



## **DIVERSify: Designing Innovative plant teams for Ecosystem Resilience and agricultural Sustainability**

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**Project Co-ordinator:** Dr Alison Karley, JHI

**Tel:** +44 (0)1382 568820

**Email:** [Alison.Karley@hutton.ac.uk](mailto:Alison.Karley@hutton.ac.uk)

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**Lead Author:** Lars Pødenphant Kiær (UCPH)

**Contributing authors:** Christoph Scherber (ZFMK), Silvia Pappagallo (ZFMK), Jana Brandmeier (ZFMK), Martin Weih (SLU), Stefano Tavoletti (UNIVPM), Diego Rubiales (CSIC), Ángel Villegas-Fernández (CSIC), Eveline Adam (SZG), Sebastian Raubach (JHI), Paul Shaw (JHI), Adrian Newton (JHI), Alison Karley (JHI)

**Reviewers:** M. Carlota Vaz Patto (ITQB), Joëlle Fustec (ESA)



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### **Executive Summary**

A comprehensive database of crop traits in monocultures and intercrops or ‘plant teams’ has been assembled from data collected from experimental trials in the DIVERSify project. Within the trials, trait data have been collected for cereal, legume, herb and grassland species grown in plant teams and monocultures under different environmental and pedo-climatic conditions. The report summarises how the database was constructed by collating and aligning trial data and metadata provided by partners in standardised templates. Storage, further development and use of the database in DIVERSify outputs is described, along with details about how the database is being made available to the scientific community as an open access data resource.





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## 1. Background

In the DIVERSify project, a central trait database is maintained containing data on crop traits across different plant species and cultivars when grown together as intercrops or ‘plant teams’. The database contains data collected within the consortium with a specific focus on crop traits measured in plot-scale field experiments in Work Package 2 (Ecological Approach to identify mechanisms and traits for optimised plant teams). Trait data was collected according to standardised protocols (Kiær et al. 2020) from co-ordinated field trials summarised in Scherber et al. (2019). The main aim of the database is to store all measured trait values for monocultures and plant teams under high- vs. low-intensity management. The first version of the database on crop traits - of plants mainly grown in individually or in monocultures - was assembled from existing open-access data (Scherber 2017). This report summarises how trait data collected from field trials is being used to develop a DIVERSify database of plant traits in monocultures and plant teams.

## 2. Data sources

### 2.1. Field trials

Trait data were collated from a large number of legume-cereal intercropping field trials established across seven countries and four pedoclimatic regions of Europe (**Table 1**; photos of example trials are shown in **Appendix 1**).

Coordination of field activities is crucial for evaluating trait and performance data from parallel field trials across sites and/or years, such as those operated in the DIVERSify project. For this purpose, we developed, for WP2 trials, a set of 47 standardized protocols for trait assessment distributed across six categories: Phenology, Morphology, Physiology, Reproduction, Yield and post-harvest, and Non-crop biodiversity. For each trait included in the handbook, method(s) of collection and units were described, and a standard name reported. To ensure that a minimum dataset was collected, given the high number of possible measurements, traits were classified as ‘essential’ (representing minimum basic data required to achieve project goals) or ‘useful’ (providing valuable additional data).

These protocols for field measurements of plant traits have been collated into a 110pp handbook with Introduction, References, and Appendices (Kiær et al. 2020) and made publicly available at the project legacy website ([www.plant-teams.org](http://www.plant-teams.org)). Besides increasing the quality of the dataset and acting as documentation for the many field assessments, it is a tool for improving future coordinated field assessments.

### 2.2. Online repositories

Using open-source software and online databases, we developed a toolset to set up and query a scalable plant trait database to be used within DIVERSify and elsewhere for the conception of





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complementary plant teams. This was used to construct a ‘virtual’ database by collating traits of species (individual plants or in monoculture stands) using publicly available trait databases (Scherber, 2017). The database is implemented in the open-source software package R (R Core Team 2017) and RStudio (RStudio Team 2017), using the TR8 library (Bocci 2015) to query plant traits across publicly available databases (Scherber 2017). We successfully extracted information for 25 numeric traits across 128 European grassland and cropland species from nine online data sources. Trait data were collated for most cereal, legume, herb and grassland species currently utilised in plant teams across Europe. The database and associated R scripts are stored both locally at ZFMK/WWU on a RAID system and on a network folder with mirror copies distributed across different server locations.

### 3. Harmonisation and management of data

Data from multiple field trials must be harmonised and documented to facilitate proper merging, analysis and sharing of datasets. More and more datasets are being shared online. However, accessibility and practical use of these datasets is encumbered by the fact that many of them lack clear semantics and metadata standardization, and existing data reporting tools (e.g. from biodiversity experiments) are inadequate to fully accommodate the specificities of intercropping data. This represents a major barrier to exchange of data on crop mixtures. Therefore, a robust approach was developed to increase consistency and quality of collated field trial data.

Data generated by partners was reported using a ‘Data Template’, a standardized Microsoft Excel file designed to accommodate intercropping data. To facilitate dataset handling, data were reported on standardised spreadsheets in a specified format (see Pappagallo et al. 2021), using standardised trait names and units of measurement. This template is not yet available as an open access resource, but it could form part of an open access publication in the future and it has been shared with partners in the ReMIX project (sister project to DIVERSify) as a resource for data collation.

Plot experiments generated a total of 24 datasets for 2017 and 2018 trials. Once these were returned by partners, datasets were first screened for errors, formatting was checked, and partner-specific differences were harmonized, described in Pappagallo et al. (2021). Formatting steps were documented using the open-source software R (version 3.6.3, R Core Team 2020) implemented in RStudio (version 1.3.959). Data formatting mainly required name and descriptors standardisation (especially among variables that were partially overlapping), and screening for evident errors and outliers. During the formatting work, two catalogues were developed. A ‘data overview’ summarized and kept track of correspondence between partner, trial type and level at which traits were measured in each year (**Figure 1**), whereas a ‘trial master’ spreadsheet was created to track metadata from all partners and years. These files have also been structured by ‘TrialID’, which enables linking to the data files for analysis. Datasets were ultimately merged according to sampling level (plot, species and individual level). Aggregated versions of all levels to plot or species level scale may also be created for analyses (Pappagallo et al. 2021).





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This intensive work generated a fully merged version of plot and species level data. In total, 61 traits were collected in year 1 (2017) trials by at least one partner, and 58 traits were collected by at least one partner in year 2 (2018) trials, out of a total of 118 reported traits. Of these, 13 traits were reported by most partners, allowing a good analytic framework to be set up across partner datasets.

DIVERSify Data Overview 2018 *for legend scroll to right*		standard crop combinations Faba-Wheat Trial						other crop combinations Faba bean-Oat Faba bean-Grass pea Dunlum wheat-Faba			standard crop combinations Pea-Barely Trial						other crop combinations Common bean-Runner bean/ Common bean-Corn/ Common bean-	COUNT total entries	COUNT entries plot level (3)	COUNT entries species level (2)	COUNT entries individual level (1)	MAX level		
Abbreviation	Importance	CSCS	JHI	SLU	SZG	UCPH	UNIVPM	WWU	SZG2	SZG3	UNIVPM2	CSCS2	JHI2	SLU2	UCPH2	UNIVPM22	WWU2	SZG4						
arthropod.abundance.perplant									1											1	0	0	1	1
biomass.gm2	core	2	2	2	2	2				2	2			2	2	2				10	0	10	0	2
canopy.height.cm	core	3	2	2	2	2	2	3	2	2			3	2	2	2	3			13	4	9	0	3
canopy.reflectance.NDVI		3				3							3							3	3	0	0	3
cover.perc	core	2	3	2	3			3	2	2			2	3	2		3			11	5	6	0	3
crop.respiration																				0	0	0	0	0
days.to.maturation	core				2					2	2									3	0	3	0	2
disease.percentage.perplant		3	2					1					2	2	2					7	1	4	2	3
disease.score		2						2					2				2	1		4	0	4	0	2
ears.pods.m2								2	1	2	2						2	1		7	0	5	2	2
flowering.date.numeric	core			2	2	2				2	2			2	2				7	0	7	0	2	
fodder.quality		3																		1	1	0	0	3
grainyield.gm2	core	2		2				2	2	2			2				2			7	0	7	0	2
grainyield.tha	core			2	2	2	2	2					2	2	2	2	2			9	0	9	0	2
growth.habit		2	2							2	2			2						5	0	5	0	2
growth.stage	core	2	2	2			2	2	2	2			2	2	2		2	2		12	0	12	0	2
herbivory.percent		2											2							4	0	2	2	2

Figure 1. Screenshot of one of the data overview files created to provide an overview of which traits were measured by which project partner at which level.

## 4. Overview of trait data

### 4.1. Field trial database

#### 4.1.1. Structure

The database contains 97,620 registrations made in a total of 30 combinations of plant teams in field trials carried out across two years in seven European countries: Austria, Denmark, Germany, Italy, Spain, Sweden, and Scotland (Table 1). It represents a total of 239 treatment combinations of site, year, input level, crop(s), and seeding rate(s), deriving from 3,732 field plots. The database currently includes a total of 15,173 entries at plot level, and 39,452 entries at species level.

The database consists of three files: Trial metadata, Plot data, and Species data. Each registration on plot or species level is affiliated with date, PlotID and TrialID, allowing the files to be linked.

Each field trial has been assigned a unique trial ID and each physical field plot has been assigned a unique plot ID, allowing tracking and analysis across time and registrations.

Trial metadata describe characteristics of the trial site (e.g. country, name and geographical coordinates), environmental conditions (e.g. weather sums, management/input level and seeding rate), and experiment (e.g. design, replicates and plot size).





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**Table 1.** Intercrops of six legume species: Faba bean (F), Common bean (C), Runner bean (R), Pea (P), Grass pea (G), Lentil (L), and five cereal species: Wheat (W), Barley (B), Oat (O), Maize (M), Sorghum (S).

Zone	Country	Partner	2017	2018
Nemoral	Sweden	SLU	F-W, P-B	F-W, P-B
Atlantic	Denmark	UCPH	F-W, P-B	F-W, F-O, P-B
Atlantic	UK	JHI	F-W, P-B	F-W, F-O, P-B, L-B
Continental	Austria	SZG	F-W, F-O, F-G, C-M, R-M, C-S, R-S	F-W, F-O, F-T, F-G, C-M, R-M, C-S, R-S
Continental	Germany	WWU	F-W, P-B	F-W, P-B
Mediterranean	Spain	CSIC	F-W, P-B	F-W, P-B
Mediterranean	Italy	UNIVPM	F-W, F-D, P-B	F-D, P-B

### 4.1.2. Plant teams and varieties

A total of 11 different plant teams are currently included in the database, encompassing combinations of six legume species and five cereal species (**Table 2**).

**Table 2.** Number of included varieties for each crop species.

Crop species	No. varieties
Pea	14
Faba bean	9
Common bean	3
Lentil	2
Grass pea	1
Runner bean	1
Barley	15
Wheat	11
Oat	5
Maize	2
Durum wheat	2
Sorghum	1
Triticale	1

### 4.1.3. Plant traits

The field trial database contains 169 uniquely named traits, describing standard agronomic performance parameters (e.g. harvested grain/biomass yield, seed quality measures, lodging), plant growth and development traits (e.g. tillering, branching, plant height, time to flowering, specific leaf area), and characteristics arising from biotic interactions (e.g. disease incidence, weed cover, herbivore damage) (**Figure 2**). Some of the traits are relevant to all the crop species assessed in the

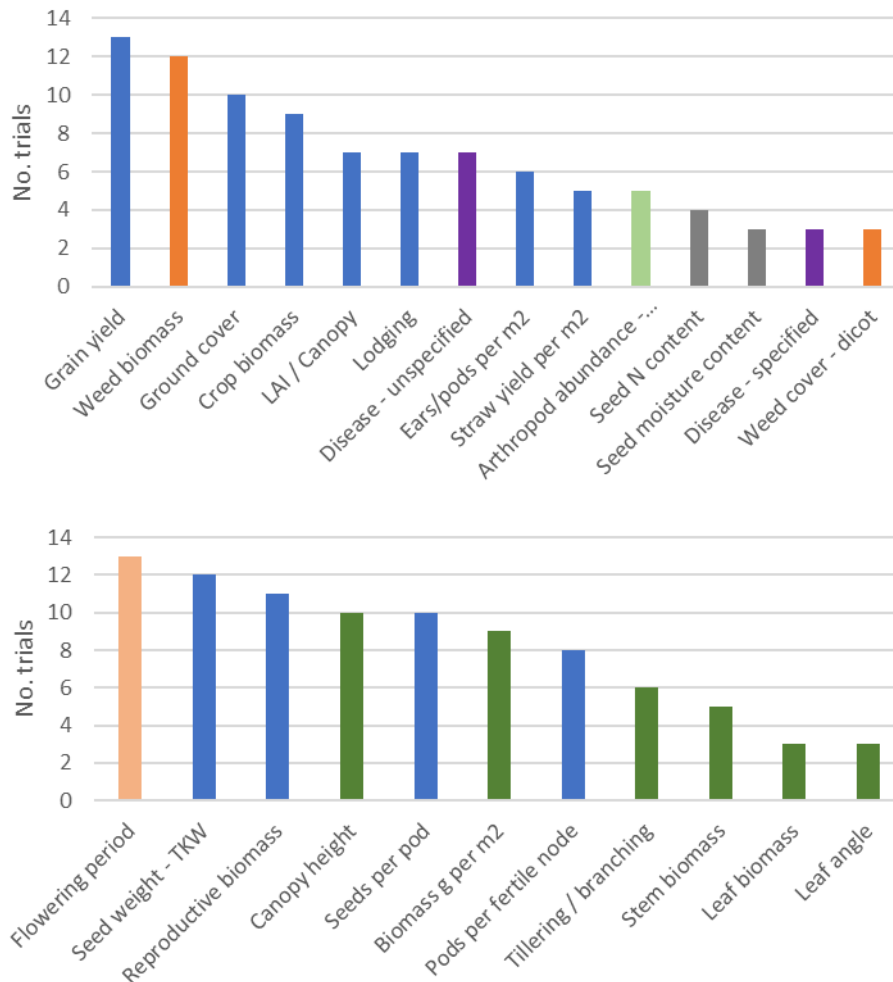






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trials, while others are crop species-specific observations, like fungal diseases or insect pests. In total, more than 40 traits or trait groups are found in the database.



**Figure 2.** Summary of plant traits collected for wheat-faba bean plant teams in the DIVERSify trait database.

## 5. Database storage and accessibility

The trait database is stored on a OneDrive site hosted by WWU/ZFMK, with duplicate copies held at JHI (see below) and UCPH. The original datasets are stored on servers of the partners who generated the data and on a SharePoint site at JHI.

### 5.1. Online repositories

The database is being made publicly available with open access under the Creative Commons license CC BY-NC-SA, via the DIVERSify community at zenodo.org ([link](#)), following an embargo period until 31<sup>st</sup>





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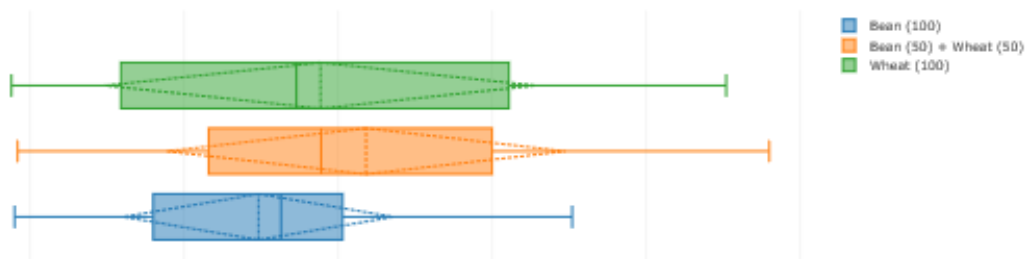
March 2023 (latest date) to allow time for project publications, although the database will be released sooner if database-associated publications are released quickly.

The database, in whole or part, will be uploaded to other repositories (e.g. dryad and/or PANGAEA) when used to support open access publications, depending on the journal requirement; the uploaded database will be registered in online registries (such as OpenAIRE and re3data.org). A scientific paper is being prepared, providing further details on the structure and querying of the dataset (Pappagallo et al., in prep).

### 5.2. Visualisation

Visualisation is a powerful approach in data exploration, helping to uncover correlations, clustering and other hidden knowledge in data. Hence, DIVERSiplotter was developed as an online tool to allow users to explore and interact with intercropping field trial data collected as part of the scientific field trials of the DIVERSify project (**Figure 3**, **Figure 4**). This expandable platform is freely available online (<https://ics.hutton.ac.uk/diversify/#/>). It currently includes integrated data for 94 traits, 11 crop species, and 48 varieties distributed among three intercropped plant teams and seven countries across Europe. Details of the tool development and use are described in Raubach et al. (2021) and Brooker et al. (2021).

#### Canopy reflectance

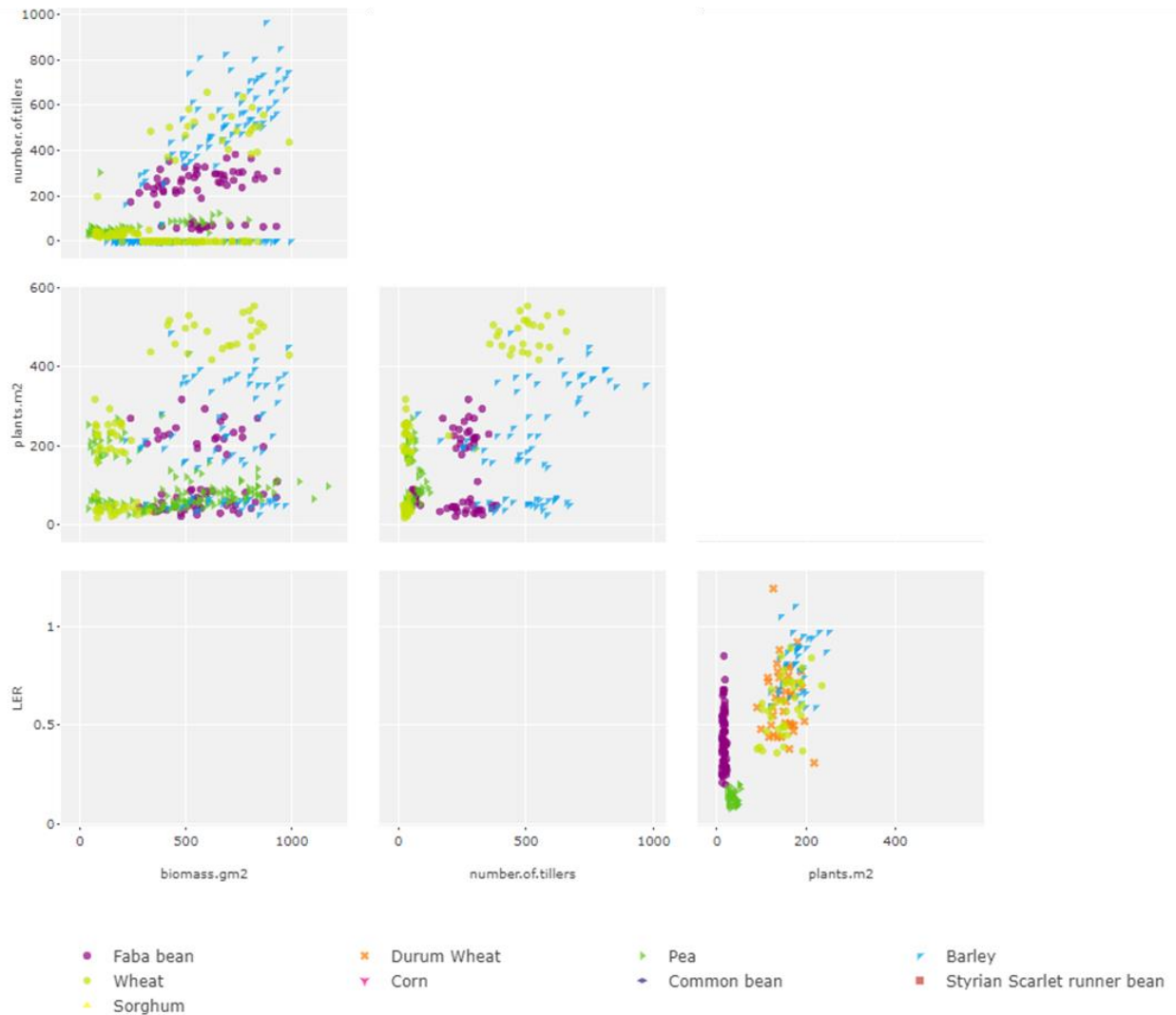


**Figure 3.** Example of species-level trait data visualization using DIVERSiplotter: Distributions of data on canopy reflectance for faba bean and spring wheat monoculture and plant teams.





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**Figure 4.** Example of individual-level data visualization using DIVERSiplotter: Scatter matrix of four trait variables (plants per m<sup>2</sup>, number of tillers per plant, biomass in gm<sup>-2</sup>, Land Equivalent Ratio - LER) plotted against each other to highlight correlations, clusters, and outliers in the data.

## 6. Outlook

The crop trait data collected in DIVERSify so far represent a unique collection at unprecedented resolution across European partners and pedo-climatic conditions. Data collected can be used for dissemination activities in scientific manuscripts and recommendations of traits suitable as breeding targets for plant team cropping. The trait database is made openly accessible via the project Zenodo site and other open access repositories. Future developments include incorporating trait data





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collected from DIVERSify WP2 trials conducted in 2019. The database could also be expanded to include trait data from individual plants/monoculture stands collected in the 'virtual' trait database and from additional phenotyping trials of crop species in monoculture that were conducted in DIVERSify to extend the range of species-level trait data available.

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## Appendix 1

Supplementary images of some of the plant teams trials conducted by DIVERSify partners.

**Figure S1.** Plots of the barley/pea intercropping experiment showing monocrops and intercropping (CSIC, April 2018).



**Figure S2.** Plots of the barley/pea intercropping experiment showing monocrops and intercropping (CSIC, April 2018).





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**Figure S3.** Images of the UNIVPM durum wheat-faba bean field trial in April 2018 (top) and in May 2018 (bottom).







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**Figure S4.** Barley-pea trial at UNIVPM in April (top) and June (bottom) 2018.

