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Automatic report
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Study ID: Jeroen_Scheper_Helianthus_annuus_France_2015

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Credit: Jeroen Scheper (WUR), David Kleijn (WUR), Isabelle Badenhauer (CEBC-CNRS), Vincent Bretagnolle (CEBC-CNRS), Ignasi Bartomeus (EBD-CSIC), Carlos Zaragoza-Trello (EBD-CSIC)

Publication: NA

Number of sites: 24

Year of sampling: 2015

Crop: Helianthus annuus

Variety: There are missing varieties (given 0 out of 24).

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: No taxa restrictions have been identified.

Abundance: Full information.

Visitation rate units: NA

Visitation rate: There are missing values (given 0 out of 24).

Yield units: seed set (number of full seeds per flowerhead)

Yield: Full information.

Alternative yield units: NA

Alternative yield: NA

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Queries
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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+observeddataset@gmail.com before the 20th of July.

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• 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 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 our information about the species groups considered is correct.
- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.