Supporting Information Methods S1 and S2

Methods S1 Studies included in the analyses: B, used in Biomass response to light/water/nutrient analysis; L, used in SLA response to light analysis; RS, used in root:shoot ratio response to nutrient/water analysis.

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Methods S2 Construction and application of species phylogenies.

The topology of the phylogenies was obtained via the online program Phylomatic (Webb & Donoghue, 2005), using the angiosperm supertree from the angiosperm phylogeny website (Stevens, 2001 onwards) as the base tree. Polytomies within families were solved as far as possible using published phylogenies obtained through molecular analysis, in particular for the Asteraceae (Goertzen *et al*., 2003; Funk *et al*., 2005; Kim *et al.*, 2005), and the Poaceae (Bouchenak-Khelladi *et al.*, 2008). Branch length estimates were obtained and included in phylogenetic trees by calibrating the topology according to ‘known’ fixed ages of the tree root and divergence at a number of tree nodes from estimates derived from multiple phylogenetic studies listed in the Angiosperm Phylogeny Website (Stevens, 2001 onwards), and using the program Phylocom version 4.1 (Webb & Donoghue, 2008). Each individual effect size was represented by a branch tip in the phylogeny, and as some species had more than one effect size, these species resembled polytomies in the phylogeny. The branch lengths of these polytomies within a species were set a nominal length (0.0001 million years), such that they did not contribute to subsequent analyses that incorporated phylogenetic relatedness. Effect sizes of trait responses were assumed to have a Gaussian error distribution throughout. In addition to the above GLS analyses, we also calculated overall mean effect sizes of trait responses and bootstrapped 95 % confidence intervals using Metawin (Rosenberg *et al.,* 2000). All GLS analyses were conducted using the program R version 2.9.1 (R Development Core Team, 2009).

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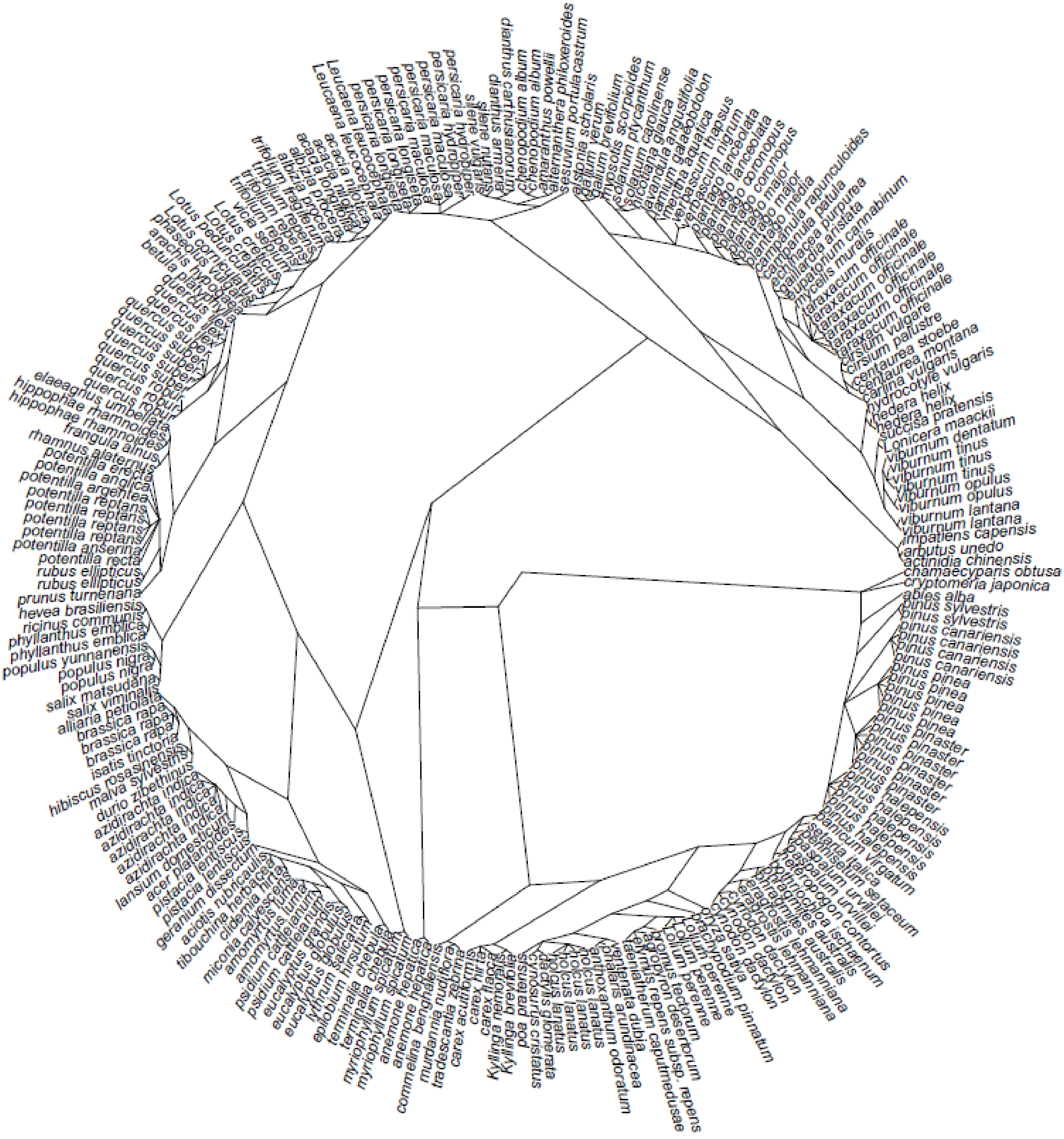
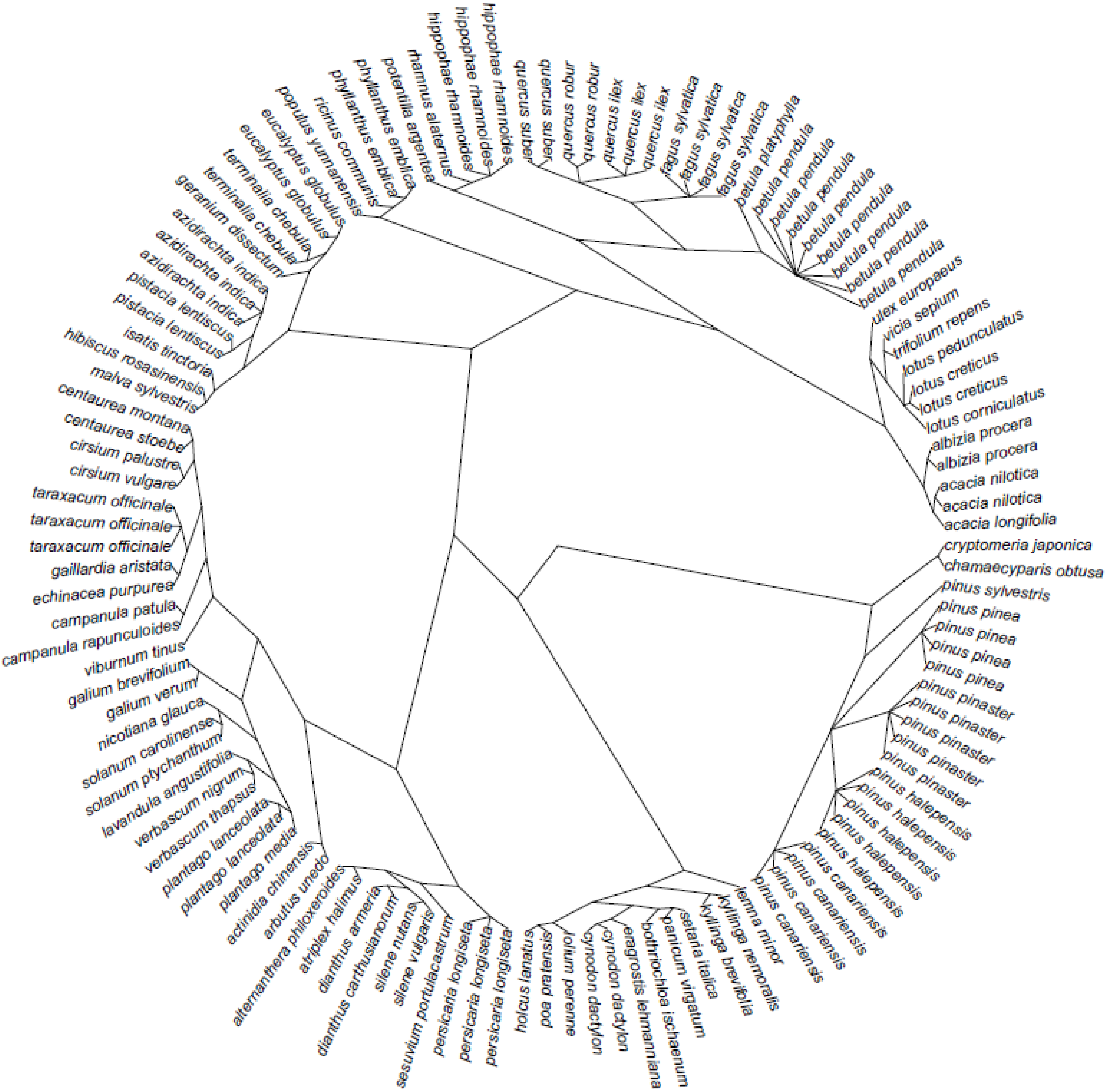
Phylogeny for biomass responses to light/nutrient/water increase. NB: branch lengths not to scale.



Phylogeny for root:shoot ratio responses to nutrient/water increase. NB: branch lengths not to scale.



Phylogeny for SLA responses to light increase. NB: branch lengths not to scale.