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Automatic report

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Study ID: Hisatomo\_Taki\_Fagopyrum\_esculentum\_Japan\_2008

Contact: htaki@affrc.go.jp

Credit: Hisatomo Taki, Forestry and forest products research institute

Publication: 10.1111/j.1744-7348.2009.00326.x/10.1016/j.baae.2010.08.004

Number of sites: 17 Year of sampling: 2008

Crop: Fagopyrum esculentum

Variety: There are missing varieties (given 0 out of 17).

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 17).

Yield units: seed set
Yield: Full information.
Alternative yield units: NA
Alternative yield: NA

## 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+observdataset@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.