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The Agrodiversity Experiment: three years of data from a multi-site plant diversity experiment in intensively managed grasslands.

METADATA

DATA SET DESCRIPTORS

A. Data set identity:

Title: The Agrodiversity Experiment: three years of data from a multi-site plant diversity experiment in intensively managed grasslands.

B. Data set identification code

Data Set Identity Code: site_info.csv biomass.csv forage_quality.csv climate.csv soils.csv

C. Data set description

Abstract:

Intensively-managed grassland systems are globally prominent ecosystems. We investigated whether experimental increases in plant diversity in grassland communities can increase their resource use efficiency. This work consisted of a coordinated, continental-scale 33 site

experiment (the Agrodiversity Experiment) that investigated plant diversity and ecosystem function in intensively-managed grassland communities. We compared the agronomic performance of monocultures and 4-species mixtures that varied in the relative abundance of the component species at sowing.

The core design for the experiment was 30 plots, representing fifteen grassland communities at two seeding densities. The fifteen communities were comprised of four monocultures (two grasses and two legumes) and eleven four-species mixtures that varied in the relative abundance of the four species at sowing (a distinctive feature of the design). There was a total of 1028 plots in the core experiment, with an additional 572 plots sown for additional treatments. Sites followed an agreed protocol, employing the same experimental methods. Certain plot management factors such as seeding rates and number of cuts were determined by local practice The four species used at any particular site depended on geographical location, but the species were chosen according to four functional traits: a fast-establishing grass, a slow-establishing persistent grass, a fast-establishing legume and a slow-establishing persistent legume. As the objective was to maximise yield for intensive grassland production, the species chosen were all high-yielding agronomic species.

The dataset contains species-specific biomass measurements (yield per species and yield of weeds) for all harvests for up to four years at 33 sites. Samples of harvested vegetation were also analysed for forage quality at 26 sites.

Analyses showed that the yield of the mixtures exceeded that of the average monoculture in >97% of comparisons. Mixture biomass also exceeded that of the best monoculture (transgressive overyielding) at about 60% of sites. There was also a positive relationship between

the diversity of the communities and aboveground biomass that was consistent across sites and persisted for three years. Weed invasion in mixtures was very much less than that in monocultures. At an analysis across four North European sites, positive yield effects were not accompanied by a reduction in either herbage digestibility or crude protein concentration. These data should be of interest to ecologists studying relationships between diversity and ecosystem function, and to agronomists interested in sustainable intensification. The large spatial scale of the sites provides opportunity for analyses across spatial (and temporal) scales. The database can also complement existing databases and meta-analyses on biodiversity-ecosystem function relationships in natural communities by focusing on those same relationships within intensively-managed agricultural grasslands. A major contribution of the design of the experiment is that it facilitates investigation of the effects of different facets of diversity (composition, richness, relative abundance and genetic diversity) on selected ecosystem functions.

D. Key words: *biodiversity; agricultural grasslands; mixtures; monocultures; ecosystem function; overyielding; plant community; species biomass; forage quality; yield*

RESEARCH ORIGIN DESCRIPTORS

The Agrodiversity experiment was a coordinated continental-scale field experiment. The coordination of the network was supported by EU COST Action 852: Quality Legume-Based Forage Systems for Contrasting Environments. Each of the 33 participating sites established at least 30 plots using the same experiment design and managed the plots according to an agreed protocol. The design of the experiment consisted of a common set of 30 plots across all sites, with additional optional plots for applying treatments. Aboveground biomass was measured at the common set of 30 plots for all harvests at all sites. Forage quality measurements were undertaken at 26 sites. Additional treatments were voluntarily undertaken by various sites. The treatments applied varied across sites and included increased genetic diversity in species, different levels of nitrogen fertilizer and different levels of cutting intensity.

The network did not have a central funding source to cover the costs of running the experiment, thus participating sites each secured funding to cover the costs incurred at their own site; COST852 provided funding for regular meetings and for scientific networking between partners. The collation of this database was supported by the Irish Research Council for Science, Engineering and Technology through a research fellowship to L. Kirwan, with additional support from Science Foundation Ireland Research Frontiers Programme (09/RFP/EOB2546).

The email addresses of people that have contributed to the data are included in the file site_info.csv. Those in the best position to answer questions concerning the data are Laura Kirwan (laura.kirwan@outlook.com) and Caroline Brophy (caroline.brophy@nuim.ie); those in

the best position to answer questions about experimental protocol are Andreas Lüscher (andreas.luescher@art.admin.ch) and Maria-Teresa Sebastià (teresa.sebastia@ctfc.es); those in the best position to answer questions concerning the experimental design are John Connolly (John.Connolly@ucd.ie) and Laura Kirwan (laura.kirwan@outlook.com).

Introduction

Ecological research on the relationship between plant diversity and ecosystem function generally shows that reductions in plant diversity of randomly-assembled communities reduce the yield of aboveground biomass (Cardinale et al. 2007). Mechanisms that underpin these relationships are attributed to improved utilisation of resources in total niche space (niche differentiation), positive interspecific interactions, and selection effects (Hooper et al. 2005). Most such experiments (as reviewed in Cardinale et al. 2007) study the effects of reductions in plant richness from relatively species-rich communities and in low-nutrient systems. In contrast, conventional agriculture in many areas maximises forage yield by planting monocultures of grasses and applying large quantities of nitrogen fertilizer, and has associated negative environmental impacts. We are interested in the role of multi-species agricultural mixtures in improving the resource use efficiency of agricultural grassland systems. If the same diversity-function mechanisms and relationships prevail in simple multi-species plant communities and under higher applications of nutrients, then increased plant diversity in species-poor agricultural systems would be expected to improve their resource-efficient provision of forage and other ecosystem services. For generality and relevance to agricultural practice, investigations of multi-species mixtures need to

be conducted at multiple sites, and require comparison against the best-performing component monoculture species (or the prevailing conventional system).

The species composition of multi-species mixtures can be strategically designed to include traits that maximise complementarity and interspecific interactions to improve resource utilisation and yield of aboveground biomass. A classic example is the combination of grass and legume species to exploit the ability of legumes to fix atmospheric nitrogen and thereby reduce reliance on application of chemical fertilizers (Nyfeler et al. 2011). However, other traits are also likely to be relevant, but are not usually explicitly tested in multi-species experiments conducted across multiple sites, years and mixture types. Here we test a temporal development trait. Fast-establishing species exhibit fast germination and growth, thereby providing adequate cover of soil and high biomass yields in the first and second year after sowing. These species often lack persistency. Slow-establishing, but persistent species exhibit slower germination and growth rate during establishment, but in the long run are highly competitive, therefore increasing in cover and biomass yields over initial years and constituting the majority of yield in the third and fourth production year and thereafter.

In this data paper, we present data from the Agrodiversity experiment, a co-ordinated continental-scale field experiment across 33 sites that was used to compare the biomass yield of monocultures and four-species mixtures (designed on the basis of specific traits) associated with intensively managed agricultural grassland systems. We addressed the following main questions (modified from Finn et al. 2013):

1. Were there yield benefits (overyielding) from diversity and, if so, did the benefits persist over three years and across sites?
2. Were the yield benefits sufficiently large for transgressive overyielding to occur?
3. Did the benefits of diversity occur and persist across the range of mixture communities used in this experiment?
4. Did both the functional traits of nitrogen acquisition and temporal development contribute to the diversity effect (the excess of mixture performance over that of the monoculture performances of component species)?
5. What were the differences in resistance to weed invasion, nutrient dynamics and forage quality among the different plant communities?
6. What were the factors affecting the stability of species composition?

Recent analyses of some of these data quantified the relationships between community diversity and aboveground biomass (Kirwan et al. 2007, Finn et al. 2013). We showed that aboveground biomass of the mixtures exceeded that of the average monoculture in >97% of comparisons, and mixture biomass also exceeded that of the best monoculture (transgressive overyielding) at about 60% of sites (Finn et al. 2013). There was also a positive relationship between the evenness of the communities and aboveground biomass that was consistent across sites (Kirwan et al. 2007) and persisted for three years (Finn et al. 2013). In an analysis across six sites, positive yield effects were not accompanied by a reduction in herbage digestibility and crude protein concentration (Sturludóttir et al. 2013).

Ultimately, we hope that further analyses of this data set will promote understanding about a) the design of multi-species mixtures for application in more resource-efficient agricultural systems

and b) how the diversity (composition, richness and relative abundance) of plant communities influences the delivery of ecosystem processes across spatial and temporal scales.

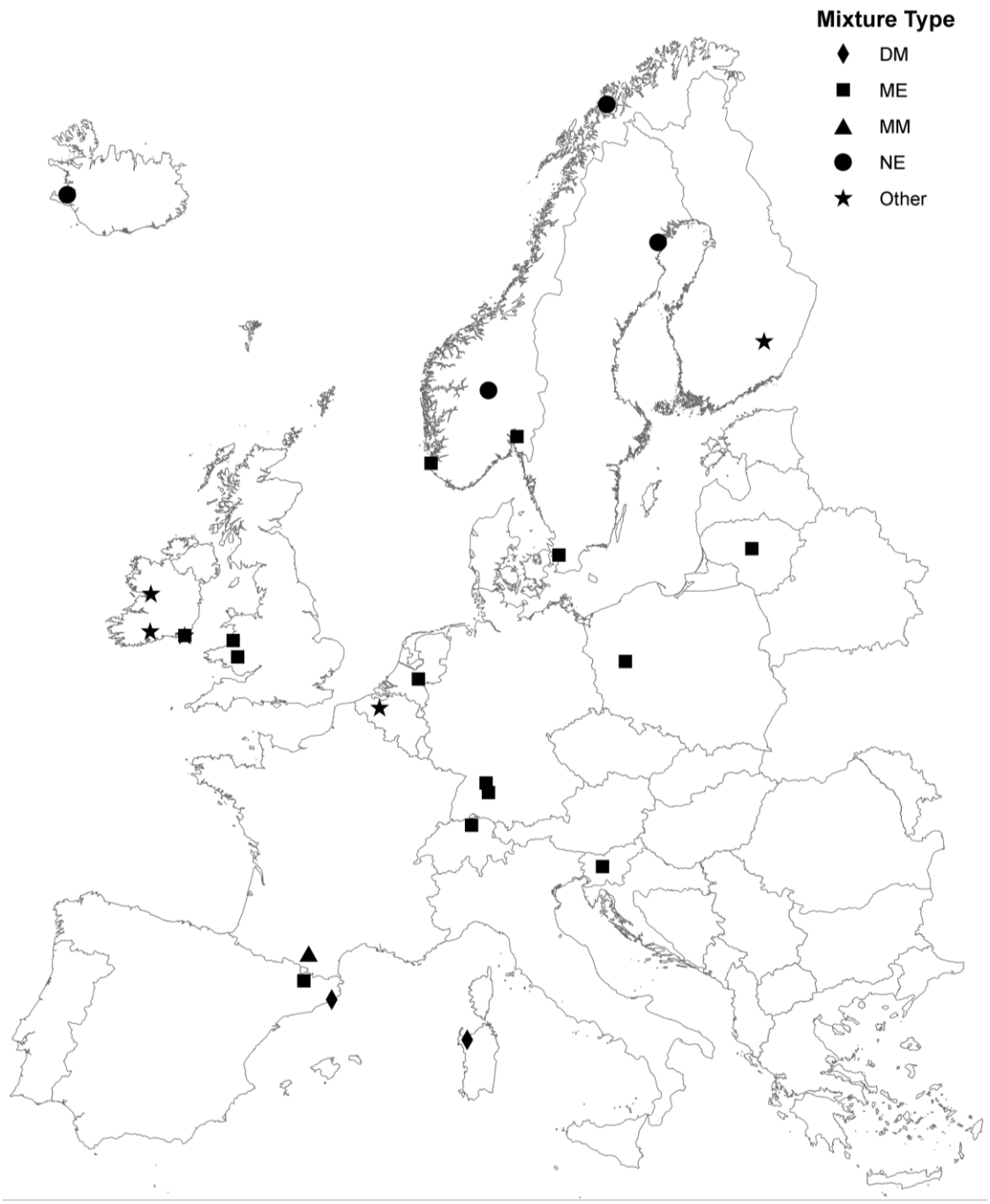

Figure 1. Map of site locations in Europe. Geographical locations of the sites are indicated for the Mid-European (ME), North-European (NE), Dry-Mediterranean (DM), Moist-Mediterranean (MM) and Other species groups. Note that there is an additional site in Canada. Coordinates for each site are contained in site_info.csv

Methods

Description of the study area and experimental design:

This was a coordinated multi-site experiment in which sites a covered a broad geographical area (Figure 1). Details of site coordinates, altitude, species and varieties used, plot management and any treatments applied are in site_info.csv.

Design of the core experiment:

The species compositions of experimental plots were selected using a simplex design for mixtures experiments (Cornell (2002) Table 1). At each site, four species were chosen according to four functional traits: a fast-establishing grass (G1), a slow-establishing persistent grass (G2), a fast-establishing legume (L1) and a slow-establishing persistent legume (L2). The species selected by individual sites are detailed in site_info.csv. The species chosen generally fell into four groups according to geographical location: Mid-European (18 sites), North-European (6 sites), Dry Mediterranean (2 sites) and Moist Mediterranean (1 site), with seven sites selecting site-specific species (Other). As the objective was to maximise yield of highly digestible forage from intensive grasslands, the chosen species were all high-yielding agronomic species.

The main treatment consisted of a core set of 30 plots, representing fifteen grassland communities at two levels of seed density. At each site, the four species were sown in monoculture, with sowing rates determined by each site according to local practice. The sowing rates of the four species were systematically varied to produce eleven mixture communities.

These fifteen communities were repeated at low and high levels of seeding density ('high' was represented by the standard seeding rate of a monoculture species at a site, with 'low' being 60% of the high seeding rate). Relative proportions of species in a mixture were manipulated by varying seeding rates of the four species at sowing, and resulted in four planned levels of evenness in the design (Table 1). This design resulted in a core set of 30 experimental plots per site (arranged in a completely randomized design).

The species richness of the communities was either one (monocultures) or four (mixtures). However within the four-species mixtures, the level of evenness was manipulated. The levels of evenness (E) were calculated using the formula $E = \frac{2s}{s-1}\sum_{i<j}^{s} P_i P_j$, where s is the maximum number of species in a community (s=4 for this experiment), and P_i is the sown relative abundance of the ith species (see Kirwan et al. 2007). This lies between 0 for monocultures and 1 for a community in which all species are represented in equal proportions.

Two sites (45 and 46) were not part of the initial network and did not use this core design. They used a variation of the design. The data from these sites is included because there is high overlap in communities with those in the core design. The same plot number is given to design points (community type) at sites 45 and 46 that are the same as those in the core design. This facilitates similar analyses and inclusion in meta-analysis. Sites 45 and 46 included two-species mixtures, whereas the core design does not.

Note on replication: Within a site, the design is not replicated. The design of the experiment was optimized for good coverage of species composition in order to facilitate the use of a response

surface regression approach. In regression analyses, one usually does not require replication and residual variation is estimated from the lack of fit of individual points to the regression model selected. However, the use of two seeding densities adds effective replication for mixture communities. The large number of individual experiments across different sites generally adds a very high level of statistical power to the overall experimental design.

Additional treatments:

Additional plots were sown at 22 sites to facilitate the assessment of an experimental treatment. The most commonly applied treatment was a wide genetic base (WGB) treatment, applied at ten sites. A nitrogen fertiliser application treatment was applied at eight sites.

A treatment to investigate genetic diversity was applied at ten sites. At these sites, the treatment plots were sown with legume species with increased intraspecific genetic diversity. The single varieties of white and red clover selected at each site were compared with a wide genetic base (WGB) treatment that consisted of composite populations of white and red clover that were each constructed from commercial varieties plus unselected material obtained from germplasm collections. Different WGB composite populations were constructed for white and red clover species for the ME and NE regions. The seed material for the WGB treatment was supplied to the participating sites and the populations supplied depended on whether the site had used the ME or NE species group for the core experiment. Further details on the composite populations and an analysis of the temporal change in genetic diversity at three sites was published in Collins et al. (2012).

At eight sites, an additional nitrogen fertiliser application level was tested. Details of the amounts of N applied at core and treatment plots are detailed in site_info.csv. The treatments applied at the other sites were cutting frequency, different legume species, and local varieties of the species.

Table 1. Description of experiment design. G1, G2, L1 and L2 represent the sowing proportions of the four species. E is the planned evenness of the community. Density is the sowing density (low is 60% of high) and is determined by each site according to local practice. Type indicates whether the design point is part of the core design, or an additional optional treatment. The core 30 plots make up the main experiment (shaded). The additional 18 treatment plots were established at 18 sites and the treatments applied are detailed in site_info.csv. Plots 49-68 are additional plots that were sown at sites 45 and 46. # Sites indicates the number of sites in which a particular community was sown.

PLOT	G1	G2	L1	L2	E	Density	Type	# Sites
1	0.7	0.1	0.1	0.1	0.64	High	Core	32
2	0.1	0.7	0.1	0.1	0.64	High	Core	32
3	0.1	0.1	0.7	0.1	0.64	High	Core	32
4	0.1	0.1	0.1	0.7	0.64	High	Core	32
5	0.25	0.25	0.25	0.25	1	High	Core	33
6	0.4	0.4	0.1	0.1	0.88	High	Core	32
7	0.4	0.1	0.4	0.1	0.88	High	Core	32
8	0.4	0.1	0.1	0.4	0.88	High	Core	32
9	0.1	0.4	0.4	0.1	0.88	High	Core	32
10	0.1	0.4	0.1	0.4	0.88	High	Core	32
11	0.1	0.1	0.4	0.4	0.88	High	Core	32
12	1	0	0	0	0	High	Core	33
13	0	1	0	0	0	High	Core	33

14	0	0	1	0	0	High	Core	33
15	0	0	0	1	0	High	Core	33
16	0.7	0.1	0.1	0.1	0.64	Low	Core	32
17	0.1	0.7	0.1	0.1	0.64	Low	Core	32
18	0.1	0.1	0.7	0.1	0.64	Low	Core	32
19	0.1	0.1	0.1	0.7	0.64	Low	Core	32
20	0.25	0.25	0.25	0.25	1	Low	Core	32
21	0.4	0.4	0.1	0.1	0.88	Low	Core	32
22	0.4	0.1	0.4	0.1	0.88	Low	Core	32
23	0.4	0.1	0.1	0.4	0.88	Low	Core	32
24	0.1	0.4	0.4	0.1	0.88	Low	Core	32
25	0.1	0.4	0.1	0.4	0.88	Low	Core	32
26	0.1	0.1	0.4	0.4	0.88	Low	Core	32
27	1	0	0	0	0	Low	Core	32
28	0	1	0	0	0	Low	Core	32
29	0	0	1	0	0	Low	Core	32
30	0	0	0	1	0	Low	Core	32
31	0.7	0.1	0.1	0.1	0.64	Low	Treatment	21
32	0.1	0.7	0.1	0.1	0.64	Low	Treatment	21
33	0.1	0.1	0.7	0.1	0.64	Low	Treatment	21
34	0.1	0.1	0.1	0.7	0.64	Low	Treatment	21
35	0.25	0.25	0.25	0.25	1	Low	Treatment	21
36	1	0	0	0	0	Low	Treatment	16

37	0	1	0	0	0	Low	Treatment	16
38	0	0	1	0	0	Low	Treatment	21
39	0	0	0	1	0	Low	Treatment	21
40	0.7	0.1	0.1	0.1	0.64	Low	Treatment	21
41	0.1	0.7	0.1	0.1	0.64	Low	Treatment	21
42	0.1	0.1	0.7	0.1	0.64	High	Treatment	21
43	0.1	0.1	0.1	0.7	0.64	High	Treatment	21
44	0.25	0.25	0.25	0.25	1	High	Treatment	21
45	1	0	0	0	0	High	Treatment	16
46	0	1	0	0	0	High	Treatment	16
47	0	0	1	0	0	High	Treatment	21
48	0	0	0	1	0	High	Treatment	21
49	0	0.5	0	0.5	0.6667	High	Additional	3
50	0	0	0.5	0.5	0.6667	High	Additional	3
51	0.5	0.5	0	0	0.6667	High	Additional	3
52	0.5	0	0.5	0	0.6667	High	Additional	3
53	0.5	0	0	0.5	0.6667	High	Additional	3
54	0	0.5	0.5	0	0.6667	High	Additional	3
55	0	0.5	0	0.5	0.6667	Low	Additional	2
56	0	0	0.5	0.5	0.6667	Low	Additional	2
57	0.5	0.5	0	0	0.6667	Low	Additional	2
58	0.5	0	0.5	0	0.6667	Low	Additional	2
59	0.5	0	0	0.5	0.6667	Low	Additional	2

60	0	0.5	0.5	0	0.6667	Low	Additional	2
61	0.88	0.04	0.04	0.04	0.2944	High	Additional	2
62	0.04	0.88	0.04	0.04	0.2944	High	Additional	2
63	0.04	0.04	0.88	0.04	0.2944	High	Additional	2
64	0.04	0.04	0.04	0.88	0.2944	High	Additional	2
65	0.88	0.04	0.04	0.04	0.2944	Low	Additional	2
66	0.04	0.88	0.04	0.04	0.2944	Low	Additional	2
67	0.04	0.04	0.88	0.04	0.2944	Low	Additional	1
68	0.04	0.04	0.04	0.88	0.2944	Low	Additional	1

Management protocol:

Plots were not grazed. The number of cuts per annum and fertilizer application levels were determined by local practice at individual sites. See Site_info.csv for details on management practices employed at each site.

The plots were not weeded and there was generally no herbicide application. However, some targeted weeding was required in some sites during the establishment phase. See Site_info.csv for details on weeding in the establishment year. Margins between plots were sprayed to prevent stoloniferous ingression from neighbouring plots.

Year 1 was defined as the first complete year after sowing. Some sites took cleaning cuts in the year of establishment (prior to year 1), but data is not recorded for these cuts. See Site_info.csv for details on cleaning cuts.

Response variables:

The response variables included in the database are total biomass, biomass of the five harvest fractions (G1, G2, L1, L2, weed) and measurements of forage quality. Analyses of total plot biomass and biomass of weed species have been published in Kirwan et al. (2007), Lüscher et al. (2008), Frankow-Lindberg et al. (2009), Nyfeler et al. (2009, 2011) and Finn et al. (2013). An analysis of forage quality at 4 sites was published in Sturludóttir et al. (2013).

Total Biomass per plot

For each plot, biomass of aboveground vegetation was measured at each harvest. This was done by cutting the whole plot and determining the fresh weight of the 'whole plant material'. A subsample of this material was taken, its fresh weight determined and the material dried at 65°C to constant weight. From the dry weight of the sample the percentage dry matter was calculated. From this, the total dry matter yield for the plot (DM/m^2) was calculated from the fresh weight of the 'whole plant material'.

Biomass of the five harvest fractions (G1, G2, L1, L2, weed)

Biomass separation was done by one of the following two methods: (see Site_info.csv for method selected for each site). The harvests at which separate determination was carried out are given in biomass.csv.

A. Fixed quadrat: A fixed 50 x 50 cm^2 quadrat was established in the middle of each plot and cut (to the standard height) separately from the rest of the plot. The plant material in the quadrat was separated into the five basic fractions: G1, G2, L1, L2, weed and dried at 65°C to constant weight. The five fractions were weighed separately.
B. Grabbed sample: Several samples of biomass were taken by hand from the plot and mixed. A sub-sample of the mixture of minimum size 200 g fresh weight was taken. The sub-sample material was separated into the five fractions: G1, G2, L1, L2, weed, dried at 65°C to constant weight and each fraction weighed.

Note on indigenous plants of experimental species (G1, G2, L1, L2): In the mixture plots indigenous (not sown) G1, G2, L1 and L2 plants cannot be separated from the sown plants of

these species and so do not form part of the weed fraction. However, in each monoculture plot, indigenous plants of the other three species are included in weed.

Forage quality

The primary forage quality analysis was carried out at the Christian-Albrechts-Universität Kiel, Kiel, Germany. Additional analysis for four North European sites was carried out at Agriculture and Agrifood Canada at Levis, Canada. This analysis of samples from the North-European sites has been published in Sturludóttir et al. (2013). In addition, N concentration of bulk samples was locally analysed by 21 sites. Forage quality data is given in forage_quality.csv. Measurements are coded _K, _C or _L to indicate whether samples were analysed at Kiel, Canada or local laboratories.

Kiel analysis: Bulk samples (not separated into component species) were analysed for 17 sites. At seven of the sites, all plots were analysed. At ten sites, samples were analysed for 18 out of the 30 experimental plots (the 12 plots in the design co-dominated by two species were omitted). Separation of the forage into the five fractions was also considered for those particularly interested in the forage quality of the different functional groups. Separated samples were analysed for eight sites. Sample material of at least 5 g per sample was prepared by drying to a constant weight at 65°C and then grinding to pass through a sieve of 1mm mesh size. Near-infrared spectroscopy (NIRS) analysis was carried out to determine the dry matter percentage of nitrogen concentration (N), ADF (acid detergent fibre) NDF (neutral detergent fibre), ELOS (enzymatic soluble organic dry matter), and ash which represents the mineral content of the sample.

Canadian analysis: Bulk samples were analysed for four sites. Samples were analysed for all plots. Samples were dried and ground and then analysed using NIRS (FOSS NIRsystems 6500, Silver Spring, MD) to determine nitrogen concentration (N), acid detergent fiber (ADF), neutral detergent fiber (NDF), *in vitro* true digestibility (IVTD) and *in vitro* cell wall digestibility (IVCWD). The latter was calculated using the following equation: IVCWD = 1000 - [(1000 – IVTD)/(NDF/1000)].

Site description variables:

Climate data

Each site provided daily climate data for the duration of their experiment. Where possible, the climate data series begins on the sowing date of the experiment at each site. The variables recorded were precipitation (mm per day), minimum daily air temperature (°C), mean daily air temperature (°C) and maximum daily air temperature (°C). The climate data is contained in climate.csv.

Soil analysis

The soil analysis was carried out at Centre Tecnològic Forestal de Catalunya, Solsona, Spain. Composite soil samples were formed by combining samples from four plots. In each sampled plot a soil volume of 5 x 5 cm^2 per 15 cm depth was taken in a systematic manner, as follows. To avoid soil contamination by litter, the first 0.5 cm of litter-soil was removed. The composite sample was dried (temperature between 20 and 40^{o}C) over two or three days. The soil aggregates

were gently ground and passed through a 2 mm sieve, discarding the fraction >2 mm. A 300 g subsample was sent to the laboratory for analysis. The percent of sand, silt, fine silt, and clay were measured and the soil type classified. In addition, percent organic matter, soil carbonates, soil electrical conductivity and soil pH were measured, along with the concentrations of calcium, potassium, nitrate, magnesium, sodium and phosphorus.

Data set description

Data from individual sites was recorded in standardized data recording spreadsheets and then collated into a central database. Data was checked using numerical and graphical summary methods. Data range was checked for each variable and pivot tables were used to check counts of measurements. The datasets were manipulated and merged using the SORT, MERGE and DATA procedures in SAS 9.1 (SAS Institute Inc., Cary, NC, USA).

Descriptions and units of measurement for the columns of data are presented in the tables below. Site-level information is contained in the comma-separated-value data files named site_info.csv, climate.csv and soils.csv. Data relating to plot-level measurements are contained in the comma-separated-value data files named biomass.csv and forage_quality.csv. Note that in all files missing data values are represented by empty cells.

Column numbers, variable names and variable descriptions for file: site_info.csv

Column	Variable Name	Variable Description	Unit
1	SITE	Site ID number	
2	Country	Country	
3	Location	Location of site within country	
4	Institute	Institute responsible for site	
5	Contact Email	Contact email of individual responsible for site	
6	Lat_Deg	Location of site (Latitude degrees)	

7	Lat_Min	Location of site (Latitude minutes)	
8	Lat_NS	Location of site (Latitude North South)	
9	Long_Deg	Location of site (Longitude degrees)	
10	Long_Min	Location of site (Longitude minutes)	
11	Long_EW	Location of site (Longitude East West)	
12	Elevation	Elevation of site	m above sea level
13	Mixture Type	Seed mixture used: ME=Mid European, NE=Northern European, DM=Dry Mediterranean, MM=Moist Mediterranean, Other=Site specific mix	
14	G1 Species	Fast establishing grass species	
15	G1 Variety	Fast establishing grass variety	
16	G2 Species	Persistent grass species	
17	G2 Variety	Persistent grass variety	
18	L1 Species	Fast establishing legume species	
19	L1 Variety	Fast establishing legume variety	
20	L2 Species	Persistent legume species	
21	L2 Variety	Persistent legume variety	
22	Sowing Date	Date the plots were established	
23	Sowing Method	Method of sowing – drilled / hand sown	

24	P at sowing	P fertiliser applied at establishment	Kg ha^{-1}
25	K at sowing	K fertiliser applied at establishment	Kg ha^{-1}
26	N at sowing	N fertiliser applied at establishment	Kg ha^{-1}
27	Annual P	P fertiliser applied per annum	Kg ha^{-1}
28	Annual K	K fertiliser applied per annum	Kg ha^{-1}
29	Annual N	N fertiliser applied per annum	Kg ha^{-1}
30	Year 1 number of harvests	Number of harvests taken in the year 1 of the experiment (year after sowing)	
31	Year 2 number of harvests	Number of harvests taken in the year 2 of the experiment	
32	Year 3 number of harvests	Number of harvests taken in the year 3 of the experiment	
33	Year 4 number of harvests	Number of harvests taken in the year 4 of the experiment	
34	Harvest Height	Cutting height when taking harvests	cm
35	Method of separation	Method of selecting subsample of biomass for separation into species components	
36	Plot Size	Size of plots	m^2
37	Area Sampled for Total Yield	Area within plot that was sampled for total aboveground biomass	m^2

38	Area Sampled for Composition	Area within plot that was sampled for separation into species components (if fixed quadrat method was used)	m^2
39	Harvesting Method	Method used to harvest biomass (manually or by machine)	
40	Treatment details	Details of treatment(s) applied (where relevant)	
41	Cleaning cut date	Date of cleaning cut (if any)	
42	Weeding details	Details of any weeding undertaken during establishment	

Column numbers, variable names and variable descriptions for file: climate.csv

Column	**Variable Name**	**Variable Description**	**Unit**
1	SITE	Site ID number	
2	DAY	Day	
3	MONTH	Month	
4	YEAR	Year	
5	DATE	Date	
6	PRECIP	Daily precipitation	mm day^{-1}
7	AIR_MIN	Minimum daily air temperature	°C
8	AIR_MEAN	Mean daily air temperature	°C

9	AIR_MAX	Maximum daily air temperature	°C

Column numbers, variable names and variable descriptions for file: soils.csv

Column	Variable Name	Variable Description	Unit
1	SITE	Site ID number	
2	CARBONATES	Soil Carbonates	%
3	EC	Soil electrical conductivity	ds m^{-1}
4	SILT	Percent silt content in soil	%
5	SILT_FINE	Percent fine silt content in soil	%
6	CLAY	Percent clay content in soil	%
7	SAND	Percent sand content in soil	%
8	OM	Percent organic matter	%
9	SOIL_TYPE	Soil type	
10	HUMIDITY	Percent humidity	%
11	CA	Calcium concentration	ppm
12	K	Potassium concentration	ppm
13	N-NO3	Nitrate concentration	ppm
14	MG	Magnesium concentration	ppm
15	NA	Sodium concentration	ppm

16	P	Phosphorus concentration	ppm
17	PH	Soil pH	

Column numbers, variable names and variable descriptions for file: biomass.csv

Column	Variable Name	Variable Description	Unit
1	SITE	Site ID number	
2	COUNTRY	Country	
3	YEAR	Year	
4	YEARN	Experimental year number	
5	NH	Number of harvests – number of times the whole plot was cut in a year	
6	HARVEST	Harvest number (within year)	
7	HARVEST_DATE	Date of harvest	
8	PLOT	Plot number as per design (1-30 = core design; 31-48 = treatment plots; 49-68 = additional plots at sites 45 and 46)	
9	TREAT	Indicator variable: 1=basic 30 plots; 2 and 3=additional treatment plots (some sites implemented two levels of additional treatments)	
10	REP	Replicate number (applies only to sites 15, 45 and 46)	

11	G1	Initial sown proportion of fast-establishing grass	
12	G2	Initial sown proportion of persistent grass	
13	L1	Initial sown proportion of fast-establishing legume	
14	L2	Initial sown proportion of persistent legume	
15	E	Initial sown evenness	
16	DENS	Indicator variable: high=high level of initial sown biomass, low = low level (60%of high)	
17	G1_Y	Harvest Dry Matter Yield of fast-establishing grass	t ha^{-1}
18	G2_Y	Harvest Dry Matter Yield of persistent grass	t ha^{-1}
19	L1_Y	Harvest Dry Matter Yield of fast-establishing legume	t ha^{-1}
20	L2_Y	Harvest Dry Matter Yield of persistent legume	t ha^{-1}
21	WEED_Y	Harvest Dry Matter Yield of weed species	t ha^{-1}
22	HARV_YIELD	Total Harvest Dry Matter Yield	t ha^{-1}

Column numbers, variable names and variable descriptions for file: forage_quality.csv

Column	**Variable Name**	**Variable Description**	**Unit**
1	SITE	Site ID number	
2	COUNTRY	Country	
3	YEAR	Year	
4	YEARN	Experimental year number	
5	NH	Number of harvests	

6	HARVEST	Harvest number (within year)	
7	HARVEST_DATE	Date of harvest	
8	PLOT	Plot number as per design (1-30 = core design; 31-48 = treatment plots; 49-68 = additional plots at sites 45 and 46)	
9	TREAT	Indicator variable: 1=basic 30 plots; 2 and 3=additional treatment plots (some sites implemented two levels of additional treatments)	
10	REP	Replicate number (applies only to sites 15 and 45)	
11	G1	Initial sown proportion of fast-establishing grass	
12	G2	Initial sown proportion of persistent grass	
13	L1	Initial sown proportion of fast-establishing legume	
14	L2	Initial sown proportion of persistent legume	
15	E	Initial sown evenness	
16	DENS	Indicator variable: high=high level of initial sown biomass, low = low level (60% of high)	
17	LOCAL_N	Indicator variable (Local lab analysis present=1, absent=0)	
18	KIEL	Indicator variable (Kiel bulk sample present=1 , absent=0)	
19	CANADA	Indicator variable (Canada bulk sample present=1 , absent=0)	

20	KIEL_SEP	Indicator variable (Kiel separated sample present=1 , absent=0)	
21	N_L	Nitrogen percent in total harvest yield (analysis performed by local lab)	% of dry matter
22	N_K	Nitrogen percent in total harvest yield (Kiel data)	% of dry matter
23	ASH_K	Ash in total harvest yield (Kiel data)	% of dry matter
24	NDF_K	Neutral Detergent Fibre in total harvest yield (Kiel data)	% of dry matter
25	ADF_K	Acid Detergent Fibre in total harvest yield (Kiel data)	% of dry matter
26	CDOMD_K	Cellulase Digestible of Organic Matter of Dry Matter in total harvest yield (Kiel data)	% of dry matter
27	ME_K	Metabolizable Energy in total harvest yield (Kiel data)	MJ ME per kg of DM
28	N_C	Nitrogen percent in total harvest yield (Canadian data)	% of dry matter
29	NDF_C	Neutral Detergent Fibre in total harvest yield (Canadian data)	% of dry matter
30	ADF_C	Acid Detergent Fibre in total harvest yield (Canadian data)	% of dry matter
31	IVTD_C	In Vitro True Digestibility in total harvest yield (Canadian data)	
32	IVCWD_C	In Vitro Cell Wall Digestibility in total harvest yield (Canadian data)	
33	N_G1_K	Nitrogen percent in G1 harvest yield (Kiel data)	% of dry matter
34	ASH_G1_K	Ash in total G1 harvest yield (Kiel data)	% of dry matter

35	NDF_G1_K	Neutral Detergent Fibre in total G1 harvest yield (Kiel data)	% of dry matter
36	ADF_G1_K	Acid Detergent Fibre in total G1 harvest yield (Kiel data)	% of dry matter
37	CDOMD_G1_K	Cellulase Digestible of Organic Matter of Dry Matter in G1 harvest yield (Kiel data)	% of dry matter
38	ME_G1_K	Metabolizable Energy in G1 harvest yield (Kiel data)	MJ ME per kg of DM
39	N_G2_K	Nitrogen percent in G2 harvest yield (Kiel data)	% of dry matter
40	ASH_G2_K	Ash in G2 harvest yield (Kiel data)	% of dry matter
41	NDF_G2_K	Neutral Detergent Fibre in G2 harvest yield (Kiel data)	% of dry matter
42	ADF_G2_K	Acid Detergent Fibre in G2 harvest yield (Kiel data)	% of dry matter
43	CDOMD_G2_K	Cellulase Digestible of Organic Matter of Dry Matter in G2 harvest yield (Kiel data)	% of dry matter
44	ME_G2_K	Metabolizable Energy in G2 harvest yield (Kiel data)	MJ ME per kg of DM
45	N_L1_K	Nitrogen percent in L1 harvest yield (Kiel data)	% of dry matter
46	ASH_L1_K	Ash in L1 harvest yield (Kiel data)	% of dry matter
47	NDF_L1_K	Neutral Detergent Fibre in L1 harvest yield (Kiel data)	% of dry matter
48	ADF_L1_K	Acid Detergent Fibre in L1 harvest yield (Kiel data)	% of dry matter
49	CDOMD_L1_K	Cellulase Digestible of Organic Matter of Dry Matter in L1 harvest yield (Kiel data)	% of dry matter
50	ME_L1_K	Metabolizable Energy in L1 harvest yield (Kiel data)	MJ ME per kg

			of DM
51	N_L2_K	Nitrogen percent in L2 harvest yield (Kiel data)	% of dry matter
52	ASH_L2_K	Ash in L2 harvest yield (Kiel data)	% of dry matter
53	NDF_L2_K	Neutral Detergent Fibre in L2 harvest yield (Kiel data)	% of dry matter
54	ADF_L2_K	Acid Detergent Fibre in L2 harvest yield (Kiel data)	% of dry matter
55	CDOMD_L2_K	Cellulase Digestible of Organic Matter of Dry Matter in L2 harvest yield (Kiel data)	% of dry matter
56	ME_L2_K	Metabolizable Energy in L2 harvest yield (Kiel data)	MJ ME per kg of DM
57	N_WEED_K	Nitrogen percent in weed species harvest yield (Kiel data)	% of dry matter
58	ASH_WEED_K	Ash in weed species harvest yield (Kiel data)	% of dry matter
59	NDF_WEED_K	Neutral Detergent Fibre in weed species harvest yield (Kiel data)	% of dry matter
60	ADF_WEED_K	Acid Detergent Fibre in weed species harvest yield (Kiel data)	% of dry matter
61	CDOMD_WEED_K	Cellulase Digestible of Organic Matter of Dry Matter in weed species harvest yield (Kiel data)	% of dry matter
62	ME_WEED_K	Metabolizable Energy in weed species harvest yield (Kiel data)	MJ ME per kg of DM

DATA-USE POLICY

The data presented here are publicly available. Those wishing to publish results from this data set should read this metadata document. The data set should be cited as: Kirwan et al. 2014. The Agrodiversity Experiment: three years of data from a multi-site plant diversity experiment in intensively managed grasslands. Ecology xx:xxx.

Three papers are currently in preparation, focusing on a) the effect of diversity on the contribution of weed species to biomass yield b) changes in the relative abundances of the mixtures and c) grassland biodiversity effects across an environmental gradient.

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