiedliche Gemeinschaften erfassten. Daher schlagen wir ihre kombinierte Anwendung vor.

Formation of gaps is a part of the natural regeneration process in temperate forests (Brokaw & Busing 2000, Vepakomma et al. 2008, Fledmann et al. 2018, Senécal et al. 2018, Keram et al. 2019). In response to this, the popularity of ‘gap-cutting’ techniques is rising, and they may become essential in modern, close-to-natural forest management practices. The employment of these techniques is still relatively new however, therefore our information and understanding regarding their mechanics is lacking (Elek et al. 2018, Keram et al. 2019). In order to assess the effects of artificial gap openings on forest ecosystems and on forest floor arthropods, ground-dwelling spiders are suitable study objects (Wise 1993, Horváth et al. 2009, Elek et al. 2016, 2018). Two of the most commonly used methods for studying this taxon are pitfall trapping and suction sampling (Samu & Sárospataki 1995, Mommertz et al. 1996, Samu et al. 1997, Woodcock 2005, Kádár & Samu 2006).

Because of their relatively cheap maintenance and low labour requirements, pitfall traps have been used to collect epigeic arthropods since the early 1900s in many habitat types (e.g., Lang 2000, Zhao et al. 2013, McCravy 2018), including forests and forest gaps. Pitfall trapping is a passive sampling technique, as is suction sampling, in that they do not use any attractant (e.g., Zou et al. 2012, McCravy 2018). This method is considered to provide data on the degree of activity rather than actual population densities of the captured species, and tend to over-represent large-bodied species and slightly under-represent diurnal species. Furthermore, this trapping technique is sensitive to several external disturbance effects

(e.g., Merrett & Snazell 1983, Topping & Sunderland 1992, Sunderland et al. 1995, Hancock & Lang 2011, Zou et al. 2011, McCravy 2018). Nevertheless, pitfall trapping tends to represent the highest percentage of the surveyed taxa, including rare species when compared to other sampling methods, making it almost essential for inventory studies (e.g., Churchill & Arthur 1999, Cardoso et al. 2008, Sabu & Shiju 2010).

In contrast to pitfall trapping, D-Vac suction sampling is considered to have relatively high cost and labour requirements, but it is far less sensitive to species activity and can provide a measure of arthropod density (McCravy 2018). On the other hand, it often under-represents large and heavy species, and species that frequently occur under the soil surface, vegetation or debris (Lang 2000, Elliott et al. 2006, McCravy 2018). This sampling process causes more disturbances (Sunderland et al. 1995). Finally, both methods are sensitive to undergrowth cover (Sunderland et al. 1995, Zou et al. 2012, McCravy 2018). Because of the reasons listed above, D-Vac suction is not as popular as pitfall trapping, but it is still widely used in entomological researches (Samu et al. 1997, Elliott et al. 2006).

While there have been numerous studies dedicated to the comparison of pitfall trapping and D-Vac suction sampling regarding various habitats, there have been none – to the best of our knowledge – that compared the two methods regarding artificial gaps in forest ecosystems. Therefore, our main goal was to conduct such a survey, focusing on the following questions:

1. Is there any difference between the communities accessed by the two sampling techniques, especially regarding species and specimen numbers, family compositions, similarity- and diversity indices and body sizes?
2. Do the communities accessed by the two different methods show differentiations between the two habitats (forest stand and gaps)?
3. Considering our findings and field experiences, is one of the sampling methods more suitable than the other to survey such study sites, or can they be used in a complementary manner?

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Materials and methods

Study sites and methods

Our data collection was carried out in West Hungary, near the town of Vép in the Gyöngyös-plain (47.22750°N, 16.78917°E, 190 m a.s.l.). The mosaic-like landscape structure of this region consists mainly of agricultural fields, permanent grasslands with anthropogenic influence (mowing) with natural vegetation, and forest patches. The studied sub-compartment was a homogenous turkey oak (*Quercus cerris* L. 1735) stand, aged 70 years (in 2014), containing 12 artificial gaps (#1–#12) opened in 2010 (approximately 15 × 30 m) (Kollár 2017). Only the gaps had understory, which was densely populated by turkey oak saplings and *Rubus* patches. Everywhere else, the forest floor was covered with threads of *Poa* species and thin leaf litter. The forestry climate category of the subcompartment is hornbeam-oak. The elevation of the terroir is 200 m, with plain geomorphology. Topsoil is deep, consisting of brown forest soil with pise texture and has no excess water.

We surveyed two artificial gaps (#7 and #9) of the sub-compartment, and the stand around them, with double-cupped Barber-type pitfall traps (PT) (Barber 1931, Woodcock 2005, Kádár & Samu 2016). They had a diameter of 90 mm at the top, and were filled with 10% acetic acid solution as a preservative. In each gap, the traps were positioned in 70 m long transects along the longitudinal axis of the gaps, with 15 traps in each transect, 5 m apart from each other. Traps N^o5 and N^o11 were at the approximate edges of the gaps (Fig. 1). Emptying of these traps took place once, after two weeks of field use, on 24. Jun. 2014.

The D-Vac suction sampling (DV) (Dietrick 1961) was carried out on 24. Jun. 2015. We surveyed six additional gaps (#1, #2, #4, #6, #10 and #11). At each gap, we sampled five, 0.1 m² areas, starting from the centres of the gaps, 5 m apart from each other, with double repetition (Fig. 1.). We chose this sampling layout of the suction sampling for the following reasons. We intended to have the same sample size (30), as the pitfall trapping (we consider the 'A' and 'B' transects repetitions of each other). We also believed that surveying the gaps and transects of the original pitfall trapping would be suboptimal, since the samplings we conducted there in previous years were quite extensive, which could have influenced a new sampling. Finally, since the D-Vac sampling took place during only a single day, we intended to survey as many addi-

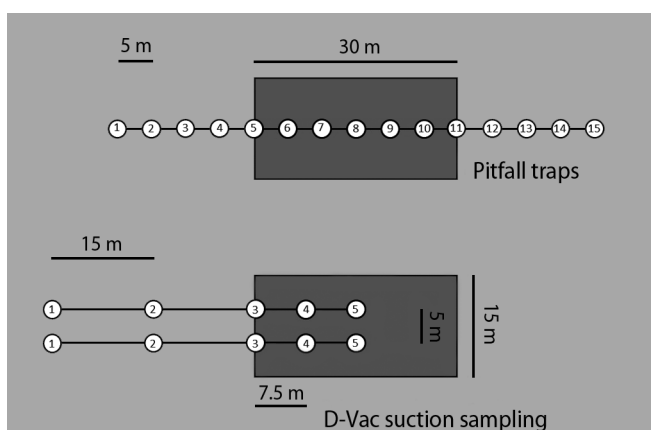


Fig. 1: Arrangement of the pitfall traps (top) and D-Vac suction samplings (bottom) at each gap (top view). Gaps represented as dark rectangles

Tab. 1: Changes in community attributes along the sampling transects. Samples located at the same relative positions in the transects are summarized. Species (S) and specimen (n) numbers represented as percentages of the total catch results (PT – pitfall trapping; DV – suction sampling, d – the distance of the sample from the centre of a gap [m]; H' – Shannon diversity; [mm] – body size; samples located inside gaps are **bold**)

Sample	d	S	n	H'	[mm]
PT.1	35	11.76	5.28	0.89	4.85
PT.2	30	14.71	2.16	1.20	5.62
PT.3	25	11.76	3.02	1.15	5.77
PT.4	20	23.53	2.05	1.89	5.34
PT.5	15	26.47	4.85	1.73	5.12
PT.6	10	38.24	7.11	2.03	5.03
PT.7	5	47.06	14.87	2.21	5.08
PT.8	0	35.29	5.28	2.24	5.55
PT.9	5	47.06	9.16	2.47	4.92
PT.10	10	26.47	6.25	1.38	5.15
PT.11	15	23.53	14.22	1.50	5.80
PT.12	20	44.12	9.81	2.08	5.71
PT.13	25	38.24	7.00	2.08	4.80
PT.14	30	20.59	5.28	1.33	4.90
PT.15	35	29.41	3.66	1.85	5.58
DV.1	45	41.46	14.99	2.66	2.66
DV.2	30	36.59	16.67	2.46	3.56
DV.3	15	34.15	18.66	2.34	2.41
DV.4	7,5	58.54	23.84	3.01	2.01
DV.5	0	43.90	25.84	2.68	1.86

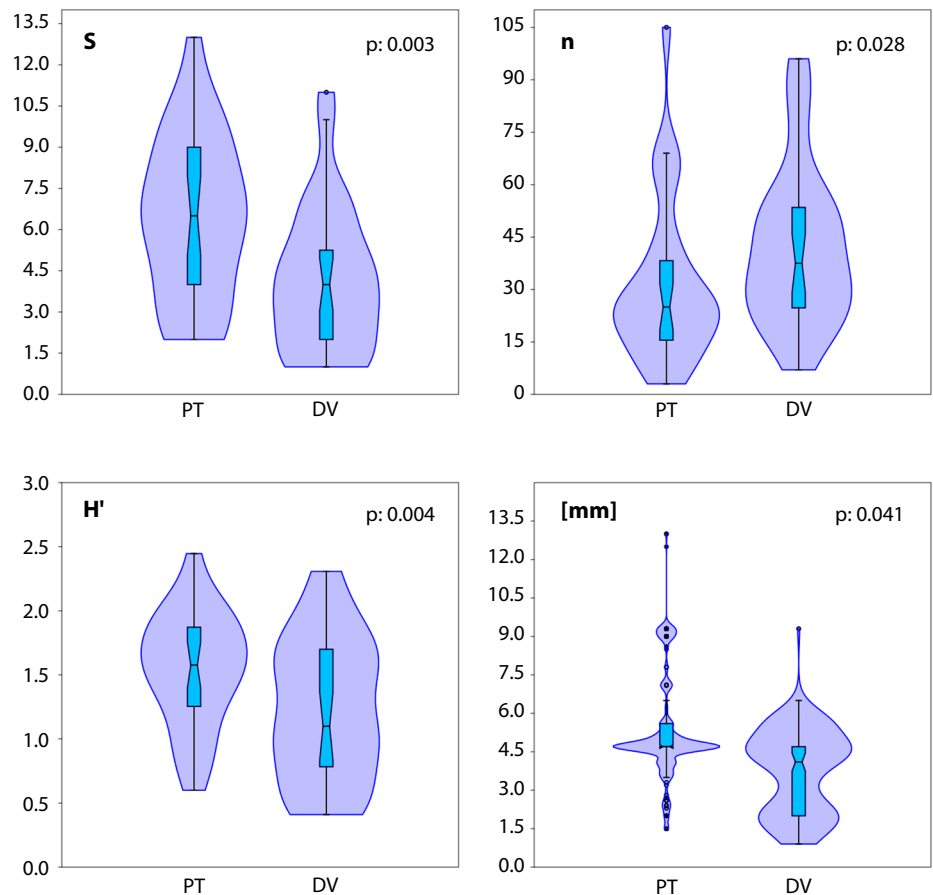
tional gaps as possible, to mitigate the unforeseeable negative effects that may occur during samplings (e.g. anthills, fallen dead wood, big game activity, etc.). The specifications of the used suction device (Stihl SH86) are as follows: a 0.8 kW (or 1.1 hp) 27.2 cm³ petrol engine with 7200 rpm speed, 770 m³/h suction capacity. A 2 litre, densely woven textile bag was used for sample collections. This device is similar in principle to the one used by Samu & Sároszpataki (1995).

In common field practice, pitfall traps are generally used for weeklong intervals, while an individual vacuum sampling only lasts for minutes. We choose to follow these practices in our survey. Since our present study is part of a larger, complex survey of the sub-compartment (Kollár 2017), we decided to keep and include the original designations of the gaps.

Data analysis

Given that we did not have the same number of samples in the different habitats, we will not make direct comparisons between their explored communities. Instead, our aim was to compare either individual samples (usually every sample, with every other sample), or the total data of both methods. We analysed the following data: numbers of species (S) and specimens (n), family and guild composition, and average body sizes [mm], which were identified by using literature data for every species (Nentwig et al. 2018). We also calculated the Shannon (H') diversity (based on natural logarithms), which is known to be sensitive to undersampling (May 1975, Beck & Schwanghart 2010), but we consider the surveyed communities well explored. To calculate this index, only data from mature specimens were used.

Fig. 2: Violin plots representing: **S**, the distribution and probability density of species numbers; **n**, specimen numbers; **H'**, Shannon diversities; **[mm]**, average body sizes of the ground-dwelling spider communities accessed by the different sampling methods; p values show the results of t-tests comparing the datasets; PT – pitfall trapping; DV – suction sampling



In order to visualise and compare the distribution of our four main data (s , n , H' , [mm]) and their probability density, we used violin plots, which are basically box plots that also show the probability density of the data at different values, usually smoothed by a kernel density estimator (Hinze & Nelson 1998). We included every individual sample (30-30) for both sampling methods (Fig. 2.). During this analysis, we also used Student's t-test to compare the datasets of the two sampling methods. We considered differences to be significant at $p < 0.05$ values.

To observe potential changes in the spider communities through the survey transect (i.e. between the gaps and forest stand) we organised the data by summarizing the samples located at the same relative positions in the transects for both methods. To make the results more comparable, we represented S and n as percentages of the total catch results (Tab. 1.).

We compared the family compositions of the two methods by species and specimen numbers, which were also represented as percentages of the total catch results (Tab. 2.). All these values were calculated by summarising the data from each sample in the same relative position. To classify the spider families into the two basic guild categories (web makers and hunters), we used the work of Cardoso et al. (2011), and we represented the data in pie charts (Fig. 3.).

Two different analyses were conducted to compare the similarities between the samples for the two methods. First, we computed the Renkonen similarity indices between the DV and PT samples (Tab. 3.). In addition, we also conducted an ordination analysis (Fig. 4.), where we applied non-metric multidimensional scaling (N-MDS). The similarity matrices were based on Bray-Curtis distance measures (Bray & Curtis 1975, Anderson & Willis 2003). The corresponding ST value

was 0.13, which is within the preferred acceptance interval (Podani 1997). The data were analysed by collecting methods and by sampling position, and only mature specimens were included. Both analyses were computed using the PAST 3.2 program (Hammer et al. 2001).

Finally, we used linear regression analysis to model the relationships between the distance from the centre of the gaps (d) and our measured data (n , S , [mm] and H'). We considered relationship to be significant at $p < 0.05$ values (Tab. 4.).

Results

The pitfall traps collected 928 (463 juvenile) specimens, representing 34 species. The suction sampling gathered 1254 (1087 juvenile) specimens, belonging to 41 species. This means an average of 2 specimens/day/trap for pitfall trapping and an average of 21 specimens/sampling (equal to 0.1 m^2) for D-Vac sampling. Eleven species occurred only in pitfall traps, while nineteen species occurred only in D-Vac samples.

The violin plots show that the mean and maximum values are higher in the pitfall samples in all four cases (S , n , H' , [mm]). The graph representing the distributions of the body sizes shows that data from the D-Vac samples are multimodal. The two peaks are in the ~ 4.5 and ~ 1.5 mm body ranges. This may indicate that the D-Vac sample collection method has assessed two different sized groups from the same community. However, the samples of from pitfall trapping seem to be mostly be the ~ 4.5 mm body range, with many outlier data points in both the minimal and the maximal ranges. Additionally, the datasets of the two methods show significant differences in the case of all four variables (Fig. 1.).

Both the S and n values are highest in the inner part of the transects (i.e. in the gaps) in the case of both methods. Addi-

Tab. 2: Family compositions. Values represented as percentages of the total catch results (PT – pitfall trapping; DV – suction sampling; highest differences in **bold**).

Taxa	Specimen number		Species number	
	PT	DV	PT	DV
Agelenidae	0.97	0.19	2.94	2.13
Atypidae	2.70	0.19	2.94	2.13
Clubionidae	0.11	0.10	2.94	2.13
Dictynidae	0.11	0.00	2.94	0.00
Dysderidae	0.22	0.10	2.94	2.13
Gnaphosidae	9.06	1.46	11.76	2.13
Hahniidae	0.00	0.19	0.00	2.13
Linyphiidae	4.31	50.58	20.59	40.43
Lycosidae	74.43	37.04	8.82	6.38
Mimetidae	0.00	0.19	0.00	2.13
Miturgidae	2.70	1.95	5.88	4.26
Mysmenidae	0.00	0.78	0.00	2.13
Philodromidae	0.54	0.39	2.94	2.13
Phrurolithidae	0.32	0.19	2.94	2.13
Pisauridae	0.11	0.00	2.94	0.00
Salticidae	0.97	2.14	8.82	6.38
Tetragnathidae	0.00	0.19	0.00	4.26
Theridiidae	0.86	1.66	11.76	10.64
Thomisidae	0.76	2.63	5.88	6.38
Zodariidae	1.83	0.00	2.94	0.00

tionally, the D-Vac data shows that the highest [mm] values are in the stands, while the lowest are in the gaps (Tab. 1.).

Examining the family-structures of the samples considering the two sampling method, it can be stated that the share of the family Linyphiidae regarding both the total species and specimen numbers were higher in the D-Vac samples.

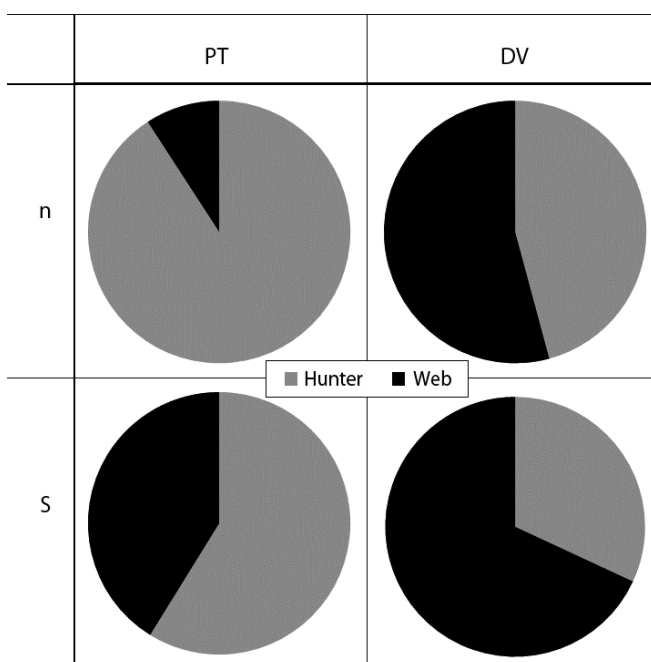


Fig. 3: Guild structure of the communities accessed by the two sampling methods (PT – pitfall trapping; DV – suction sampling; S – species number; n – specimen number)

Tab. 3: Renkonen similarity index values between the samples of the two methods. Samples located at the same relative positions in the transects are summarized (PT – pitfall trapping; DV – suction samplings; numbers in brackets represent the distance [m] of the sample site from the centre of the gaps; highest values in **bold**)

	DV.1(0)	DV.2(7.5)	DV.3(15)	DV.4(30)	DV.5(45)
PT.1(35)	0.21	0.26	0.32	0.15	0.09
PT.2(30)	0.21	0.29	0.29	0.23	0.17
PT.3(25)	0.18	0.26	0.29	0.12	0.09
PT.4(20)	0.39	0.46	0.48	0.24	0.25
PT.5(15)	0.25	0.26	0.40	0.20	0.13
PT.6(10)	0.32	0.43	0.58	0.33	0.23
PT.7(5)	0.33	0.50	0.49	0.35	0.29
PT.8(0)	0.37	0.53	0.46	0.34	0.28
PT.9(5)	0.34	0.45	0.54	0.37	0.34
PT.10(10)	0.29	0.42	0.41	0.25	0.25
PT.11(15)	0.30	0.37	0.40	0.28	0.17
PT.12(20)	0.21	0.26	0.40	0.20	0.09
PT.13(25)	0.25	0.32	0.45	0.20	0.18
PT.14(30)	0.25	0.26	0.32	0.15	0.09
PT.15(35)	0.25	0.29	0.29	0.24	0.16

We got the same results for the family Gnaphosidae in the pitfall samples. Furthermore, the share of the family Lycosidae in the total specimen numbers was higher in the pitfall samples (Tab. 2.). Additionally, the guild analysis showed that the majority of the spiders (considering both S and n) were hunters in the pitfall traps, and web builders in the D-Vac samples (Fig. 3.).

The Renkonen similarity values showed that four of the D-Vac samples show the highest similarities to those pitfall samples which are located in the gaps (Tab. 3.).

In the ordination analysis, the samples of the two methods are organised into two distinct groups. Both the largest similarities and largest dissimilarities can be seen in case of the pitfall traps. The superimposed minimum spanning tree indicate fairly good 2D solutions (Fig. 4.).

According to the regression analysis, the distance of the sampling sites shows significant relationships with specimen number, species number and diversity in case of the pitfall traps; and only with specimen number in case of suction samplings. All these values show negative connection. The R^2 values are generally low, the highest being 0.38 (Tab. 4.).

Discussion

The total sample size of the pitfall traps may be considered lower than expected. The specific reason for this is unknown, but some factors may be partially responsible: the dry microclimate of the investigated forest, the big game activity in the area and the carabid attractive properties of the acetic acid.

Both the total and the relative catching numbers were higher using the suction sampling method. The formation of two distinct groups can be interpreted in the ordination analysis as the two methods accessed somewhat different communities, which is in line with the findings of Samu & Sároszpataki (1995), Green (1999) and Cardoso et al. (2008). The reason the D-Vac samples were mostly similar to the gap located pitfall samples (according to the Renkonen indices), might be that the gap located pitfall traps caught more small

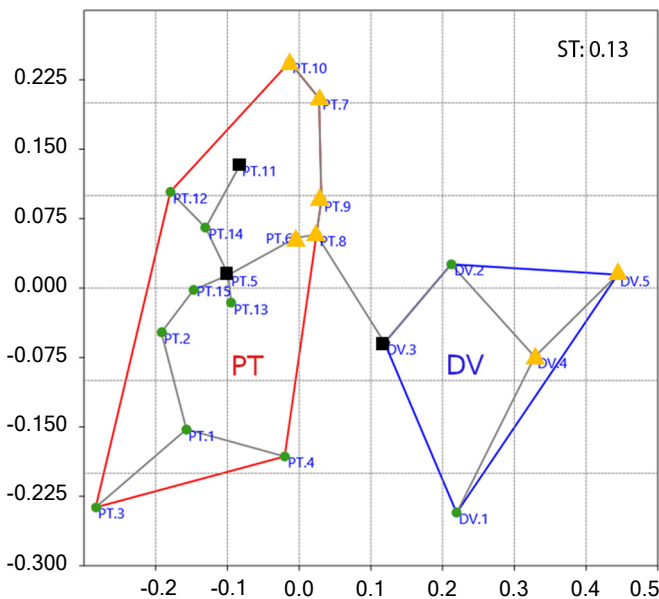


Fig. 4: Ordination analysis. Non-metric multidimensional scaling (NMDS) based on Bray-Curtis dissimilarity. Dots represent the sampling sites in the transects, with minimum spanning tree. Samples located at the same relative positions in the transects are summarized (PT – pitfall trapping; DV – suction sampling; circles – forest located samples; squares – edge located samples; triangles – gap located samples)

and/or web-building specimens. Examining the family structures, Linyphiidae was more represented in the D-Vac samples, while Lycosidae and Gnaphosidae were more represented in the pitfall samples. Underrepresentation of Lycosidae in D-Vac samples has been reported in multiple studies (Merrett & Snazell 1983, Dinter 1995). The distribution of body size data showed that the pitfall traps could catch larger species on average, as has been shown in several previous papers (Sunderland et al. 1995, McCravy 2018). The changes in community characteristics along the transects, and the results of the regression analysis show that the effects of the gap openings were more prominent regarding species numbers, specimen numbers and diversity indices, especially using pitfall traps.

Multiple reasons may have caused the differences observed between the sampling methods. One of the more obvious is the duration of each sampling. While pitfall traps were active for 14 days (and nights), the suction sampling took place during one day (in daytime). This means that less abundant and/or nocturnal species (i.e. Gnaphosidae) are more likely to be caught by pitfall traps. The disturbance (vibrations) caused by the suction device may also be responsible for the underrepresentation of hunting spiders (i.e. wolf spiders) in these samples. In addition, smaller and lighter species (Linyphiidae) may be easier to catch using suction sampling, which is in line with the findings of Mommertz et al. (1996). In addition,

the D-Vac suction may be unable to access those specimens that are under debris (leaf litter, dead wood, stone), or in the topsoil at the time of the samplings (Sunderland et al. 1987).

In summary, we suggest that for ground-dwelling spiders in forest ecosystems – partly because of its habitat's higher structural complexity – the D-Vac suction sampling is more suitable for short-term examinations, while pitfall traps can more effectively conduct the research requiring longer durations. Overall, both methods seem to be adequate to explore the effects of gap openings, but they access somewhat different attributes of the spider community. Pitfall trapping was more sensitive towards larger and/or active hunting species, while suction sampling resulted in a higher abundance of web building and/or smaller species. Therefore, in order to gain a more detailed picture on the ground-dwelling spider community of a given area, we suggest their combined use, perhaps with a pitfall focus due to this cheap maintenance and low labour requirements.

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Tab. 4: Linear regression analysis. We considered relationships to be significant at $P < 0.05$ values (D – distance from the centre of the gaps; independent variable; I – intercept; n – specimen number; S – species number; [mm] – average body size; H' – Shannon diversity; PT – pitfall trapping; DV – suction sampling)

	PT				DV				
	R ²	P	I	D	R ²	P	I	D	
n	0.1466	0.0367	45.7368	-0.7930	n	0.1376	0.0436	51.6882	-0.5071
S	0.3480	0.0006	9.3421	-0.1576	S	0.0361	0.3147	4.7902	-0.0303
[mm]	0.0010	0.8708	5.2534	0.0015	[mm]	0.1152	0.0665	1.6619	0.0216
H'	0.3843	0.0003	2.0101	-0.0250	H'	0.0460	0.2549	1.3711	-0.0072

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