Data Article

Meta-analysis dataset of soil extracellular enzyme activities in intercropping systems

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A R T I C L E   I N F O

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A B S T R A C T

This dataset accompanies the meta-analysis entitled “Intercropping increases soil extracellular enzyme activity: A meta-analysis” Curtright and Tiemann (2021). Sustainable agriculture practices often aim to increase plant diversity. One means of doing this is through intercropping, where two or more plants are grown in the same field at the same time. Aboveground plant diversity may result in changes to the functioning of belowground microbial communities. Soil enzyme activities are frequently used as indicators of soil health and descriptors of soil nutrient cycling. While some studies have described the effect of intercropping on soil enzyme activities, results vary widely. To assess the overall effect that intercropping has on soil enzyme activities and describe the largest sources of variation, we performed a global meta-analysis of all studies found in the literature reporting enzyme activities in an intercropping system. Data were collected using exhaustive keyword searches on studies published through January 2021. We provide here a dataset of 969 observations across 100 studies. In addition to average enzyme activities in intercropping, metadata on environmental, edaphic, and agronomic properties were also collected.

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Specifications Table

| Subject                  | Agricultural Microbiology |
|--------------------------|---------------------------|
| Specific subject area    | Plant diversity, enzyme activities |
| Type of data             | Table                     |
| How data were acquired   | Systematic literature search and data extraction |
| Data format              | Raw                       |
| Parameters for data collection | Search terms in ISI Web of Science (all databases): (intercrop* OR interseed*) AND (enzyme OR urease OR *sidase OR protease OR *terase OR *genase OR sucrase OR *olase OR *ulase OR *idase OR *ulase)

Met following criteria:
1. had an intercropping treatment with control
2. was an agricultural system
3. measured the activity of at least one soil extracellular enzyme

Description of data collection

Data were extracted from published studies. If data were only presented in graphs or plots, numeric values were obtained using WebPlotDigitizer [2].

Data source location

Global, majority of studies happened to be located in Asia while very few were from North America or Europe

Data accessibility

With the article

Related research article

A.J. Curtright, L.K. Tiemann, Intercropping increases soil extracellular enzyme activity: A meta-analysis, Agric. Ecosystems and Environ. 319 (2021),
doi:10.1016/j.agee.2021.107489. [1]

Value of the Data

- This dataset compiles nearly 1000 observations across 100 studies reporting the effect of intercropping on soil enzyme activities. Associated metadata are included in a standardized form with common units.
- Data will assist those interested in determining how plant diversity in agricultural systems affects soil enzyme activities.
- Data are available for meta-analysis and for identifying literature gaps (e.g. studies in North America are currently underrepresented) that would benefit from additional original research.

1. Data Description

Table S1: Dataset of 969 observations across 100 studies reporting the effects of intercropping on soil enzyme activities. The dataset includes studies published through January 2021. Each observation includes data for a pair of control and treatment groups. Control groups contained a “main crop” grown in monoculture. The paired treatment group included the “main crop” as well as one or more “intercrops”. Soil enzyme data are provided in the units presented in the study and were used to calculate a unitless response ratio for meta-analysis. The response ratio indicates the relative increase (or decrease) in enzyme activity of the intercropping treatment relative to the monoculture control. For each observation, environmental, edaphic, and agro-nomic information as well as publication details are provided, if available.

Table S2: Description of the column names used in Table S1.

2. Experimental Design, Materials and Methods

Data were obtained through a systematic literature review. Studies were located using ISI Web of Knowledge using the following search terms: (intercrop* OR interseed*) AND (enzyme OR urease OR *sidase OR protease OR *terase OR *genase OR sucrase OR *olase OR *ulase OR
Abstracts were screened to find papers that met the following criteria: 1) had an intercropping treatment with a paired monoculture control, 2) was an agricultural system, which included agroforestry, and 3) measured the activity of at least one soil extracellular enzyme. Studies published through January 2021 were included. The workflow of the literature review and meta-analysis is presented in Fig. 1.

Fig. 1. PRISMA flow diagram adapted from Moher et al. [9], describing the workflow of the review and meta-analysis process.
Enzyme activities as well as associated metadata were extracted from the studies. If data were only reported on graphs, the values were extracted using WebPlotDigitizer [2]. Within studies, independent observations were considered as unique combinations of an enzyme activity and intercropping pair. To ensure independence of observations, only one observation per year, per enzyme, per study was included in the meta-analysis, even if multiple observations were provided in the original study. When multiple observations over the course of a year were reported, an averaged value was used.

Enzyme activity was collected as the reported average and variation. All variation data were converted to standard deviation for meta-analysis. If only mean separations were reported, standard deviations were back calculated from the smallest significant difference, using the indicated group size, significance level, and multiple-comparisons correction method. If no multiple-comparisons correction was specified, means were assumed to have been separated by Fisher’s LSD (which would result in the most conservative back-calculated estimate of the standard deviation). If studies were missing data on variation, authors were contacted. If standard errors or standard deviations could not be obtained, either in the paper or upon contact, standard deviations were imputed based on the average CV of the remaining dataset [3].

Metadata associated with each study were also extracted and these included: latitudinal zone, type of experiment (greenhouse or field), mean annual precipitation, mean annual temperature, soil texture (% clay, % silt, % sand), pH, soil organic matter, soil organic carbon, total N and P, available N and P (i.e. extractable inorganic N or P), N fertilizer amount, P fertilizer amount, plant biomass or yield, length of study, sample type (rhizosphere or bulk soil), sampling depth, main crop, intercrop, and microbial biomass. Methodological information was also extracted, including general information on the enzyme assay protocol and whether fresh or air-dried soil was used.

Data were collected in two rounds: initial and during revision. The initial dataset contained publications published before early 2018. Upon revision of the manuscript, the dataset was updated with all studies published through January 2021. For the first round of studies, if soil textural data was not reported in the study, this information was obtained from other studies reported from the same field site or from the Harmonized World Soil Database v1.2 [4].

Response ratios were calculated for enzyme activity, plant biomass/yield, and microbial biomass carbon. These calculations were performed using OpenMEE (Build Date: 2015-11-15), an open source software platform that provides a graphical user interface built around the metafor R package [5]. Response ratios were calculated in OpenMEE for each observation by taking the natural log of the average values ($\bar{x}$) of the monocrop (control) and intercrop treatments, as described in Formula 1. For enzyme activity and microbial biomass carbon, the variance for the response ratio was calculated according to Formula 2.

$$RR = \ln \frac{\bar{x}_{inter}}{\bar{x}_{mono}}$$

$$var(RR) = \frac{SD_{mono}^2}{n_{mono} \times \bar{x}_{mono}^2} + \frac{SD_{inter}^2}{n_{inter} \times \bar{x}_{inter}^2}$$

Enzymes were categorized prior to performing meta-analysis. We categorized enzymes based on the type of substrate they react with or the nutrient that is released with activity. Hydrolytic C enzymes are those that target relatively easy to access forms of C with a regularly repeating polymeric structure (invertase, cellulase, cellobiohydrolase, $\beta$-glucosidase, and $\beta$-xylosidase); oxidative C enzymes included peroxidase, phenoloxidase, and polyphenoloxidase; N enzymes included N-acetyl-glucosaminidase, proteases, peptidases, and urease; P enzymes included both alkaline and acid phosphatases as well as phytase. A “general” category of enzymes was also included for enzymes routinely used as indicators of overall microbial activity but not associated with the acquisition of particular nutrients [6–8]. This category included dehydrogenase and catalase as well as fluorescein diacetate (FDA) degradation activities.

To determine the role of plant type on the intercropping effect, we grouped observations according to the type of plant used as the main crop (or monocrop) and the intercrop. In our
analysis, each observation consisted of a treatment (i.e. a main crop grown with an intercrop) compared to a control (i.e. the main crop grown in monoculture). Accordingly, the main crop was defined as the crop that was grown in monoculture in the control group. Any particular species of plant could therefore be considered as the main crop or intercrop depending on how it was used in the study. For example, if the intercrop treatment included maize grown with soybean and the control group was only maize, then maize would be considered the main crop and soybean the intercrop. On the other hand, if the intercropped treatment was compared to a control group consisting of soybean by itself, then maize would be considered the intercrop and soybean the monocrop. These treatment designations were defined according to the crops grown during the growing season(s) reported by the study. Additional elements of diversity, such as the use of rotations, were not specifically included in our analysis.

Plants were grouped according to the following categories: the grasses category included grains as well as forage grasses; legumes included pulses, oilseeds, and forages; woody species included shrubs and trees; the forbs category included non-woody plants that did not fall into the grasses or legumes categories. The same categories were used to group main crops and intercrops.

Meta-analysis and sub-group comparisons were also performed in OpenMEE, using the following options-Analysis Method: Continuous random-effects; Random-Effects Method: DerSimonian-Laird; Confidence Level: 95.0%. Meta-regressions, also in OpenMEE, were performed with the following options-Model Type: Random effects; Random-Effects Method: Restricted maximum likelihood estimator; Analysis Type: Parametric; Confidence Level: 95.0%.

**Ethics Statement**

The authors declare that this submission follows the ethical requirements for publication in Data in Brief.

**CRediT Author Statements**

**Andrew J. Curtright:** Conceptualization, Formal analysis, Investigation, Writing – review & editing, Writing – original draft, Visualization; **Lisa K. Tiemann:** Conceptualization, Writing – review & editing, Writing – original draft.

**Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.

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**Supplementary Materials**

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.dib.2021.107284.
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