

Ecography

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Supplementary material

Appendix 1 *The non-native naturalized species (“invaders”) recorded.*

Appendix 2 *Plots of MDNS and DNNS vs. species richness.*

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Appendix 1 The non-native naturalized species (“invaders”) recorded

Table A1. List of non-native species recorded and used for analyses, with indication of the sampling resolution at which they were sampled. All species are neophytes according to the classification by Celesti-Grapow et al. 2009.

Species	Family	Status	4m ²	64m ²	35km ²
<i>Acacia saligna</i> (Labill.) H.L.Wendl.	Fabaceae	Inv	X	X	X
<i>Agave americana</i> L.	Asparagaceae	Inv	X	X	X
<i>Ailanthus altissima</i> (Mill.) Swingle	Simaroubaceae	Inv			X
<i>Amaranthus retroflexus</i> L.	Amaranthaceae	Inv			X
<i>Ambrosia coronopifolia</i> Torr.&A.Gray	Asteraceae	Inv			X
<i>Amorpha fruticosa</i> L.	Fabaceae	Inv			X
<i>Artemisia verlotiorum</i> Lamotte	Asteraceae	Inv			X
<i>Bidens frondosa</i> L.	Asteraceae	Inv			X
<i>Canna indica</i> L.	Cannaceae	Nat			X
<i>Carpobrotus acinaciformis</i> (L.) L.Bolus	Aizoaceae	Inv	X	X	X
<i>Carpobrotus edulis</i> (L.) N.E.Br.	Aizoaceae	Inv	X	X	X
<i>Cenchrus incertus</i> Curtis	Poaceae	Inv		X	X
<i>Chenopodium ambrosioides</i> L.	Chenopodiaceae	Inv			X
<i>Commelina communis</i> L.	Commelinaceae	Inv			X
<i>Cortaderia selloana</i> (Schult.) Asch.&Graebn.	Poaceae	Inv			X
<i>Datura stramonium</i> L.	Solanaceae	Inv			X
<i>Dichondra micrantha</i> Urb.	Convolvulaceae	Nat		X	X
<i>Erigeron bonariensis</i> L.	Asteraceae	Inv			X
<i>Erigeron canadensis</i> L.	Asteraceae	Inv	X	X	X
<i>Erigeron sumatrensis</i> Retz.	Asteraceae	Inv		X	X
<i>Eucalyptus camaldulensis</i> Dehnh.	Myrtaceae	Nat		X	X
<i>Ipeion uniflorum</i> (Graham) Raf.	Liliaceae	Nat			X
<i>Lantana camara</i> L.	Verbenaceae	Nat			X
<i>Ligustrum lucidum</i> Aiton	Oleaceae	Nat			X
<i>Lonicera japonica</i> Thunb.	Caprifoliaceae	Inv			X
<i>Mirabilis jalapa</i> L.	Nyctaginaceae	Inv			X
<i>Myoporum tenuifolium</i> G.Forst.	Scrophulariaceae	Inv			X
<i>Oenothera adriatica</i> Soldano	Onagraceae	Inv			X
<i>Oenothera biennis</i> L.	Onagraceae	Inv	X	X	X
<i>Oenothera suaveolens</i> Desf.exPers.	Onagraceae	Inv			X
<i>Opuntia ficus-indica</i> (L.) Mill.	Cactaceae	Inv		X	X
<i>Oxalis articulata</i> Savigny	Oxalidaceae	Inv		X	X
<i>Oxalis pes-caprae</i> L.	Oxalidaceae	Inv			X
<i>Parthenocissus quinquefolia</i> (L.) Planch.	Vitaceae	Inv			X
<i>Paspalum distichum</i> L.	Poaceae	Inv			X
<i>Passiflora coerulea</i> L.	Passifloraceae	Nat			X
<i>Phoenix canariensis</i> Chabaud	Arecaceae	Nat			X
<i>Phyla nodiflora</i> (L.) Greene	Verbenaceae	Nat			X
<i>Phytolacca americana</i> NA	Phytolaccaceae	Inv			X
<i>Pittosporum tobira</i> (Thunb.) W.T.Aiton	Pittosporaceae	Nat	X	X	X
<i>Populus canadensis</i> Moench	Salicaceae	Nat			X
<i>Robinia pseudoacacia</i> L.	Fabaceae	Inv		X	X
<i>Senecio angulatus</i> L.	Asteraceae	Inv			X
<i>Senecio inaequidens</i> DC.	Asteraceae	Inv			X
<i>Symphotrichum squamatum</i> (Spreng.) G.L.Nesom	Asteraceae	Inv			X
<i>Ulmus laevis</i> Pall.	Ulmaceae	Nat			X
<i>Veronica persica</i> Poir.	Scrophulariaceae	Inv		X	X
<i>Vitis rupestris</i> Scheele	Vitaceae	Nat			X
<i>Xanthium orientale</i> L.	Asteraceae	Inv	X	X	X
<i>Xanthium spinosum</i> L.	Asteraceae	Inv		X	X
<i>Yucca gloriosa</i> L.	Asparagaceae	Nat		X	X

Nomenclature and Invasion status according to:

Celesti-Grapow et al. 2009. Inventory of the non-native flora of Italy. *Plant Biosystems*, 143: 386-430
 Conti et al. 2005. An Annotated Checklist of the Italian Vascular Flora. Palombi Editori, Roma, Italia.

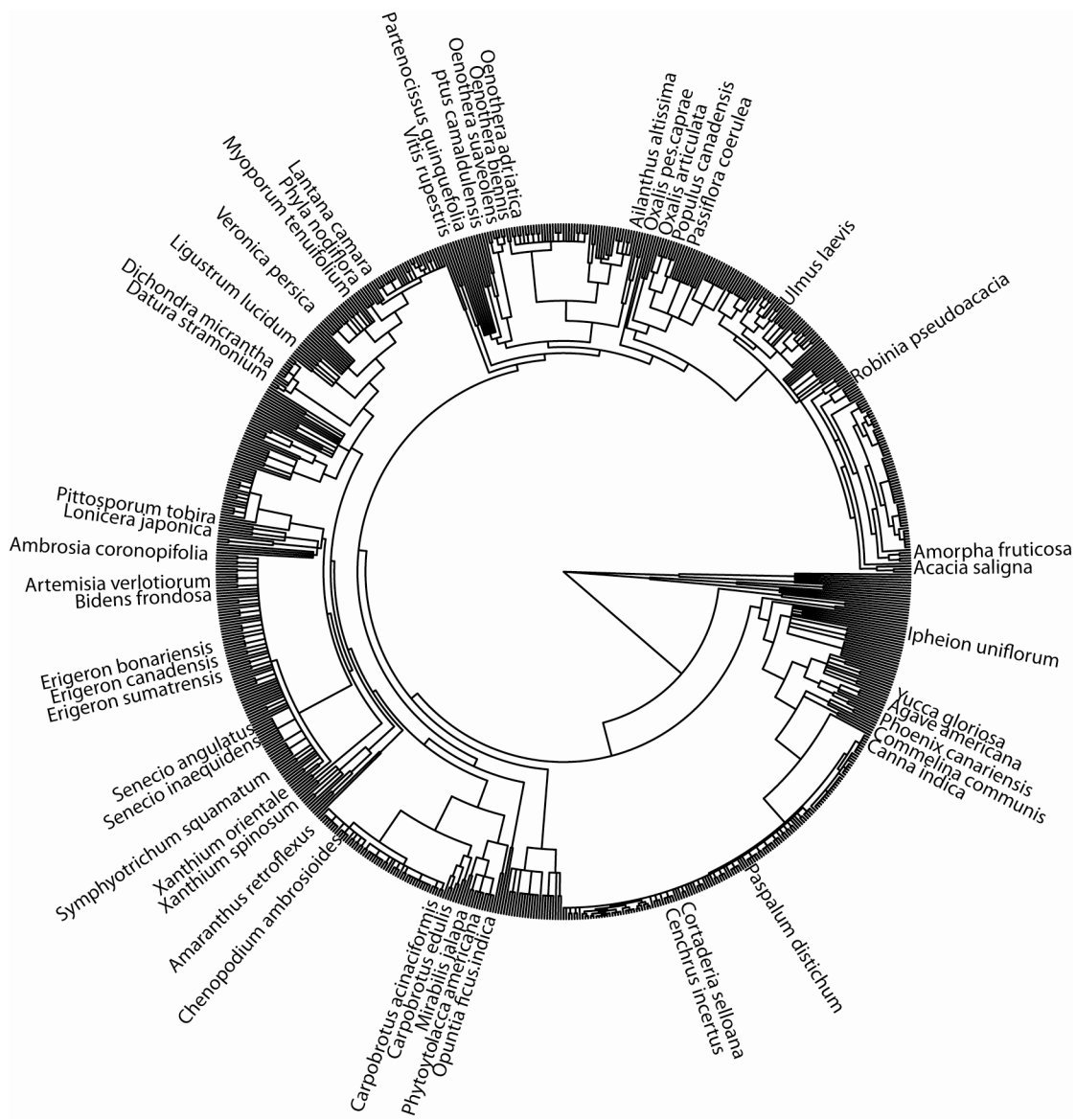


Fig. A1 The position of non-native naturalized species (“invaders”) on the supertree.

Appendix 2 Plots of MDNS and DNNS vs. species richness

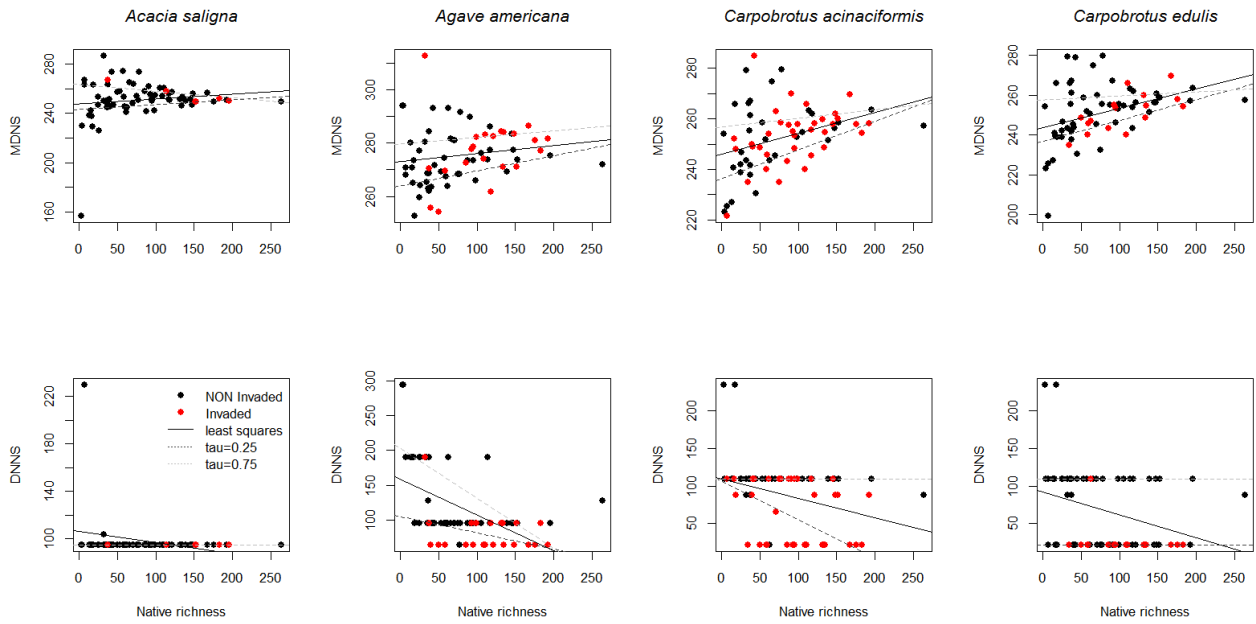


Fig. A2 Examples of plots of MDNS (first row) and DNNS (second row) vs. species richness, with fitted regression line and quantile regressions at $\tau=0.25$ and $\tau=0.75$ to show the general trends. Represented are the relationships at the coarse scale for the four most common invasive species in the study area.

Appendix 3 Sensitivity test of the potential effect of the polytomies in the phylogeny on the overall results of the analyses.

Methods

Given that the phylogenetic tree constructed by the software Phylomatic contained several polytomies at the species and genus levels, it was necessary to check whether the phylogenetic resolution affected the MDNS and DNNS metrics. We therefore performed a sensitivity test in which polytomies were randomly resolved to measure their influence on the metrics. We generated 100 phylogenetic trees with the polytomies resolved using the Polytoomy Resolver software developed by Kuhn et al. (2011). For each simulated tree, we randomly resolved the polytomies from the original supertree by applying a birth-death (Yule) bifurcation process within each necessary genus or family. From these randomly resolved trees we then produced a distribution of metrics (MDNS/DNNS), averaged across sites, for each of the 8 alien species found at all three spatial resolutions. We finally compared the observed values of the metrics (i.e. unresolved polytomies) with these distributions (i.e. resolved polytomies).

Results

We found that in most of the cases the value of the metric calculated from the unresolved tree (used for the main analyses in the paper) was very close to the mean of the values from the randomly resolved phylogenies and that the variation of the distributions was moderate (Fig. A3). We were therefore confident on using the unresolved tree for the analyses through the paper.

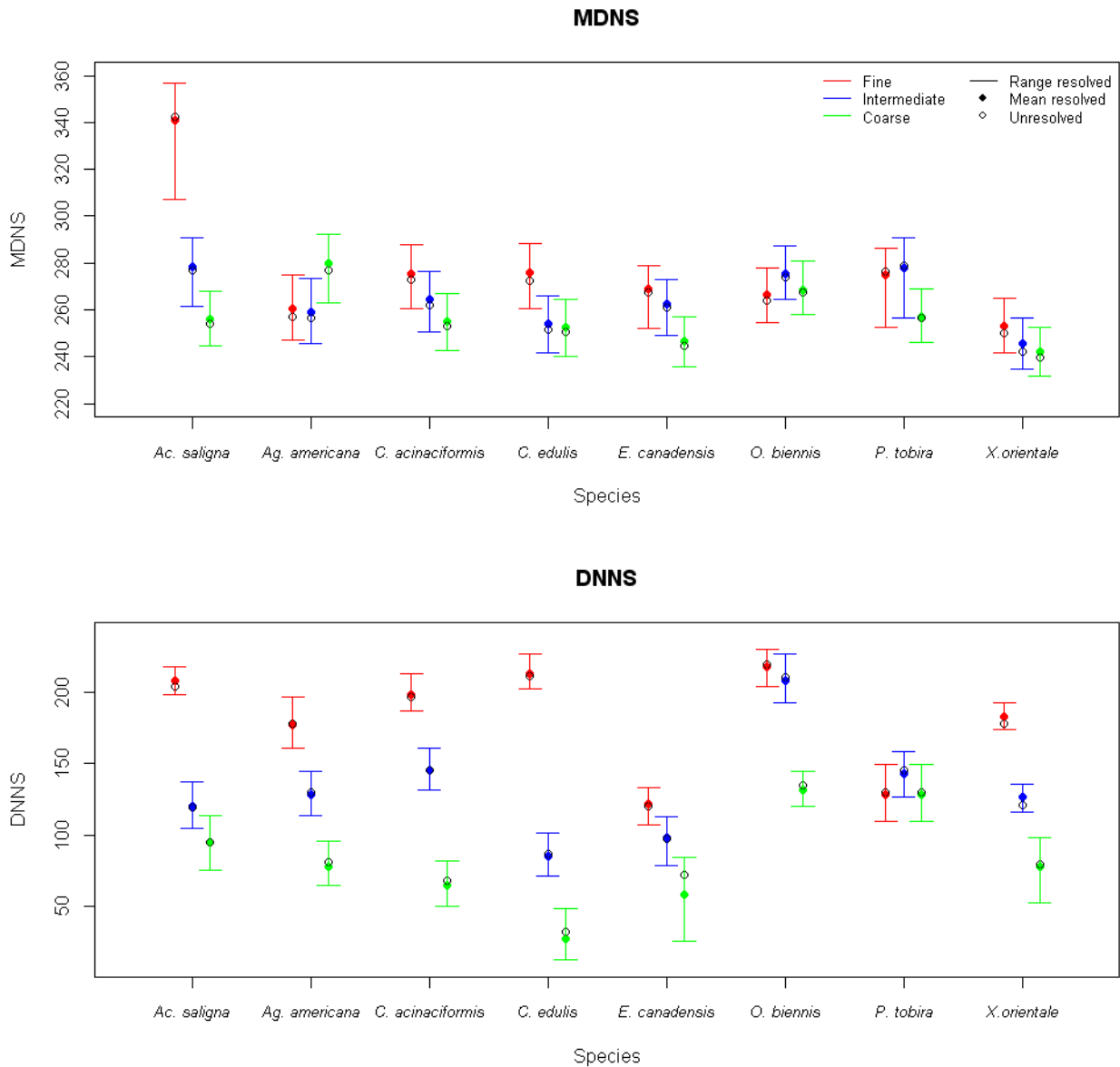


Fig. A3. Sensitivity test of the effects of polytomies in the phylogeny on MDNS (upper panel) and DNNS (lower panel). Plotted are for the eight alien species found at all resolutions the range and mean of metrics from 100 randomly resolved trees and the value of the metric without resolving the polytomies.

References

Kuhn, T.S., et al. 2011. A simple polytomy resolver for dated phylogenies. - *Methods in Ecology and Evolution* 2: 427-436.

Appendix 4 Link between phylogeny and ecological characteristics.

Methods

To corroborate the baseline assumption that closely-related species shared similar ecological characteristics, we checked for a phylogenetic signal of some selected traits for a subset of species.

We measured five traits linked to the leaf-height-seed (LHS) plant strategy scheme (Westoby 1998) and to plant responses to the harsh coastal environment: Leaf thickness (mm), specific leaf area (SLA - the ratio of leaf area on dry weight measured as mm^2/mg), plant height at maturity (cm), seed mass (mg of air dried propagules) and seed shape (measured as the variance of the three dimensions of length, breadth and thickness). The two leaf traits tend to be intercorrelated but may not always capture the same functions and are mostly indicators of leaf life span. For example, higher SLA is associated with shorter leaf life span, higher leaf nitrogen, higher photosynthetic capacity, shorter nutrient residence times and higher relative growth rates (Westoby et al. 2002). Plant height (height of flowering shoot) relates to both competitive ability and tolerance of disturbance (Westoby et al. 2002). Finally the two seed traits are a proxy of dispersal ability and germination.

Traits were measured from the field on a subset of 47 dominant species out of the 264 species recorded at the fine scale (4m^2 plots). This subset of species was chosen by selecting the most common and abundant species within each habitat along the sea-inland gradient on the basis of previous studies (see Carboni et al. 2011; Acosta et al. 2011) and of the complete vegetation database used in this study. We estimated that the selected species collectively made up at least 80% of the maximum standing live biomass of each habitat (estimated through the cumulative cover of all species available for the 4m^2 plots. See Carboni et al. 2011 for details on cover estimation). This threshold has been shown to ensure a satisfactory description of overall community properties (Pakeman & Quested, 2007).

Each attribute was obtained by measuring at least 10 replicate samples per species and averaging. Traits were log-transformed to meet the assumption of normality. We calculated phylogenetic signal using Abouheif's test (1999) designed to detect phylogenetic autocorrelation in quantitative traits (function `abouheif.moran` in the R-based package 'adephylo'). A recent sensitivity analysis (Münkemüller et al. 2012) showed that Abouheif's test is one of the best performing methods for measuring and testing phylogenetic signal under a variety of models of trait evolution. Note that the aim of our study was not to compare the strength of phylogenetic signal across different phylogenies or traits, for which Blomberg's K might be more appropriate. We used a pruned phylogeny containing only the 47 dominant species for this test.

Results

Table A2. Test of Abouheif (function `abouheif.moran` in the R-based package 'adephylo') for 5 traits measured on a subset of 47 dominant species: Leaf thickness (mm), specific leaf area (SLA - mm² mg⁻¹), plant height at maturity (cm), seed mass (mg) and seed shape.

Trait	Obs	Std.Obs	P value
Leaf thickness	0.294	2.913	0.004
SLA	0.113	1.123	0.137
Height	0.149	1.560	0.061
Seed mass	0.186	1.936	0.035
Seed shape	0.355	3.586	0.002

We found a significant phylogenetic signal for leaf thickness, seed mass and seed shape (Table A2).

Plant height at maturity also exhibited a marginally significant phylogenetic signal.

In summary, most of the traits examined seemed to be more similar for closely-related species than under random expectation, reflecting all aspects of the leaf-height-seed (LHS) plant strategy scheme.

References

Abouheif, E. 1999. A method for testing the assumption of phylogenetic independence in comparative data. - *Evolutionary Ecology Research* 1: 895-909.

- Acosta, A., Carranza, M.L. & Izzi, C.F. 2009. Are there habitats that contribute best to plant species diversity in coastal dunes? - *Biodiversity and Conservation* 18: 1087-1098.
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Appendix 5 Patterns of specific invaders and likely interactions involved.

At the finest resolution the invaders *A. saligna* and *C. acinaciformis* were more distantly related to the native community than expected by chance (with $p < 0.025$) and *X. orientale* had a very similar, marginally significant pattern ($p = 0.05$). All three of these invaders were quite abundant in our study area. They are invasive in Italy (Celesti et al. 2009) and, more specifically, they are also invasive on coastal dunes (Weber 2005, Carboni et al. 2011). Furthermore they are also all strong competitors (Witkowski 1991, Suehs et al 2004, Sintès et al 2007, Weber 2005). With our data it is not possible to conclusively say whether the absence of phylogenetically close invaders in the communities is a precondition for invasion or the result of competitive displacement. Given that all overdispersed invaders were strong competitors it is actually likely that phylogenetically closest native neighbors were displaced due to the higher competitive ability of incoming invaders.

Furthermore, we found that invaders avoiding close relatives at the fine scale included both herbaceous (*X. orientale*) and woody species (*A. saligna*), which invaded different habitats of the coastal dune zonation along the sea-inland gradient, from the beach (*X. orientale*) to the mobile and transition dunes (*C. acinaciformis*) up to the backdune Macchia (*A. saligna*). Therefore invaders with an overdispersed distribution did not share a common strategy, but were rather sorted along the sea-inland environmental gradient.

Interestingly, in the case of *C. acinaciformis*, the invader did not co-occur with close relatives at the fine scale, but it was instead more phylogenetically close to its native neighbors at the coarse scale. Overall, this implies that the shift from greater overdispersion of invaders to greater clustering across scales does not only reveal the varying proportion of non-random patterns. To the contrary it also reflects different co-occurrence patterns of single invaders depending on the scale of observation.

References

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