Model results description: IBC-grass

**Summary:**

The dominant stabilizing mechanism within this version of IBC-grass is intraspecific negative density dependence, with equalizing mechanisms – or weak stabilization – emerging from differences in trait values along several focal axes:

1) competition vs. survival in adverse conditions (*Gmax*),

2) maximum size vs. dispersal (*MaxMass*),

3) specific leaf area vs. defense against herbivores,

4) size-structure (allocation towards woody stems vs. leaves, *LMR*),

5) clonal life-history, and inter-spacer distance (*meanSpacerLength*).

Coexistence without negative density dependence when competitive dominants are present is temporally fleeting, though the time to extinction for the inferior species is directly related to their traits. With negative density dependence, the competitive ability of the superior competitors is diminished as they grow in abundance, thus enabling comparatively less-fit species to also persist. Simulations were run with relatively low levels of soil resources, and the dominant species within the mixtures tended to be stress-tolerant and slow growing, as well as clonal in their life-history with a large maximum size (Fig. 1). Within monoculture, a slow life-history was the most critical trait endowing biomass (Fig. 2). In general, species with moderate to higher monoculture biomasses tended to dominate community mixtures (Fig. 3), and those with higher monoculture biomasses are almost guaranteed to persist within the mixtures for significantly longer (Fig. 4).

**Realized Shannon diversity and species richness:**

Across planted-species richness treatments: During both the metacommunity and isolation phase, there is a slight, positive relationship between realized Shannon diversity and the mixture’s total biomass (Fig. 5). This is likely because, as the number of species with high monoculture biomasses increases within the mixture (a sampling effect), the total biomass also increases. Larger species mixtures will contain more of these species, and thus reach higher biomass as well. There is not a significant change in total biomass when seed addition is removed. This is likely because Shannon diversity only slightly decreases once the propagule pressure is removed.

Between planted-species richness treatments:

During the metacommunity phase, treatments with low initial species richness tend to present a positive relationship between biodiversity and total biomass (Fig. 5). Because without negative density dependence this relationship is reversed (Fig. 6), this effect likely emerges because when a species is in monoculture, its total maximal biomass is reduced because of intraspecific competition. As the number of species within the mixture is increased, this relationship tends to flatten; once an individual is surrounded by interspecific neighbors rather than conspecifics, its biomass is no longer limited by density dependence. During the isolation phase – once external seed addition is withdrawn – the intra-richness treatment slopes become more negative. The mechanism likely underlying this effect is that as the propagule pressure is removed, competitive dynamics will reduce the abundance of the sub-dominant species. Thus, the higher-biomass mixtures will necessarily have to be dominated by higher-biomass species.

**Functional dispersion:**

Similar to realized Shannon diversity, there is a positive relationship between functional dispersion and total biomass within IBC-grass, that is relatively stable between richness treatments regardless of propagule pressure (Fig. 8). Between richness treatments, functional dispersion does not change significantly in high richness treatments, while it flips from insignificant and positive to significantly negative with external seed rain removed. The mechanism underlying this effect likely mirrors that of Shannon diversity, in that the total mixture biomass for low-richness treatments will be greatly dependent on the monoculture biomass of the dominant species.



Figure . Marginal effect of Gmax, MaxMass, and mean spacer length on a species’ total biomass within mixture, predicted using random forest (package randomForest) partial dependency plots (package PDP). Variables were selected as they are the three most important predictors of a species’ biomass in mixture. Random forest pseudo R-squared: 0.87, correlation to testing dataset: 0.95.



Figure . Marginal effect of Gmax, MaxMass, and SLA on a species’ total biomass in monoculture, predicted using random forest (package randomForest) partial dependency plots (package PDP). Variables were selected as the top three most important predictors of a species’ monoculture biomass. Random forest pseudo R-squared: 0.98, correlation to testing dataset: 1.



Figure . Monoculture biomass vs. average biomass in 32-species mixture. Each color represents a species, while individual points represent mixtures in which that species is present.



Figure . Monoculture biomass vs. average time to extinction in 32-species mixture. Each color represents a species, while individual points represent mixtures in which that species is present. Seed rain is eliminated in year 100.



Figure . The relationship between realized Shannon diversity and total community biomass **with negative density dependence present**. Colored lines refer to the fits within-richness treatments, while the black lines refer to the larger trend, inclusive of all planted-species richness treatments. Total biomass is scaled from 0 – 100. The assembly stage is defined as the first 100 iterations of the simulation, in which external seed addition is present. The isolation stage is defined as the following 100 iterations, once external seed addition has been excluded. Ribbons represent the 95%, 80% and 50% credibility intervals of the fits, while estimates with dashed lines include a slope of 0 with their 89% highest density intervals, suggesting that they are not statistically significant.



Figure . The relationship between realized Shannon diversity and total community biomass **with negative density dependence absent**. Colored lines refer to the fits within-richness treatments, while the black lines refer to the larger trend, inclusive of all planted-species richness treatments. Total biomass is scaled from 0 – 100. The assembly stage is defined as the first 100 iterations of the simulation, in which external seed addition is present. The isolation stage is defined as the following 100 iterations, once external seed addition has been excluded. Ribbons represent the 95%, 80% and 50% credibility intervals of the fits, while estimates with dashed lines include a slope of 0 with their 89% highest density intervals, suggesting that they are not statistically significant.



Figure 7. The relationship between richness total community biomass. Colored lines refer to the fits within-richness treatments, while the black lines refer to the larger trend, inclusive of all planted-species richness treatments. Total biomass is scaled from 0 – 100. The assembly stage is defined as the first 100 iterations of the simulation, in which external seed addition is present. The isolation stage is defined as the following 100 iterations, once external seed addition has been excluded. Ribbons represent the 95%, 80% and 50% credibility intervals of the fits, while estimates with dashed lines include a slope of 0 with their 89% highest density intervals, suggesting that they are not statistically significant.



Figure 8. The relationship between functional dispersion and total community biomass. Colored lines refer to the fits within-richness treatments, while the black lines refer to the larger trend, inclusive of all planted-species richness treatments. Total biomass is scaled from 0 – 100. The assembly stage is defined as the first 100 iterations of the simulation, in which external seed addition is present. The isolation stage is defined as the following 100 iterations, once external seed addition has been excluded. Ribbons represent the 95%, 80% and 50% credibility intervals of the fits, while estimates with dashed lines include a slope of 0 with their 89% highest density intervals, suggesting that they are not statistically significant.