

# Evaluation of Efficiency of Schoenly Trap for Collecting Adult Sarcosaprophagous Dipterans

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**ABSTRACT** Communities of adult sarcosaprophagous dipterans were evaluated using both Schoenly traps (BST) baited with rabbit carcasses and the traditional forensic methodology (TradC) in the Sabana de Bogotá, Colombia. During 42 sampling days, 2,726 adult dipterans were collected (2,291 by BST and 435 by TradC) belonging to 31 morphospecies (31 by BST and 23 by TradC) and 14 families (14 by BST and 10 by TradC). Significant differences in the species abundance, richness, diversity, and dominance were found between BTC and TradC. BST collected more individuals and species than TradC. Rank correlations and matched rank-abundance plots indicated a significant nesting of the dipteran community collected by TradC with respect to BST captures. By comparing the structure and composition of the collected communities, only those collected by BST showed repeatability of the results. The above-mentioned information allows us to consider BST as a superior methodology to perform inventories of Diptera imagoes associated with carcasses. In the community collected by BST, the most abundant and rich families were Calliphoridae, Muscidae, Phoridae, and Sarcophagidae, all of them necrophagous species associated with carcasses. Calliphoridae and Muscidae were dominant in the first stages of decomposition (fresh and active decomposition), and Phoridae was the principal family during decomposition, dry remains, and bones stages.

**KEY WORDS** forensic entomology, Schoenly trap, Diptera, Sabana de Bogotá-Colombia

The arrival of arthropods and other groups of invertebrates in a decaying substrate (e.g., a carcass in the case of forensic investigations) follows a structured and predictable sequence, which depends on both the environmental conditions and the composition of the sarcosaprophagous faunal community of the area of interest (Catts and Goff 1992, Goff and Odom 1987, Payne 1965, Payne et al. 1968, Rodriguez and Bass 1983). The assessment of these two main variables and their relationship with the successional process is one of the main sources of information for forensic entomology, which aims to determine indicator species, which span a wide time window, thereby providing relevant forensic information concerning, for example, the postmortem interval.

The heterogeneity of the tropics, manifested by its diversity of species and its environmental heterogeneity (e.g., temperature and relative humidity), makes it impossible to extrapolate or generalize entomological information gathered in temperate regions (e.g., Palearctic or Nearctic) or even other tropical regions. The recent work on forensic entomology in tropical

countries, which has mainly focused on filling the gap in our knowledge of the tropical sarcosaprophagous fauna (Baumgartner and Greenberg 1984, Baumgartner and Greenberg 1985, Moura et al. 1997, Carvalho et al. 2000, de Carvalho and Linhares 2001, Wolff et al. 2001), has emphasized this limitation, but it is clear that the job is far from being complete.

Until now, inventories of this type of fauna have usually been based on what we term herein as “traditional collection methodology,” which involves direct manual capture, by using common entomological methods (e.g., nets, brush, tweezers, and aspirators) of the fauna that is directly associated to the carcass at the time of the visit. Despite its limitations and problems, this method has been the preferred approach to making base line inventories of sarcosaprophagous fauna in Palearctic, Nearctic, and Neotropical zones (Payne 1965, Payne et al. 1968, Rodriguez and Bass 1983, Lord and Burger 1984, Anderson and VanLaerhoven 1996, VanLaerhoven and Anderson 1999, Wolff et al. 2001).

There are three main limitations associated with this methodological approach: first, it only takes into account the fauna present at the moment of the visit; second, it depends heavily on the ability and expertise of the collector; and third, it needs close contact and manipulation of the bait, so that the sampling process itself may alter the conditions of development of the organisms already established in the carcass, altering

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the successional process. Because of these problems and their interactions, the obtained inventories may be biased and incomplete, not providing an accurate representation of the invertebrate community associated with the carcass.

One way of avoiding such problems and limitations is the use of sampling devices or traps. Among various traps or devices for making inventories of the adult sarcosaprophagous fauna (Schoenly 1981, Schoenly and Reid 1983, Morón and López-Méndez 1985, Morón et al. 1986, Arnaldos et al. 2001, Arnaldos et al. 2004), the demographic bait trap designed by Schoenly (1981) seems to be the most promising. The Schoenly trap is an omnidirectional collection device that traps all fauna that accedes to, develops in, and emerges from the bait. Moreover, there is never direct contact with the bait; thus, all the arthropod fauna can be collected in a sequential way without altering the successional process. It also avoids any collector bias and reflects the entire time spectrum of the process (Schoenly 1981, Schoenly and Reid 1983).

Schoenly (1991) and Schoenly et al. (1991) briefly commented on the collection efficiency of their trap, and they pointed to how the number of species and functional group richness collected with more conventional techniques can be included within the larger range of taxa collected with their trap. The same authors also emphasize the advisability of comparing captures obtained with their device with those collected by the traditional method in the same locality.

Therefore, the aim of the present work was to assess the effectiveness of the baited Schoenly trap (BST) to collect adult dipterans and to compare its results with those obtained using the traditional methodology (TradC). We also conducted a numerical evaluation of the successional process to determine how community composition and diversity of the adult dipteran community changes during the decomposition process.

We centered our attention on dipterans, which are one of the key sarcosaprophagous faunal groups, and, along with coleopterans, they have a long-documented and well-known relationship with decaying materials, ranging from animal carcasses to decaying vegetation (Schoenly 1981, Schoenly and Reid 1983, Baumgartner and Greenberg 1984, Baumgartner and Greenberg 1985, Goddard and Lago 1985, Morón and López-Méndez 1985, Morón et al. 1986, Catts and Haskell 1990, Davies 1990, Greenberg 1991, Fisher et al. 1998, Faucherre et al. 1999, Anderson 2000, Disney 2005). Being one of the key groups associated to a decaying carcass, they are often used in forensic entomology to estimate the postmortem interval.

### Materials and Methods

**Study Area.** The study area was located in a rural area of Tenjo, Cundinamarca (Andean region of Colombia; 04° 52' 27" N, 74° 08' 54" W, at an altitude of 2,600 m. The precipitation regime is bimodal-tetrastational, with an annual average rainfall of 780.2 mm, and

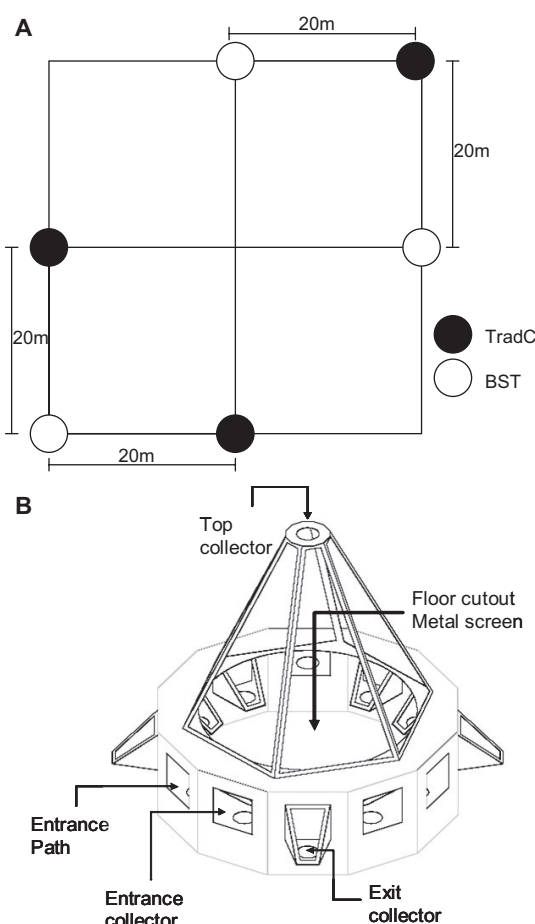


Fig. 1. (A) Diagram showing the disposition of traps in the experimental site and the. (B) Basic scheme of the Schoenly trap.

a monthly average of 65 mm, reaching a maximum (95.6 mm) in April, and a minimum (32.2 mm) in January. The annual average temperature is 13.5°C, with a maximum of 14.1°C in April and May and a minimum value of 13.1°C in December and January (weather station of Granja Providencia 2120598, Tenjo Municipality).

Almost all of the plains in the area have been transformed from their natural state for agricultural or recreational use. Currently, the area can be characterized by abundant extensions of pine groves (*Pinus patula* Schltdl. & Cham.) and milk cattle pastures dominated with *Pennisetum clandestinum* Hochst. ex Chiov. There are also large extensions of maize (*Zea mays* L.) and potatoes (*Solanum tuberosum* L.). The study site is adjacent to a wetland dominated by emergent rushes of *Polygonum* sp. L., and shore species, such as *Lemna* sp. L. and *Eichornia crassipes* Kunth.

**Data Collection.** In the study site, three enclosures similar to those used in other studies (Payne 1965, Payne et al. 1968, Early and Goff 1986, Smith 1986, De Jong and Chadwick 1999) were set up following the

Table 1. Dipteran groups or taxa in each the decomposition stage

Family	Species/Morph	BST					TradC				
		Fres	Act	DAdv	DryRm	Bon	Fres	Act	DAdv	DryRm	Bon
Calliphoridae	<i>Comptosmyiops</i> sp.1 Townsend	2	29	4							
	<i>Eudasyphora</i> sp.1 Townsend		9	4				2			
	<i>Lucilia</i> sp.1 Robineau-Desvoidy	3	788	182	125	2	9	69			9
	<i>Morelia</i> sp.1 Robineau-Desvoidy		9	1	7		3	8	1		3
	<i>Phaenicia sericata</i> Meigen	2	176	54	29	9	7	23			7
	<i>Protocalliphora</i> sp.1 Hough	8	57	2	1	2	2	36			2
Cecidomyiidae	aff. <i>Porricondyla</i> sp.1 Rondani		1								
	Cecidomyiidae sp.1	1	1								
Chironomidae	Chironomidae sp.1		2	2	1	1	4	2			4
	<i>Kermosmittia</i> sp.1 Thienemann & Kruger	1	6			2	3	2	2		3
	<i>Paratandipes</i> sp.1 Paratendipes Kieffer	1	3		2		1				1
Drosophilidae	Drosophilidae sp.1	1									
	Drosophilidae sp.2		22	5				5			
Empididae	Diptera sp.21	3			1						
Muscidae	<i>Fannia</i> sp.1 Robineau-Desvoidy	5	98	13	22	3	4	31			4
	<i>Fannia</i> sp.3 Robineau-Desvoidy	5	44	1	9	18	9	11			9
	<i>Hydrotaea</i> sp.1 Robineau-Desvoidy		7	15	4	1		9			
Mycetophilidae	<i>Musca domestica</i> L.	2	4	1	8		2	2			2
	<i>Epicyptha</i> sp.1 Winnertz		8	2	3	4		3			
	<i>Paleoplatyura</i> sp.1 Meunier		6		1	1					
Phoridae	<i>Borrophaga</i> sp.1 Enderlein	11	28	3	3	4	4	1			4
	Phoridae sp.1		3	3				3			
	Phoridae sp.2					1					
Psychodidae	Phoridae sp.3	3	8	49	8	18	4	47	4	4	4
	<i>Telmatoscopus</i> sp.1 Eaton		1								
Sarcophagidae	<i>Anolisimyia blakeae</i> Dodge			2	2	2					
	<i>Microcerella</i> sp.1 Macquart	1	7	2			7	4			7
	<i>Sarcophagula</i> sp.1 F.	2	47	7	4	5	11	16			11
Sepsidae	<i>Sepsis punctum</i> F.		8		4	4		1			
Sicaridae	<i>Corynoptera</i> sp.1 Winnertz	3	11	7	2	7	4	6	1		4
Simuliidae	Simuliidae sp.1			1					2		
Sphaeroceridae	<i>Leptosera</i> sp.1 Oliver	1	8	7	16	6	33	12			33

Fres, fresh stage; Act, active decay; DAdv, advanced decay; DryRm, dry remains; and Bon, bones.

TradC. Three modified BSTs were placed in the same area. The traps were located in a quadrangular pattern in an alternate sequence, ensuring that all traps were submitted to the same light intensity, shading, and air and soil temperatures. The distance between traps was 20 m (Fig. 1A). This distance has been shown to be sufficient for avoiding an overlapping effect of attraction by the bait (Tullis and Goff 1987, Richards and Goff 1997). Each of the BST and the TradC was baited with a headless skinned rabbit (to enhance attraction) of 2.5 kg.

The Schoenly traps used are dodecahedral boxes (the only characteristic similar to the original design by Schoenly, 1981) of 68-cm diameter (larger than the original trap), constructed of galvanized aluminum (a different material from that proposed by Schoenly) and with a series of openings in the top that allow ventilation and dissipation of the bait odor (Fig. 1B). The trap floor had a cutout with attached 1.5-cm<sup>2</sup> mesh size metal screen, between the carcass and the soil surface, allowing the natural movement of fauna between the bait and the soil.

Fieldwork was carried out for 42 d (6 wk), from 27 April 2003 to 7 June 2003. The sampling sequence was established following the protocol of the American Council of Forensic Entomology, as proposed by Catts

and Haskell (1990). The sampling frequency was as follows: every 12 h during the first 14 d; every 48 h during the following 6 d; and every 72 h during the following 21 d. During the sampling period, measurements of air temperature (°C) and absolute humidity (g × m<sup>-3</sup>) were registered hourly, inside and out side each trap, by using automated data-loggers. In comparison, internal and external trap conditions were significantly correlated (linear regressions:  $r^2 = 0.820$ ,

Table 2. Comparison between BST and TradC

Measurement	BST	TradC
Taxa (S)* <sup>a</sup>	26 ± 1	17 ± 3
Individuals* <sup>b</sup>	764 ± 78	145 ± 42
Dominance (D)* <sup>c</sup>	0.26 ± 0.07	0.12 ± 0.02
Simpson (1 - D)* <sup>d</sup>	0.74 ± 0.07	0.88 ± 0.02
Shannon (H)* <sup>e</sup>	2.04 ± 0.20	2.39 ± 0.21
Evenness (e <sup>H/S</sup> )* <sup>f</sup>	0.30 ± 0.05	0.66 ± 0.05

Comparisons were made using Mann-Whitney *U* test. Results marked with \* are significantly different ( $P < 0.005$ ).

<sup>a</sup>  $U = 0.0$ ,  $df = 3$ ,  $P = 0.04$ .

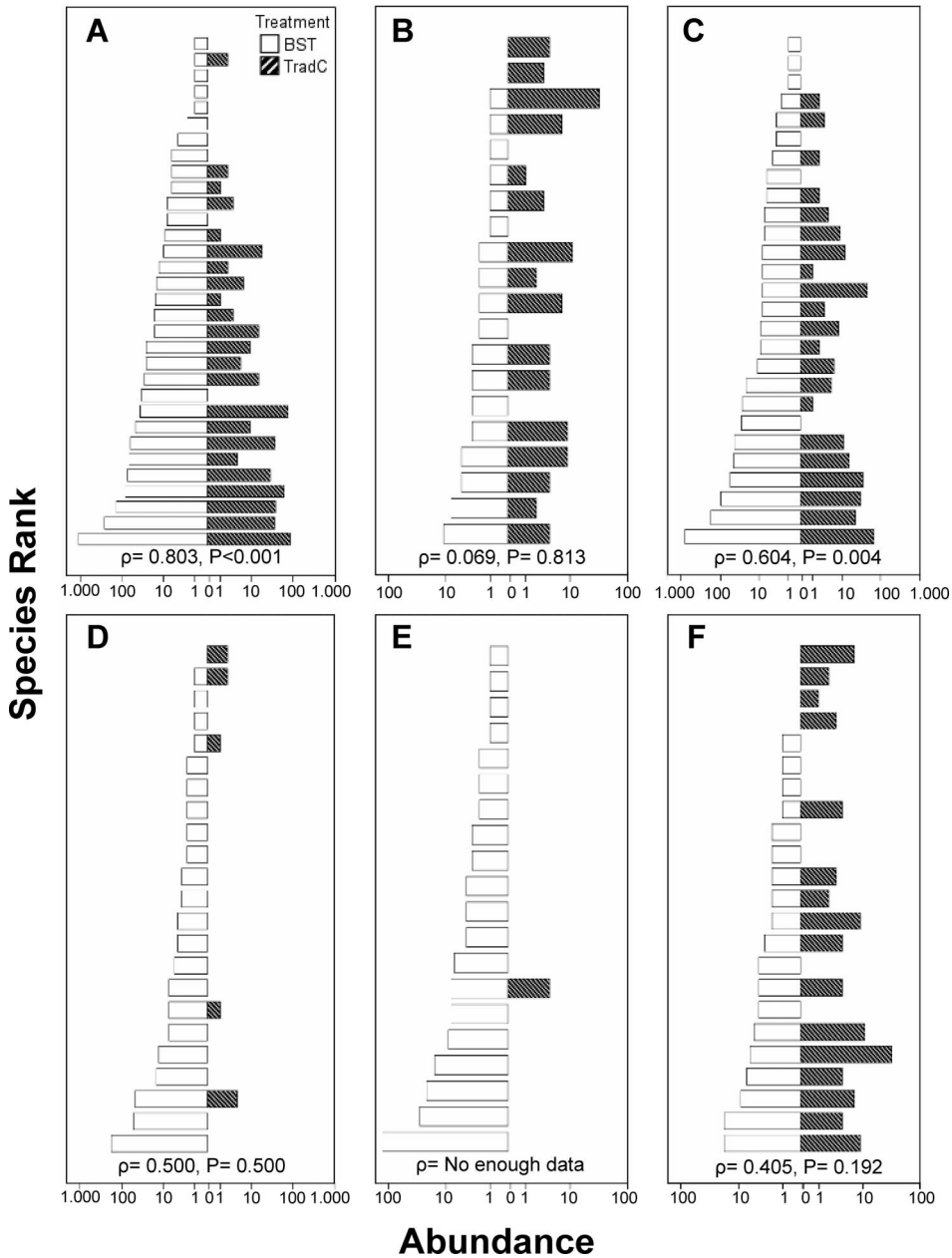
<sup>b</sup>  $U = 0.0$ ,  $df = 3$ ,  $P = 0.04$ .

<sup>c</sup>  $U = 0.0$ ,  $df = 3$ ,  $P = 0.04$ .

<sup>d</sup>  $U = 0.0$ ,  $df = 3$ ,  $P = 0.04$ .

<sup>e</sup>  $U = 1.0$ ,  $df = 3$ ,  $P = 0.12$ .

<sup>f</sup>  $U = 0.0$ ,  $df = 3$ ,  $P = 0.04$ .



**Fig. 2.** Matched rank-abundance plots of collected dipteran species from BST and TradC. Samples for each method were totalled over all sampling dates (A), segregated according to the decomposition stage: fresh stage (B), active decay (C), advanced decay (D), dry remains (E), and bone (F). Baited Schoenly traps were used as the reference methodology.

$P < 0.001$  for temperature and  $r^2 = 0.4303$ ,  $P < 0.001$  for humidity). Both temperature ( $F = 6.693$ ;  $df = 1,960$ ;  $P < 0.010$ ) and absolute humidity ( $F = 11.833$ ;  $df = 1,960$ ;  $P = 0.001$ ) differed between internal trap and external conditions, although average differences in temperature ( $2.3 \pm 2^\circ\text{C}$ ) and absolute humidity ( $0.70 \pm 0.71 \text{ g} \times \text{m}^{-3}$ ) can be consider rather small.

The collection procedure varied according to each method. For TradC, adult flies were collected during a period of 10 min (e.g., 5 min of direct collection with

brushes and tweezers and 5 min of collection by entomological net). Individuals present on top and under the carcass, together with these hidden in folds or flying over the bait were collected. Additionally, visual counts of identifiable species associated to the bait and nearby were conducted to complement the inventory.

For BSTs, the collection bottles filled with Morrill solution (Morrill 1975) (four side bottles for incoming organisms, four side bottles for outgoing organisms, and one top collector for outgoing flying organisms;

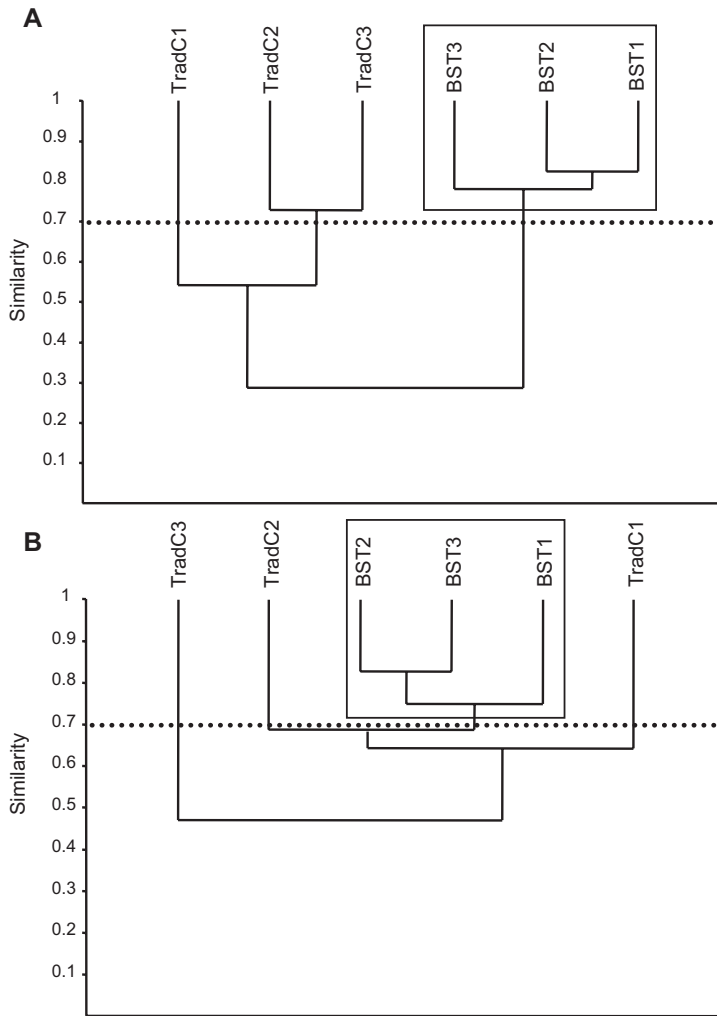


Fig. 3. Comparisons of the structure and composition of the collected community with BST and TradC; (A) Cluster analysis using Bray-Curtis algorithm and pair linkage. (B) Cluster analysis using the Jaccard index and pair linkage. Boxes in the results show the differential formation of two main groups, with BST showing sufficiently high similarity between replicates to be considered one treatment. Dashed lines mark the significance level of 70%.

Fig. 1B) were withdrawn and replaced by a new series of bottles. For each trap, individual containers were labeled with the date, hour of collection, and trap from which it was obtained.

For identification of the decomposition stages, the appearance (e.g., size of the body, decomposition stage, percentage of the remaining tissue) and the smell of each bait (e.g., no odor, rotten, rancid) were assessed for each visit. Also, the presence of larvae, their degree of development, and the presence of other groups of arthropods (e.g., coleopterans, spiders, collembolans) were recorded.

As suggested by Schoenly and Reid (1987) and Schoenly (1992), this information was used in parallel to the changes in taxonomic composition to accurately pinpoint the seral stages boundaries of the decomposition process. Thus, duration of each seral stage was determined by combining the information of the phys-

ical appearance of the body and the inventory of the entire community collected with BST (dipterans and other groups at the same time). This information was analyzed using multivariate analysis techniques (e.g., clusters and principle components analysis [PCA]) to group sampling intervals according to similarities in both the community structure and the response to environmental factors.

**Data Analysis.** To compare the efficiency of BST and TradC, the maximum, minimum, and average values of species richness, specimen abundance, Shannon-Weaver diversity, and Simpson dominance were compared graphically and statistically. We used a non-parametric test (Mann-Whitney *U* test) to determine statistical differences between collecting devices (Sokal and Rohlf 1995, Brower et al. 1997, Zar 1999).

The Shannon-Weaver diversity index (Shannon 1948) is a measurement of the information with which

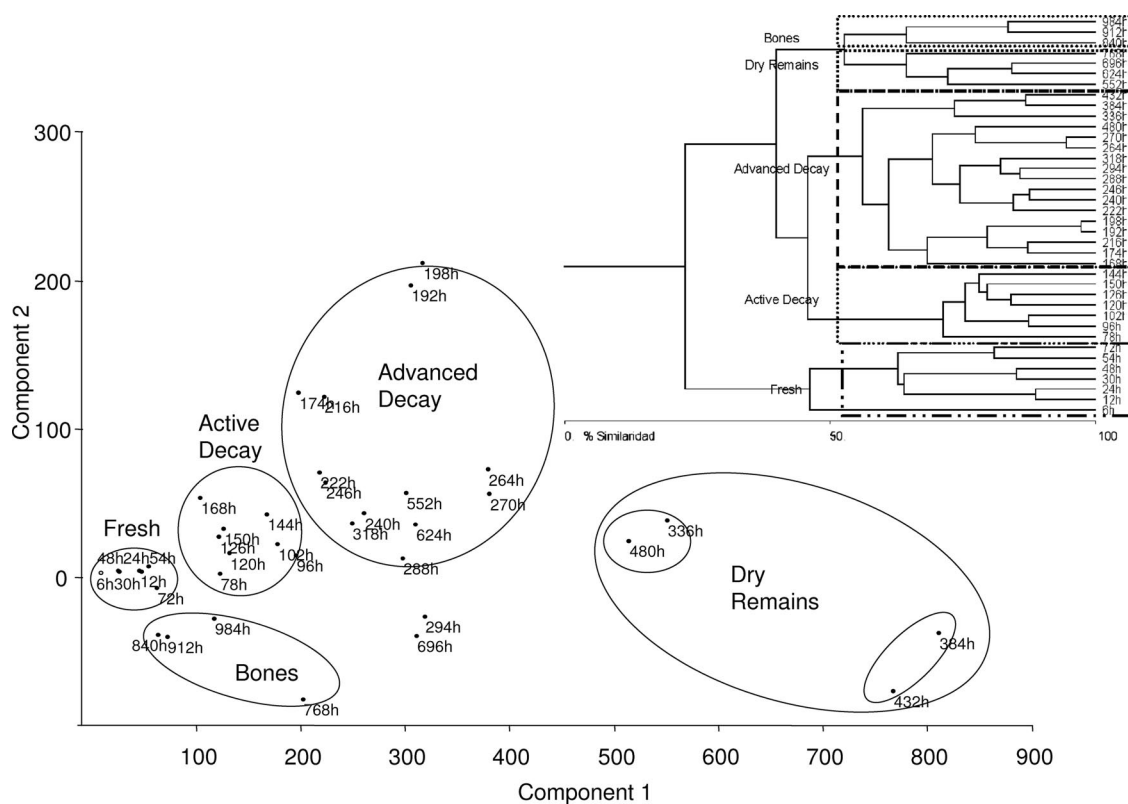


Fig. 4. Seral stages of the decay process. Stages were defined using multivariate analysis (PCA). Accumulated variance by the first two eigenvalues 83.37% (75.17% by the 1st and 8.2% by the 2nd). Inset, seral stages determination using Bray-Curtis analysis. Five stages were determined due to similarities in community structure between sampling dates. Names of each seral stage were given by using the traditional terminology for comparison purposes.

the diversity of a system is determined according to the degree of order (or disorder) present in the system-community (Ludwig and Reynolds 1988, Magurran 1988, Brower et al. 1997). This index is calculated using equation 1:

$$H' = \sum p_i \log p_i \quad [1]$$

where  $p_i$  is the proportion of the  $i$ th species from the total pool of species.

The Simpson index of dominance (Simpson 1949) is a measurement of the dominance of a given species (or a group of species). It can be defined as the probability with which two individuals selected from the same sample belong to the same species or category. This index is calculated using equation 2:

$$D_s = 1 - \frac{\sum n_i(n_i - 1)}{N(N - 1)} \quad [2]$$

where  $N$  is the total number of collected individuals and  $n_i$  is the relative abundance of the  $i$ th species or category.

Similarity of the collected communities was assessed using multivariate clustering techniques. The Bray-Curtis (equation 3) and Jaccard (equation 4) indices were used to constrict similarity clusters with a weighted average grouping technique (Brower et al. 1997, Ludwig and Reynolds 1988, Zar 1999):

$$I_{BC} = 1 - \frac{\sum |x_i - y_i|}{\sum (x_i + y_i)} \quad [3]$$

$$CC_J = \frac{c}{s_1 + s_2 - C} \quad [4]$$

where  $x_i$  is the relative abundance of the  $i$ th species in community 1;  $y_i$  is the relative abundance of the  $i$ th species in community 2;  $s_1$  and  $s_2$  are the number of species in communities 1 and 2, respectively; and  $c$  is the number of species common to communities 1 and 2:

These comparisons determined the similarity in composition (i.e., collected species) and structure (i.e., recorded species and their relative abundance) between the communities. These comparisons were also performed between replicates to assess the homogeneity between independent samplings performed by BST or TradC.

The overlap of species between sampling techniques was assessed using both "matched rank-abundance plots" (Longino and Colwell 1997), a graphical method of examining overlap of species between sampling methods; and statistical comparisons of the level of correlation of the species ranks using the Spearman rank correlation coefficient ( $\rho$ ). Matched rank-abundance plots consist of standard rank-abundance plots



Table 3. Description and duration of the observed seral stages during the decomposition process

Stage	Duration	Description
Fresh	72 h (3 d)	This stage started with the carcass placement and ended with the first evidence of blowing. No odors were detectable and no physical apparent changes in the body were evident. A large amount of dipterans were observed visiting the body.
Active decay	78 h (3 d)	Blowing of the body and intense activity of anaerobic bacteria, dipterans larvae. This activity caused a large loss of biomass and liquefaction of the carcass tissues is observed. An intense odor is perceived.
Advanced decay	330 h (14 d)	During this stage, dipteran larvae reached the last developing stage and start to migrate. Also, large amounts of coleopteran larvae were observed. Most of the carcass tissue was removed by the end of this stage, and an intense odor to raw fat characterized the stage.
Dry remains	288 h (12 d)	The remaining carcass tissue dried, and several dry tissue feeders were observed. Odors diminished during the duration of the process until no odors were perceived. At the end of the period, dipterans emerged.
Bones	144 h (6 d)	Throughout this stage, total removal of the dry tissues of the body occurred until bones were exposed and were the last remaining body tissues. No odors were perceived during this stage.

Each stage was named by its physical appearance and following stage definitions by Catts and Haskell (1990).

for a reference method (BST in our case) against which the corresponding abundances of an alternative method are compared (TradC in our case). Matched rank-abundance plots allow a quick visual inspection of the degree of correspondence in the collected community between two methods.

The seral stages of the successional process were determined using two multivariate statistical techniques: clusters and PCA (Jongman et al. 1995). Stages were determined using the data from the collected sarcosaprophagous community (using all the collected groups), the environmental data (temperature and relative humidity), and the descriptions of the carcass appearance.

Comparisons of the species richness, the abundance of individuals, Shannon–Weaver diversity, and Simpson dominance of the seral stages also were made using a nonparametric statistics (Mann–Whitney *U* test) to test for significant differences (Sokal and Rohlf 1995, Brower et al. 1997, Zar 1999).

Results and Discussion

**General Results and Comparisons of Respective Devices.** The total number of collected individuals was 2,726 (for both BST and TradC methods). These be-

long to 14 families and 31 morphospecies, assuming the concept of morphospecies proposed by Oliver and Beattie (1996).

Total number of individuals collected at each stage of the decay process for BST and TradC are shown in Table 1. A clear difference in species richness and number of individuals was evident between methods; BST collected 68% more individuals (2,291 compared with 435) and 52% more species (31 compared with 23) than TradC. When the species richness, abundance of individuals, Shannon–Weaver diversity index, and Simpson dominance values were statistically compared (Table 2), significant differences were observed between the two methods.

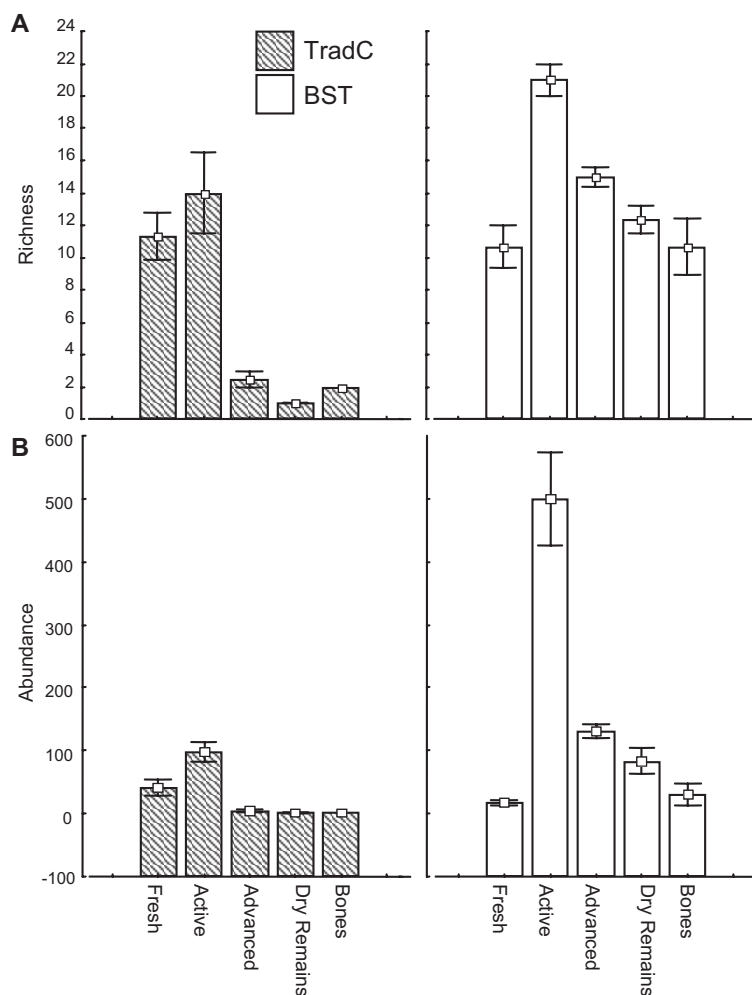
Matched rank-abundance plots for BST and TradC show for the entire collected community both a high degree of overlap in the collected community between methodologies (Fig. 2A), and a significant positive correlation across methods ( $\rho = 0.803, P < 0.001$ ). Matched abundance plots show that species caught as singletons (e.g., taxa represented as single specimens) by Trad C, were consistently caught in moderate to larger numbers by BST. Additionally, it is important to highlight that the dipteran community captured by TradC is a completely nested subset of the community collected by BST (Fig. 2A); although within each seral

Table 4. Comparison between the seral stages of observed decay process by using BST and TradC

Measurement	Fresh (mean ± SD)	Active decay (mean ± SD)	Advanced decay (mean ± SD)	Dry remains (mean ± SD)	Bones (mean ± SD)
Taxa (S) <sup>a</sup>	17 ± 2	27 ± 2	22 ± 1	20 ± 2	19 ± 3
Individuals <sup>b</sup>	54 ± 7	1499 ± 130	394 ± 20	252 ± 37	92 ± 29
Dominance (D) <sup>c</sup>	0.100 ± 0.03	0.302 ± 0.10	0.253 ± 0.07	0.276 ± 0.05	0.108 ± 0.01
Simpson (1 - D) <sup>d</sup>	2.548 ± 0.03	1.894 ± 0.10	1.992 ± 0.07	1.928 ± 0.05	2.531 ± 0.01
Shannon (H) <sup>e</sup>	0.899 ± 0.20	0.697 ± 0.23	0.746 ± 0.22	0.723 ± 0.18	0.891 ± 0.14
Evenness (e <sup>H/S</sup> ) <sup>f</sup>	0.751 ± 0.04	0.246 ± 0.09	0.333 ± 0.08	0.343 ± 0.04	0.661 ± 0.12

Comparison were made using Kruskal–Wallis test. Results marked with \* are significantly different ( $P < 0.05$ ).

<sup>a</sup> H = 10.75, df = 15,  $P = 0.03$ .  
<sup>b</sup> H = 11.52, df = 15,  $P = 0.02$ .  
<sup>c</sup> H = 10.30, df = 15,  $P = 0.04$ .  
<sup>d</sup> H = 10.30, df = 15,  $P = 0.04$ .  
<sup>e</sup> H = 6.80, df = 15,  $P = 0.15$ .  
<sup>f</sup> H = 11.86, df = 15,  $P = 0.02$ .



**Fig. 5.** Comparison of the species richness (A) and abundance (B) of BST and TradC methods on each one of the five determined seral stages of the decay process. Comparisons between the treatments showed significant differences between treatments when seral stages were taken into account for species richness ( $F = 59.77$ ,  $df = 4$ ,  $P < 0.01$ ) and abundance ( $F = 15.20$ ,  $df = 4$ ,  $P < 0.01$ ).

stage of the decomposition process, abundance ranks were significantly different between methodologies (Fig. 2B–F).

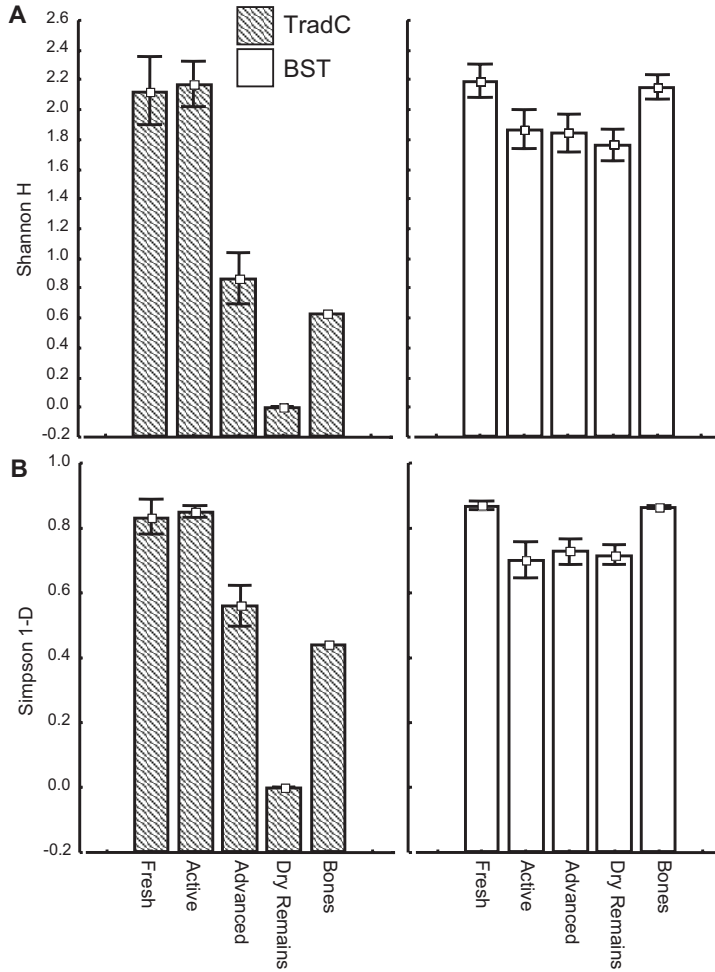
Significant differences were also found between community structure of the sarcosaprophagous community collected by BST and TradC (dissimilarity above 65%). Analogous comparisons of the community structure (Fig. 3A) and composition (Fig. 3B) between replicates for each treatment pointed to a great variability in the TradC methodology, with significant differences between replicates. This was not the case with BST, in which the communities collected by each of the replicates were very similar (i.e., similarity above 70%; Fig. 3A and B).

Taking into account the richness, abundance, diversity, and dominance (Table 2), together with the community structure and composition of both methods, it can be seen how the community collected by

BST is more complex and structured than that obtained by TradC. This difference can be attributed to the TradC community being biased toward conspicuous and abundant groups that are only observed during the sampling event, whereas the BST community shows higher richness and abundance, which represent a higher complexity in the trophic structure of the sarcosaprophagous community. These differences confirmed the differences existing between the methods and the superiority of BST for collecting adult dipterans in a decaying corpse.

Comparisons with other studies carried out in tropical areas by using the TradC method (Early and Goff 1986, Richards and Goff 1997, Carvalho et al. 2000, de Carvalho and Linhares 2001, Wolff et al. 2001) indicates a higher species richness in the BST community collected in this study. This is despite the use of larger baits (e.g., pigs weighing 2.5–25 kg) and the longer collection times in compared studies. These





**Fig. 6.** Comparison of Shannon diversity (A) and Simpson dominance (B) of BST and TradC communities on each of the five determined seral stages of the decay process. Comparisons between the treatments showed significant differences between treatments when seral stages were taken into account for Shannon diversity ( $F = 18.28$ ,  $df = 4$ ,  $P < 0.01$ ) and Simpson dominance ( $F = 37.40$ ,  $df = 4$ ,  $P < 0.01$ ).

differences, together with the superior collection efficiency of BST, suggest that this is the best choice for making inventories of the sarcosaprophagous fauna (in sensu stricto) associated with a decaying carcass.

**Global Study of the Sarcosaprophagous Community and Description of the Successional Process.** Five seral stages (Fig. 4) were defined using multivariate techniques (clusters and PCA), named according to the physical condition of the bait during the time frame of the stage (i.e., odor, physical appearance, presence of larvae and adults of other groups) and following the classification of Catts and Haskell (1990) and Catts and Goff (1992). Thus, the following names were given to the respective stages: fresh, active decay, advanced decay, dry remains, and bones.

A description and the length of each stage are recorded in Table 3. The stages reflect changes in the structure and composition of the sarcosaprophagous community as a result of transformation of the re-

source (i.e., the carcass), and the effects of the environmental variables (e.g., temperature and precipitation). The reported stages match the stages described by Anderson and VanLaerhoven (1996), Arnaldos et al. (2001, Payne (1965), and Wolff et al. (2001), and they partially agree with those described by Early and Goff (1986), Richards and Goff (1997), and Tullis and Goff (1987), which jointly consider both active and advanced stages.

The differences between the seral stages that we report here (Fig. 4; Table 3) and those recorded in others studies are mainly due to the method used to delimit the time frame of each stage. The multivariate methods as suggested by Schoenly and Reid (1987) and Schoenly (1992) take into account changes in the community composition as a result of environmental factors and the changes in the community structure, this being the cause of the time lag between our stages and those reported in other studies, which depend on the appearance of the bait.

Results from analyses of variance (ANOVAs) comparing abundance, Shannon diversity, and Simpson dominance between devices (BST and TradC) and stages (fresh, active decay, advanced decay, dry remains, and bones) confirmed the significant differences between the devices, and the changes in the community during the decay process (species richness:  $F = 59.765$ ,  $df = 4$ ,  $P < 0.01$ ; total abundance:  $F = 15.202$ ,  $df = 4$ ,  $P < 0.01$ ; Shannon diversity:  $F = 18.275$ ,  $df = 4$ ,  $P < 0.01$ ; and Simpson dominance:  $F = 37.400$ ,  $df = 4$ ,  $P < 0.01$ ). The comparison of abundance and richness of adult dipterans between devices and in each decomposition stages (Table 4) were also significantly different. The maximum value for both variables was found during the active and advanced decay stages and the lowest values during the dry stage (Fig. 5A).

The variation in total abundance and total species richness, together with the differences between stages of the Shannon diversity (Fig. 6A) and Simpson dominance (Fig. 6B) indices illustrates the changes taking place in the adult dipterans community during the decay process. This variation in the community structure is the result of changes in the condition of the corpse which attract other orders of insects.

All the above-mentioned evidence provides ample grounds to recommend BST as the most effective device for characterizing the sarcosaprophagous succession, because of the larger number of species and individuals collected during each stage and throughout the process, which permitted a more reliable characterization of the successional process.

Very few studies on sarcosaprophagous fauna have used a collection device; among those that do, we highlight Schoenly (1981), Schoenly and Reid (1983), Schoenly et al. (1991), and Arnaldos et al. (2001, 2004), which used the Schoenly demographic trap, and Morón and López-Méndez (1985), Morón et al. (1986), and Morales et al. (1998), which used the NTP-80 trap. None of these studies attempts a comparison with other methodologies, and, for the trap NPT-80, its design is directed at collecting coleopterans only; thus, a direct comparison of results with ours is not possible.

A comparison between studies carried out in different areas is not a priori indicative of the efficiency of a given device, due to the differences in the fauna as a result of various parameters (e.g., environmental factors, biogeographical region, seasonality, ecosystem type, and microclimate). Moreover, good knowledge of the regional and local fauna is necessary in forensic entomology; thus, extensive inventories of the sarcosaprophagous fauna need to be made using a uniform and unbiased method that removes collector-related errors.

This is the case with Schoenly traps, which can provide ample databases of sarcosaprophagous species for a broad range of forensic entomology applications, in a cheap, quick, and unbiased way. This is of special concern in forensic practice, where estimation of the postmortem interval can be made according to the composition of the fauna present at the time of finding

of the corpse (Catts and Goff 1992, Catts 1992). For this reason, the removal of collection bias, during the collection of baseline information takes on tremendous importance.

The Schoenly trap is clearly the most effective method of collecting adult sarcosaprophagous dipterans, reflecting the entire community species richness of this group. It can be considered as the most suitable methodology for conducting extensive inventories of adult sarcosaprophagous dipterans and for identifying all the species associated to the carcass during each stage of the decay process.

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