

Data fields are as follows:

phylo.name

Taxonomic name, matches labels of tips in the phylogeny. The phylogeny is published as supplementary data with the paper.

Species notes

Sequencing for the phylogeny revealed that a few species were misidentified. These are in the correct position within the phylogeny, but the names are incorrect. The notes identify those species.

Data from the harvests used in plant growth analysis (weights are in g, area in cm<sup>2</sup>):

leaf.fresh.weight.g

leaf.dry.weight.g

root.dry.weight.g

stem.dry.weight.g

leaf.area.cm.sq

experiment

Because we wished to compare more species than we could fit into the growth chamber at one time, we split the experiment into two halves, run sequentially.

To statistically control for differences between these two halves of the experiment, the analysis includes “replicate” as a factor in the analysis of the growth data – A or B.

all.dry.weight.g

Total dry weight for each plant harvested (total of leaf.dry.weight.g + root.dry.weight.g + stem.dry.weight.g).

block

Experimental block (1-8).

harvest.minus.germ.date

Duration of growth in days, calculated as the harvest date minus the germination date.

average.seed.weight

Mean seed weight for the species.