
Automatic report

Study ID: Yi_Zou_Brassica_napus_China_2015

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Number of sites: 18 Year of sampling: 2015 Crop: Brassica napus

Variety: There are missing varieties (given 0 out of 18).

Location: Full information.

Country: All reported countries are OK.

Field size: Full information.

Management: Full information.

Sampling period: There are missing sampling periods.

Richness: Full information.

species groups considered: all visitors considered. Data was obtained by using pantraps

Abundance: There are missing values (given 0 out of 18).

Visitation rate units: NA

Visitation rate: There are missing values (given 0 out of 18).

Yield units: Fruit set (%) Yield: Full information.

Alternative yield units: Seed set Alternative yield: Full information.

Queries

Instructions: Please, edit this file and answer the following queries within the document, one by one. Then send the edited 'Summary_report_and_queries' (with your comments) and your 'Data_ownership' (excel) file to alfonso.allen.perkins+observdataset@gmail.com before the 20th of July.

- Please check that credit information is correct and add the corresponding affiliations and acknowledgements/funding information in your 'Data_ownership' (excel) file.
- If your study is already published, please check that its DOI is correct.
- If possible, please provide the names of missing crop varieties.

- If possible, please provide the sampling start month and sampling end month for each field, respectively, and use a numeric format (for example, 1 for January, 2 for February and so on).
- There are sites without abundance records. Please, check that such information is correct. See also the information about OBServ data processing in your 'First read me General report' pdf file.
- There are sites without visitation rate records. Please, check that such information is correct. See also the information about OBServ data processing in your 'First read me General report' pdf file.
- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.