

## **Appendix S1:** Incorporation of phylogenetic information

### *1. Representing phylogenetic information with principle coordinates*

In contrast with principal component analysis (PCA), where the distance among objects is treated within the algorithm as Euclidian, in PCoA any distance measure can be used. The matrix that serves as the basis for computing the ordination is calculated a priori. We calculated a patristic distance matrix of the plant species using the phylogenetic supertree from Durka (2002). Since we lack information on branch length we set all branch lengths to unity for the calculation (Faith 1992), so that the patristic distance represents the number of branches between two species across the phylogenetic tree. For each subset of species we performed separate analyses to extract the phylogenetic structure of the data. Due to the composition of the data the last few dimensions could yield negative eigenvalues; we therefore restricted our analysis to the number of dimensions with positive variances. Furthermore, axes with more variance indicate major phylogenetic structures in the cladogram (Diniz-Filho *et al.* 1998). Therefore, we only used the PCos cumulatively accounting for up to 80% of variation in the data to test for significance on species' grid cell frequency. We assumed that the axes of higher order represent white noise or species' phylogenetic idiosyncrasies, i.e. variation between very closely related species and just the first few ones account for large phylogenetic trends and phylogenetic autocorrelation. However, the limit of 80% was set arbitrarily.

### *2. Partitioning the variation between traits and phylogeny*

Variation partitioning (Legendre & Legendre 1998; Desdevises *et al.* 2003) was applied for variables significant in CS and/or PI analyses. Variation related only to phylogeny quantifies the strength of association between invasion success and other, phylogenetically conservative traits, which are not included in the respective model. Variation related only to the trait shows the extent to which the covariation between invasion success and trait can be found repeatedly within different phylogenetic lineages. Variation attributed jointly to phylogeny and trait quantifies the extent to which invasion success is linked to the phylogenetic conservatism of the trait in question (see also Westoby *et al.* 1995). Different subsets of species were used in the single trait models. As the variation explained by phylogeny is dependent on the subset of species it is not possible to compare the degree of phylogenetic dependence of traits between models that use different subsets.

## References for Appendix S1

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