Oikos

**OIK-03969**

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# Appendix 1

Table A1. List of grassland species sown in the experiment. Nomenclature follows Wisskirchen and Haeupler (1998).

| Non-legume forbs (n = 32) | | Legumes (n = 9) | | Graminoids (n = 13) | |
|---|---|---|---|---|---|
| Family | Species | Family | Species | Family | Species |
| Anthericaceae | *Anthericum ramosum* | Fabaceae | *Anthyllis vulneraria* | Cyperaceae | *Carex flacca* |
| Apiaceae | *Peucedanum oreoselinum* | | *Dorycnium germanicum* | Juncaceae | *Luzula campestris* |
| | *Pimpinella saxifraga* | | *Genista tinctoria* | Poaceae | *Agrostis capillaris* |
| Asteraceae | *Achillea millefolium* | | *Hippocrepis comosa* | | *Brachypodium pinnatum* |
| | *Buphthalmum salicifolium* | | *Lotus corniculatus* | | *Briza media* |
| | *Centaurea jacea* | | *Medicago lupulina* | | *Bromus erectus* |
| | *Centaurea scabiosa* | | *Securigera varia* | | *Dactylis glomerata* |
| | *Hieracium pilosella* | | *Trifolium pratense* | | *Festuca ovina* |
| | *Leontodon hispidus* | | *Vicia cracca* | | *Festuca rubra* |
| | *Leontodon incanus* | | | | *Helictotrichon pratense* |
| Campanulaceae | *Campanula rapunculoides* | | | | *Helictotrichon pubescens* |
| | *Campanula rotundifolia* | | | | *Koeleria pyramidata* |
| Cistaceae | *Helianthemum nummularium* | | | | *Poa angustifolia* |

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|---|---|---|---|---|---|---|---|
| Globulariceae | *Globularia cordifolia* | | | | | | |
| Lamiaceae | *Betonica officinalis* | | | | | | |
| | *Clinopodium vulgare* | | | | | | |
| | *Prunella grandiflora* | | | | | | |
| | *Prunella vulgaris* | | | | | | |
| | *Teucrium montanum* | | | | | | |
| | *Thymus praecox* | | | | | | |
| | *Thymus pulegioides* | | | | | | |
| Linaceae | *Linum perenne* | | | | | | |
| Plantaginaceae | *Plantago lanceolata* | | | | | | |
| | *Plantago media* | | | | | | |
| Rosaceae | *Agrimonia eupatoria* | | | | | | |
| | *Filipendula vulgaris* | | | | | | |
| | *Potentilla tabernaemontani* | | | | | | |
| | *Sanguisorba minor* | | | | | | |
| Rubiaceae | *Asperula cynanchica* | | | | | | |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
|  | *Galium album* |  |  |  |  |  |  |
|  | *Galium verum* |  |  |  |  |  |  |
| Scrophulariaceae | *Veronica chamaedrys* |  |  |  |  |  |  |

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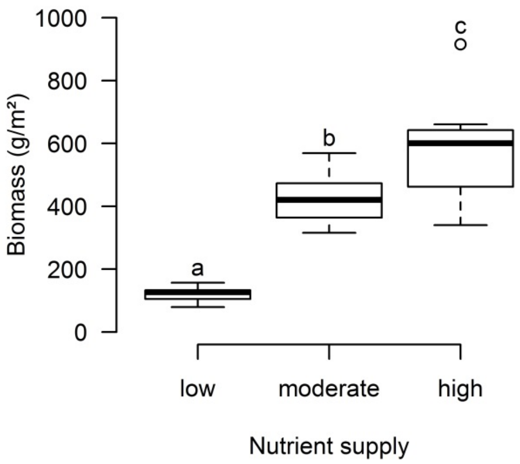

Figure A1. Biomass of experimental grasslands with contrasting levels of soil nutrient supply in the third year after establishment. Different letters indicate significant differences among nutrient levels ($p < 0.05$); p-values are from permutation t-tests with 999 permutations and corrected for multiple comparisons following Benjamini and Hochberg (1995).

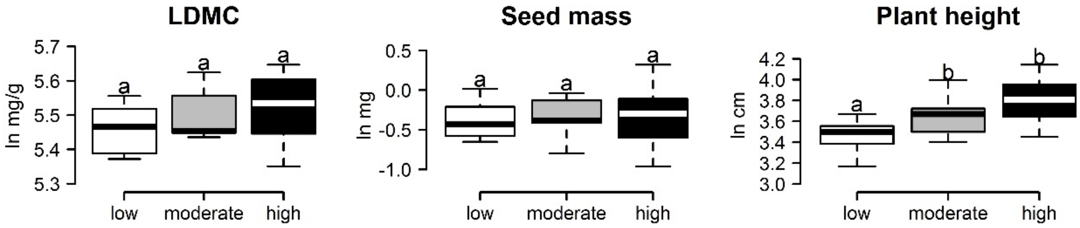

Figure A2. Community weighted mean (CWM) trait values in grassland plots (0.25 m²) after three years with contrasting nutrient supply. Different letters indicate significant differences ($p < 0.05$) among nutrient treatments, evaluated using permutation t-tests with 9999 permutations (LDMC, leaf dry matter content).

Footnote: Trait values are from databases (Jäger 2007, Kleyer et al. 2008, Hintze et al. 2013). Maximum (seed mass, height) or minimum (LDMC) values were used for calculations, after trait values from experiments and unrealistically high or low values had been removed. Values were ln-transformed to reduce outliers prior to the calculation of CWMs. Database values conserve species rankings based on field-measured trait values well (Kazakou et al. 2014), and interspecific rather than intraspecific trait variation was found to explain much larger amounts of total trait variation in an experiment using some of the species found in our study, with similar site conditions and located close (~2.5 km) to our field site (Andrade et al. 2014). Additionally, comparing self-measured seed mass values of the sown species with values extracted from databases, we found a very high correlation of $r = 0.95$. As LDMC values for *Oenothera biennis* agg. and *Thymus pulegioides* were not available from databases, we used values from the closely related, morphologically and ecologically similar species *Oenothera erythrosepala* and *Thymus serpyllum*, respectively.

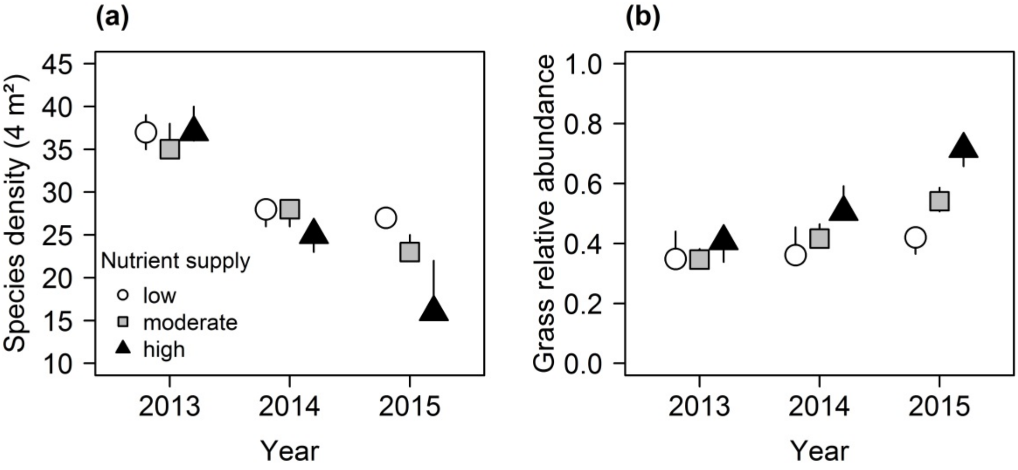

Figure A3. Effects of soil nutrient supply on temporal dynamics of (a) species density and (b) grass relative abundance in experimental grasslands plots (4 m²). Symbols are median values, bars are upper and lower quartiles.

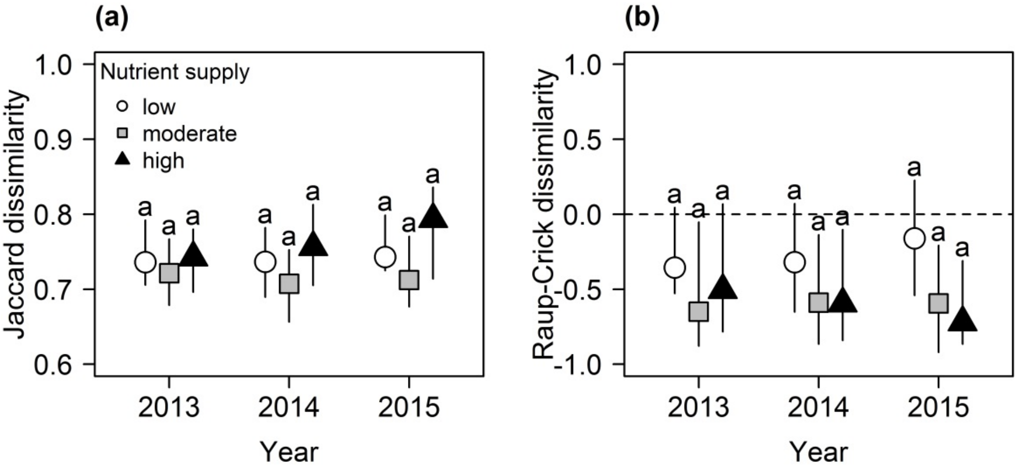

Figure A4. Temporal change in beta diversity among grassland plots (4 m²) within contrasting nutrient treatments. Beta diversity was measured as (a) raw turnover in species composition using Jaccard's dissimilarity, or (b) using a modified Raup–Crick dissimilarity metric, indicating the degree to which the observed number of shared species between communities deviates from a null-expectation. In (b), values close to 0 indicate that communities share as many species as expected from random sampling. Values approaching –1 indicate communities share more species than expected, whereas values approaching 1 indicate communities share less species than expected from random sampling. Both can be interpreted as niche-based assembly mechanisms, reflecting either environmental filtering (–1) or spatial aggregation (1). Symbols are median values, bars are upper and lower quartiles. Different letters indicate significant differences ($p < 0.05$) in beta diversity among treatments within years, based on permutational distance-based tests for homogeneity of multivariate dispersions (Anderson 2006). In (b), these differences were assessed before Raup–Crick dissimilarities were rescaled to range between –1 and 1. Note the opposing temporal trends of Raup–Crick dissimilarity in low versus high nutrient treatments in (b).

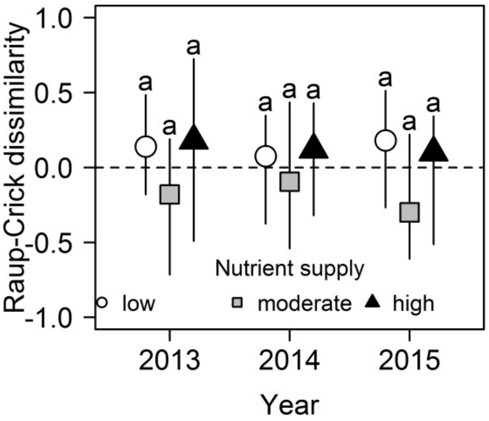

Figure A5. Temporal change in grass species beta diversity among replicate plots (4 m²) at contrasting levels of soil nutrient supply. Beta diversity was measured using a modified Raup–Crick dissimilarity metric, indicating the degree to which the observed number of shared grass species between communities deviates from a null-expectation. Symbols are median values, bars are upper and lower quartiles. Common letters indicate non-significant differences ($p > 0.05$) in beta diversity among treatments within years, based on permutational distance-based tests for homogeneity of multivariate dispersions (Anderson 2006).

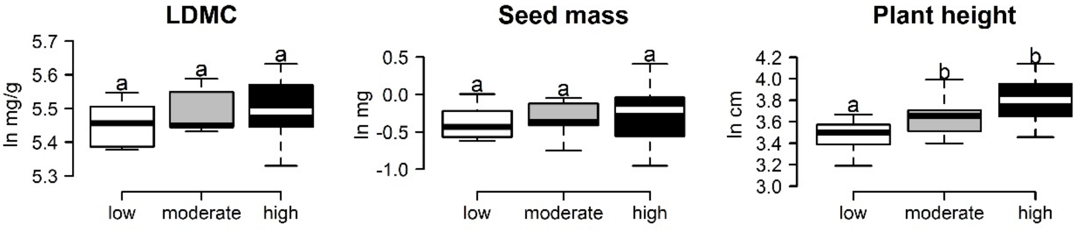

Figure A6. Community weighted mean (CWM) trait values in grassland plots (4 m²) after three years with contrasting nutrient supply. Different letters indicate significant differences ($p < 0.05$) among nutrient treatments, evaluated using permutation t-tests with 9999 permutations. LDMC = leaf dry matter content. For detailed methods see footnote of Fig. A2.

# References

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# Appendix 2

## Recruitment of new species in the plots

To demonstrate that dispersal into the plots occurred, we counted the number of newly encountered (i.e. successfully recruited) species per plot and census, as shown in Fig A7. Actual dispersal rates were probably higher than suggested by the number of new recruits for at least three reasons: Firstly, it is unlikely that every immigrating seed (species) successfully established in the subsequent year. Secondly, if only few individuals of a species were present in a plot and died between two censuses, but the population of this species in this plot was rescued by immigration from another plot, this did not count as a new species encounter in this analysis. Thirdly, when seeds of individuals from outside the plot established but the species was already present in the plot, this did also not count as a new recruit here.

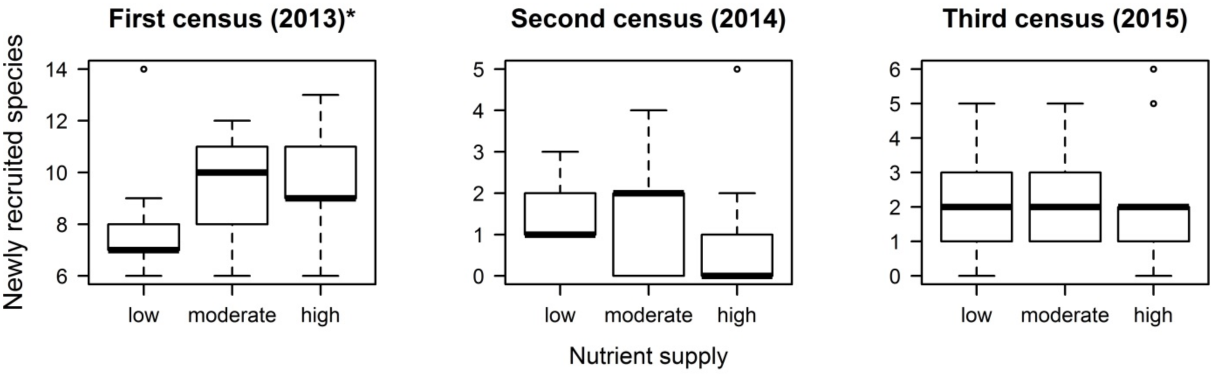

Figure A7**.** Newly encountered species in the plots per census and nutrient treatment. *, For the first census, only species that dispersed into the plot on their own accord (i.e. they were not sown) are shown.

To test whether plot spatial arrangement influenced the number of newly recruited species, we grouped the plots of each block into three classes, according to the number of edges adjacent to neighboring plots (in brackets): central plots (4 edges), plots in the corners (2), and plots in the middle of each side of the block (3). We used a generalized linear model with a Poisson distribution to model the number of newly recruited species per plot as a function of fertilization level, plot location, the interaction of these two factors, and year. In this model, only year had a significant effect ($p < 0.05$), showing that plot spatial arrangement did not influence recruitment patterns.

## Beta deviation based on the abundance-based null model of Stegen et al. (2013)

A recent simulation study by Tucker et al. (2016) suggested that beta deviation obtained from the abundance-based null model of Stegen et al. (2013) would be a more reliable index to discern community assembly mechanisms. This null model shuffles individuals among plots, while keeping constant the observed number of individuals per species in the pool. Beta diversity between each pair of random communities is then calculated using Bray-Curtis dissimilarities. Repeating this procedure n times provides a distribution of expected pairwise beta diversity. Subsequently, pairwise beta deviation is calculated as the observed minus the mean expected Bray–Curtis dissimilarity. There are however two problems when applying this approach to our study. First, we measured species abundance as the number of occurrences in 0.1×0.1-m squares and not as the number of individuals in the 0.5×0.5-m permanent plots. In addition, based on our field observations and especially so in high-nutrient plots, the numbers of individuals of dominant species were considerably higher than suggested by the number of occupied 0.1×0.1-m squares. Thus, it is difficult to interpret abundance-based beta deviations in our case where single incidences of square occupancy would be shuffled rather than individuals, and the degree of deviations from null expectations is likely underestimated in fertilized plots. Second, the approach of Tucker et al. (2016) yields negative beta deviations when observed beta diversity is smaller than mean expected beta diversity. Although this is a meaningful property of the index, it prevents evaluations of statistical differences in beta diversity among experimental treatments using PERMDISP. This is so because the method requires non-negative distances values (dissimilarities) as input to compute distance-to-centroid values that are then compared among treatments. Statistical tests comparing just the k×(k–1)/2 raw pairwise beta deviations (k is the number of plots) of treatments are not valid, because these individual values are not independent of one another (Anderson et al. 2006).

Still, the results of this abundance-based approach showed a tendency similar to the Raup–Crick null-model approach: niche-based processes tended to be more important in the plots with high nutrient supply, i.e. higher beta deviations (Tucker et al. 2016; Fig. A8).

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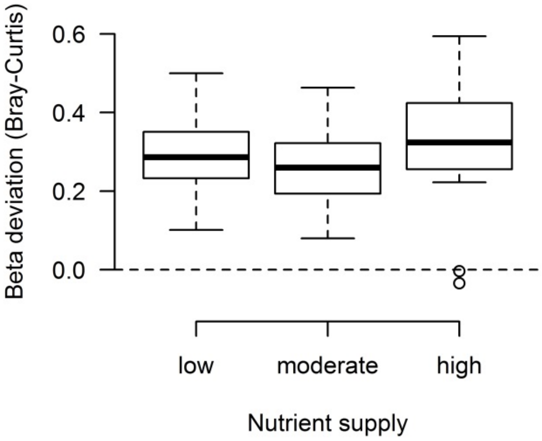

Figure A8. Beta deviation values based on Bray–Curtis dissimilarities among grassland plots (0.25 $m^2$) after three years with contrasting nutrient treatments. This index is less suited for our data and statistical approach (see main text), and results should be interpreted considering these caveats. Statistical differences among treatments based on ANOVA are not reported, because individual beta deviation values are not independent of one another

## References

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