Data preparation

Cedar Creek Ecosystem Science Reserve

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Data source

Data from *Grassland ecosystem recovery after soil disturbance depends on nutrient supply rate*.

Disturbance treatment

The **Disturbance treatment** was replicated in the three old-fields (A, B, C) in a completely randomised block design (two treatments in each of three fields for a total of 6 35 × 55 m large plots). In April 1982, in each of the fields, one of these two 35 × 55 m areas was selected to be disturbed with a 45 cm diameter disk harrow pulled by a tractor 20 times in one direction, 20 times perpendicularly and 5 times diagonally to the first passes. Following the disking, the soil was hand raked to smooth the soil and remove any remaining vegetation, so that subsequent colonisation was solely from seeds or small rhizome fragments. Within each of the 6 large plots, the 54 small plots were arrayed in 6 × 9 grid with 1 m buffers between each plot. Aluminium flashing was buried to depth of 30 cm around each plot to prevent horizontal movement of nutrients and spreading of plants through vegetative growth.

The nutrient treatments

The **nutrient treatments** were replicated six times in a completely randomised design in each of the 35 × 55 m plots (54 4 × 4 m small plots) yielding 324 (6 x 54) plots.

In our analyses, we focus on two nutrient treatments: 1. Control (no nutrients; Treatment I) and 2. Other Nutrients and 9.5 g of N (Treatment F) (Table S1).

(We present analyses of the full N gradient in Figures S7 to S10 and Table S4. In brief, choosing a higher or lower N addition rate would change the strength of the N effect, but would not change the direction of the effects or change the strength of the interactions with the disking.)

Sampling and analysis

At peak biomass (mid-July to late August), all aboveground biomass was clipped in a 3 m by 10 cm strip (0.3 m 2) in each plot. Note that there were 4 years when the disturbed plots were not sampled or only sampled in a single field. The biomass was sorted into dead, previous year's growth (litter) and live, current year's growth (live biomass). Live biomass was sorted to species, dried to constant mass at 40°C, and weighed to the nearest 0.01 g. We estimated total aboveground biomass as the summed biomass of all non-woody species in each 0.3 m^2 sample, converted to g m^{-2}. We excluded woody biomass, because our goal was to estimate annual productivity and most of the woody biomass is from previous year's growth. Woody plant biomass composed less than 1% of total biomass across the data set.

Species richness is the number of species in each 0.3 m^2 sample. We quantified plant diversity as the Effective Number of Species based on the Probability of Interspecific Encounter (ENS_{PIE}), a measure of diversity that is more robust to the effects of sampling scale and less sensitive to the presence of rare species than species

richness (Jost, 2006, 2007; Chase and Knight, 2013). ENS_{PIE} is equivalent to the Inverse Simpson's index of diversity which is calculated as $1/\sum_{i=1}^{S} p_i^2$ where S is the total number of species (i.e. species richness) and p_i is the proportion of the community biomass reesented by species i (Jost, 2006, 2007; Chase and Knight, 2013). Simpson's evenness (E) satisfies the main requirements of an evenness index (Smith and Wilson, 1996). In addition, it is directly related to ENS_{PIE} through the relationship $E = ENS_{PIE}/S$ (Smith and Wilson, 1996), thus we can factor diversity directly into its richness and evenness components through the relationship: $ENS_{PIE} = S*E$.

Across all data, ENS_{PIE} was positively correlated with richness ($r = 0.63$) but uncorrelated with evenness ($r = 0.03$). Richness and evenness were negatively correlated ($r = -0.60$). All analyses were conducted in R (v. 3.5.3; R Foundation for Statistical Computing, Vienna, Austria). Mixed effects models were fit using the lmer function in the lme4 library. We $\log_{10}$ transformed all response variables prior to analysis to stabilise the variance of the residuals. In addition, the transformed data tested for proportional changes in the variables, which was the most biologically relevant given the among field and among year variability. In all models, among field and among year variability were treated as random effects. In the analyses of individual groups of species (e.g. annual or perennial plants), we analysed $\log_{10}$ (biomass + 1), because there were some plots with zero mass of certain groups. All model specifications are included with each table of results (Tables S5–S7).

Variables