Remarkable TACHINID DIVERSITY from Malaise trap samples in southern BRAZIL

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Introduction

Here, I report on Tachinidae recovered from two 6m Malaise traps from the Southern Atlantic Forest of Brazil, in the states of Paraná and Santa Catarina. The traps were erected in March 2015 by Allen Norrbom (U.S. National Museum of Natural History (USNM)) and Marcoandre Savaris (Universidade de São Paulo) to sample tephritid flies. This sampling was part of a larger collaborative project between Norrbom, Luciane Marinoni (Universidade Federal do Paraná, DZUP), and her students M. Savaris and Silvana Lampert, which was focused on Tephritidae, particularly the genus *Anastrepha*. Norrbom and technicians sorted much of the material to family, including Tachinidae. I borrowed this material from the USNM to examine the diversity and composition of the tachinid fauna. The traps collected a surprising number of estimated species (212) over a sampling period of less than one week, indicating a highly diverse tachinid fauna. I briefly examine the diversity and community composition of these communities.

Site details

Both sites are located in southern Brazil, in the general region of the southern Serra do Mar (Serra Geral) characterized by a Cfb-Oceanic Koppen climate type, which consists of a temperate oceanic climate with warm summers. This region consists of the southern portion of Brazil's Atlantic Forest (*Mata Atlântica*), a biome that is famous for its biodiversity and endemism, as well as for its highly endangered status (Eisenlohr *et al*. 2015, Ribiero *et al*. 2009). The Serra do Mar region has fared better than other Atlantic Forest areas in retaining about a third of its original forest cover, although this decreases as one moves inland (e.g., Araucaria region with 12.6% remaining, Interior region with 7% remaining; Ribiero *et al*. 2009). The sampling sites are located in the subtropical Araucaria moist forest ecoregion (also known as Paraná pine forest or mixed ombrophylous forest). One trap was located near the southern border of the state of Paraná, just north of Santa Catarina (FCC) in the Serra do Mar biogeographical sub-region, and the other was located near the southeastern border between Santa Catarina and Rio Grande do Sol (PNAS), in the Araucaria sub-region. The traps were situated approximately 340 km apart (Fig. 1).

FCC

BRAZIL: Paraná: Palmas, Linha Alegria, Fazenda Cerro Chato, 1224m, 26.50252°S, 51.67033°W, Malaise on hill in campo, 3–4 Mar 2015, M. Savaris & A.L. Norrbom [area with grass & shrub vegetation and gallery forest along a river]. This trap was placed in a region of pastureland with scattered forest patches and *Araucaria* gallery forest along the Rio Chopim (Fig. 1). Specifically, it was erected near the river in an area of grass and shrub vegetation next to the gallery forest. Fazenda Cerro Chato is a working ranch in a larger area of grassland with scattered patches of forest that is neighbored by larger areas of moist *Araucaria* forest. The trap was erected for two days, 3–4 March, 2015.

PNAS

BRAZIL: SC: Parque Nacional Aparados da Serra, Rio do Boi, river crossing, 29.20231°S 50.05032°W, 209m, Malaise, 6–9 Mar 2015, A. L. Norrbom & M. Savaris.

This trap was placed in El Parque Nacional Aparados da Serra. This small, ca. 10,000 Ha, scenic park was one of Brazil's first national parks and is characterized by dense *Araucaria* forest and deep canyons. The Malaise trap was placed at the bottom of Itaimbezinho Canyon, beside the Rio do Boi, which was surrounded by forested canyon slopes (Fig. 1). It was run for four days, from 6–9 March, 2015.

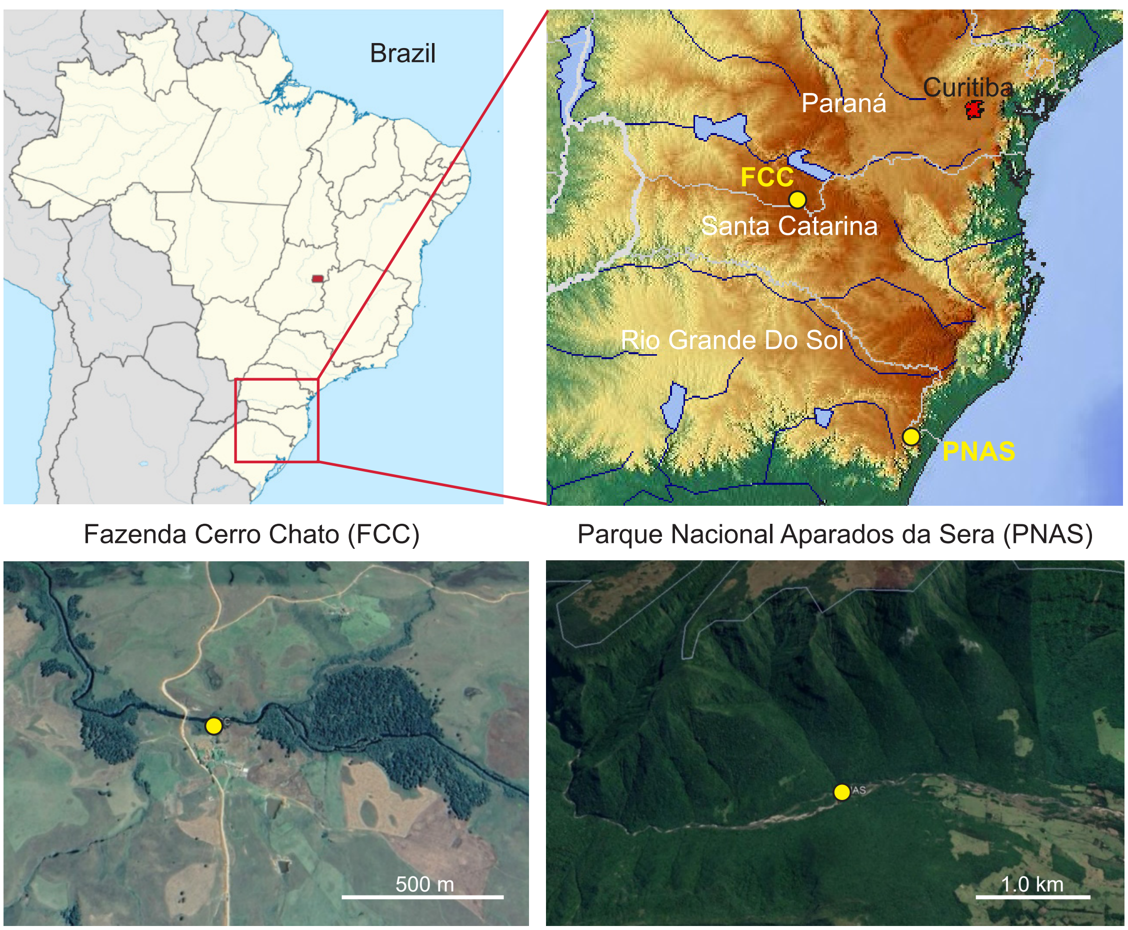


Figure 1. *Top*: Location of the trapping sites in southern Brazil. At left is an outline map of Brazil including states and at right is a zoomed in relief map with the sampling locations indicated by yellow circles. *Bottom*: Google Earth satellite views of the area surrounding each of the sites (not to same scale), with Fazenda Cerro Chato (left) situated in an open rangeland area with patchy forest and Parque Nacional Aparados da Sera, being surrounded by protected forest land.

Methods

Tachinid specimens were stored in vials with 70% ethanol for several years before I brought them to my laboratory at Wright State University, Dayton, OH, USA. I chemically dried the specimens in ethyl acetate before they were mounted on points or glued to pins (some large specimens were pinned before drying). Specimens were sexed and identified to genus with the help of keys in Wood & Zumbado (2010), Wood (1985) and Townsend (1927), and by comparisons with specimens in the Stireman (JOSC) collection at Wright State University. In assigning species to genera, I used the broad generic concepts of Wood & Zumbado (2010), and it is possible that some specimens may actually belong to other related named genera. Thus, in many cases the generic assignments are tentative, and this is often indicated by "G. nr." or "?". In some cases, the genus of a specimen could not be determined (even tentatively) and these are indicated as "nr. genus X" or "unknown genus". Comprehensive generic keys for Brazilian tachinids are lacking except for the works of Townsend (1927, 1936–1941), in which the keys tend to be difficult to use and outdated in terms of synonymy. Townsend's (1927) key to muscoid genera of the humid tropics (which does not explicitly cover the region sampled) was useful, but this work must be used with care as it appears to be based on limited representatives of each genus and my specimens often did not key to the correct genus. To make matters worse, it lacks illustrations and the abbreviations used for characters (to cut down on the length of couplets) must first be learned.

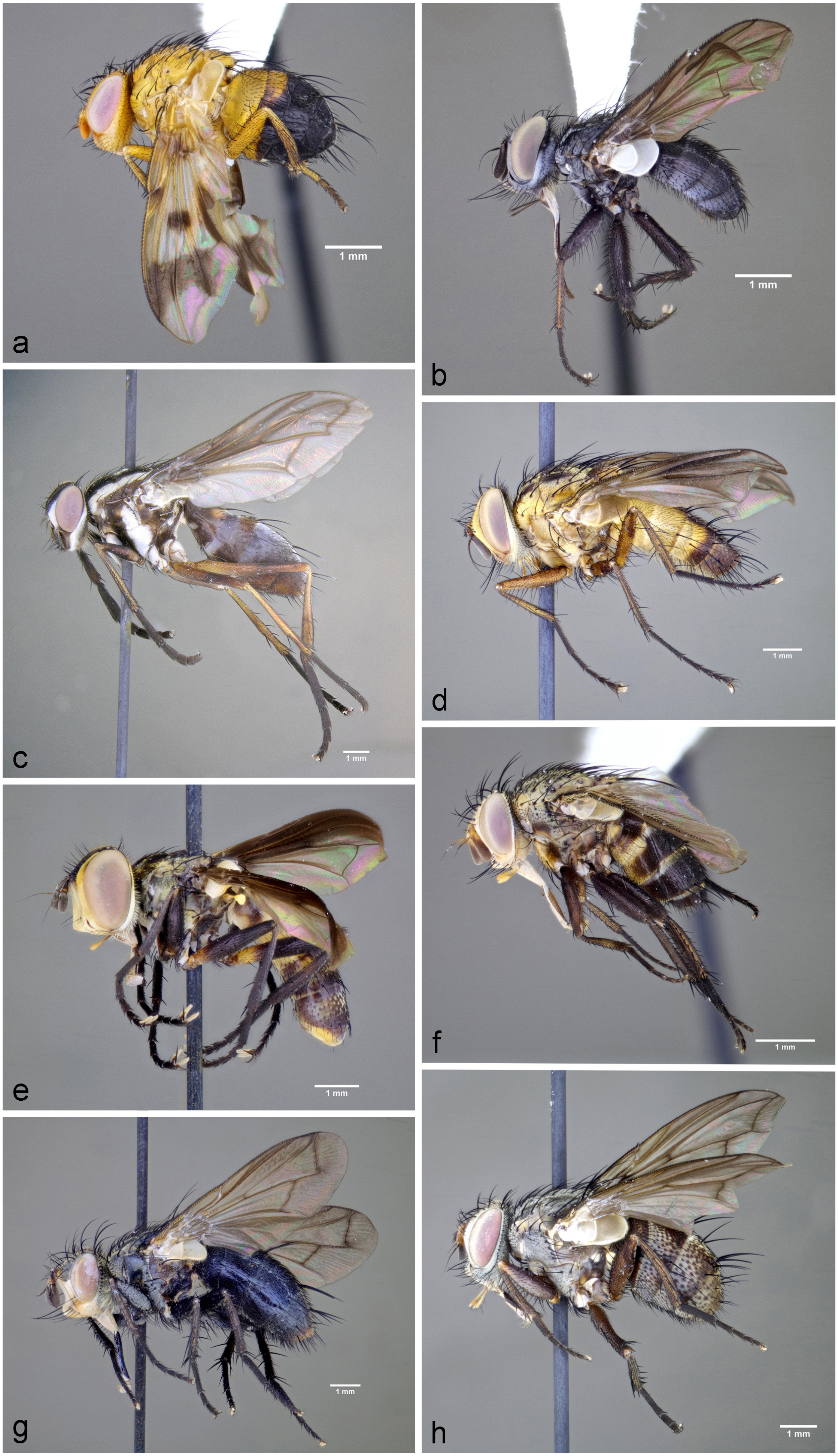
Once a tentative generic identification was established, specimens were sorted into morphospecies on the basis of external morphology. Such morphospecies designations are subject to several sources of error including the artificial separation of sexually dimorphic species or aberrant individuals and the lumping of morphologically cryptic species or those only separable by examination of terminalia. I have made notes in several instances where it is possible that two apparent morphospecies could represent one genetic species as well as where I may have lumped multiple genetic species into a single morphologically variable one. Genetic analyses of tachinid taxa have revealed both patterns; i.e., morphologically variable species that have been artificially separated (Lee *et al*. 2020) as well as cryptic species (Smith *et al*. 2007, Fleming *et al*. 2019). I probably erred in both directions, but if there is an overall bias in my morphospecies designations, it is probably towards underestimating the total number of species.

Data manipulation and quantification was conducted using the R programming language v. 3.6.0 (R core team 2019). Species rarefaction, interpolation, and extrapolation were conducted using the *iNEXT* package (Chao *et al*. 2014, Hsieh *et al*. 2016).

Results & Discussion

Over the six total trap-days, the combined traps collected 473 individual tachinids, comprising 266 males and 207 females. These specimens were divided among 212 morphospecies (Appendix 1), with 121 found at FCC (278 individuals; 2 days) and 115 found at PNAS (195 individuals, 4 days). A sample of some of the taxa that were recovered is shown in Fig. 2 (see discussion).

Figure 2 (see following page)**.** A sample of the genera and morphospecies collected. Dexiinae: **a**. *Euoestrophasia* nr. *townsendi* sp. 1 (♀) (Dufouriini). **b**. *Epigrimyia* sp. 1 (♂) (Epigrimyiini). **c**. *Euanthoides* sp. 1 (♀) (Sophiini). Exoristinae: **d**. *Eucelatoria* (or G. nr.) sp. 1 (♂) (Blondeliini). Phasiinae: **e**. *Xanthomelanopsis* sp. 2 (♂) (Gymnosomatini). Tachininae: **f**. *Actia* sp. 5 (♀) (Siphonini). **g**. *Copecrypta* sp. 1 (♀) (Tachinini). **h**. New genus 12 sp. 1 (♀) (Polideini).


a
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As is suggested by the species and specimen totals, most species were represented by just one or a few individuals in each trap (Fig. 3). A total of 133 species were recorded only once, and an additional 32 only twice. This high number of singletons suggests that we have just scratched the surface of tachinid diversity in these areas. Species rarefaction curves support this conclusion, displaying high slopes and no sign of reaching an asymptote (Fig. 4). Extrapolated richness estimates for each sampling site at twice the actual sample sizes predict species richness of 172 and 190 species for PNAS and FCC respectively. Total species richness estimates based on the Chao estimator (Chao 1987) are 273 (95% CI: 196–422) for PNAS and 324 (229–504) for FCC. These diversity estimates rival that of any other site that has been examined thus far, even tropical forest sites (see Burington *et al*. 2020). For example, a single 2m Malaise trap that was operated for over a year in Ohio (U.S.) found a total of 117 species (Chao est. 190; Inclán and Stireman 2011), and another 2m Malaise trap operated in the Ecuadorian Andes (ca. 2000m) for six weeks recovered 138 species (Chao est. 240) (Burington *et al*. 2020). Even more impressive is that the tachinid species richness of these Brazilian Atlantic Forest sites is comparable to that recovered from other trapping studies despite only a few days of sampling versus months in other cases (Burington *et al*. 2020). Interestingly, although fewer species were recorded from the PNAS site, rarefaction curves for the current Brazilian trap samples resulted in a higher slope and potentially higher asymptote for this site relative to FCC.

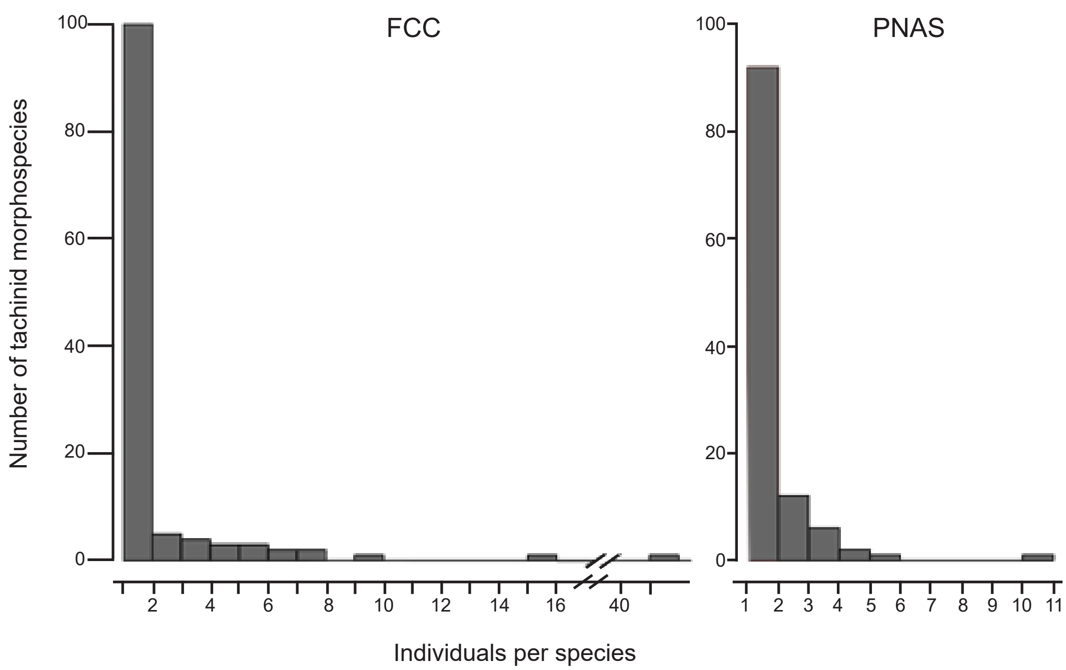

Figure 3. Histograms of the number of individuals per species in trap samples from each of the two sites (FCC left and PNAS right).

One factor contributing to the high diversity from these samples is the type of trap used. Anecdotal observations by myself and colleagues (e.g., J.E. O'Hara, G.A. Dahlem) suggest that the large 6m Malaise traps can be exceedingly effective at collecting tachinids, even when the results of other collecting methods, including standard 2m Malaise traps, are poor.

Only 22 species (about 10% of the total) were shared between the two sampling sites, resulting in high dissimilarity estimates (Bray-Curtis distance = 0.860, Jaccard distance = 0.925, where a value of one indicates maximum dissimilarity). However, this should not necessarily be interpreted as high species turnover or beta diversity between the sampling locations because so many of the species were represented by only one or a few individuals. More extensive sampling at each site could reveal many more shared species as the communities are more thoroughly characterized.

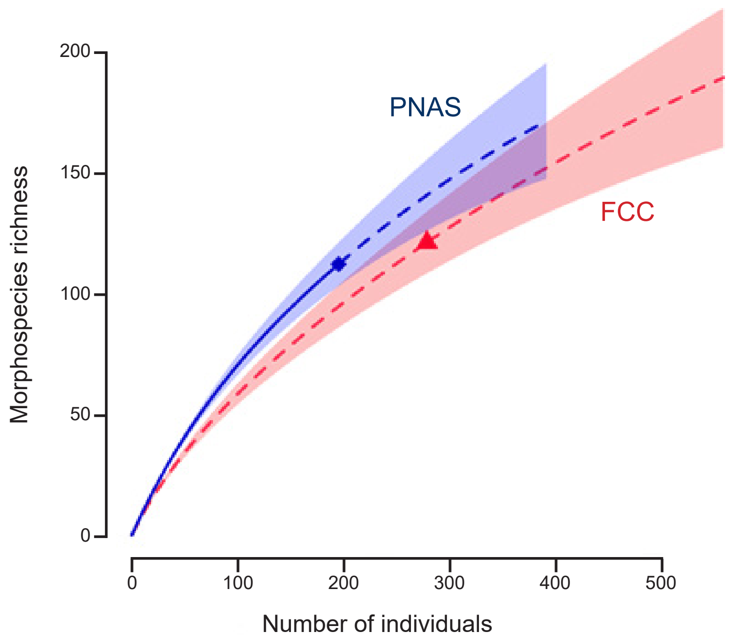

Figure 4. Rarefaction curves of species richness calculated for each site with 95% bootstrap confidence intervals (colored regions) using *iNEXT* (see text). Symbols indicate the observed values of species richness and total number of individuals. Dotted lines indicate extrapolated richness values to twice the observed number of individuals.

Composition

Trap samples of both communities were dominated by the tribes Blondeliini and Siphonini (Fig. 5; Appendix 1). These two tribes made up well over half of all recorded species and individuals. The rank of other tribes with regard to species richness and abundance was also similar between the two sites, with some exceptions. I briefly summarize some of the taxonomic patterns below.

Dexiinae (Fig. 2a–c)

Voriini comprised the third most species rich tribe at both sites, largely due to the genus *Campylocheta*, which was represented by an estimated 10 species. Otherwise, there were relatively few Dexiinae, except for a species of *Prosena* found at FCC, which was the most abundant species recovered with 41 individuals (this resulted in Dexiini being the fourth ranked tribe in terms of abundance at FCC). Perhaps the most notable dexiines were the odd-looking *Euanthoides* spp. (Sophiini), with their boldly marked bodies, petiolate abdomens and extremely short, sunken, antennae (Fig. 2c). Four species of Dufouriini were collected, including three species of *Euoestrophasia* (all from FCC; Fig. 2a). The presence of the genus *Epigrimyia* (Epigrimyiini; Fig. 2b) at FCC was somewhat unexpected, as the genus was not previously known from South America (O'Hara *et al*. 2020), although its relative *Beskia aelops* (Walker), which was also collected, is known from throughout the Americas.

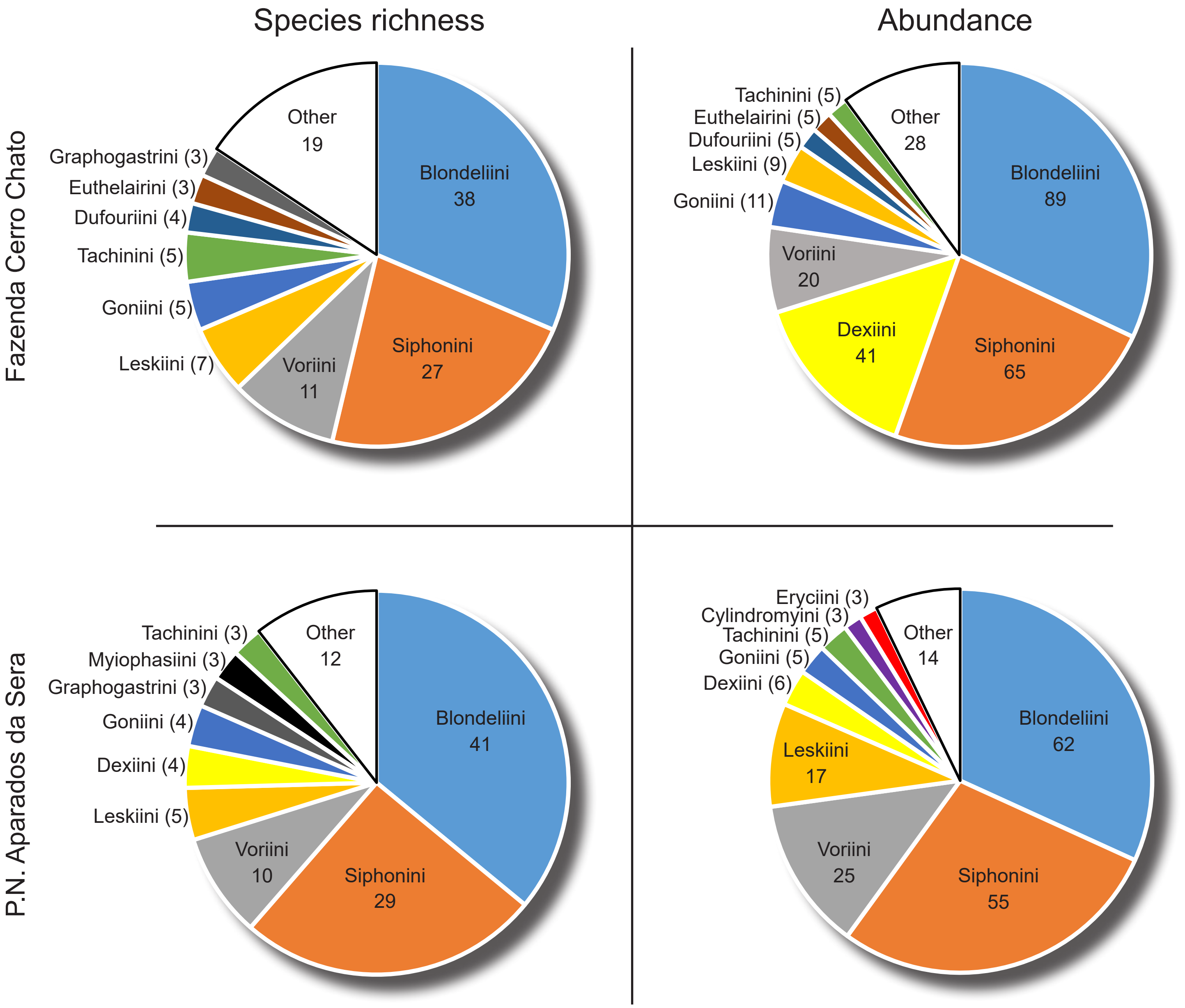

Figure 5. Pie charts showing the relative dominance of tachinid tribes in terms of species richness (left) and number of individuals (right) for traps at each sampling site (top: Fazenda Cerro Chato, bottom: P.N. Aparados da Serra). Numbers of species or individuals are given after tribe names.

Exoristinae (Fig. 2d)

Within the Blondelliini, the dominant genera included *Chaetostigmoptera* (7–8 spp.), *Eucelatoria* (8), *Lixophaga* (13), and *Myiopharus* (13). As stated previously, some of these generic placements are tentative and there were several blondeliines in which the genus was unclear (e.g., Fig. 2d). Goniini (8 spp.) and Eryciini (3 spp.) appeared to be under-represented given the large numbers of described species within these tribes, and Exoristini were entirely absent.

Phasiinae (Fig. 2e)

Very few phasiines were collected between the two traps, with only eight species in six genera being recorded (12 individuals, ~ 2.5% of the total; see Appendix 1). Of note was the finding of two species of *Xanthomelanopsis* (Fig. 2e) and two species of the unusual phasiine *Neobrachelia*.

Tachininae (Fig. 2f–h)

Siphonini dominated the contribution of the subfamily Tachininae to trap samples. *Siphona* was the most species rich genus in the samples, with 28 apparent species, although *Actia* (10 spp.; Fig. 2f) and *Ceromya* (8) were also well represented. Other tachinine groups that were relatively well represented include the Leskiini (12 spp.) and Graphogastrini (6 spp., all *Phytomyptera*). The relative lack of Tachinini (7 spp.) was notable for such a large tribe, although several species of *Copecrypta* (Fig. 2g) were collected. Of the two Polideini collected, one represents an unnamed genus (Fig. 2h, N. Genus 12; Perilla-López pers. comm.).

Interpretation and conclusions

It is clear from this preliminary study of Malaise trap samples from southern Brazil that this region harbors a rich and diverse tachinid fauna. It is surprising that more than 200 species were recovered from these traps over a span of only six days, and extrapolations from rarefaction hint at a much richer total fauna. As mentioned previously, part of the explanation for this great diversity of tachinids collected may be the high efficacy of 6m Malaise traps versus smaller traps or other survey methods. In addition, at both sites the traps were placed near waterways alongside gallery forests that could represent major flyways for tachinids. In this way, the traps may have sampled a much larger area than expected based on their size. I found it interesting that the FCC site harbored more species, given that it was sampled for a shorter period of time and the area is locally more impacted by grazing and other intensive land uses. However, this area likely possesses a greater variety of habitats including gallery forest, shrubby areas, grasslands, and pastures, which may enhance local tachinid diversity. The PNAS site, on the other hand, was surrounded by relatively unbroken forest, although just outside the park boundaries forest clearing and other human impacts are evident. Still, rarefaction analyses indicated that the PNAS site may actually possess greater diversity than FCC at comparable sample sizes of individuals, suggesting that the more intact forested site may hold more species. As indicated previously, the species turnover between the two sites was very high, but this may partly be an artifact of the large numbers of singletons, doubletons, etc.

The patterns of taxonomic composition of the sampled tachinids are difficult to interpret. The two sites had similar relative abundance and richness of tachinid tribes, suggesting that observed patterns are not just due to the local conditions of the traps. On the other hand, we know very little about how Malaise trap catches are biased relative to local community composition. The traps caught many individuals and species of smaller bodied taxa (e.g., Blondeliini, Siphonini, *Phytomyptera*, *Campylocheta*), which hand collecting is likely biased against. The paucity of Goniini+Eryciini, is however striking. A cursory examination of other tachinid trap data in the Neotropics (from upland sites) supports the dominance of Blondeliini and Siphonini and a relatively low diversity of Goniini and Eryciini, however Tachinini tend to comprise a much higher fraction of species in these other datasets (J.O. Stireman, unpub. data). Finally, it should be remembered that the traps were out for only a very short period at a particular time of year (early March). Sampling over a larger temporal scale may reveal a much different taxonomic composition as well as many additional species.

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Appendix 1. Table of species

Tachinid genera and morphospecies recorded from two traps in southern Brazil. M = number of males, F = number of females, Tot = total individuals, FCC = Fazenda Cerro Chato, PNAS = Parque Nacional Aparados da Serra (x's indicate species presence).

Species	M	F	Tot	FCC	PNAS	Notes
SUBFAMILY DEXIINAE						
Tribe Dexiini						
Billaea sp. 1	0	1	**1**		x	
Billaea sp. 2	0	1	**1**		x	
Leptodexia (?) sp. 1	0	1	**1**		x	
Myiomima (or G. nr.) sp. 1	2	1	**3**		x	
Prosena sp. 1	35	6	**41**	x		
Tribe Dufouriini						
Ebenia sp. 1	0	1	**1**		x	
Euestrophasia aperta (B. & B.)	1	0	**1**	x		
Euestrophasia nr. *townsendi* Guimarães sp. 1	0	3	**3**	x		
Euestrophasia nr. *townsendi* Guimarães sp. 2	0	1	**1**	x		
Tribe Epigrimyiini						
Beskia aelops (Walker)?	1	0	**1**	x		
Epigrimyia sp. 1	2	0	**2**	x		
Tribe Sophiini						
Euanthoides sp. 1	0	1	**1**	x		not *E. petiolata* Tnsd.
Euanthoides sp. 2	1	0	**1**	x		M of sp. 1?
Tribe Telothyriini						
Telothyria sp. 1	3	1	**4**	x		>1 sp.?
Telothyria sp. 2	1	0	**1**		x	
Telothyria sp. 3	0	1	**1**		x	F of sp. 2?
Tribe Uramyini						
Itaplectops sp. 1	1	0	**1**		x	
Tribe Voriini						
Arrhinactia sp. 1	0	1	**1**	x		
Campylocheta sp. 1	0	1	**1**	x		
Campylocheta sp. 2	0	1	**1**		x	
Campylocheta sp. 3	1	2	**3**		x	
Campylocheta sp. 3a	1	0	**1**		x	
Campylocheta sp. 4	8	2	**10**	x	x	
Campylocheta sp. 4a	3	0	**3**	x	x	= sp. 4?
Campylocheta sp. 4b	0	1	**1**		x	
Campylocheta sp. 5	3	2	**5**		x	
Campylocheta sp. 6	1	2	**3**		x	
Campylocheta sp. 7	3	1	**4**		x	= sp. 4 or sp. 5?
Cyrtophloeba/*Minthoplagia* sp. 1	0	2	**2**	x		
Micronychiops sp. 1	3	0	**3**	x		

Species	M	F	Tot	FCC	PNAS	Notes
Neosolieria sp. 1	1	0	**1**	x		
Neosolieria sp. 2	0	1	**1**		x	
Phasiophyto sp. 1	0	1	**1**	x		
Spathidexia sp. 1	0	2	**2**	x		
Trafoia or G. nr. sp. 1	1	0	**1**	x		
G. nr. *Trochilodes* sp. 1	0	1	**1**	x		
SUBFAMILY EXORISTINAE						
Tribe Blondeliini						
Admontia or G. nr. sp. 1	1	0	**1**	x		
Admontia sp. 1	1	0	**1**	x		
Anisia sp. 1	4	1	**5**	x		F diff., >1 sp. ?
Borgmeiermyia or G. nr. sp. 1	1	7	**8**	x	x	
Borgmeiermyia or G. nr. sp. 2	0	1	**1**		x	
Calodexia sp. 1	0	3	**3**		x	
Calodexia sp. 2	0	1	**1**		x	
Calodexia sp. 3	1	1	**2**		x	
Calolydella sp. 1	0	1	**1**	x		
Celatoria sp. 1	0	1	**1**	x		
Celatoria sp. 2	0	2	**2**	x		
Chaetodoria sp. 1	2	0	**2**	x		
Chaetona sp. 1	0	1	**1**		x	
Chaetonodexodes sp. 1	0	1	**1**		x	
Chaetostigmoptera G. nr. sp. 1	0	3	**3**		x	
Chaetostigmoptera sp. 1	0	2	**2**		x	
Chaetostigmoptera sp. 1a	0	1	**1**		x	
Chaetostigmoptera sp. 2	1	0	**1**	x		
Chaetostigmoptera sp. 3	8	0	**8**	x		
Chaetostigmoptera sp. 4	1	0	**1**		x	
Chaetostigmoptera sp. 5	0	4	**4**	x		
Chaetostigmoptera? sp. 6	1	1	**2**	x		
Erythromelana cf. *leptoforceps* (Inclán)	2	0	**2**		x	
Eucelatoria cf. *strigata* (van der Wulp)	0	2	**2**		x	
Eucelatoria sp. 1	11	6	**17**	x	x	F diff., >1 sp.?
Eucelatoria sp. 3	0	1	**1**		x	
Eucelatoria sp. 4	0	1	**1**	x		
Eucelatoria sp. 4a	1	0	**1**	x		
Eucelatoria sp. 4b	0	1	**1**		x	
Eucelatoria sp. 5 *aurata* (Tnsd.) grp.	0	1	**1**		x	
Eucelatoria sp. 6 *tinensis* (Tnsd.) grp.	0	1	**1**		x	
Eucelatoria sp. 7	0	1	**1**		x	
Italispidea sp. 1	1	0	**1**	x		
Italispidea sp. 2	4	0	**4**		x	1M diff., >1 sp.?
Leptostylum sp. 1	0	1	**1**		x	
Lixophaga (or *Calolydella*) sp. 1	1	0	**1**	x		

Species	M	F	**Tot**	FCC	PNAS	Notes
Lixophaga sp. 1	1	0	**1**	x		
Lixophaga sp. 2	10	0	**10**	x		
Lixophaga sp. 2b	0	1	**1**		x	F of sp. 2?
Lixophaga sp. 3	1	2	**3**		x	
Lixophaga sp. 5	0	2	**2**	x		
Lixophaga sp. 6	0	1	**1**		x	
Lixophaga sp. 7	0	1	**1**	x		
Lixophaga sp. 8	2	0	**2**	x		
Lixophaga sp. 9	1	0	**1**	x		
Lixophaga sp. 10	0	1	**1**	x		
Lixophaga sp. 11	0	1	**1**	x		
Lixophaga sp. 12	0	1	**1**	x		
Lydinolydella or G. nr. sp. 1	1	0	**1**	x		*Opsomeigenia*?
Myiodoriops (or *Lixophaga*) sp. 1	4	0	**4**	x		nr. *Erythromelana*
Myiopharus sp. 1	0	4	**4**		x	1F diff., >1 sp.?
Myiopharus sp. 2	1	2	**3**		x	
Myiopharus sp. 2a	1	0	**1**	x		
Myiopharus sp. 3	0	1	**1**		x	
Myiopharus sp. 4	0	3	**3**	x		
Myiopharus sp. 5	0	1	**1**		x	
Myiopharus sp. 6	3	1	**4**		x	
Myiopharus sp. 7	1	0	**1**	x		
Myiopharus sp. 8	0	1	**1**		x	
Myiopharus sp. 9	0	1	**1**		x	
Myiopharus sp. 10	0	1	**1**	x		
Myiopharus sp. 11	0	1	**1**		x	
Myiopharus sp. 12	1	0	**1**		x	
Phyllophilopsis (G. nr.) sp. 1	1	0	**1**		x	
Steleoneura/*Trigonospila* G. nr. sp. 1	0	1	**1**		x	
Thelairodoriopsis sp. 1	0	1	**1**		x	
Zaira or G. nr. sp. 1	0	1	**1**	x		
Zaira or G. nr. sp. 2	0	2	**2**	x	x	
Blondeliini unk. G. 1 nr. *Eucelatoria* sp. 1	2	0	**2**	x		
Blondeliini unk. G. 2 nr. *Celatoria*? sp. 1	1	0	**1**	x		
Blondeliini unk. G. 3 nr. *Leptostylum* sp. 1	0	1	**1**		x	
Unknown genus (Blondellini?) sp. 1	0	1	**1**	x		
Tribe Eryciini						
Ametadoria sp. 1	1	1	**2**		x	
Drino sp. 1	1	0	**1**	x		
Zizyphomyia (G. nr.?) sp. 1	0	1	**1**		x	
Tribe Euthelairini						
Neomintho/*Pelecotheca* sp. 1	2	0	**2**	x		
Pelecotheca sp. 2	1	1	**2**	x	x	
Pelecotheca sp. 3	2	0	**2**	x		

Species	M	F	Tot	FCC	PNAS	Notes
Tribe Goniini						
Choeteprosopa sp. 1	0	1	**1**		x	
Chrysoexorista sp. 1	0	1	**1**	x		
Hyphantrophaga (G. nr.?) sp. 2	1	0	**1**	x		
Hyphantrophaga sp. 1	0	2	**2**		x	
Leschenaultia sp. 1	0	1	**1**		x	
Patelloa sp. 1	0	6	**6**	x		
Patelloa sp. 2	0	1	**1**	x		
Patelloa sp. 3	1	2	**3**	x	x	
SUBFAMILY EXORISTINAE						
Tribe Cylindromyiini						
Neobrachelia sp.	2	0	**2**		x	
Neobrachelia sp. 2	0	1	**1**		x	
Tribe Gymnosomatini						
Gymnoclytia sp. 1	1	1	**2**	x		
Xanthomelanopsis sp. 1	1	0	**1**		x	
Xanthomelanopsis sp. 2	1	1	**2**	x		
Tribe Leucostomatini						
Clairvillia sp. 1	1	0	**1**	x		
Tribe Phasiini						
Phasia sp. 1	0	1	**1**	x		
Tribe Strongygastrini						
Strongygaster sp. 1	0	2	**2**	x		
SUBFAMILY TACHININAE						
Tribe Ernestiini						
Linnaemya sp. 1	0	1	**1**		x	
Tribe Graphogastrini						
Phytomyptera sp. 1	1	0	**1**	x		
Phytomyptera sp. 1b	1	0	**1**	x		
Phytomyptera sp. 2	1	0	**1**		x	
Phytomyptera sp. 3	1	0	**1**	x		
Phytomyptera sp. 4	0	1	**1**		x	
Phytomyptera sp. 5	0	1	**1**		x	
Tribe Leskiini						
Clausicella sp. 1	1	0	**1**	x		
Clausicella sp. 2	0	2	**2**		x	
Clausicella sp. 2a	1	0	**1**	x		
Genea (*Geneopsis*) sp. 2	1	0	**1**	x		
Genea sp. 1	3	0	**3**	x		
Ginglymia sp. 1	8	3	**11**		x	>1 sp.? M = F?
Ginglymia sp. 2	1	0	**1**		x	
Leskia sp. 1	1	0	**1**	x		
Leskia sp. 2	1	0	**1**	x		

Species	M	F	**Tot**	FCC	PNAS	Notes
Trochiloleskia G. nr. sp. 1	0	1	**1**	x		
Trochiloleskia G. nr. sp. 2	0	1	**1**		x	
Urumyobia sp. 1	0	2	**2**		x	
Tribe Megaprosopini						
Acronacantha (G. nr.) sp. 1	0	1	**1**	x		
Tribe Minthoini						
Actinochaeta sp. 1	0	1	**1**		x	
Paradidyma sp. 1	0	1	**1**	x		
Paradidyma sp. 2	0	1	**1**	x		
Tribe Myiophasiini						
Cholomyia sp. 1	0	1	**1**	x		
Cholomyia sp. 2	0	1	**1**		x	
Cholomyia sp. 3	0	1	**1**		x	
Cholomyia sp. 4	0	1	**1**		x	
Gnadochaeta sp. 1	1	0	**1**	x		
Tribe Polideini						
Chrysotachina cf. *willistoni* Curran	1	0	**1**	x		
N. Genus 12 sp. 1	0	1	**1**	x		
Tribe Siphonini						
Siphona (*Pseudosiphona*) sp. 14	1	2	**3**	x	x	
Siphona (*Pseudosiphona*) sp. 15	1	0	**1**	x		
Siphona (*Pseudosiphona*) sp. 16	1	0	**1**	x		
Siphona (*Pseudosiphona*) sp. 17	0	1	**1**		x	
Siphona (*Pseudosiphona*) sp. 18	0	5	**5**		x	
Siphona (*Pseudosiphona*) sp. 19	10	1	**11**	x	x	
Siphona (*Pseudosiphona*) sp. 20	1	1	**2**	x		
Siphona (*Pseudosiphona*) sp. 20a	1	0	**1**	x		= sp. 20?
Siphona (*Pseudosiphona*) sp. 21	0	1	**1**		x	
Siphona (*Pseudosiphona*) sp. 22	0	1	**1**	x		
Siphona (*Pseudosiphona*) sp. 23	1	0	**1**	x		
Siphona (*Siphona*) sp. 1	1	1	**2**	x		
Siphona (*Siphona*) sp. 2	1	0	**1**		x	
Siphona (*Siphona*) sp. 2a	6	0	**6**	x		
Siphona (*Siphona*) sp. 3	0	3	**3**		x	
Siphona (*Siphona*) sp. 3a	3	0	**3**	x		M of sp. 3?
Siphona (*Siphona*) sp. 4	1	0	**1**	x		
Siphona (*Siphona*) sp. 5	0	3	**3**	x		
Siphona (*Siphona*) sp. 6	3	0	**3**	x	x	
Siphona (*Siphona*) sp. 6a	1	1	**2**	x	x	= sp. 6?
Siphona (*Siphona*) sp. 7	5	2	**7**	x	x	2 spp.?
Siphona (*Siphona*) sp. 8	2	4	**6**		x	
Siphona (*Siphona*) sp. 8a	6	2	**8**	x	x	= 8a?, or > 1 sp.?
Siphona (*Siphona*) sp. 9	1	2	**3**	x	x	
Siphona (*Siphona*) sp. 10	2	1	**3**	x	x	F diff. sp.?

Species	M	F	Tot	FCC	PNAS	Notes
Siphona (*Siphona*) sp. 11	1	0	**1**	x		
Siphona (*Siphona*) sp. 12	1	0	**1**		x	
Siphona (*Siphona*) sp. 13	0	1	**1**	x		
Tribe Tachinini						
Archytas? sp. 1	1	0	**1**	x		
Copecrypta sp. 1	0	2	**2**	x	x	
Copecrypta sp. 2	0	1	**1**		x	= sp. 1?
Copecrypta sp. 3	3	0	**3**		x	
Gymnommopsis? sp. 1	1	0	**1**	x		
Neosarromyia sp. 1	1	0	**1**	x		
Parepalpus sp. 1	0	1	**1**	x		
Totals	**266**	**207**	**473**			