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The insect fauna of Acacia species in Mkomazi Game Reserve, north-east Tanzania

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Introduction

The last 15 years have seen an immense increase in knowledge of insect communities in tropical forest tree canopies (Erwin, 1982, 1983; Moran & Southwood, 1982; Adis *et al*., 1984; Stork, 1987a,b, 1991; Morse *et al*., 1988; Basset, 1991a,b, 1996; Basset & Kitching, 1991). However, insect communities in tropical savannah tree canopies are still comparatively poorly studied. No large-scale study has yet been conducted anywhere in an African savannah habitat (Erwin, 1995), although savannahs cover over 40% of the surface of the tropics (Cole, 1986; Solbrig, 1996). Consequently, there are virtually no estimates of insect diversity in this habitat (Lewinsohn & Price, 1996). To assess habitats for their relevance for conservation, ecological inventories provide an essential tool for environmental management (Campbell, 1993) and insects are a major component in every terrestrial habitat. However, studying arthropod communities in savannah habitats is difficult because of a lack of clear habitat boundaries (Lewinsohn & Price, 1996). In contrast, trees provide an excellent framework for insect community research, because they can be considered a discrete ecological unit (Southwood & Kennedy, 1983). Trees also have great niche diversification because of structural complexity (Lawton, 1978, 1986; Lawton & Price, 1979), are a stable resource (Southwood, 1978) and their inhabitants are all more or less trophically interlinked (Moran & Southwood, 1982). As Moran & Southwood (1982) conclude, ‘in almost all respects it is easier to sample arboreal communities more completely, more widely and more accurately, [. . .], than it is to sample other very complex communities’. This is especially true for savannah tree canopies where the overlap to neighbouring trees is lower than in forest habitats.

This study analyses the insect community associated with thirty-one trees of six *Acacia* species in Mkomazi Game Reserve, north-east Tanzania using a mist-blowing technique. It is the biggest insect sample ever taken from a tropical savannah habitat. Sampling effort and its effect on species richness as well as abundance patterns and the distribution of diversity, abundance and biomass among insect taxa are analysed.

Materials and Methods

Study site

Mkomazi Game Reserve (37°35′–38°45′E and 3°50′–4°25′S) is located in north-east Tanzania at the Tanzanian–Kenyan border next to the Tsavo (West) National Park in the north. It covers an area of ⊤ 3250 km^2 of semiarid tropical savannah habitat with an annual precipitation between 300 mm at the eastern end of the Reserve and 900 mm in the central and western parts. Temperatures vary between 23.1 and 37.8 °C. The distribution of precipitation is bimodal with the long rains between March and mid-May and the short rains between late October and December (Coe, 1995). The altitude varies between 240 and 1609 m above sea-level and the savannah is dominated by trees of the genera *Acacia* and *Commiphora*.

Insect sampling

Thirty-one trees of six species of *Acacia* were sampled between 30 December 1995 and 18 January 1996 in the north-west of Mkomazi Game Reserve. Samples were taken using a *Hurricane Minor* petrol-driven mist blower (Cooper-Pegler Ltd), fitted with an ultra-low-volume delivery nozzle to spray a mist of undiluted Pybuthrin 216 into the canopy, a pyrethroid formulation synergized with piperonyl butoxide. Only trees under 10 m height were sprayed in the morning when leaf surfaces were dry. Three bursts from three directions were given, with a total spraying time of 30 s, and knocked-down insects were sampled using 1-m^2 funnel-shaped trays over a standard drop-time of 1 h. Catches were separated from debris and stored in 70% alcohol. Material was sorted to order and family level and morphotyped into recognizable taxonomic units (RTUs, CSIRO, 1991). Larvae were excluded from the analysis to avoid counting two developmental stages as different RTUs. Five randomly chosen individuals of each RTU were measured to the nearest 0.01 mm, the median being used to calculate the dry biomass per RTU using the formula in Moran & Southwood (1982).

Data analysis

The cumulative area RTU relationship was described by power regression to reveal the exponent for the relationship.

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Table 1. Summary statistics of the thirty-one *Acacia* tree samples analysed in the study.

Species	No. sampled	Area sampled (m^2)	Number of RTUs Mean	Min.	Max.	Number of individuals Mean.	Min.	Max.
A. etbaica	1	3.00	58	–	–	652	–	–
A. mellifera	4	6.28	62	35	79	386	210	592
A. nilotica	12	23.72	98	65	188	1445	400	2998
A. reficiens	4	8.28	86	65	103	1099	814	1485
A. senegal	8	16.00	107	78	145	1786	1497	2716
A. tortilis	2	4.00	105	84	125	872	439	1304
Total	31	61.28	93	35	188	1326	210	2998

A true richness estimator was used that provided information on the true number of species, derived from a number of samples. Chao's estimator 2 (Chao, 1984) takes the general form:

$$S = S_{\text{obs}} + (L^2/2M) \qquad (1)$$

where S is the true species richness of all trees sampled, S_{obs} is the observed number of species of all trees combined, L is the number of species present on only one tree and M is the number of species present on only two trees.

The abundance pattern of the community was described with a rank abundance graph following Hughes (1986), Morse *et al.* (1988) and Basset & Kitching (1991). A regression of the form:

$$y_i = a x_i^{-b} \qquad (2)$$

was fitted, where a and b are constants to predict the abundance (y) from the rank number (x) of the ith species.

Results

Composition of the fauna

A total of 41 099 insect specimens, belonging to fourteen orders, 133 families and 492 RTUs was recognized. The average insect density was 666 m^{-2} and the mean number of RTUs per tree was ninety-three. The number of RTUs varied five-fold between individual trees, and the number of individuals showed a 14-fold variation (Table 1).

The true richness estimator shows that 77% of the insect fauna is represented in the samples from the trees (Fig. 1). Similar percentages were found for the four main orders (around 80%) with the exception of Diptera, where Chao 2 estimated that only 53% were represented in the sample. The exponents of the power regressions lay between 0.30 (Diptera) and 0.47 (Coleoptera).

Table 2. Distribution of RTU richness, abundance and biomass among the fourteen insect orders present in the study. The family Formicidae was separated from the rest of Hymenoptera.

Taxon	Number of RTUs	Number of individuals	Biomass share (%)
Collembola	4	537	0.1
Thysanura	2	29	0.2
Blattodea	9	78	0.7
Mantodea	13	88	15.3
Orthoptera	24	500	6.5
Phasmatodea	3	31	10.3
Psocoptera	11	2943	1.1
Hemiptera	121	11875	10.1
Thysanoptera	14	10288	2.0
Neuroptera	4	8	0.2
Coleoptera	113	2197	6.6
Diptera	58	1029	1.0
Lepidoptera	11	288	0.5
Formicidae	14	7467	26.9
Hymenoptera	91	3741	2.2
Larvae			16.4

The RTU richness (Table 2) was highest for Hemiptera, followed by Coleoptera, Hymenoptera and Diptera. The other orders had negligible numbers of RTUs. The most diverse families were Cicadellidae, Chrysomelidae, Miridae and Formicidae (7.9, 5.5, 4.1 and 2.9% of total RTU richness, respectively). In terms of abundance, Thysanoptera and the ants (family Formicidae) became much more important than Coleoptera, but Hemiptera had the highest abundance. The families with highest abundance were Thripidae, Formicidae, Cicadellidae and Miridae (19.2, 18.2, 12.3 and 12.1% of total abundance, respectively). The picture changed again for the biomass distribution. The highest share was obtained by Formicidae, followed by larvae and Mantodea. Although praying mantids had minor RTU richness and abundance shares, their biomass share was large as most of the largest insects collected belonged to that order. The same is true to a lesser extent for Phasmatodea.

The rank abundance graph (Fig. 2) revealed that most RTUs were present with only one individual. The negative power regression provides a good fit ($R^2 = 0.957$, d.f. = 490, $P < 0.0001$). For the four main orders, the results were similar.

Discussion

The cumulative area–RTU relationship follows, in most cases, the pattern proposed by MacArthur & Wilson (1967), and exponents between 0.3 and 0.35 are commonly found in other

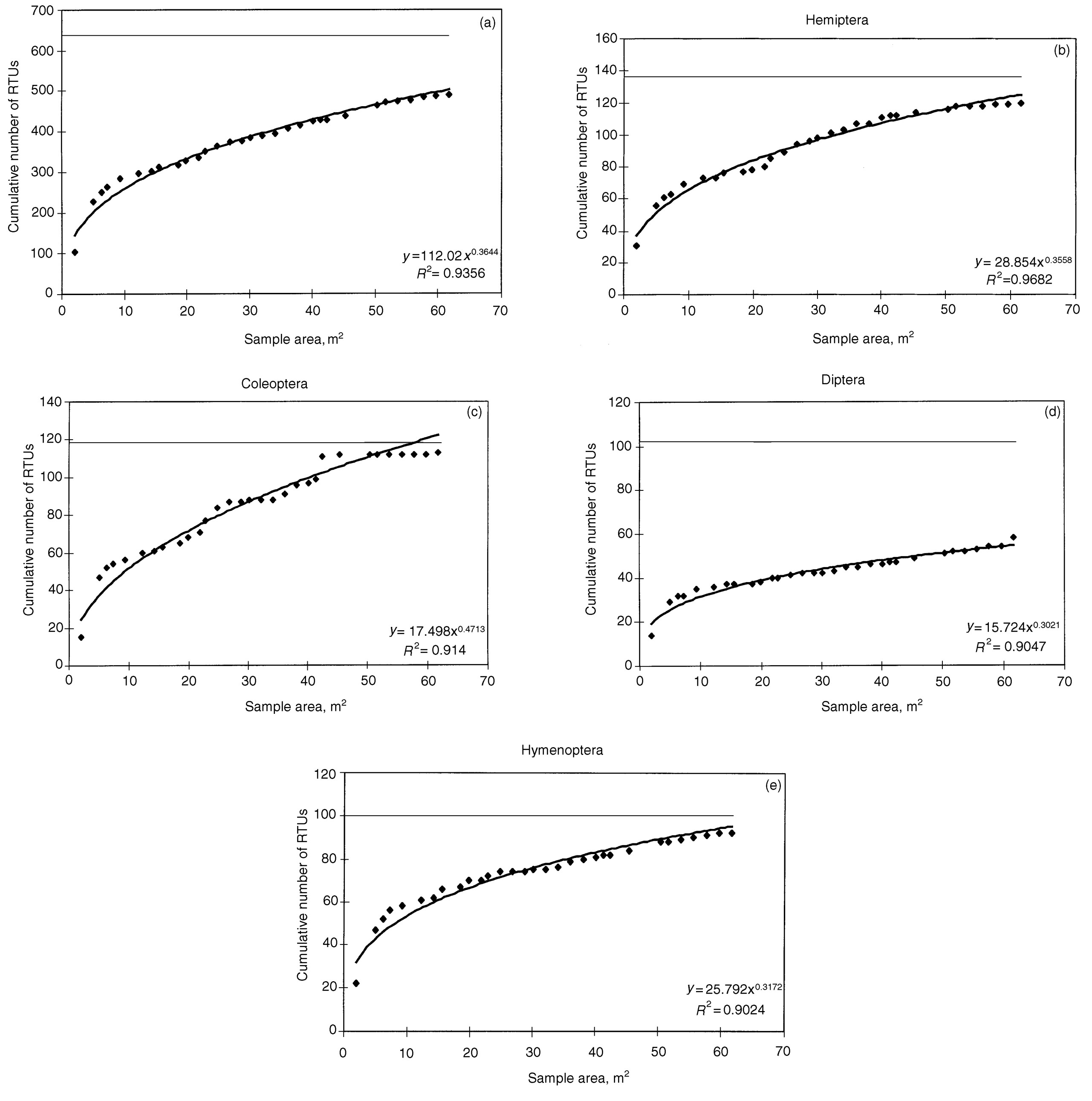

Fig. 1. Cumulative area-RTU curves for the entire insect fauna (a) and the four main orders (b–e). The horizontal line is an asymptote of a true richness estimator from a non-parametric approach (Chao, 1984).

taxa and areas (Ricklefs, 1990). The exponent of 0.47 for Coleoptera is very high, coinciding with this order having the highest biodiversity of all taxa, measured by the α index (Krüger, 1997).

The estimator of true RTU richness suggests that a representative sample of the insect community has been analysed. Diptera are an exception where Chao 2 indicates that only 53% of the true richness has been sampled. This might be for two reasons: for large Diptera the time between contact with the insecticide and paralysis could be long enough for them to leave the tree, and the general problem of the validity of morphotyping could play a role. It is likely that the true RTU richness is underestimated by lumping sibling species together, especially in the family Cecidomyiidae (Simandl, 1993; J. D. Ismay, personal communication). Treating males and females of species with a high sexual dimorphism as separate species biases in the other direction and therefore all results must be interpreted with caution. Throughout the morphotyping process, a conservative approach was applied, so that underestimation is much more likely than overestimation. Because there is no alternative to morphotyping given the time constraints (Erwin, 1995), and in most studies morphotyping

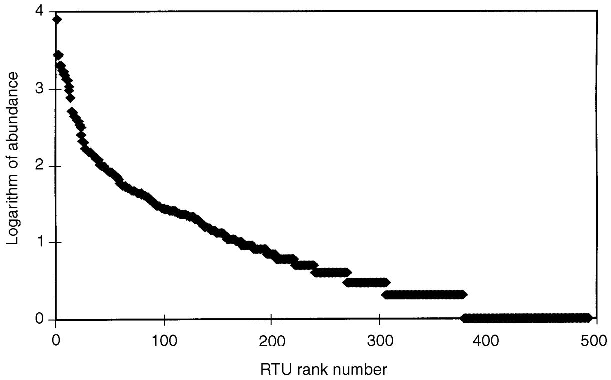

Fig. 2. Rank abundance graph of the entire fauna, the relation being fitted best by $y = 7715.7 + x^{-0.9841}$ (note that the y-axis is displayed on a log scale for convenience).

has been considered a very robust tool (Southwood *et al.*, 1982; Stork, 1991; Erwin, 1995), it is probable that the results presented here are reasonably reliable.

The rank abundance plot revealed exponents similar to those found by Morse *et al.* (1988) who reported an exponent of –0.98 and Basset & Kitching (1991) who found exponents of –1.36 and – 1.37. The value in this study (–0.98) was very similar. More data on insect communities from these habitats are needed urgently to address the question of how much tree canopies of these habitats have in common with tropical forest canopies and how much with temperate canopies. This study indicates that the abundance of ants and diversity of Coleoptera parallels that of other tropical studies (Adis *et al.*, 1984; Stork, 1991), while the diversity of chewing species (mainly Chrysomelidae, Orthoptera, Phasmatodea) is typical of more temperate faunas (Basset & Arthington, 1992).

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