Correlations between higher-taxon richness and species richness in the British Isles flora

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ABSTRACT

It has been suggested that the biodiversity of areas may be compared using the number of higher taxa present rather than by compiling full species lists. This would reduce sampling problems especially in the tropics with their high species richness. Data from British Isles regional Floras are used to examine the relationship between species richness and higher taxa richness for flowering plants. Positive correlations were found between species richness and genus richness ($r_s = 0.97$) and species richness with family richness ($r_s = 0.89$). Richness of species in a small number (15) of the most species-rich genera was highly correlated with total species richness ($r_s = 0.91$) and could be used as an alternative to higher taxa in comparing sites. Such relationships, validated on the well studied British flora, could be of great use in less well studied areas such as tropical forests. The study also illustrates the importance of regional Floras as a data base for use in studies of biodiversity.

KEYWORDS: regional Floras, biodiversity, higher taxa, species richness.

"The ultimate task of the systematist is not merely to describe the diversity of the living world but also to contribute to its understanding." Mayr (1997).

INTRODUCTION

One of the key problems of conservation biology is how to identify the most important areas for biodiversity so that they can receive protection (Williams & Gaston 1994; Wilson 1992). An ideal data set on which to base such a decision would include full species lists for all areas under discussion. However, even for biologically well known countries such as Britain, this has not been achieved for many groups. The problem is much greater in the tropics, the home of the greatest terrestrial biodiversity (Wilson 1992); here estimates of the total number of species are very large. For example, estimates of the number of insects based on extrapolation from beetle data (reviewed by May (1988) and Gould 1996)) give values of up to 50 million species. Studies based on extrapolation from other insect orders give smaller, but still very large numbers (Hodkinson & Casson 1991). Whatever the true number, it is clear that full species lists will not be achieved, even for the apparently less diverse flowering plants, which have an estimated 250,000 species (Holdgate 1991).

This raises the question of how areas can be compared when full species lists are not available. A number of approaches have been described, including: i. use of correlation between biodiversity and environmental variables (e.g. soil or water chemistry); ii. relationships between indicator groups and total biodiversity; iii. using higher taxa to compare sites (Williams & Gaston 1994); and iv. combining data from groups of widely differing organisms (Vane-Wright *et al.* 1994). This paper concentrates on the use of higher taxa, based on the idea that relationships between species richness and number of higher taxa can be used to compare sites. Such an approach has been widely used in palaeontology, where making comparisons at the species level is often difficult (Gaston & Spicer 1998). This approach, if successful, would be in many cases logistically more realistic and more cost-effective than compiling full species lists (Andersen 1995; Gaston & Williams 1993; Williams & Gaston 1994).

This paper aims to investigate the relationship between species richness and higher taxon (family

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	Number of:				
		families	genera	species	species in
Area	Reference				large genera
Suffolk	Simpson, 1982	118	622	1643	221
Kent	Philp, 1982	119	657	1643	216
Dorset	Good, 1984	110	585	1473	223
Glamorgan	Wade et al., 1994	126	570	1460	213
Jersey	Le Sueur, 1984	120	585	1448	201
Durham	Graham, 1988	113	546	1421	220
Somerset	Roe, 1981	110	572	1413	223
Angus	Ingram & Noltie, 1981	105	491	1192	212
Leicestershire	Primavesi & Evans, 1988	98	505	1171	189
East Yorkshire	Crackles, 1990	104	476	1133	184
Shropshire	Sinker et al., 1985	110	475	1089	186
Derbyshire	Clapham, 1969	101	478	1089	186
South Lancashire	Savidge et al., 1963	103	479	1063	185
Staffordshire	Edees, 1972	98	436	1017	171
Anglesey	Roberts, 1982	102	450	1004	188
Cheshire	Newton, 1971	100	427	913	152
Radnorshire	Woods, 1993	99	387	871	157
Connemara & Burren	Webb & Scannell, 1983	94	387	818	160
Outer Hebrides	Pankhurst & Mullin, 1991	81	321	696	148
Shetland	Scott & Palmer, 1987	79	300	627	93

TABLE 1. NUMBERS OF FAMILIES, GENERA AND SPECIES RECORDED IN 20 BRITISH AND IRISH REGIONAL FLORAS

and genus) richness, for the well studied British flora, to test the correlation between species and higher taxa richness. It also considers the importance of the more species-rich genera in such relationships.

METHODS

The long history of biological recording in Britain, often carried out by non-professional biologists (Allen 1976) makes it one of the best studied countries in the world. This provides data sets which can be used to test relationships between species richness and higher taxon richness. This study used data on flowering plants from a subset of the regional Floras produced for Britain and Ireland (Table 1), most of which cover a single Watsonian vice-county. This system dates from 1852 and divides Britain into 112 vice-counties (Ireland is covered by an additional 40). The idea was to create a set of areas of more equal size than the administrative counties, into which the country could be divided for biological recording. These vice-counties are still somewhat unequal in size with between three and six per 100 km² (Vincent 1990). While such sizes are large by the standard of British reserves they are more comparable in size with some existing and proposed tropical protected areas (Janzen 1994; Wilson 1992).

In 20 such regional Floras the numbers of species, genera and families of flowering plants were counted. As Ratcliffe (1984) pointed out, humans have introduced a large number of non-native species to Britain and altered the distribution of many native plants. No attempt was made to distinguish native from non-native species, all species listed in a given Flora as growing in the area were counted. The coverage of apomictic microspecies of *Rubus* and *Taraxacum* is very variable between different Floras, and therefore in this study they were counted as two species *R. fruticosus* agg. and *T. officinale* agg. The apomictic microspecies of the genus *Sorbus* were also excluded from the calculations. Such microspecies are really clonal lineages and can be regarded as single

TABLE 2. LARGE GENERA, DEFINED AS ONES	WITH 20 OR MORE SPECIES IN BRITAIN
AND IRELAND LISTED F	BY STACE (1991)

Excluding Sorbus with its many apomictic microspecies

Genus	Number of species
Carex	74
Cotoneaster	45
Salix	35
Trifolium	32
Ranunculus	31
Potamogeton	29
Juncus	28
Chenopodium	27
Veronica	26
Geranium	24
Rumex	23
Saxifraga	22
Euphrasia	21
Allium	20
Rosa	20

evolutionary individuals rather than good species (Janzen 1977); as such they should probably not be considered as important as other species in biodiversity surveys (see Gould (1996) for an alternative view of microspecies).

Species are not evenly distributed between higher taxa; for example a small number of plant genera are unusually species-rich (Cronk 1989; Webb 1991). A good example is *Carex* in the British Isles (Table 2). To investigate this, the numbers of species in large genera were recorded for each Flora; large genera are defined as those with 20 or more species listed by Stace (1991). It should be noted that one of these genera, *Cotoneaster*, is composed almost entirely of introduced species.

RESULTS AND DISCUSSION

Data from 20 regional Floras are shown in Table 1. There are significant correlations (using the non-parametric Spearman rank correlation coefficient) between species richness and genus richness ($r_s = 0.97$, p<0.001) and species richness and family richness ($r_s = 0.89$, p<0.001). Both higher taxon levels investigated are therefore highly correlated with species richness, with variation in genus richness accounting for more of the variation in species richness ($r^2 = 0.94$) than is accounted for by family richness ($r^2 = 0.79$). These patterns are found even though the regional Flora data are potentially "noisy", with different levels of accuracy and detail between different Floras. This suggests that this approach may work with data sets from areas of the world where "noise" is introduced due to the local flora being incompletely known.

The results of this study provide an example of a data set with a good positive correlation between higher taxon richness and species richness. Other published examples include relationships between family and species richness for: British ferns and British butterflies among 100-km squares, Australian passerine birds using $5^{\circ} \times 5^{\circ}$ grid squares and northern and central American bats using grid squares of c. 611,000 km² (Williams & Gaston 1994). However, Anderson (1995), working on genus richness as a surrogate for species richness in Australian ants, found that "except in limited circumstances, genus richness ... appears to be an unreliable surrogate for species richness in local Australian ant faunas. This may apply more generally to taxa in which relatively small numbers of genera can contribute a large proportion of species."

When the number of species in large genera are compared with total species richness in this British Isles data set a very strong positive correlation was found ($r_s = 0.91$, p< 0.001). This means

that if data were only collected on numbers of species in these 15 genera it would be almost as useful a predictor ($r^2 = 0.83$) for comparing areas as a full species list. If such a relationship holds for richer floras which are less well known taxonomically it suggests an option of just recording data from a subset of all genera i.e., the large ones. In the British Isles data set, removing the large genera has little effect on the relationships between higher taxa as, with the exception of the mainly non-native *Cotoneaster*, all large genera occur in each of the regional Floras studied.

The only approach to validating such heuristic rules is an empirical one, testing these rules at a variety of sites and with a variety of taxa. It is hoped that relationships such as this, tested on the British flora, will also work on tropical forest vegetation. These forests are thought to contain some 40% of the world's flora (Archibold 1995); mean values of over 230 plant species per 0.1 ha have been described for some of these forests (Crawley 1997). For such areas, comparing lists of higher taxa is a much more realistic possibility than attempting to compile full species lists. The British flora would suggest that comparing sites at the family level could be a good guide to their relative species richness. Comparison at the genus level would provide greater accuracy but would also require more taxonomic work.

This study also highlights the importance of regional Floras as biodiversity data sets. Such Floras contain a wealth of data which can be used in many different studies. An attempt to replicate these results using tropical Floras would be of great interest if/when enough data are available.

The quotation from Ernst Mayr at the start of this paper suggests that data from plant systematics (and biogeography) can add to our understanding of the world as well as merely describing its variety. It can also contribute to its preservation by providing ways of evaluating the biodiversity of different sites as illustrated by this study.

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