SI Text

Experimental Design. We used a grass-shrub steppe ecosystem to create a plant-species richness gradient by removing plant species and portions of individuals. By removing plant species, we changed the original species number of the experimental units to generate a gradient of 1, 2, 4, and 6 species with all possible assemblages replicated. By removing portions of individuals, we obtained equal cover along the species gradient and avoided confounding diversity with abundance changes. To create the gradient, we first selected 84 5 × 5m plots containing the six target species, three grass species: *Stipa speciosa* Trin et Ruprecht, *Stipa humilis* Cav., and *Poa ligularis* Nees ap. Steud; and three shrub species: *Mulinum spinosum* (Cav.) Pers., *Adesmia campestris* (Rendle) Rowlee, and *Senecio filaginoides* DC. The six target species were the dominants among a pool of 62 species in the Patagonian steppe (1), and accounted for 94% of aerial cover and 97% of ANPP (SI Table 3). Later, we randomly assigned biodiversity treatments to plots. To implement treatments, first we removed species from the plots and left only target species; then, we removed portions of individuals with wedges of different angles to equalize the cover to the average cover of monocultures. In this way, we generated a species-richness gradient that initially had similar cover ($P > 0.05$) but different numbers of species. We followed a sequential procedure to estimate the percentage of plot reduction needed so all plots would start the experiment with the same cover. First, we chose 84 plots with the six dominant species (2). We ensured that all species were present in the plots using the line interception technique along four parallel 5-meter lines (3). Second, we randomly assigned the species richness and composition treatments to the plots, and we removed target species; at this point, monocultures were ready. Third, we recorded vegetation cover for all plots, and estimated the average of the 18 monocultures (three replicates per each of the six species). Finally, we estimated the reduction percentage needed to equalize the cover of plots containing mixture of species with the average cover of monoculture plots. To achieve this reduction percentage, we used wedges that ranged from 18° to 342°, with steps of 18°, which corresponds to 5% of the vegetation cover (SI Fig. 8). For example, in plot number 1, we assigned two species, *Mulinum spinosum* and *Stipa speciosa*, and plot cover after removing the other species was 0.11 cm per plant per cm^{-1}; to reduce 40% of the cover, we applied an angle of 144° to all of the individuals in the plot and we achieved a final cover of 0.07 cm per plant per cm^{-1}. All removals were mechanically performed; grasses were manually removed including tillers and roots, and shrubs were cut at the crown level. The sandy and unstructured soils helped to pull grasses with their roots; however, deep shrub roots were impossible to remove. Other species different from the six target species represented a small fraction of vegetation cover with an average of only 2.5% of total cover. The Patagonian steppe has a total of 62 vascular plant species; and our 5 × 5 m plots had an average of 12.3 species per plot, which were estimated by using a species area curve developed for the steppe ($S = CA^z$; C = 5.6, z = 0.25 adapted from 1).

The aim of equalizing vegetation cover at the beginning of the experiment was to avoid confounding a gradient of species richness with a gradient of biomass. The removal of portions of individuals equalized biomass along the species richness gradient (SI Fig. 3). After we removed target species and portions of individuals, we estimated biomass using the line-interception technique in four parallel five-meter lines (3) and specific calibrations for the Patagonian steppe (4). We found that biomass along the gradient of species had a slope nondifferent from zero (slope ± 1SE: -0.15 ± 0.45 g m^{-2} species number^{-1}; $P > 0.74$) (SI Fig. 3). At the beginning of the experiments, plots differed in the number or composition of species, but neither in the biomass left nor in the amount biomass removed (SI Fig. 3 *B* and *C*).

To estimate aboveground-net-primary production, we calculated the difference between green biomass at the beginning of the growing season and its peak (5, 6). We estimated green biomass, with vegetation cover and a nondestructive method calibrated at a species level for the Patagonian steppe that relates plant cover to biomass (4).

Relative Yield Total (RYT)

The RYT, or replacement index, is used to evaluate changes in the yields of species in mixtures compared to monocultures (7-10). The RYT is calculated as $RYT = \sum_{i=1}^{N} RY_i = \sum_{i=1}^{N} \frac{O_i}{M_i}$, where O_i is the yield of a species in a mixture, M_i is the yield of a species in monoculture, RY_i is the relative yield of *i* species, and *N* is the number of species in the mixtures. Values of RYT = 1 indicate that species in a mixture yield the same as in monocultures (8, 10); values of RYT >1 indicate that species in a mixture had relatively higher ANPP compared with monocultures and could result from the increase in some or all species. A condition for the RYT index is that species density or biomass for monocultures and for mixtures should be the same at the beginning of the growing season (7). In single-growing-season-experiments, this condition could be easily accomplished, but in experiments that lasted several growing seasons in which species in mixture had different yield than monocultures this condition would no longer be maintained. The experiments that we used for the comparison presented here resulted from several growing seasons, and in all these experiments productivity increased with biodiversity (9, 11-13). We used the ratio between the RYT of the current year divided by the RYT of the previous year (SI Box1).

SI BOX1: The Relative Yield Total (RYT) for Experiments with >1 Year of Data. The RYT has as condition that monocultures and mixtures have the same initial density or biomass (7). In experiments in which productivity increases with diversity, this condition does not hold true after the first year in which a biodiversity effect is observed. One way to correct this unwanted bias is by dividing the RYT of current year by the RYT of previous year. The RYT for year 1 is

$$RYT_1 = \sum_i^N RY_{i1} = \sum_i^N \frac{O_{i1}}{M_{i1}}$$

where O is mixture yield, M is monoculture yield, RY is relative yield of i species, and N is the number of species in the mixtures. The initial amount of i species in the mixture is

$$O_{i0} = \frac{M_{i0}}{N}$$

were M_{i0} is the initial amount on the monoculture. The yield of i species in the first year could be expressed as

$$O_{i1} = O_{i0} a_{i1} = \frac{M_{i0}}{N} a_{i1}$$

$$M_{i1} = M_{i0} b_{i1}$$

where a_{i1} is the increase in biomass of the *i* species in mixture from year 0 to 1. Similarly, b_{i1} is the increase in biomass of *i* species in monoculture from year 0 to 1. RYT for the year 1 could be expressed as

$$RYT_1 = \sum_{i}^{N} \frac{M_{io} a_{i1}}{N\, M_{i0} b_{i1}} = \sum_{i}^{N} \frac{a_{i1}}{N\, b_{i1}}$$

The ratio a_{i1}/b_{i1} could be interpreted in the same way as the value of RYT, if they are higher or lower than one, species *i* respond to the presence of its neighbors, but if it equal to one it grows the same as in the monoculture. The RYT is the average of the performance among species. For the year 2 we have

$$RYT_2 = \sum_{i}^{N} RY_{i2} = \sum_{i}^{N} \frac{O_{i2}}{M_{i2}}$$

The yield of species *i* for year 2 in mixture and monoculture is

$$O_{i2} = O_{i1} a_{i2} = \frac{M_{i0}}{N} a_{i1} a_{i2}$$

$$M_{i2} = M_{i1} b_{i2} = M_{i0} b_{i1} b_{i2}$$

Replacing in the formula for the RYT on the year 2

$$RYT_2 = \sum_{i}^{N} \frac{M_{i0} a_{i1} a_{i2}}{N\, M_{i0} b_{i1} b_{i2}} = \sum_{i}^{N} \frac{a_{i1} a_{i2}}{N\, b_{i1} b_{i2}} = \sum_{i}^{N} \frac{RY_{i1} a_{i2}}{b_{i2}}$$

For the year 2, the RYT is the average of the product between current and past year of the change in biomass ratio for *i* species growing in mixture or in monoculture. If $RYT_1>1$ and in the second year all species grow the same in mixture or monocultures ($a_{i2}/b_{i2} = 1$ for every species), $RYT_2 = RYT_1>1$. It is possible to correct the RYT_2 dividing the RY_{i2} by the product of $N\, RY_{i1}$

$$RYTcorr_2 = \sum_i^N \frac{1}{N\, RY_{i1}} RY_{i2} = \sum_i^N \frac{1}{N\, RY_{i1}} \frac{a_{i1}a_{i2}}{N\, b_{i1}b_{i2}} = \sum_i^N \frac{1}{N\, RY_{i1}} \frac{RY_{i1}a_{i2}}{b_{i2}} = \sum_i^N \frac{a_{i2}}{N\, b_{i2}}$$

Note that $RYTcorr_2$ is a similar expression than RYT_1.

When data were available we applied the correction mentioned above. However, sometimes we acceded only to the average data and we did the best guess to $RYTcorr_2$, which is

$$RYTcorr_2^* = \frac{RYT_2}{RYT_1}$$

$RYTcorr_2^*$ equals $RYTcorr_2$ in the particular case in which every species have the same response in the mixture in the previous year.

$$If\ \frac{a_{i1}}{b_{i1}} = c_1 \forall i \therefore RYT_1 = \sum_i^N RY_{i1} = \sum_i^N \frac{a_{i1}}{N\, b_{i1}} = \sum_i^N \frac{c_1}{N} = c_1$$

$$RYTcorr_2 = \sum_i^N \frac{1}{N\, RY_{i1}} RY_{i2} = \sum_i^N \frac{1}{N \frac{c_1}{N}} \frac{c_1 a_{i2}}{N\, b_{i2}} = \sum_i^N \frac{a_{i2}}{N\, b_{i2}}$$

$$RYTcorr_2^* = \frac{RYT_2}{RYT_1} = \frac{\sum_i^N \frac{c_1 a_{i2}}{N\, b_{i2}}}{c_1} = \frac{c_1 \sum_i^N \frac{a_{i2}}{N\, b_{i2}}}{c_1} = \sum_i^N \frac{a_{i2}}{N\, b_{i2}} \Rightarrow RYTcorr_2^* = RYTcorr_2$$

$RYTcorr_2^*$ is the best guess based on two variables of what happens with 2N variables. How well $RYTcorr_2^*$ represent $RYTcorr_2$ would depend on the asymmetry among species on the a_{t-1}/b_{t-1} ratio and the number of species in the mixture.

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