**Supporting Information: Text S1**

Phylogeny for the Massachusetts and Wisconsin spring floras

We first assembled two phylogenies for all of the species at each of our two sites using Phylomatic [1], which assumes the APG III angiosperm phylogeny backbone [2] (See Supporting Information Figures 1a and b). We additionally resolved a small number of unresolved relationships in these trees using DNA sequence data from GenBank. To do this we used a mega phylogeny inferred for a study on the relationship between phylogenetic distance on and plant species’ invasiveness (Schaefer et al., *in prep*). GenBank nucleotide data for 17 DNA regions were downloaded and data matrices for the entire flora of the continental United States were assembled and aligned using the PHLAWD computer package [3]. These DNA matrices were then analyzed using Maximum Likelihood as implemented in RAxML v7.2.8 [4]. Here, we greatly reduced this mega phylogeny to produce phylofloras for each of our two sites using the name.check function in the *geiger* package version 1.3-1 and the drop.tip function in the *ape* package version 3.0-5 [5]. These phylogenies were then used to resolve the remaining nodes in the Phylomatic tree described above, most of which were within a small number of genera. Finally, divergence times were then estimated for each of these phylogenies using dates from Wikstrom et al. [6] as implemented using the bladj algorithm of Phylocom [7]. The tree files for each location are available on the Primack Lab website.

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**Supporting Information Figure S1a.** Phylogeny of Massachusetts spring-flowering plant species used in the analyses.

**Supporting Information Figure S1b.** Phylogeny of Wisconsin spring-flowering plant species used in the analyses.