
Supplementary Methods.**Description of the R2G2_20140601 super tree, a dated phylogenetic tree of all vascular plant families for phyloecological studies.**

We hand-constructed a supertree R2G2_20140601 with stable node dates that includes the accepted vascular plant families of angiosperms, gymnosperms, and pteridophytes. The goal was to create an age-stable supertree that could be readily used to create phylogenetic topologies for any list of plant species worldwide. We used tools in Phylocom³⁶ and Phylomatic v.4.2

(<http://phylodiversity.net/phylocom/>) to create and date the tree. The supertree includes 4,789 terminal taxa from 51 orders, 419 families, 259 other named clades, 2,320 genera, and an additional 1,515 fixed internal nodes. Accepted names and spellings follow The Plant List (www.theplantlist.org) as of 18 April 2014. We provide the tree as a dated Newick file R2G2_20140601.new.txt.

Sources for topology.

The angiosperm topology is based on the Bremer and Angiosperm Phylogeny Group³⁸ classification (APGIII) as updated at the Angiosperm Phylogeny website of the Missouri Botanic Gardens (www.mobot.org/MOBOT/research/APweb/). The gymnosperm topology was taken from Chaw, et al.³⁹ and the fern topology from Lehtonen⁴⁰. Additional topological structure was added for several orders: Alismatales⁴¹, Liliales⁴², Commelinales⁴³, Zingiberales⁴⁴, and Ranunculales⁴⁵. We included within-family topological structure for a number of large and important

groups with available exhaustive topologies: Pinaceae⁴⁶, Cupressaceae⁴⁷, Poaceae⁴⁸, Fabaceae⁴⁹, Asteraceae⁵⁰, Solanaceae⁵¹, Ericaceae⁵², Arecaceae⁵³, Araceae⁵⁴, Rosaceae⁵⁵, Fagaceae^{56,57}, and Meliaceae⁵⁸. When appropriate, additional subfamily structure was sometimes supplemented from information presented on the Angiosperm Phylogeny Website.

Making phylogenetic distances stable for derived trees.

An important feature for the development and use of our PhyloSusceptibility model was that pairwise phylogenetic distances would be stable among trees derived from the R2G2_20140601 supertree, no matter what species comprised the list. That is, the estimated phylogenetic distance between species A and species B should be the same, regardless of whether it was calculated from a small tree with a few closely related families or a broad tree that includes angiosperms and gymnosperms. This stability is not necessarily the case with the standard Phylomatic and bladj approach (<http://phylodiversity.net>), because the nodes are dated on the derived tree by interpolating among a limited number of major nodes of given minimum ages⁵⁹. As such, phylogenetic distance estimates can vary somewhat depending on which major nodes are included in the derived tree. To avoid this problem, we first updated and expanded the list of minimum ages of named nodes (mostly from references found in Stevens, P.F. 2014. Angiosperm Phylogeny Website, version 13. <http://www.mobot.org/MOBOT/research/APweb/>). We then created a full version of R2G2_20140601 and used Phylomatic and bladj to interpolate ages for all remaining nodes in the supertree. We gave arbitrary (but permanent) names to

every unnamed node in the supertree, and then exported the full file of estimated ages of all nodes.

When we then use Phylomatic to derive a tree topology for a particular species list based on the supertree R2G2_20140601, we can use the `bladj` function of Phylocom and the R2G2_ages file to provide a stable age structure to the derived tree. This is essential for applying the PhyloSusceptibility model, because the coefficients for the logistic regression were derived from a set of 210 plant genera with phylogenetic distances derived from the R2G2_20140601 tree.

Derived trees first match the genera in the plant species list to named genera in the tree; if the genus is not specifically named in the supertree (as is usual for smaller families), genera are placed as polytomies within that family. One limitation of estimating phylogenetic distances using R2G2_20140601 is that phylogenetic distance estimates for closest relatives will vary somewhat depending on the number of species in such polytomies in the sample. However, correcting this would require a fixed topology with more than 15,000 terminal nodes. This limitation did not have any effect on the analyses presented in this study.

Why we chose the Phylomatic approach to estimating phylogenetic distances.

By using a supertree approach, we may not have as precise an estimate of phylogenetic distances as if we had built a unique community phylogeny based on multi-gene DNA sequences for the plant species in our grassland⁶⁰. However, the

value of the PhyloSusceptibility model is that it can be applied to any set of species from around the world, most particularly with novel combinations of plant species. By building a supertree with a stable age structure, we were able to apply the less refined but more broadly applicable Phylomatic approach here. This will also enable other researchers to more readily test these relationships in their own systems in ways that are directly comparable.

Resolving polytomies in derived tree for analyses in this paper

The phylogenetic tree of wild meadow and experimental plant species derived from the master tree R2G2_20140601 for this paper contained six unresolved polytomies of 3-4 genera or species. To improve the resolution of the calculated phylogenetic distances between those closely related species, we searched the literature for modern phylogenetic treatments of those clades that would permit better resolution. When available, we grafted the resolved topology onto the phylogenetic tree for use in all analyses.

We were able to resolve the topologies of three polytomies:

Asteraceae:Cichorieae (*Lactuca*, *Hypochaeris*, *Sochus*, *Taraxacum*)⁶¹

Apiaceae (*Foeniculum*, *Conium*, *Eryngium*)⁶²

Trifolium (*T. dubium*, *T. angustifolium*, *T. subterraneum*)⁶³

The following three polytomies could not be further resolved:

Bromus (*B. pubescens*, *B. kalmia*, *B. hordeaceus*, *B. diandrus*). The current state of phylogenetic understanding indicates reticulate evolutionary patterns and two of the species in our tree have not yet been examined systematically.

Rumex (*R. altissimus*, *R. salicifolius*, *R. acetosella*) Phylogenetic placement of two of these species has not yet been clearly determined.

Pseudognaphalium (*P. obtusifolium*, *P. californicum*, *P. sp.*) One of the three species could not be identified to species because it never flowered.

The analyses presented in this paper were all conducted with the tree presented in Extended Data Figure 1 (with the first three polytomies resolved). However, we conducted all analyses as well using the tree as derived directly from R2G2_20140601 (with six polytomies). Although the phylogenetic distances among particular pairs of closely related species changed, distances among pairs of species within-without those clades remained unaffected. Because the data from each site are composite measures across the assemblage of species, and then the data used in the regression analyses were means across sites of those composites, the effects of small changes in phylogenetic distances in the resolved polytomies were almost undetectable. For Figure 2b, only one mean Q10 phylogenetic distance changed by more than 1My (*Taraxacum campylodes* changed from 65.8 to 64.4 My from its neighboring plants). Only four species showed any change in mean weighted abundances in Figures 2c or 2d, and the largest change was by 0.011. For Figure 3, the largest change in phylogenetically predicted disease was 0.00069. None of the statistics changed appreciably for any of the analytical results presented in the

paper. This indicates that although trees derived directly from R2G2_20140601 through Phylomatic will inevitably have some polytomies in less resolved clades, the additional effort to resolve those polytomies may not have a substantial effect on analytical outcomes.

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