The influence of phylogeny on functional grouping of species: a case study in herbaceous communities of Southern Spain

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ABSTRACT: Ecological and evolutionary processes take place at very different time scales. Most efforts in understanding the influence of evolutionary history on ecosystem processes have been focused on the adaptive value of functional traits. However, it must be kept in mind that many of these traits are not randomly distributed among species since they are influenced by kinship and by processes of convergent or parallel evolution. The aim of this work was to determine which of the variables important for grouping species were determined by phylogeny and to what extent. The phylogenetic distance matrix of 31 plant species was obtained from both molecular and taxonomic data, which rendered very similar results. The most important traits for the segregation of the species were those related to reproduction and to foliar morphology. Phylogenetic relationships between species explained the differences observed in both types of variables, but they never explained more than 50 % of the total variance. This suggests the existence of microevolutionary processes that were undetected by the phylogenetic relationships considered in addition to the macroevolutionary processes already included in the phylogeny itself.

1 INTRODUCTION

Ecological and evolutionary processes take place at very different time scales. Most efforts in understanding the influence of evolutionary history on ecosystem processes have been focused on the adaptive value of functional traits, see Tilman (1988). However, it must be kept in mind that many of these traits are not distributed at random among species since they are influenced by kinship as can be seen in Harvey and Pagel (2000).

2 MATERIAL AND METHODS

We have selected 31 vascular plant species co-occurring in motorway slopes in Málaga (southern Spain). The values for 27 variables of each species were gathered from the literature. The role of each variable in determining functional groups was established using principal components analysis. Regarding phylogeny, three distance matrices were built using taxonomic classification and molecular information using two basic models in phylogenetic studies. With respect to functional traits, five Euclidean distance matrices were built, either considering all variables or using those belonging to each group as shown in Table 1a. To determine the similarity between matrices, a Mantel test was carried out (Mantel Nonparametric Test Calculator version 2.0, 1999).

3 RESULTS AND DISCUSSION

Correlation between taxonomic and molecular distance matrices was highly significant (Table 1a). This result validates the usage of taxonomic classification since loss in precision was low and it is more practical for large numbers of species. Traits having more influence in the segregation of species were reproductive ones and those related to leaf morphology (Table 1b). Differences observed in variables related to reproduction and to leaf morphology were explained by kinship relationships among species but they never explained more than 50 % of the total variance (Table 1a). Differences in spatial occupation and geographical distribution of the species were not significantly related to the degree of kinship although they were important in segregating species in functional groups (Tables 1a and 1b). We suggest that sharing characteristics relative to reproduction and to leaf morphology is affected by the previous evolutionary history, while sharing characteristics related to spatial occupation or geographical distribution, could be the result of a process of convergence or parallelism and they may play an important role for local adaptation of different taxa to the environment.

Table 1. a) Mantel correlation coefficient between taxonomic and molecular and functional distance matrices. (*, p<0.05). b) Main variables segregating species and their weights in axis 1 and 2. Axis 1 accounted for 16. 93 % and axis 2 accounted for 12.74 % of the total variance.

a)

Molecular matrices	Taxonomic matrix
"p-Distance" Model	0.82 (*)
"Kimura-2" Model	0.60 (*)

Functional matrices	Taxonomic matrix
Total Variables	0.31 (*)
Ocupation/Architect.	0.06
Foliar Morfology	0.20 (*)
Reproduction	0.45 (*)
Biogeography	-0.10

b)

Axis 2 (12.74 %)	Axis 1 (16.93 %)
Ramification 0.72	Seed size 0.79
Stem epidermis 0.72	Plant size 0.58
Foliar epidermis 0.65	Dispersion way 0.57
Foliar length 0.43	Foliar abundance 0.5
Dispersal type 0.42	Flower distribution 0.47
Lobulation 0.39	Spinescence 0.43
Persistence 0.37	Flower type 0.4
Leaf situation – 0.71	Leaf epidermis 0.36
	Stem texture – 0.69
	Distribution – 0.64
	Sexuality – 0. 45

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