

CHARACTERIZATION OF ARTHROPOD ASSEMBLAGE  
SUPPORTED BY THE CHINESE TALLOW TREE (*SAPIUM SEBIFERUM*)  
IN SOUTHEAST TEXAS

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**Abstract.**—Arthropod abundance, species richness and trophic structure were measured on the introduced species Chinese Tallow tree (*Sapium sebiferum* (L.) Roxb.) in southeast Texas. Samples were collected using sweep nets between June and October of 2001. A total of 811 individuals and 160 arthropod species were caught. Orders Diptera, Acari, and Araneida were abundant on *Sapium*, while orders such as Thysanoptera, Neuroptera, Orthoptera were present in much lower relative abundances. The order Hemiptera was markedly low in abundance and species richness. Compared to available data on native ecosystems, predators and detritivores were relatively abundant while herbivores and total arthropod diversity were relatively low on *Sapium*. These results suggest that *Sapium* has not yet acquired an insect fauna comparable to native plants in Texas.

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Arthropods represent a significant proportion of faunal community diversity and have vital roles in ecosystem functioning (Wilson 1992; Price 1997). A number of ecosystem services are performed by arthropods, such as nutrient recycling, seed dispersal, herbivory, and pollination (Proctor & Yeo 1972; Petruszewicz & Grodzinski 1975; Davidson & Morton 1981; Jones et al. 1994). Introduced plant species have been shown to alter ecosystem functioning, reduce native diversity, and promote extinction of native species (Vitousek 1986; Liebhold et al. 1995; Mack et al. 2000), and through changes in vegetation structure, composition and host quality, they may affect arthropod assemblages. Insect diversity is frequently correlated with the diversity of plants (Schowalter 1995; Siemann 1998) and architectural complexity of a habitat (Strong et al. 1984). When previously diverse habitats are converted to monospecific stands of non-native plants, insect species richness will often be lower.

Factors that influence arthropod colonization rates on introduced plant species may affect subsequent community composition and structure. Strong et al. (1984) suggested that taxonomic, phenological, biochemical, and morphological similarities between introduced and native plants, as well as geographic range, may influence how quickly introduced plants are colonized by native arthropods. However, arthropod host

choice is typically driven by physiological and behavioral adaptations in response to host plant quality (Price 1997; Schowalter 2000). Host plants considered low quality for arthropod growth and development, are typically highly defended and/or nutritionally poor (Price et al. 1980). Host choice usually divides herbivorous insects into two categories, generalists and specialists (Feeny 1976). Generalists capitalize on the most abundant and obvious resource, whereas specialists possess increased efficiency but reduced resource choice (Feeny 1976; Brown 1984). Therefore, generalist arthropods are thought to be more commonly found on introduced plant species than native species (Strong et al. 1984; Lankau et al. 2004), but little empirical evidence supports this assertion.

*Sapium sebiferum* (L.) Roxb. (Euphorbiaceae) also known as *Triadica sebifera*, invades coastal tallgrass prairie, disturbed areas, and intact floodplain forests in east Texas (Bruce et al. 1997). The enemy release hypothesis has been used to explain the success of some introduced species including *Sapium* (Elton 1958; Keane & Crawley 2002; Siemann & Rogers 2003a). It asserts that alien species are introduced without their co-evolved specialist herbivores and pathogens. This release from natural enemies may give alien species a competitive advantage over native plants (Elton 1958; Groves 1989; Lodge 1993; Tilman 1999). Indeed, there is evidence that herbivore loads are lower on introduced plant species than native species (Southwood et al. 1982; Strong et al. 1984; Yela & Lawton 1997). Furthermore, biological control agents can sometimes control alien plant populations (Goeden & Louda 1976; Groves 1989). If the enemies release hypothesis is valid, insects may play an important role in the invasion of *Sapium*.

The objective of this study was to characterize the arthropod community by quantifying arthropod taxonomic richness and abundance on a monospecific stand of *Sapium*, growing on a former coastal prairie in southeast Texas, and comparing to data from native habitats in southeastern Texas (Birch 1975; McFadden 1978; Cameron & Byrant 1999). It was predicted that: (1) fewer herbivore species would be found on *Sapium* than in native communities if *Sapium* is avoided by North American herbivores, and (2) the arthropod community structure on *Sapium* would be different from that found in native habitats, as *Sapium* has been present for a shorter time and is therefore less likely to have acquired a full insect fauna.

## MATERIALS AND METHODS

*Focal study species.*—Originally from Asia, Chinese tallow tree (*Sapium sebiferum*) was introduced to Georgia in the late eighteenth century and subsequently into Texas in the early 1900's (Bruce et al. 1997). *Sapium* is a dominant invasive species in the southeastern United States (Flack & Furlow 1996; Bruce et al 1997). Once established it can form dense monospecific stands with little understory vegetation (Bruce et al. 1997). It experiences low levels of herbivory in Texas (Siemann & Rogers 2001; 2003a; 2003b) but the diversity and composition of associated arthropods in Texas is not known.

*Study site.*—The study was conducted at the University of Houston Coastal Center (henceforth known as UHCC), a 374 ha research area, located 50 km SE of Houston, Texas. Most of the research site consists of *Sapium* stands in areas that originally would have been tallgrass prairie. This study was conducted in a monospecific *Sapium* stand that was estimated to be 30 years old.

*Sampling protocol.*—This *Sapium* stand was sampled 16 times between 8 June and 24 October 2001. The sampling frequency was devised for taxa that emerge for only short periods and, or have short life spans. On each sampling occasion, four samples were collected randomly from *Sapium*. Each sample was collected along a 16 m transect. Transects were selected for minimal undergrowth to minimize the influence of other plant species on the focal arthropod community. Each transect was sampled for arthropods using 30 swings of a sweep net (15 inches diameter) that reached 5.8m into the canopy (see Siemann 1998 for comparisons of sampling methods affecting relative abundance and species richness). Sampling was conducted at approximately the same time of day and under similar weather conditions (dry and warm).

*Arthropod identification.*—Arthropod specimens were sorted under magnification and identified to either species or morphospecies within family or genus, and abundance, and trophic group was recorded by taxon. Individuals from the order Araneida (spiders) were often not identified beyond order due to their taxonomic complexity and lack of a local reference collection. Morphospecies have been shown to correlate with arthropods identified by entomologists (Oliver & Beattie 1996), and this technique is often effectively utilized in the characterization of communities (Ingham & Samways 1996; Siemann 1998; Symstad et al. 2000).

*Determination of trophic level.*—For each species or morphospecies, a trophic group was determined for the developmental stage at which the individual was caught by referring to relevant literature (Arnett 1960 1993; Borror & White 1970; McAlpine et al. 1981; 1987; Schuh & Slater 1995). The functional groups were the following: herbivore, detritivore, predator, parasite, omnivore, non-feeding, and unknown. Herbivores included any arthropod feeding primarily on living plant material. Omnivores were defined as individuals feeding on plants and animals. The group 'unknown' was assigned for those whose trophic grouping could not be determined through lack of available knowledge or insufficient taxonomic determination. Little is known about feeding habits for some taxonomic groups, especially those without agricultural or medical importance. There are some arthropods that only feed in their larval stage; therefore, a non-feeding group was included.

*Data from previous studies.*—The native sites and habitats sampled by Cameron & Byrant (1999) were located near Sealy, Texas, approximately 110 km NW of the *Sapium* study site (UHCC). They sampled using a beating net for woody areas and a sweep net in herbaceous vegetation. The beating nets usually have heavier canvas fabric that collects smaller individuals than a sweep net. The habitats included: riparian woodland with ungrazed pasture and savanna woodland (RW1), dense riparian woodland with less open grassland (RW2), bottomland woodland with dense herbaceous understory (BW3), fluvial woodland with open understory with periodic flooding and bordered by pasture (FWP4), dense drier woodland with woody understory (DW5), grazed pasture with a few woody species (GP6), abandoned pasture with patches of riparian woodland (PW7), and coastal prairie with no woody vegetation, surrounded by agriculture and grazing (CP8). Cameron & Byrant (1999) did not include non-insect arthropods in their study so these groups were excluded from the UHCC data (including *Sapium* data) for comparative analyses.

Two studies from UHCC on arthropod communities were also included in this study (Birch 1975; McFadden 1978). Arthropod data from high (HDB) and low densities (LDB) of *Baccharis halimifolia* L. were utilized from an earlier study by Birch (1975). Like *Sapium*, *Baccharis* is both common and woody, yet *Baccharis* is native to the area. Birch (1975) sampled the stands on four occasions in 1975, using a D-vac. Siemann (1998) found that relative richness and abundance values for D-vac and sweep net samples were strongly correlated. McFadden (1978) collected arthropod data in the coastal prairie at

UHCC (UHCP) every two months, a total of seven times in the year, using a sweep net. Sampling effort was standardized for McFadden (1978), Birch (1975), and Cameron & Byrant (1999) by using relative rather than absolute values. Birch (1975) and McFadden (1978) are the only available studies on arthropod communities at the UHCC.

*Data analyses.*—To assess the differences in the *Sapium* insect community from those in native Texas habitats, a non-metric multidimensional scaling (NMS) ordination was conducted using relative abundance of seven insect orders from *Sapium*, high and low densities of *Baccharis* (Birch 1975), coastal prairie (McFadden 1978), and eight native sites studied by Cameron & Bryant (1999). Araneida and Acari were excluded. NMS is a non-parametric, iterative technique based on ranked distances among sites (McCune & Grace 2002). The number of dimensions was determined by a minimal stress (departure from monotonicity). The distance matrix of sites used for ordination was  $1-D_s$ , in which  $D_s$  is Sørensen's similarity index. Using the distance matrix output by PC-ORD Version 4, the distance ordination was conducted in SAS V.8 (SAS Institute 2000) with routine PROC NMS.

## RESULTS

A total of 811 individuals and 160 species in 15 orders of arthropods were caught in a total of 1920 sweeps. Some orders were abundant on *Sapium*, such as Acari (mites), Araneida (spiders), and Diptera (flies), which accounted for 78% of the individuals in the community (Table 1). The most diverse orders were Diptera (36% species richness) and Acari (13% species richness). Coleoptera (beetles), Homoptera (leafhoppers), Hymenoptera (wasps and ants) and Psocoptera (barklice) were less abundant on *Sapium*. Eight orders were rarely encountered (Collembola (springtails), Dictyoptera (mantids and cockroaches), Ephemeroptera (mayflies), Hemiptera (true bugs), Lepidoptera (moths and butterflies), Neuroptera (lacewings), Orthoptera (grasshoppers and crickets), and Thysanoptera (thrips). Twenty immature individuals were caught, of which 13 were Orthoptera, and the remainder were Coleoptera, Homoptera, and Thysanoptera.

A species accumulation curve was constructed to determine the number of species collected versus sampling effort for the data on *Sapium*. Three saturating equations were fitted to the curve (Tablecurve 2D, Systat, Point Richmond CA). They indicated that the total number of species in the community was 189 (first order intermediate kinetic

Table 1. Abundance and species richness of arthropods by taxonomic order summed over all samples.

Order	Abundance	Species Richness
Acari	165	20
Araneida	248	—
Coleoptera	25	14
Collembola	1	1
Dictyoptera	2	2
Diptera	222	57
Ephemeroptera	1	1
Hemiptera	2	2
Homoptera	36	16
Hymenoptera	39	16
Lepidoptera	4	4
Neuroptera	14	7
Orthoptera	13	6
Psocoptera	36	11
Thysanoptera	3	3
TOTAL	811	160

function), 191 (simple equilibrium, net rate and equilibrium concentration function), or 208 (first order intermediate kinetic function with equilibrium) which suggests the sampling effort on *Sapium* caught 85%, 84%, or 77% of the species respectively. A species-sweep curve constructed by McFadden (1978) showed that 1000 sweeps would contain 85% of the diversity. Cameron & Byrant (1999) also estimated they collected 85% of the diversity (based on McFadden 1978). Birch (1975) did not create a sampling curve.

The most abundant family encountered was Oripodidae (beetle or armored mites), which accounted for 14% of total arthropod community abundance (Table 2). Chironomidae (non-biting midges), Lauxaniidae (Lauxaniid flies), and Dolichopodidae (long legged flies) were also relatively common (Table 2). The most diverse (species rich) among these were Dolichopodidae and Chironomidae. Other common families were Psocidae (common barklice), Sciaridae (dark winged fungus gnats), Formicidae (ants) and Coccidae (scales) (Table 2).

Only two families were encountered that might be considered as specialist herbivores. These were Coccidae (scales) and Cicadellidae (leafhoppers) both in the order Homoptera. Homoptera are often known to stay on host plants where their eggs are laid.

Predators (326 individuals) and detritivores (241 individuals) together represented 70% of the arthropod assemblage supported by *Sapium*. Herbivores were considerably less abundant and composed only 7% of

Table 2. Fifteen most abundant families sampled from *Sapium*. The families listed account for 53% of total arthropod community abundance and 55% of total species richness.

Order	Family	Abundance	Species Richness
Acari	Oripodidae	115	5
Diptera	Chironomidae	61	12
Diptera	Lauxaniidae	60	9
Diptera	Dolichopodidae	53	13
Psocoptera	Psocidae	25	6
Diptera	Sciaridae	18	8
Hymenoptera	Formicidae	16	4
Homoptera	Coccidae	14	5
Homoptera	Cicadellidae	11	5
Hymenoptera	Braconidae	11	3
Diptera	Chloropidae	10	6
Orthoptera	Gryllidae	9	4
Neuroptera	Chrysopidae	8	3
Psocoptera	Pseudocaeciliidae	8	3
Coleoptera	Coccinellidae	7	2

all *Sapium* community arthropods (58 individuals). Insect relative abundance for the additional trophic categories were 3% for omnivores and parasites, 10% unknown, and 8% non-feeding on *Sapium*. However, species richness was more evenly proportioned among the trophic categories. Detritivores were the most species rich (43 species or morphospecies) but only represented 27% of the community diversity. Both herbivores and predators had similar levels of diversity, representing 20% and 17% respectively.

The arthropod community on *Sapium* differed from the communities found on native sites sampled by Birch (1975), McFadden (1978), and Cameron & Byrant (1999) (Table 3). After Acari and Araneida data were removed, relative species richness and abundance were recalculated to make all the data sets comparable. The relative richness of herbivores (29%) was approximately 50% less on *Sapium* than on native vegetation (native herbivore range 49-67%). In contrast, both predator and detritivore relative richness was higher on *Sapium* (24% and 38% respectively) than the native site averages (12% and 16% respectively). The average relative species richness for predators from native sites was 12% (range 6-19%), and the average for detritivores (native sites) was 16% (range 7-24%). Parasites on *Sapium* were similar in their relative species richness (9%) compared to the native sites (range 8-21%). Cameron & Byrant (1999) did not present results on the trophic distribution of arthropod abundance.

Table 3. Arthropod relative species richness by trophic group for *Sapium* samples in this study (“*Sapium*”) and habitats sampled by Birch (1975), McFadden (1978), and Cameron & Byrant (1999). Refer to methods for description of sites.

Sites	Herbivore %	Predator %	Parasite %	Detritivore %
RW1	57	9	15	20
RW2	57	7	11	24
BW3	55	12	16	17
FWP4	61	11	12	17
DW5	59	11	9	21
GP6	58	6	14	22
PW7	67	8	10	15
CP8	54	13	16	16
UHCC prairie	67	19	8	7
HD <i>Baccharis</i>	56	10	21	12
LD <i>Baccharis</i>	49	14	21	16
<i>Sapium</i>	29	24	9	38

The comparison of community composition of *Sapium* and native sites sampled by Birch (1975), McFadden (1978), and Cameron & Byrant (1999) showed both differences and similarities in the relative abundance of orders (Table 4). Arthropod relative abundance on *Sapium* was comparable within the range of relative abundance at native sites for Homoptera, Coleoptera, Orthoptera, Hymenoptera, and Lepidoptera (Table 4). However the relative abundance found on *Sapium* was higher for Diptera and ‘others’, and lower for Hemiptera (Table 4).

The NMS ordination of relative abundance of orders indicated that the insect community on *Sapium* differed substantially from that of native sites (Figure 1). A 3-dimensional solution was found. However, a two dimensional graph is presented, for ease of interpretation (Figure 1). A total of 38 iterations were run for the final solution, and the final stress was 0.08196. A final stress value between 0.1 and 0.05 is generally interpreted as a good ordination with negligible risk of inferring false conclusions (McCune & Grace 2002). The UHCC sites were distinctly separated from Cameron & Byrant’s (1999) sites along dimension 1 (Figure 1). The *Sapium* site was located at the extremes of both axes (Figure 1). The grazed pasture site (GP6) was the most similar native site to *Sapium* in insect community (Sørensen’s similarity index (SSI) = 0.75), followed by UHCC coastal prairie (UHCP) (SSI = 0.56), while abandoned pasture with patches of riparian woodland (PW7) was the most different (SSI = 0.31).



Table 4. Relative abundance of insects (Acari and Araneida excluded) by order from the native habitats sampled by Birch (1975), McFadden (1978), Cameron & Byrant (1999), and for *Sapium* samples in this study. These values are the percentage of each order within each site. 'Others' include all other orders not already listed. Refer to methods for site abbreviations. HOM=Homoptera, HEM=Hemiptera, COL=Coleoptera, ORT=Orthoptera, DIP=Diptera, HYM=Hymenoptera, LEP=Lepidoptera.

Sites	HOM	HEM	COL	ORT	DIP	HYM	LEP	Others
RW1	13.2	39.0	33.1	3.6	6.9	3.8	0.3	0.4
RW2	29.8	11.6	14.6	26.0	11.8	5.1	1.0	0.0
BW3	23.0	8.7	47.3	7.5	8.3	4.3	0.6	0.3
FWP4	12.0	2.7	66.3	7.6	7.0	4.1	0.1	0.5
DW5	20.0	18.8	21.0	10.0	25.0	4.0	1.0	1.0
GP6	12.1	16.4	6.9	11.9	49.5	3.2	0.0	0.0
PW7	28.1	1.8	23.5	37.6	5.7	2.9	0.3	0.1
CP8	4.0	38.7	6.2	23.2	21.7	6.2	0.3	0.1
UHCC prairie	15.7	14.1	20.1	4.4	20.0	20.7	1.6	3.2
HD <i>Baccharis</i>	34.0	19.3	3.9	0.3	9.7	31.8	0.5	0.5
LD <i>Baccharis</i>	17.8	39.7	1.9	0.0	11.6	23.4	1.0	4.7
<i>Sapium</i>	9.0	0.5	6.3	3.3	55.8	9.8	1.0	14.3

## DISCUSSION

Consistent with the enemies release hypothesis, *Sapium* woodlands in southeastern Texas supported communities depauperate in herbivores and specialists, and were instead composed primarily of predators and detritivores (Table 1, Table 3). These data support earlier predictions of fewer herbivores and a differing arthropod community structure on *Sapium* compared to native habitats. The differences in arthropod abundance and species richness between *Sapium* woodlands and native habitats were substantial (Figure 1, Table 3). Nevertheless, *Sapium* may be in the early stages of acquiring a more typical insect assemblage. Other work has shown that introduced plants may take up to 300 years to support an insect fauna indistinguishable from native plants (Strong 1974; Strong et al. 1984). Therefore the difference in the fauna documented on *Sapium* might be consistent with only 100 years of colonization time in Texas.

A large proportion of the species or morphospecies were infrequently encountered on *Sapium*, suggesting either a high number of transient individuals or rare individuals. This is considered typical in arthropod communities (Siemann et al. 1999).

The differences in arthropod communities between *Sapium* woodlands and native habitats might reflect unusual taxonomic, phenological,

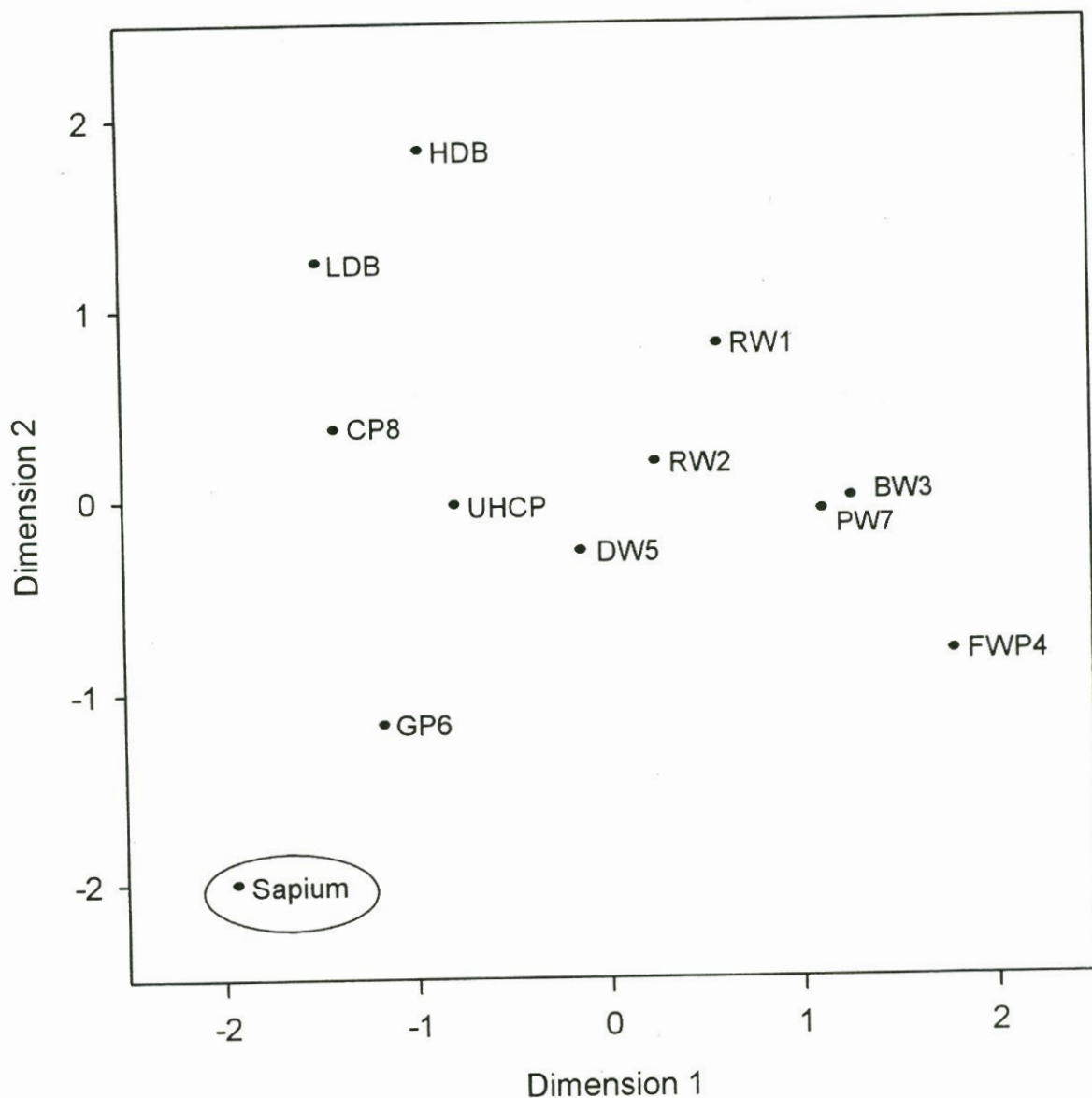


Figure 1. Non-metric multi dimensional scaling ordination of the relative abundance of the seven major insect orders (see Table 4) sampled from *Sapium*, UHCC coastal prairie (McFadden 1978), high and low densities of *Baccharis* (Birch 1975), and the eight native habitats from Cameron & Byrant (1999). Refer to methods for site abbreviations.

biochemical, and morphological properties of the exotic species (Strong et al. 1984). Taxonomically, there are no other native tree species belonging to the Euphorbiaceae family, although there are a number of herbs such as *Euphorbia bicolor* (snow-on-the-prairie) and *Croton capitatus* (woolly croton). However, phenologically and morphologically it is similar to the native mid-sized, broad-leaved deciduous trees, such as *Celtis laevigata* (Bush & Van Auken 1986; Bruce et al. 1997), suggesting that *Sapium* is not unusual in this regard. *Sapium*'s ability to form dense monospecific stands and reduce habitat complexity in the

understory is unprecedented in this region, thus simple plant architecture and or low local plant diversity might account for reduced arthropod diversity and abundance.

Of all the native habitats examined, the grazed pasture site was most similar in arthropod composition to *Sapium* woodlands (Figure 1, Table 4). Both *Sapium* and grazed pasture are unnatural types of habitat. Originally the *Sapium* sampling location would have been coastal tall-grass prairie approximately 100 years ago, although 90 hectares of coastal prairie has now been restored. The UHCC coastal prairie site (McFadden 1978) was the second most similar native site, while the coastal prairie (Cameron & Byrant 1999) was the fourth most similar. *Sapium* woodlands may have recruited some arthropods from adjacent prairie habitat, and this may account for some degree of similarity between the arthropod community composition of *Sapium* and native coastal prairie sites sampled by McFadden (1978) and Cameron & Bryant (1999).

Comparisons to Birch (1975), McFadden (1978), and Cameron & Byrant (1999) are informative. However, there are differences between the approaches that should be noted (also see methods). First, sampling was conducted at different times and years. Birch (1975), McFadden (1978), and Cameron & Byrant (1999) all sampled in the mid to late 1970's, although there have been no significant, sudden, or large scale changes (such as land use change) in the UHCC vicinity. Furthermore Cameron & Byrant (1999) only sampled in the spring. Generally, insect communities increase in abundance at the beginning of the growing season and decrease at the end of the growing season, yet many populations display substantial fluctuations. *Sapium* arthropod data (total abundance and species richness) exhibited no significant pattern of variation among the sampling periods. Secondly, sampling efforts could differ, but are difficult to quantify or compare. Thirdly, Birch (1975) also used a D-vac in addition to a sweep net (see Siemann 1998). Although there are differences in approaches, the overall relative results should not be greatly influenced by them, especially considering that both McFadden (1978) and Cameron & Byrant (1999) state they collected 85% of the diversity, which is comparable with the *Sapium* data (77-84%). This would suggest that their results are representative of the communities they sampled. Finally, the authors determined trophic data for McFadden (1978) from an appendix of the most common 95 species and morphospecies (from a total of 535). It was assumed that the

complete data would have been driven by the most abundant species and morphospecies and so the trophic data determined would reflect this. These factors may have influenced the contrast between the insects found on *Sapium* and in native habitats, but the data indicate a paucity of herbivores found on *Sapium*.

In conclusion, *Sapium* woodlands seem to presently support an atypical arthropod fauna, with Diptera (flies), Acari (mites) and Araneida (spiders) as the dominant orders. *Sapium*'s fauna is mostly composed of predators and detritivores with very few herbivores. The apparent relative lack of a herbivorous food chain supports the prediction and may have important implications in ecosystem functioning. Although *Sapium* woodlands in southeastern Texas appear to have acquired few herbivores in the 100 years it has been present, it is expected that arthropod diversity and possibly abundance will continue to increase on *Sapium* and the composition of associated arthropod fauna will change to be more similar to native communities over time. Perhaps the accumulation of a more robust herbivore fauna will limit *Sapium*'s success as an invader in the future.

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