

Supporting information to Teixeira et al., Functional diversity and invasive species influence soil fertility in experimental grasslands

Supporting Information may be also found in the online version of this article:

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Figure S1: Effects of functional dispersion on *Solidago* plants emergence and aboveground biomass. Figure **(a)** shows *S. gigantea* emergence, while **(b)** represents results for *S. gigantea* biomass varying according to the functional dispersion index. Aboveground biomass was collected at the end of the experiment (16 weeks), while emergence was evaluated during the second week of the experimental period for each one of the communities, invaded or not. For the dependent variables, F-values are presented in the text (*** $p \leq 0.001$; ** $p \leq 0.01$; * $p \leq 0.05$; . $p \leq 0.10$; ns $p > 0.10$).

Figure S2: Functional classification for a set of 54 grassland plant species by trait similarity into three functional groups.

Figure S3: Regression analysis for the functional dispersion and functional redundancy indexes [1,2]. The figures show the functional dispersion index **(a)** and the functional redundancy index **(b)** according to the number of functional groups composing the experimental communities and the correlation between functional dispersion and functional redundancy **(c)**.

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24 **Table S2:** Functional trait characteristics of the native species occurring in the mesocosm
25 communities used for the calculation of the functional dispersion index. Zero (0) and 1 values
26 represent the presence/absence of categorical functional traits. Quantitative functional traits
27 are represented by mean values for each species. Species relative abundances were
28 determined by multiplying the 3 g m^{-2} of native species sown (i.e. 0.48 g of seeds which
29 means, approximately, 0.054 g for each one of the native species present) by its mean seed
30 mass to obtain the number of seeds per native species. Mean seed mass information (given in
31 mg) was obtained from BiolFlor database [3,4]. For the species *Buphthalmum salicifolium* L.
32 we used the thousand seed mass obtained from Rieger-Hofmann GmbH (Catalogue
33 2016/2017) to calculate the mean seed mass.

Supplementary File 1: Functional diversity and biotic resistance

S1.1. Functional dispersion effects on Solidago plants emergence and aboveground biomass

Although no statistical differences were found ($F = 0.3$, $df = 8$, $p > 0.05$ for *Solidago* biomass; and $F = 0.4$, $df = 8$, $p > 0.05$ for emergence of *Solidago* plants), emergence of *Solidago gigantea* showed a slightly negative tendency when in communities with higher functional dispersion. However, such effects were not strong enough to affect invasive plants emergence rates by competition (Fig. S1).

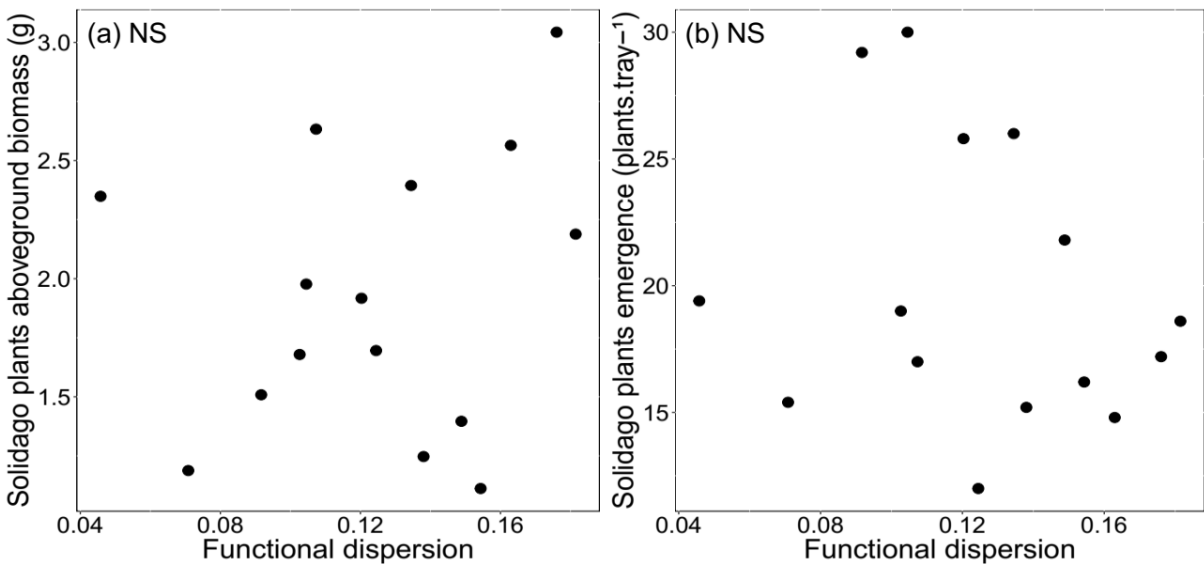


Figure S1: Effects of functional dispersion on *Solidago* plants emergence and aboveground biomass. Figure (a) shows *S. gigantea* biomass, while (b) represents results for *S. gigantea* emergence varying according to the functional dispersion index. Aboveground biomass was collected at the end of the experiment (16 weeks), while emergence was evaluated during the second week of the experimental period for each one of the communities, invaded or not. For

the dependent variables, F-values are presented in the text (*** $p \leq 0.001$; ** $p \leq 0.01$; * $p \leq 0.05$; . $p \leq 0.10$; NS $p > 0.10$).

Supplementary File 2: Material and methods extended

S2.1. Plant species and functional traits selection

Solidago gigantea (Asteraceae) was used as a model species, given that is known to be problematic in disturbed areas such as roadsides and newly re-vegetated areas [5]. Seeds from *S. gigantea* were collected from seven (clonal) stands along River Isar near Freising, southern Germany (48°24'N, 11°41'E). Before the experiment, the seeds were tested for viability under controlled conditions consisting in an 8 h night at 12 °C and a 16 h day at 20 °C and resulting in a germination success of $73.6 \pm 4.5\%$. The experimental pool of native species was based on a set of 54 native grassland species occurring with a frequency $\geq 10\%$ in a dataset comprising more than 100 surveys of calcareous grasslands in the agricultural landscape north of Munich, Germany [6]. The native seed material was obtained from the local seed producer Johann Krimmer (Pulling, Germany).

Functional group classification was performed using trait information for the set of 54 native grassland species (Table S1, Fig. S2). For doing so, eight traits were found to be suitable proxies for species dispersal, establishment success, growth, persistence and competitive ability [7–9], i.e. specific leaf area (SLA), leaf dry matter, life form, shoot morphology, morphology of vegetative organs, canopy height at maturity, seed mass and longevity (Table S1, Fig. S2). This was done, because SLA, canopy height at maturity and seed mass are correlated with invasiveness [10], and several traits are correlated to

competition among plant species, i.e. SLA, seed mass and canopy height at maturity. We collected the functional traits information from the BiolFlor [3,4] and LEDA databases [11].

S2.2. Functional groups clustering

Statistical analyses for the functional grouping were performed using Infostat software [12]. Previous to clustering analysis, all non-numerical functional traits were transformed into dummy variables (binary values). Subsequently, the trait information was converted to continuous values using a principal coordinate analysis using Jaccard's distance measure and saving the first five principal coordinates [13]. Based on the collected data for all functional traits, a cluster analysis was conducted using Gower's similarity coefficient among species and Ward as the linkage method [14,15]. The classification of all species led to three statistically different functional groups (Fig. S2).

To prove that clusters were significantly different, a multivariate analysis of variances was performed with the same variables. Null hypothesis of equal vector means was rejected ($F = 13.6$, $p < 0.0001$) and mean vector comparisons showed significant differences among the clusters (Table S1). Finally, we calculated functional dispersion and redundancy indexes [1,2] to check for the functional dissimilarity in our experimental communities (Appendix S2, Fig. S3).

87 **Table S1:** Functional trait characteristics for each functional group. Values of quantitative functional traits represent mean ($\pm$ SD).

Functional traits	Functional group		
	FG 1	FG 2	FG 3
Longevity	Perennial	<u>Perennial</u> + biannual + annual	Perennial
Life form	<u>Hemicryptophytes</u> , geophytes, chamaephytes	<u>Hemicryptophytes</u>	<u>Hemicryptophytes</u> , chamaephytes
Shoot morphology	<u>Hemi-rosette</u> , erosulate	<u>Hemi-rosette</u>	<u>Erosulate</u> , rosette
Root morphology	<u>Runner</u> , rhizome, tuft, pleicorm	<u>Pleiocorm</u> , runner	<u>Pleiocorm</u> , rhizome, runner
Seed mass (g)	1.60 $\pm$ 1.72	2.44 $\pm$ 1.64	1.97 $\pm$ 3.27
Canopy height (m)	0.37 $\pm$ 0.18	0.33 $\pm$ 0.22	0.27 $\pm$ 0.19
SLA (mm ⁻² mg ⁻¹)	22.6 $\pm$ 9.2	21.5 $\pm$ 7.2	23.2 $\pm$ 6.0
Dry leaf mass (mg g ⁻¹)*	268 $\pm$ 78 ^b	240 $\pm$ 44 ^{b,a}	203 $\pm$ 52 ^a

88 Dry leaf mass was the only quantitative trait to significantly differ among communities (ANOVA test; $F = 5.34$; $p \leq 0.05$). Values with a
89 common letter are not significantly different ($p > 0.05$).

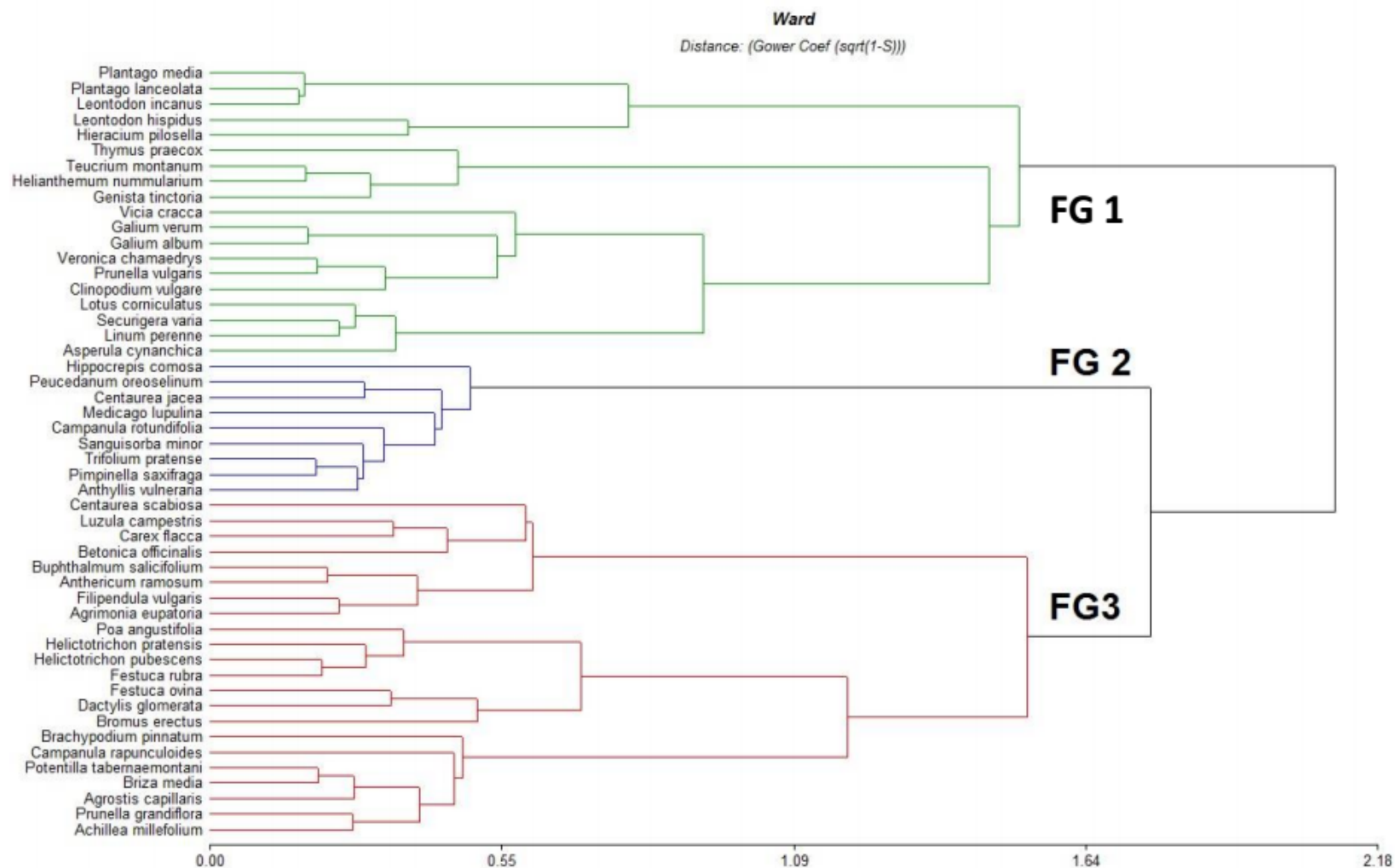


Figure S2: Functional classification for a set of 54 grassland plant species by trait similarity into three functional groups.

92 S2.3. Composition of the plant communities

93 **One functional group**

94 *Replica 1 = FG1*

Nr	Species	Family	FG
1	<i>Prunella vulgaris</i>	Lamiaceae	1
2	<i>Plantago media</i>	Plantaginaceae	1
3	<i>Helianthemum nummularium</i>	Cistaceae	1
4	<i>Genista tinctoria</i>	Fabaceae	1
5	<i>Asperula cynanchica</i>	Rubiaceae	1
6	<i>Veronica chamaedrys</i>	Scrophulariaceae	1
7	<i>Lotus corniculatus</i>	Fabaceae	1
8	<i>Hieracium pilosella</i>	Asteraceae	1
9	<i>Vicia cracca</i>	Fabaceae	1

95 *Replica 2 = FG2*

Nr	Species	Family	FG
1	<i>Anthyllis vulneraria</i>	Fabaceae	2
2	<i>Campanula rotundifolia</i>	Campanulaceae	2
3	<i>Centaurea jacea</i>	Asteraceae	2
4	<i>Hippocrepis comosa</i>	Fabaceae	2
5	<i>Medicago lupulina</i>	Fabaceae	2
6	<i>Peucedanum oreoselinum</i>	Apiaceae	2
7	<i>Pimpinella saxifraga</i>	Apiaceae	2
8	<i>Trifolium pratense</i>	Fabaceae	2
9	<i>Sanguisorba minor</i>	Rosaceae	2

96 *Replica 3 = FG3*

Nr	Species	Family	FG
1	<i>Betonica officinalis</i>	Lamiaceae	3
2	<i>Poa angustifolia</i>	Poaceae	3
3	<i>Festuca rubra</i>	Poaceae	3
4	<i>Agrimonia eupatoria</i>	Rosaceae	3
5	<i>Prunella grandiflora</i>	Lamiceae	3
6	<i>Helictotrichon pubescens</i>	Poaceae	3
7	<i>Agrostis capillaris</i>	Poaceae	3
8	<i>Achillea millefolium</i>	Asteraceae	3
9	<i>Potentilla tabernaemontani</i>	Rosaceae	3

97

98 *Replica 4 = FG3*

Nr	Species	Family	FG
1	<i>Helictotrichon pubescens</i>	Poaceae	3
2	<i>Dactylis glomerata</i>	Poaceae	3
3	<i>Agrostis capillaris</i>	Poaceae	3
4	<i>Anthericum ramosum</i>	Anthericaceae	3
5	<i>Potentilla tabernaemontani</i>	Rosaceae	3
6	<i>Helictotrichon pratense</i>	Poaceae	3
7	<i>Brachypodium pinnatum</i>	Poaceae	3
8	<i>Festuca rubra</i>	Poaceae	3
9	<i>Bupthalmum salicifolium</i>	Asteraceae	3

99 *Replica 5 = FG 1*

Nr	Species	Family	FG
1	<i>Teucrium montanum</i>	Plantaginaceae	1
2	<i>Helianthemum nummularium</i>	Cistaceae	1
3	<i>Galium album</i>	Rubiaceae	1
4	<i>Asperula cynanchica</i>	Rubiaceae	1
5	<i>Genista tinctoria</i>	Fabaceae	1
6	<i>Linum perenne</i>	Linaceae	1
7	<i>Vicia cracca</i>	Fabaceae	1
8	<i>Prunella vulgaris</i>	Lamiaceae	1
9	<i>Veronica chamaedrys</i>	Scrophulariaceae	1

100

101 **Two functional groups**

102 *Replica 1 = FG 1 + FG 3*

Nr	Species	Family	FG
1	<i>Leontodon incanus</i>	Asteraceae	1
2	<i>Achillea millefolium</i>	Asteraceae	3
3	<i>Linum perenne</i>	Linaceae	1
4	<i>Plantago media</i>	Plantaginaceae	1
5	<i>Brachypodium pinnatum</i>	Poaceae	3
6	<i>Lotus corniculatus</i>	Fabaceae	1
7	<i>Genista tinctoria</i>	Fabaceae	1
8	<i>Festuca ovina</i>	Poaceae	3
9	<i>Bromus erectus</i>	Poaceae	3

103 *Replica 2 = FG 1 + FG 3*

Nr	Species	Family	FG
1	<i>Helictotrichon pubescens</i>	Poaceae	3
2	<i>Teucrium montanum</i>	Plantaginaceae	1
3	<i>Agrostis capillaris</i>	Poaceae	3
4	<i>Veronica chamaedrys</i>	Scrophulariaceae	1
5	<i>Hieracium pilosella</i>	Asteraceae	1
6	<i>Genista tinctoria</i>	Fabaceae	1
7	<i>Prunella grandiflora</i>	Lamiceae	3
8	<i>Vicia cracca</i>	Fabaceae	1
9	<i>Brachypodium pinnatum</i>	Poaceae	3

104 *Replica 3 = FG1+FG2*

Nr	Species	Family	FG
1	<i>Veronica chamaedrys</i>	Scrophulariaceae	1
2	<i>Sanguisorba minor</i>	Rosaceae	2
3	<i>Clinopodium vulgare</i>	Lamiaceae	1
4	<i>Teucrium montanum</i>	Plantaginaceae	1
5	<i>Lotus corniculatus</i>	Fabaceae	1
6	<i>Medicago lupulina</i>	Fabaceae	2
7	<i>Anthyllis vulneraria</i>	Fabaceae	2
8	<i>Leontodon incanus</i>	Asteraceae	1
9	<i>Trifolium pratense</i>	Fabaceae	2

105

106 *Replica 4 = FG2+FG3*

Nr	Species	Family	FG
1	<i>Helictotrichon pratense</i>	Poaceae	3
2	<i>Anthyllis vulneraria</i>	Fabaceae	2
3	<i>Achillea millefolium</i>	Asteraceae	3
4	<i>Prunella grandiflora</i>	Lamiceae	3
5	<i>Medicago lupulina</i>	Fabaceae	2
6	<i>Sanguisorba minor</i>	Rosaceae	2
7	<i>Trifolium pratense</i>	Fabaceae	2
8	<i>Festuca ovina</i>	Poaceae	3
9	<i>Bromus erectus</i>	Poaceae	3

107 *Replica 5 = FG 1 + FG 2*

Nr	Species	Family	FG
1	<i>Sanguisorba minor</i>	Rosaceae	2
2	<i>Genista tinctoria</i>	Fabaceae	1
3	<i>Asperula cynanchica</i>	Rubiaceae	1
4	<i>Clinopodium vulgare</i>	Lamiaceae	1
5	<i>Peucedanum oreoselinum</i>	Apiaceae	2
6	<i>Linum perenne</i>	Linaceae	1
7	<i>Prunella vulgaris</i>	Lamiaceae	1
8	<i>Pimpinella saxifraga</i>	Apiaceae	2
9	<i>Anthyllis vulneraria</i>	Fabaceae	2

108

109 **Three functional groups**

110 *Replica 1 = FG 1 + FG 2 +FG 3*

Nr	Species	Family	FG
1	<i>Festuca rubra</i>	Poaceae	3
2	<i>Dactylis glomerata</i>	Poaceae	3
3	<i>Poa angustifolia</i>	Poaceae	3
4	<i>Hippocrepis comosa</i>	Fabaceae	2
5	<i>Campanula rotundifolia</i>	Campanulaceae	2
6	<i>Medicago lupulina</i>	Fabaceae	2
7	<i>Leontodon incanus</i>	Asteraceae	1
8	<i>Hieracium pilosella</i>	Asteraceae	1
9	<i>Teucrium montanum</i>	Plantaginaceae	1

111 *Replica 2 = FG 1 + FG 2 +FG 3*

Nr	Species	Family	FG
1	<i>Festuca rubra</i>	Poaceae	3
2	<i>Poa angustifolia</i>	Poaceae	3
3	<i>Centaurea scabiosa</i>	Asteraceae	3
4	<i>Sanguisorba minor</i>	Rosaceae	2
5	<i>Pimpinella saxifraga</i>	Apiaceae	2
6	<i>Anthyllis vulneraria</i>	Fabaceae	2
7	<i>Asperula cynanchica</i>	Rubiaceae	1
8	<i>Lotus corniculatus</i>	Fabaceae	1
9	<i>Vicia cracca</i>	Fabaceae	1

112 *Replica 3 = FG 1 + FG 2 +FG 3*

Nr	Species	Family	FG
1	<i>Centaurea scabiosa</i>	Asteraceae	3
2	<i>Dactylis glomerata</i>	Poaceae	3
3	<i>Potentilla tabernaemontani</i>	Rosaceae	3
4	<i>Medicago lupulina</i>	Fabaceae	2
5	<i>Campanula rotundifolia</i>	Campanulaceae	2
6	<i>Anthyllis vulneraria</i>	Fabaceae	2
7	<i>Galium album</i>	Rubiaceae	1
8	<i>Leontodon incanus</i>	Asteraceae	1
9	<i>Helianthemum nummularium</i>	Cistaceae	1

113

114 *Replica 4 = FG 1 + FG 2 +FG 3*

Nr	Species	Family	FG
1	<i>Betonica officinalis</i>	Lamiaceae	3
2	<i>Potentilla tabernaemontani</i>	Rosaceae	3
3	<i>Poa angustifolia</i>	Poaceae	3
4	<i>Trifolium pratense</i>	Fabaceae	2
5	<i>Sanguisorba minor</i>	Rosaceae	2
6	<i>Anthyllis vulneraria</i>	Fabaceae	2
7	<i>Galium album</i>	Fabaceae	1
8	<i>Teucrium montanum</i>	Plantaginaceae	1
9	<i>Leontodon incanus</i>	Asteraceae	1

115 *Replica 5 = FG 1 + FG 2 +FG 3*

Nr	Species	Family	FG
1	<i>Festuca ovina</i>	Poaceae	3
2	<i>Brachypodium pinnatum</i>	Poaceae	3
3	<i>Agrostis capillaris</i>	Poaceae	3
4	<i>Campanula rotundifolia</i>	Campanulaceae	2
5	<i>Pimpinella saxifraga</i>	Apiaceae	2
6	<i>Centaurea jacea</i>	Asteraceae	2
7	<i>Leontodon incanus</i>	Asteraceae	1
8	<i>Genista tinctoria</i>	Fabaceae	1
9	<i>Prunella vulgaris</i>	Lamiceae	1

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S2.4. Functional dispersion and functional redundancy indexes

We calculated two indexes of functional diversity: **i.** The functional dispersion (Fdis) index using the dbFD function in the FD package in R [1], and **ii.** the functional redundancy (Fred) index using the R function called ‘uniqueness’ [2]. For calculating the indexes, we used plant traits obtained from the BiolFlor [3,4] and LEDA databases [11] as presented in Table S2. Both measures can be calculated including categorical and numerical traits and provide opposite insights on the how functional diversity is distributed amongst our experimental communities. As previously described, Fdis represents the mean distance in the multidimensional trait space comparing the values of individual species to the value of all species. In other words, Fdis indicates the degree in which plant species occupy the multidimensional trait space. Fdis can correct for different abundances among species, thus controlling possible effects of more abundant species. Another important aspect is that Fdis is not affected by the species richness values in different communities [1].

On the other hand, Fred represents the similarities amongst species composing a given community in terms of their functional traits and, consequently, their performances. Since ecosystem functioning under stressful conditions (e.g. invasions) would require the occurrence of species with similar performances, we can expect Fred to be an important component of diversity ensuring ecosystem functions over time [2]. However, despite high values of Fred can indicate that ecosystem functioning would be less affected by species loss, it can also occur when there is a weak relationship between species richness and functions [16].

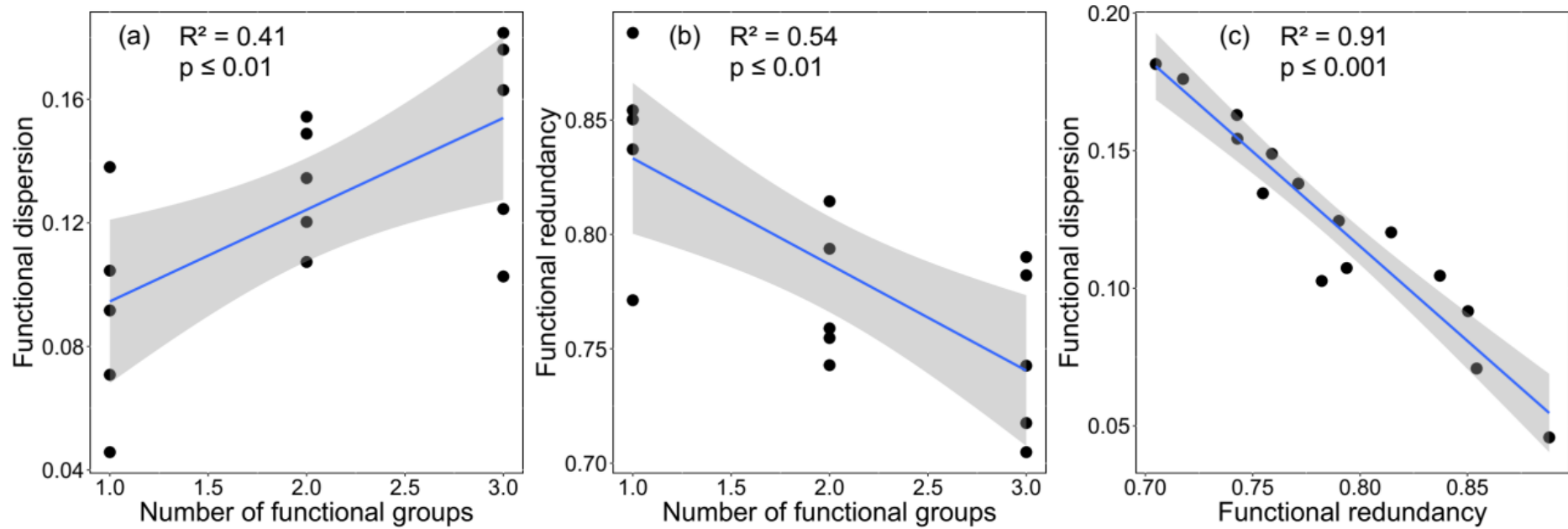
Afterwards, we correlated these functional diversity indexes to the number of functional groups resulting from the cluster analysis based on plant traits using a linear model. We also correlated (using the same type of linear model) the Fdis and Fred indexes to check if they were positively or negatively correlated (Fig. S3). The number of functional groups was log-transformed prior to the analysis to fulfill the linear model assumptions. This analysis showed that both functional diversity indexes were significantly correlated to the levels of functional diversity determined by the cluster analysis using plant traits (Fig. S3). Fdis significantly increased with the number of functional groups composing the plant communities ($R^2 = 0.41$, $p \leq 0.01$, Fig. S3a), while the Fred index decreased with the number of functional groups in our experimental communities ($R^2 = 0.45$, $p \leq 0.01$, Fig. S3b). Finally, a negative correlation was found between the indexes, indicating that both measures represent opposite aspects of functional diversity and that one cannot maximize them at the same time when trying to restore a given plant community ($R^2 = 0.99$, $p \leq 0.001$, Fig. S3c).

Table S2: Functional traits characteristics of the native species occurring in our experimental communities used for the calculation of the functional dispersion index. Zero (0) and 1 values represent the presence/absence of categorical functional traits. Quantitative functional traits are represented by mean values for each species. Species relative abundances were determined by multiplying the 3 g m⁻² of native species sown (i.e. 0.48 g of seeds which means, approximately, 0.054 g for each one of the native species present in our communities) by its mean seed mass to obtain the number of seeds per native species. Mean seed mass information (mg) was obtained from BioFlor database [3,4]. For the species *Bupthalmum salicifolium* L. we used the thousand seed mass obtained from Rieger-Hofmann GmbH (Catalogue 2016/2017) to calculate the mean seed mass.

Native grasslands species	seed mass	cannopy height	life long perennial	life long biannual	life long annual	life form hemicryptophytes	life form geophytes	life form chamaephytes	life form hph	root morphology rhizome	root morphology runner	root morphology pleiocorm	root morphology tuft	shoot morphology hemi-rosette	shoot morphology rosette	shoot morphology erosulate	non-legume	legume	grass	sla	dry leaf mass
<i>Achillea millefolium</i>	0.13	0.3955	1	0	0	1	0	0	0	0	1	0	0	1	0	0	1	0	0	19.475	185.5
<i>Agrimonia eupatoria</i>	3.61	0.3	1	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	17.85	339.5
<i>Agrostis capillaris</i>	0.07	0.25	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	33.2	263
<i>Anthericum ramosum</i>	3.81	0.2875	1	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	23.51	161.45
<i>Anthyllis vulneraria</i>	3.31	0.2	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	18.85	170
<i>Asperula cynanchica</i>	0.97	0.2375	1	0	0	1	0	0	0	0	0	1	0	0	0	1	1	0	0	28.06	329.32
<i>Betonica officinalis</i>	1.39	0.375	1	0	0	1	0	0	0	1	0	0	0	0	0	1	1	0	0	25.45	227.705
<i>Brachypodium pinnatum</i>	3.38	0.6	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	27.33	397
<i>Briza media</i>	0.35	0.165	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	25.85	295.57
<i>Bromus erectus</i>	4.59	0.5	1	0	0	1	0	0	0	1	0	0	1	1	0	0	0	0	1	20.725	353
<i>Bupthalmum salicifolium</i>	0.46	0.35	1	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	25.72	181.45
<i>Campanula rapunculoides</i>	0.11	0.375	1	0	0	1	0	0	0	0	1	0	0	1	0	0	1	0	0	54.74	135.545
<i>Campanula rotundifolia</i>	0.07	0.19	1	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	36.7	255.5
<i>Carex flacca</i>	0.95	0.275	1	0	0	0	1	0	0	1	1	0	0	1	0	0	0	0	1	15	332.095
<i>Centaurea jacea</i>	1.53	0.85	1	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	15.65	219.59
<i>Centaurea scabiosa</i>	6.17	0.825	1	0	0	1	0	0	0	1	0	1	0	1	0	0	1	0	0	18.45	197
<i>Clinopodium vulgare</i>	0.45	0.425	1	0	0	1	0	0	0	0	1	0	0	0	0	1	1	0	0	23.6	258

<i>Dactylis glomerata</i>	0.9	0.454	1	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	31.75	212
<i>Festuca ovina</i>	0.33	0.1525	1	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	1	19.29	309.74
<i>Festuca rubra</i>	0.79	0.45	1	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	1	17	273
<i>Filipendula vulgaris</i>	0.72	0.35	1	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	13	295
<i>Galium album</i>	0.53	0.45	1	0	0	1	0	0	0	0	1	1	0	0	0	1	1	0	0	24.09	162.37
<i>Galium verum</i>	0.57	0.425	1	0	0	1	0	0	0	0	1	1	0	0	0	1	1	0	0	22.25	227
<i>Genista tinctoria</i>	3.86	0.45	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	16.17	248
<i>Helianthemum nummularium</i>	1.08	0.1155	1	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	14.5	237.5
<i>Helictotrichon pratense</i>	3.11	0.65	1	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	1	9.85	318
<i>Helictotrichon pubescens</i>	1.91	0.6	1	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	1	21.3	264
<i>Hieracium pilosella</i>	0.15	0.06	1	0	0	1	0	0	0	1	1	0	0	0	1	0	1	0	0	24.29	188
<i>Hippocrepis comosa</i>	3.9	0.14	1	0	0	1	0	0	0	0	1	1	0	1	0	0	0	1	0	15.75	235.66
<i>Leontodon hispidus</i>	0.99	0.235	1	0	0	1	0	0	0	1	0	0	0	0	1	0	1	0	0	22.17	143.64
<i>Leontodon incanus</i>	1.4	0.1	1	0	0	1	0	0	0	0	0	1	0	0	1	0	1	0	0	21.36	157.22
<i>Linum perenne</i>	2.18	0.45	1	0	0	1	0	0	0	0	0	1	0	0	0	1	1	0	0	25.88	200.98
<i>Lotus corniculatus</i>	1.46	0.2	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	1	0	29.5	158
<i>Luzula campestris</i>	0.74	0.27	1	0	0	1	0	0	0	1	1	0	0	1	0	0	0	0	1	24.85	245.74
<i>Medicago lupulina</i>	1.76	0.325	1	1	1	1	0	0	0	0	0	1	0	1	0	0	0	1	0	29.2	196
<i>Peucedanum oreoselinum</i>	3.83	0.5	1	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	16.27	259.32
<i>Pimpinella saxifraga</i>	1.13	0.3	1	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	17.12	285.5
<i>Plantago lanceolata</i>	1.8	0.15	1	0	0	1	0	0	0	0	0	1	0	0	1	0	1	0	0	16.82	140.605
<i>Plantago media</i>	0.36	0.05	1	0	0	1	0	0	0	0	0	1	0	0	1	0	1	0	0	18.7	137
<i>Poa angustifolia</i>	0.21	0.36	1	0	0	1	0	0	0	0	1	0	1	1	0	0	0	0	1	15.55	424.5
<i>Potentilla tabernaemontani</i>	0.63	0.1	1	0	0	1	0	0	0	0	1	0	0	1	0	0	1	0	0	16.75	315
<i>Prunella grandiflora</i>	0.78	0.1325	1	0	0	1	0	1	0	0	1	0	0	1	0	0	1	0	0	20.11	174.37
<i>Prunella vulgaris</i>	0.7	0.145	1	0	0	1	0	1	0	0	1	0	0	0	0	1	1	0	0	33.01	165
<i>Sanguisorba minor</i>	5.08	0.2	1	0	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	22	313.96
<i>Securigera varia</i>	5.4	0.425	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	1	0	32.9	168.33
<i>Teucrium montanum</i>	0.91	0.2	1	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	17.93	264.12
<i>Thymus praecox</i>	0.15	0.07	1	0	0	0	0	0	1	0	1	0	0	0	0	1	1	0	0	14.82	234
<i>Trifolium pratense</i>	1.36	0.275	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	21.5	225.13

<i>Veronica chamaedrys</i>	0.19	0.25	1	0	0	1	0	1	0	0	1	0	0	0	0	1	1	0	0	32.21	215.38
<i>Vicia cracca</i>	14.29	0.75	1	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	22.04	219.49



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161 **Figure S3:** Regression analysis for the functional dispersion and functional redundancy indexes [1,2]. The figures show the functional dispersion
 162 index **(a)** and the functional redundancy index **(b)** according to the number of functional groups composing the experimental communities and
 163 the correlation between functional dispersion and functional redundancy **(c)**.

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