

# Regional species richness of families and the distribution of abundance and rarity in a local community of forest Hymenoptera

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## 9 Abstract

Recent investigations about the relationship between the number of species of taxonomic lineages and regional patterns of species abundances gave indecisive results. Here, it is shown that mean densities of species, of a species rich community of forest Hymenoptera (673 species out of 25 families) were positively related to the number of European species per family. The fraction of abundant species per family declined and the fraction of rare species increased with species richness. Species rich families contained relatively more species, which were present in only one study year (occasional species), and relatively fewer species present during the whole study period (frequent species).

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16 Keywords: Hymenoptera; Parasitoids; Community structure; Rarity; Species richness; Singletons; Ecological drift

# 18 1. Introduction

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19 The question of how evolutionary history influences the 20distribution and abundance of species at local and regional 21 scales has recently gained much interest. A series of studies dealing with birds and mammals showed that vulnerability to 22 23 extinction is not randomly distributed and that species poor 24 lineages contain higher proportions of regionally rare species, which are potentially in danger of becoming extinct 25 26 (Russel et al., 1998, Purvis et al., 2000a, 2000b). On the other 27 hand, Schwartz and Simberloff (2001) reported an opposite 28 trend for North American vascular plants. They found that species poor taxa contain fewer numbers of regionally rare 29 30 species.

All of these studies dealt with abundance or spatial distribution patterns at regional or continental scales and used regional or global rarity as a metric for estimating extinction probabilities. However, whether species richness of taxa influences patterns of abundance and therefore of community structure at the local, ecosystem scale is largely unknown. Additionally, there is an obvious lack of analyses about

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groups others than vertebrata (Schwartz and Simberloff 38 2001). 39

40 The present paper tries to fill this gap in our knowledge. A local community of forest Hymenoptera is used to infer 41 whether regional species richness is related to patterns of 42 local abundance. Hymenoptera are one of the largest arthro-43 pod taxa. In Europe, about 16,000 species in 80 families have 44 been described so far (Ulrich, 1999a) and local habitats like 45 forests contain more than 500 species (Hilpert, 1989, Ulrich, 46 1998). This extraordinary high local and regional species 47 richness makes the group an ideal candidate for the study of 48 the relation between species richness of lineages and local 49 abundance patterns. 50

# 2. Methods

The compilations of Ulrich (1999a, 1999b, 2001a) are 52 used to infer species numbers of European Hymenopteran 53 families and included the recent new estimate for the Ichneu-54 monidae of Horstmann (2002). In total, about 16,000 species 55 of European Hymenoptera have been described (Ulrich, 56 2001a). However, the exact number of Hymenoptera is even 57 for Europe still unknown and the percent of undescribed 58 species may be up to 20% for some families of Microhy-59 menoptera (Ulrich 1999a, Horstmann 2002, personal com-60

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munication). However, the problem of taxonomic incompleteness affects nearly all larger families of this group to a
more or less equal degree (Ulrich, 1999a, 1999b). The use of
estimates given in Ulrich (1999a, 2001a) instead of numbers
of described species does not change the results presented
below (data not shown).

Data about local Hymenopteran densities and species 67 68 numbers are based on a long-term quantitative sampling program for estimating arthropod densities and biomasses in 69 70 a beech forest (Fagus sylvatica) located on a limestone 71 plateau approximately 420 m above sea level in the vicinity 72 of Göttingen in Lower Saxony, Germany (Schaefer, 1991). 73 The vegetation can be classified as a Melico-Fagetum subas-74 sociation Lathyrus vernus. The herb layer is well developed 75 and consists mainly of spring geophytes that usually disap-76 pear in summer. Mercurialis perennis and Allium ursinum 77 dominate. A distinct shrub layer is missing. Ulrich (1998, 2001a) provided detailed descriptions of the study site and 78 79 the sampling program.

80 From 1980 to 1987 Hymenoptera of this forest were quantitatively sampled with emergence traps (Ulrich, 1998, 81 82 1999b, 2001a). Each trap covered a forest floor of 0.25 m<sup>2</sup> 83 (1984 and 1985; in both years five such traps were run),  $1 \text{ m}^2$ (1981 and 1982: 12 traps, 1983 and 1986: four traps, and 84 1987: 16 traps), and 3.2 m<sup>2</sup> (1981: 10 traps). In total 85 86 43,695 specimens from 720 species and 30 families of Hy-87 menoptera were sampled during the eight study years and of 88 them 695 species could be identified at least to genus level. 89 A study that is based on emergence densities, have to 90 control for individuals that were enclosed under the traps 91 during placement but did not emerge. These individuals 92 might bias mean densities, hence samples obtained directly 93 after the placement of traps were therefore excluded. Ex-94 cluded were also all nest-building aculeate species because 95 they were not sampled quantitatively (in total 22 species out 96 of the families Vespidae, Formicidae, Sphecidae, Megachil-97 idae, and Apidae). The following analysis is therefore based 98 on catches of 33,806 individuals from 673 species.

99 Mean annual emergence densities per species were com-100 puted as the total number of individuals per family and year divided by the area sampled by the traps and by the actual 101 number of species of the respective family found in the 102 103 forest. All species represented by only a single individual 104 (singletons) were classified as rare. In total 198 species 105 belong to this group. All species of the upper density quartile 106 were classified as abundant. These are all species (in total 159) of which at least 20 individuals were obtained. The 107 108 second density quartile contains all species (148) represented 109 by 5-19 individuals.

Following Ulrich and Ollik (2004) all species, which were found in only one of the sampling years, were classified as being occasional (in total 338 species). Frequent species are those found in at least six of the eight study years (in total 114 72 species).

115 The use of frequencies of rare or abundant species might 116 be misleading at low total species numbers due to Poisson sampling errors. To minimize such errors such frequencies117were computed only for families having more than 10 Euro-118pean species. Therefore, (Figs. 2–4) leave out the Embolemi-119dae (two European species, one rare species in the beech120forest) and the Heloridae (one European species present also121in the forest).122

The non-parametric statistics, the non-linear and the mul-123tiple regression (GLM mode) modules of STATISTICA 5124(Statsoft, 1997) were used for statistical analysis. Errors refer125always to standard deviations. Species numbers, body weight126and density data were log-transformed prior to multiple regression.127

3. Results

A regression between mean local density per species and 130 log species richness of European Hymenopteran families 131 explained 17% of the total variance when only families found 132 in the forest were included (Fig. 1A). Including all European 133 families raised the coefficient of determination to 31% 134 (Fig. 1B). Spearman's rank coefficient indicates in both cases 135 to a significant positive correlation between mean density 136

Hymenopteran families do not only differ in species richness but also include a wide range of body sizes ranging from 139

and log species richness (p < 0.01).



Fig. 1. Plots of mean local emergence densities (individuals m<sup>-2</sup> species<sup>-1</sup>) of forest Hymenopterous species on the corresponding number of European species per family. (A) Only families found in the beech forest. Least square regression:  $Y = (0.22 \pm 0.09)\ln(X) + (0.14 \pm 0.49)$ ;  $R^2 = 0.17$ ; Spearman's rank r = 0.51; p(t) = 0.004. (B) All European families included. Least square regression:  $Y = (0.22 \pm 0.04)\ln(X) - (0.29 \pm 0.16)$ ;  $R^2 = 0.31$ ; Spearman's rank r = 0.60; p(t) < 0.0001.

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W. Ulrich / Acta Oecologica 🔳 (2004) 1 1 abun Cant species В Δ 0.8 0.8 singletons Fraction of Fraction of 0.6 0.6 0.4 0.4 0.2 0.2 0 0 1000 10000 1 10 100 1 10 100 1000 10000 Number of species Number of species

Fig. 2. (A) Plots of the fraction of singletons on the corresponding number of European species per family. Non-linear least square regression:  $Y = (0.07 \pm 0.02)\ln(X) - (0.15 \pm 0.13)$ ;  $R^2 = 0.28$ ; Spearman's rank r = 0.58; p(t) = 0.002. (B) The fraction of abundant species (the upper quartile) was negatively correlated with the corresponding number of European species per family. Non-linear least square regression:  $Y = (-0.09 \pm 0.04)\ln(X) + (0.81 \pm 0.19)$ ;  $R^2 = 0.22$ ; Spearman's rank r = -0.48; p(t) = 0.02.



Fig. 3. (A) Plots of the fraction of occasional species (species found in only one of the study years) on the corresponding number of European species per family. Non-linear least square regression:  $Y = (0.07 \pm 0.04)\ln(X) + (0.17 \pm 0.21)$ ;  $R^2 = 0.14$ ; Spearman's rank r = 0.49; p(t) = 0.01). (B) The fraction of frequent species (species found in at least six study years) was negatively correlated with the corresponding number of European species per family. Non-linear least square regression:  $Y = (-0.09 \pm 0.03)\ln(X) + (0.67 \pm 0.19)$ ;  $R^2 = 0.23$ ; Spearman's rank r = -0.44; p(t) = 0.03).



Fig. 4. Plots of the fraction of species with intermediate densities (species of the second quartile) on with the corresponding number of European species per family. Non-linear least square regression:  $Y = (0.05 \pm 0.02)\ln(X) - (0.12 \pm 0.10)$ ;  $R^2 = 0.27$ ; Spearman's rank r = 0.61; p(t) = 0.001.

140 very small Mymaridae to large Ichneumonidae or Symphyta.

141 Any species number-density regression has therefore to con-142 trol for possible underlying density-body weight relation-

143 ships (Gaston and Kunin, 1997). In order to do this multiple

144 regression was used with log-transformed species number

and body weight data as independent variables. (Table 1) 145 shows that after separating the body weight effect, the relation between mean log-density and log species number still 147 remains significant ( $p_{\text{species number}} = 0.03$ ). 148

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The fraction of singletons was positively (Fig. 2A; Spearman's r = 0.58; p = 0.002) and the fraction of abundant species negatively (Fig. 2B; Spearman's r = -0.48; p = 0.02)) 151 correlated with species richness. These results hold after 152 controlling for mean body weight. The significance levels for 153 the species richness effect were in both cases below 0.02 154 (Table 1). 155

Larger families contained higher proportions of occasional (Fig. 3A; Spearman's r = 0.49; p = 0.01) but lower 157 proportions of frequent species (Fig. 3B; Spearman's r 158 = -0.44; p = 0.03). Again both results hold after controlling 159 for mean body weight (Table 1). 160

The above results seem contradictory. Species rich families had higher mean densities per species than species poor ones. On the other hand, in these families frequencies of abundant species were lower and frequencies of singletons higher. Such a pattern is only possible if there are accompanying changes in abundance patterns of species with interme-166

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#### Table 1

Multiple regressions using frequencies and log-transformed mean densities as dependent and log-transformed species numbers and mean body weights as independent variables point to species richness as a major variable that influences patterns of local abundances

	Beta	Std. Error	В	Std. Error	t	р		
Mean density								
Constant			0.47	0.48	1.04	0.310		
Body weight	-0.18	0.19	-0.11	0.11	-0.97	0.340		
Species richness	0.42	0.19	0.26	0.11	2.23	0.030		
Fraction of abundant speices								
Constant			1.05	0.31	3.27	< 0.01		
Body weight	0.24	0.20	0.04	0.03	1.25	0.220		
Speices richness	-0.47	0.22	-0.09	0.04	-2.41	0.020		
Fraction of singletons								
Constant			-0.20	0.23	-0.86	0.400		
Body weight	-0.01	0.19	-0.01	0.03	-0.04	0.960		
Speices richness	0.55	0.19	0.08	0.03	2.96	< 0.01		
Fraction of occasional species								
Constant			-0.35	0.37	-0.94	0.360		
Body weight	-0.26	0.20	-0.04	0.03	-1.28	0.210		
Speices richness	0.42	0.20	0.09	0.03	2.04	0.050		
Fraction of frequent species								
Constant			0.94	0.29	3.24	<0,01		
Body weight	0.33	0.19	0.05	0.03	1.71	0.100		
Speices richness	-0.49	0.19	-0.09	0.03	-2.58	0.020		
Fraction of species in the second quartile								
Constant			-0.22	0.17	-1.33	0.200		
Body weight	-0.15	0.19	-0.01	0.02	-0.79	0.430		
Speices richness	0.55	0.19	0.05	0.02	2.95	<0,01		

167 diate densities that counterbalance these opposite trends.

168 This was indeed the case. (Fig. 4) shows a strong correlation

169 of the fraction of species of the second abundance quartile

170 with species number per family. Again, this correlation re-

171 mained statistically significant after controlling for mean

172 body weight (Table 1).

## 173 4. Discussion

174 There are apparently no comparable studies that tried to 175 relate local patterns of abundance and community structure 176 to the species richness of taxonomic units. However, recent investigations on the relation between species richness of 177 178 taxa and abundance patterns at the regional scale gave inde-179 cisive results while either pointing to a negative relation in 180 plants (Schwartz and Simberloff, 2001) or to a positive relation in some mammals (Purvis et al., 2000a). The present 181 182 study shows that both trends might be observed in the same data set when using different measures of abundance. This 183 184 has potential implications for studies that try to assess extinction risks for instance on the basis of IUCN abundance and 185 186 frequency classes. Using total abundances or frequency classes might give contrary impressions about the depen-187 188 dence of extinction vulnerability on taxon size.

189 The 'mystery of singletons' in arthropod samples has 190 gained much attention (Novotny and Basset, 2000, Ulrich, 191 2001b). The high number of singletons has mainly been 192 explained by high local and regional dispersion abilities 193 resulting in higher numbers of transient species or tourists and by sampling artifacts (Shmida and Wilson, 1985, Hub-<br/>bell and Foster, 1986, Novotny and Bassett, 2000). The above<br/>results point to species richness of taxonomic lineages and<br/>therefore to evolutionary history as an additional variable<br/>that might influence rarity at the local scale.194<br/>195

Table 1 does not point to any body weight effect on density 199 as reported in other studies (Gittleman and Purvis, 1998; 200 Belgrano et al., 2002). Indeed, the local density-body weight 201 distribution has a negative slope (Ulrich, 2001a, Ulrich, 202 2004). However, the size differences between and inside the 203 taxa that form the classical 'Microhymenoptera' are rela-204 tively small and the body size effect is weak (Ulrich, 2001a). 205 Additionally, the lumping of species into families with wider 206 size distributions further levels the body weight effect. 207

Nevertheless, there are two possible caveats in the present 208 study. First, the analysis assumes that eclector samples are 209 sufficiently accurate to allow comparisons to be made con-210 cerning differences in mean densities among families. Previ-211 ous studies (Thiede, 1977, Funke, 1983, Ulrich, 2001a) have 212 213 shown, that parasitic Hymenoptera (the vast majority of the species) spend at least one stage of their live cycle (often the 214 pupal stage) in the soil or near the ground. These species 215 should be sampled quantitatively. Based on a mix of sample 216 techniques Ulrich (2001a) showed that of the 720 species 217 found in the forest less than 20 spend their whole live cycle in 218 219 the canopy of trees. Furthermore 20-30 bi- or polyvoltine species spend at least one generation solely in the canopy. 220 These species (5–6% of total) are potentially undersampled. 221 Because these species come from different families their low 222 frequency should not influence overall density estimates. 223

224 A second caveat might be a possible sample bias against 225 species rich families. If species of these families are under-226 represented in local samples (for instance due to their very 227 low densities) estimates of mean species densities would also 228 be biased towards higher mean densities in species rich 229 families. However, this would only be a problem if there 230 were severe sample bias, but there is no indication, that this 231 occurred. Jackknife estimates of total species numbers and 232 local species—area curves point to rather equal rates of 233 unrecorded species among families (Ulrich, 2001a and in 234 preparation). In fact, due to the well known negative abun-235 dance-body weight relation (Ulrich, 1999c) this type of 236 sample bias is more related to mean body weight. In this 237 respect, such a bias might occur in the Ichneumonidae with 238 its mainly larger species of low mean abundances (Ulrich, 239 1999c). However, to account for the correlation in (Fig. 1) the 240 fraction of unrecorded species in the largest families must be 241 at least five times the fraction in smaller families. The close 242 linear regression between local (forest) and European species 243 numbers (Ulrich, 2001a and in preparation) makes such a 244 bias improbable.

245 Recently, Magurran and Henderson (2003) and Ulrich and 246 Ollik (2004) found that the division of local communities 247 into frequent and occasional species might improve our un-248 derstanding of what factors influence local patterns of spe-249 cies abundances. The present works adds to this picture. 250 (Fig. 3) showed that at the local scale, species rich lineages 251 have higher proportions of occasional but lower proportions 252 of frequent species. Frequent species are either those that 253 persist in a community over longer time periods or have high 254 migration abilities so that local extinctions are immediately 255 counterbalanced. Differences between small and large lineages in regard to patterns of temporal persistence in a 256 257 community might therefore tell something about their evolu-258 tionary history. Unfortunately, up to now it proved to be 259 impossible to work out an unequivocal phylogenetic system 260 of Hymenopteran lineages at and above the family level (Dowton et al., 1997; Ronquist, 1999; Carpenter, 2000; Vil-261 262 helmsen, 2001). Furthermore, there is no consensus about the 263 status and the phylogenetic position of most of the super-264 families (Ronquist, 1999). This poor state of the art prohibits 265 a deeper analysis of the evolutionary significance of the 266 present findings. In particular, it would be of interest to see 267 whether patterns of local abundance are not only related to 268 species richness but also to the phylogenetic age of a lineage. 269 Nevertheless, the patterns reported here call for an expla-270 nation. Of course, one might think about a simple statistical 271 artifact. Local and regional species numbers of Hy-272 menopteran families are highly correlated (Ulrich, 1999b, 273 2001a), and regionally species rich families are most often 274 also species rich at the local scale. Now assume that temporal 275 variability is a simple log-normally distributed random num-276 ber. Then species of species rich families will have a higher 277 probability to reach very high densities. One hundred nu-278 merical simulations of this simple model using the observed 279 species numbers and realistic ranges of maximum and minimum densities resulted in 24 statistically significant (at p 280 < 0.05) correlations between regional species richness and 281 mean local density per species. This model might therefore 282 account for the relationship of (Fig. 1), but fails to explain the 283 remaining patterns. In particular, it predicts a positive correlation between species richness and the fraction of abundant 285 species contradicting the observed pattern (Fig. 2). 286

Nevertheless, it remains to be shown whether stochastic 287 models might explain the observed relationships. In this 288 respect it would be interesting to see whether the neutral 289 model approach of Hubbell (2001) predicts similar relation-290 ships between regional species diversity and patterns of local 291 community structure. Hubbell (2001) showed that his eco-292 logical drift model results in close positive correlations be-293 tween regional and local abundances and phylogenetic age. 294Additionally, his model predicts that phylogenetic older lin-295 296 eages should be more species rich. From these two assumed patterns it is only a short step to the prediction of a positive 297 relationship between local abundance and species richness of 298 299 lineages. However, whether the other patterns reported here 300 also follow from ecological drift is still not clear. To study this, intensive and CPU-time consuming simulations with 301 larger assemblages under different speciation regimes are 302 303 necessary.

Of course, the present results refer only to one community304of forest Hymenoptera; it remains to be shown whether they305can be generalized. For this task complete local abundance306data about other species rich taxa like Diptera, Carabidae,307Lepidoptera, Arachnida, or Aves are necessary.308

Last, the present results shed light on a neglected group of species, those having intermediate densities. Most studies 310 dealing with conservation and biodiversity concentrated on rare species (Gaston and Kunin, 1997). It seems that to get unequivocal results about patterns of rarity and abundance 313 these intermediate species have to be included into our analyses. 315

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