Arthropod communities in two primary forest types of New Caledonia sampled by fogging

Eric Guilbert & Jean Chazeau

Abstract. Interest in wondering how high is the diversity of life has increased during the last decade, and scientists attempted to answer this question by estimating the richness using various methods. This study presents an estimate of the richness of canopy arthropods at family level, in four different forests in New Caledonia, sampled by insecticidal fogging. The arthropod community structure of the four forests can be easily characterized at family level using correspondence analysis. Their cumulative richness distribution is calulated by bootstrap. Then, the estimate of their richness is attempted by modelling cumulative richness distribution. The model found here is a cubic proportional model. The maximum richness is 117 families for two sclerophyllous forests, and 119 for two dense evergreen forests.

Key words. Biodiversity, arthropod community, fogging, canopy, richness estimate.

Introduction

How many species are there on earth? The urgency in obtaining an answer to this question is required by the increasing rate of destruction of biotopes and its flora and fauna by man. Since a few years, many scientists are trying to give an answer (Stork, 1988; Erwin, 1982; May, 1988). We know, by an inventory of the fauna and flora all around the world, that about 1.8 million species have been described. Everybody agrees that many species remain undescribed; but nobody knows how many species we still have to discover. Diversity can be measured by many ways, as mentioned by Cousins (1991), each one having its own limitations. Nevertheless, some scientists attempted to predict biodiversity, using either literature (Gaston, 1991), samples (Erwin, 1983) or mathematical tools (Baltanas, 1992; Palmer, 1990). The highest estimates of the earth's richness in species have been made by projection from fogging samples. Erwin (1983) proposed a total number of 30 million arthropod species. Based on Erwin's calculation, Stork (1988) estimated the total number of animal species at somewhere between 7 and 80 millions. In attempting to answer the question posed above, there are 2 different strategies: the first is to continue to describe species. This is the best way to obtain a precise answer; but certainly not the quickest. The second strategy is to estimate the

H. Ulrich (ed.): Tropical biodiversity and systematics. Proceedings of the International Symposium on Biodiversity and Systematics in Tropical Ecosystems, Bonn, 1994. Zoologisches Forschungsinstitut und Museum Alexander Koenig, Bonn, 1997.

biodiversity with such tools as samples of communities and mathematical models. This is not the most precise way, but it can give an answer quickly. The aim of this study is to try to estimate quickly the richness of canopy arthropod communities sampled by fogging, in four sites belonging to two forest types in New Caledonia. It will present briefly the arthropod communities, at family level. Then, it will show how to perceive quickly the richness of those forests, by using cumulative richness distribution of family richness.

Sampling sites

The canopy arthropods have been sampled in four sites in two forest types in New Caledonia. Two sites are relictual sclerophyllous forests: Pindaï (North Province, alt. 30 m) on limestones and conglomerates and Mt. Nondoué (Païta, South Province, alt. 110 m) on schists. The other two sites belong to the dense evergreen forest in Rivière Bleue Provincial Park (South Province, alt. 160 m). One of the sites is on ultramafic alluvium (P6), and the other one is on a deep slope on peridotitic colluvium (P7). The vegetation of all these sites has been described (Jaffré & Veillon, 1990; Jaffré et al., 1993).

Methods

The arthropods have been sampled by insecticidal fogging. We use a portable fogging machine (Dyna-fog Golden Eagle Backpack 2980) to generate a fast killing, pyrethrin based fog (Cyfluthrin, water and polyhydric alcohols). The fogger was manipulated from the ground level. We placed randomly 40 collectors of one square meter each, which were white plastic sheets, at 0.5 to 0.8 m above the ground. All the arthropods which had dropped onto the sheets in the first two hours after fogging, were collected by washing the sheets with water and a wetting agent (tipol), and were stored in 95 % alcohol. The specimens were sorted out and counted at order level for all arthropods and at family level for Araneae, Hymenoptera, Hemiptera, Orthoptera, Coleoptera and Diptera.

Each site was sampled four times a year to cover seasonal variations. The first sampling was done during the dry season (30 June / 16 July 1992); its results are analysed here.

Before analysing the community structure, we selected the families which show significant differences in distribution among the 4 sites. Fourteen families were selected. The community structure has been analysed by correspondence analysis, to see whether it was possible to discriminate the sites by their taxonomic structure at family level.

An estimator proposed for taxa richness by Heltshe & Forrester (1983), the first order jackknife, has been used to estimate the richness (RE) of the community:

$$RE = RO + RR * (n - 1) / n.$$

It takes into account the number of taxa observed (RO) and the number of taxa which appear in only one quadrat (RR). N is the number of quadrats. This estimator gives a better estimate than some others according to Palmer (1991) and Baltanas (1992).

The richness has been estimated for an increasing surface by adding sampling units one by one. To obtain a cumulative richness distribution, we used a non-parametric method: the bootstrap. The procedure samples randomly with replacement array an increasing number of units (2 to 40 units). It makes for each pulling 500 iterations and gives the mean estimate at every surface taken.

Various models found in the literature (Connor & McCoy, 1979; Lauga & Joachim, 1987) were tested to describe and predict the family richness estimated by the linear less-squared regression method. They were transformed by an autoregressive method into a polynomial model when the residuals showed a characteristic distribution (Tomassone et al., 1992). All statistical analyses were performed by SAS (SAS Institute Inc., 1985), and Mathlab (The Math Works Inc., 1993) packages.

Results

Over the 4 foggings, a total of 64642 individuals were collected and sorted to 164 families. The numbers of families for each individual site were 110, 115, 114 and 116 in Rivière Bleue P7, Rivière Bleue P6, Païta and Pindaï, respectively.

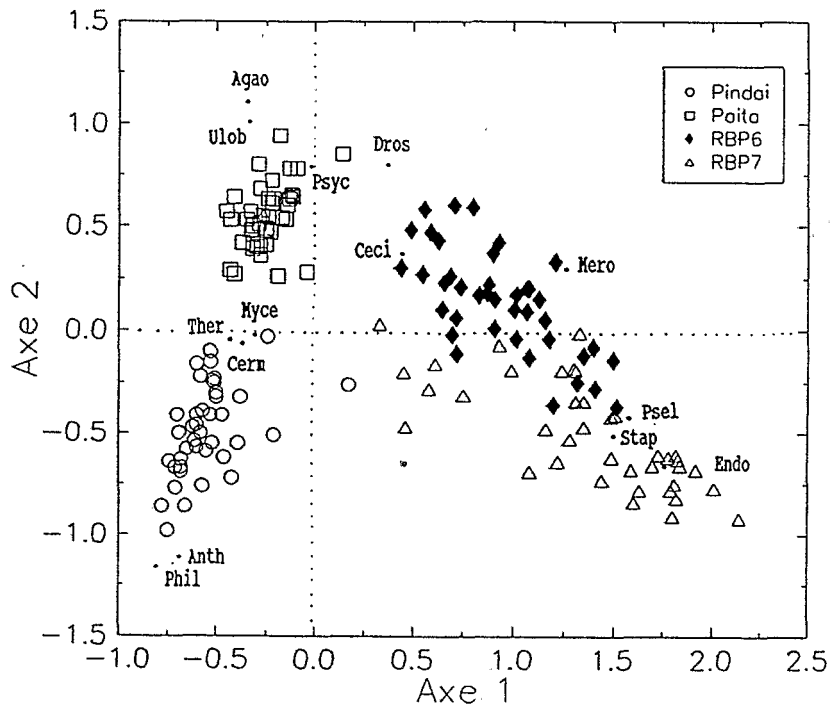

Figure 1: 1–2 Factors map of the correspondence analysis of the four sites, each represented by 40 sampling units, and the 14 families taken into account. Agao: Agaontidae, Anth: Anthibidae, Ceci: Cecidomyiidae, Cerm: Cerambycidae, Dros: Drosophilidae, Endo: Endomychidae, Mero: Merophisidae, Myce: Mycetophilidae, Phil: Philodromidae, Psel: Pselaphidae, Psyc: Psychodidae, Stap, Staphylinidae, Ther: Theridiidae, Ulob: Uloboridae.

The 3 first axes of the correspondence analysis explain 66,33 % of the variance. In the first axis (37.67 % of the variance), the 2 forest types represented each by 80

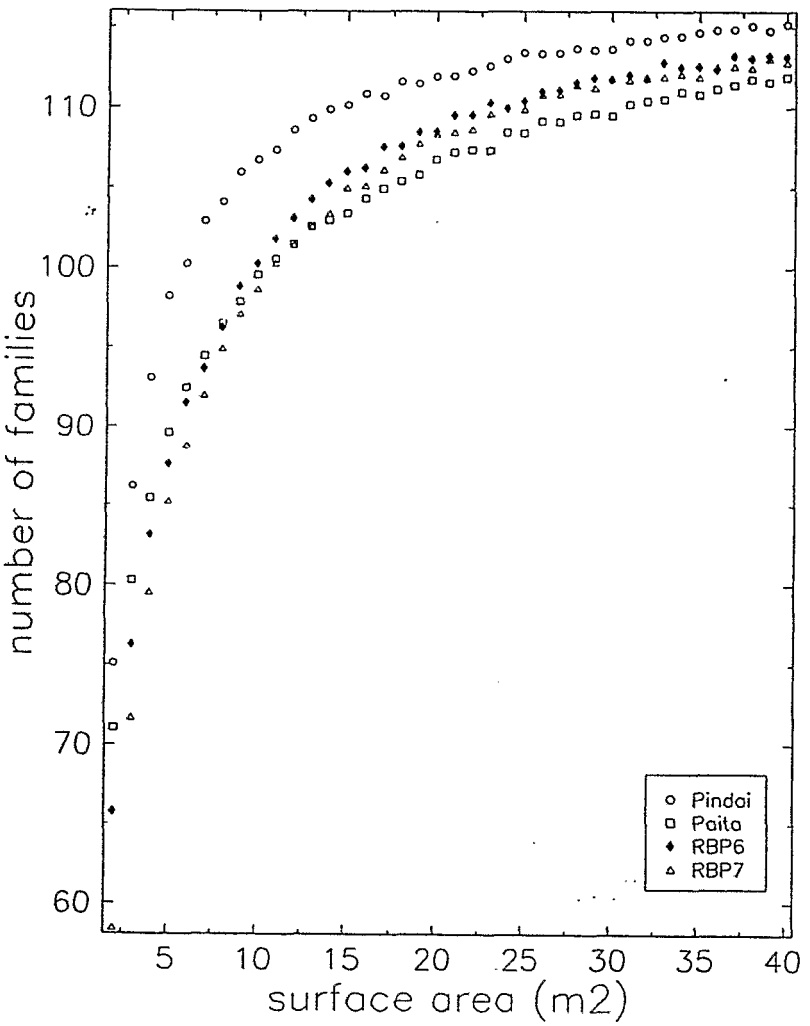

Figure 2: Cumulative family richness (RE) distribution of the four sites, estimated by bootstrap.

sampling units are well separated (figure 1). The coleopteran families Staphilinidae and Pselaphidae and the aranean family Theridiidae all together, contribute for more than 72 % to the first axis. The two coleopteran families characterize the two sites in dense evergreen forests, and the aranean family characterizes the two sites in sclerophyllous forests. Along the second axis (18.93 % of the variance), the 2 sites in sclerophyllous forests are separated whereas the two sites in dense evergreen forests flow together (figure 1). The two aranean families, Uloboridae and Philodromidae contribute to 49.5 % to this partition. The two dense evergreen

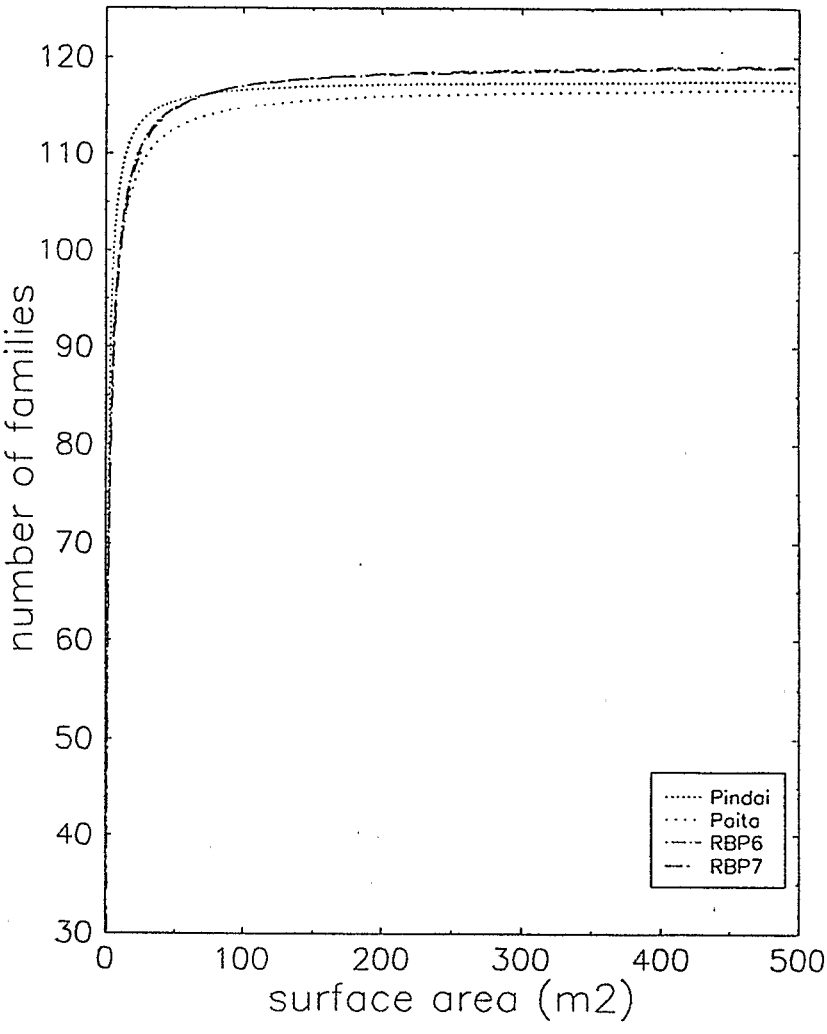

Figure 3: Family richness of the four sites predicted among the surface area by a cubic proportional model.

sites are separated along the third axis (9.73 % of the variance). This separation is characterized by the Merophisidae (Coleoptera) and the Cecidomyiidae (Diptera) (60.3 % of the contribution). The other axes do not show any remarkable structure between the four sites.

The curve of the family richness estimated (RE) vs the surface area shows a typical taxa/area relation (figure 2). It reaches 112, 113, 113 and 115 families for the whole collecting surface of Païta, both Rivière Bleue sites and Pindaï,

respectively. This estimate is not far from the total number of families sampled in each site (114, 110, 115 and 116 families for Païta, Rivière Bleue P7, Rivière Bleue P6 and Pindaï, respectively). The same curve for family richness observed (RO) gives lower values than the real numbers of families except for P7, although the difference is small (110, 110, 114 and 114 families for Païta, Rivière Bleue P7, Rivière Bleue P6 and Pindaï, respectively). As RE under-estimates the true richness (Palmer, 1991), we use the cumulative richness distribution obtained with RE for modelisation.

The model which fits best with the estimate is a cubique proportional model:

$$RE^{-1} = a*S^{-3} + b*S^{-2} + c*S^{-1} + d.$$

RE is the Richness Estimated, S is the surface, a, b, c are three parameters and d the intercept estimated by regression. More than 99.8 % of the variance (R^2) is explained by the model, and the Durbin-Watson D is around 2 for the different sites. The simple and the quadratic proportional models show an R2 higher than 99.8 %; but they all show a correlation between the residuals. In addition, the Durbin-Watson D is lower for the quadratic model. With this model the richness reaches a plateau approaching the asymptote which represents the maximum richness. This asymptote is at 117 families for sclerophyllous forests and at 119 families for dense evergreen forests (figure 3).

Conclusion

The four sites show differences in both family composition and family abundances. The sclerophyllous forests are characterized by Aranean families such as Theridiidae, Uloboridae and Philodromidae; and Coleopteran families such as Pselaphidae, Staphylinidae and Merophisidae characterize dense evergreen forests. Therefore we can characterize by their community structure at family level, either different forest types or different forests in a same forest type. We could have taken into account "rare" taxa to characterize the sites; but the presence of "rare" taxa could be a consequence of the sampling method used: these "rare" taxa may be "accidental" taxa.

To estimate quickly the richness of those sites, and predict it for the biotope considered, we combine here two methods: the use of an estimator and the extrapolation of a taxa–area curve. The richness has been estimated by extrapolation of a taxa–area curve; but to make the curve, we used an estimate of the number of taxa instead of the number of taxa observed.

The model proposed in this study is only mathematical: the biological sense of the parameters is not known. The parameters a and b of the model are statistically close to zero (tested by T-test). A more simple model should have been preferable,

but such models over-estimate the richness for high sampling surface. Our model can fit differently when applied to other communities; and when applied at lower taxonomic level. Here, it has been applied for a small sampling surface, which however provides a stable sample. Consequently, the validity of our model must be tested further by field verifications.

Endemicity, taxonomic and functional relations between families, distribution, etc. are not taken into account. We considered here the richness at family level. It is obviously not the more precise level for measuring such a value. Of course biodiversity cannot be reduced to a number of species, and still less to a number of families. Vane-Wright et al. (1991) have explored the use of taxonomic distinctiveness in measuring diversity. The problem of this method is that there is not always sufficient taxonomic knowledge for groups of taxa in unexplored biotopes. In addition, such taxonomic approaches need big teams of specialists and time. The increasing and speeding up destruction of natural biotopes does not allow us to wait for such tools. In this sense, the family level represents a good alternative. A simple count of taxa is not the best information, but the first information about biodiversity we need; and it should help us in choosing quickly areas to be studied and then protected, or protected first, and then studied.

Acknowledgements

We are indebted to J. Najt and S. Tillier for comments on the manuscript and to M. Baylac for statistic assistance. This study is supplied by the Muséum National d'Histoire Naturelle program, "Biodiversité terrestre en Nouvelle-Calédonie", and the ORSTOM program, "Caractérisation des peuplements des forêts et maquis non anthropisés". It is part of a PhD study.

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