Figure Legends

Figure 1: Raw data (gm-2) plotted as circles (shoots) and triangles (roots). Error bars show mean biomass (gm-2) +/- 1 SE for shoots (purple error bars) and roots (brown error bars). The panels are faceted by treatment combinations: intensity of defoliation on top (lenient 15 cm or severe 5 cm on top), and frequency of defoliation labeled on the right hand side (2 wk or 4 wk). The x-axis groups responses by cultivar: A = Argentine, P = Pensacola, T9 = Tifton-9, and UF-R = UF-Riata.

Figure 2: Fixed effects from varying-intercepts/varying-slopes Gamma regression model. Coefficients are plotted on the log-link scale and include a median (point), 50% (thick line) and 95% (thin line) credible intervals for a) shoot production, b) root production and c) root allocation. Where the entire 95% credible interval falls above or below zero, we can interpret that as a 97.5+% Bayesian probability of that coefficient having a positive or negative effect on the response, respectively.

Figure 3: Varying-intercepts from the Gamma regression model for root production. Coefficients represent deviations of each cultivar (A = Argentine, P = Pensacola, T9 = Tifton-9, and UF-R = UF-Riata) from the overall mean (fixed effect coefficient), and are thus naturally centered at 0, where negative values represent lower than average performance, and positive values higher than average performance. Plots include a median (point), and 50% (thick line) and 95% (thin line) credible intervals. Where the entire 95% credible interval falls above or below zero, we can interpret that as a 97.5+% Bayesian probability of the cultivar having a higher or lower overall root production compared to the mean among all cultivars.

Figure 4: Pairwise contrasts among each cultivar (A = Argentine, P = Pensacola, T9 = Tifton-9, and UF-R = UF-Riata) for the varying intercepts of the root allocation model. Plots include a median (point), and 50% (thick line) and 95% (thin line) credible intervals. Where the entire 95% credible interval falls above or below zero, we can interpret that as a 97.5+% Bayesian probability of the first cultivar having a higher root allocation than the second cultivar.

Figure 5: a) Predicted versus observed scatterplot for root production as predicted by shoot production as an aboveground proxy, and b) predicted versus observed scatterplot for root production as predicted by defoliation treatment, cultivar identity, and shoot production. For reference, the 1:1 line of “perfect fit” is plotted along with an in-sample median Bayesian R2 for both predictive models.