
Automatic report

Study ID: Hajnalka_Szentgyorgyi_Fagopyrum_esculentum_Poland_2005

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Credit: Hajnalka Szentgyorgyi

Publication: 10.1016/j.agee.2009.05.001

Number of sites: 6 Year of sampling: 2005

Crop: Fagopyrum esculentum

Variety: There are missing varieties (given 0 out of 6).

Location: There are missing locations (given 0 out of 6).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 6).

Management: Full information.

Sampling period: Full information.

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 6).

Yield units: kg/ha

Yield: There are missing values (given 4 out of 6).

Alternative yield units: NA

Alternative yield: NA

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 area of each field [in hectares].

- If possible, please provide the latitude and longitude of the missing locations [in decimal degrees].
- 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.
- There are sites without yield. Please, check that such information is correct. If possible, please provide the missing values (or the corresponding z-scores).
- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.