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Automatic report
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Study ID: Rachael_Winfree_Citrullus_lanatus_USA_2010

Contact: rwinfree@rutgers.edu

Credit: Rachael Winfree, Neal M. Williams, Jonathan Dushoff, and Claire Kremen

Publication: 10.1111/j.1461-0248.2007.01110.x

Number of sites: 18

Year of sampling: 2010

Crop: Citrullus lanatus

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

Location: Full information.

Country: All reported countries are OK.

Field size: There are missing field sizes (given 0 out of 18).

Management: Full information.

Sampling period: Full information.

Richness: There is not enough taxonomic resolution to estimate richness.

species groups considered: NA

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

Visitation rate units: visits per flower per time

Visitation rate: Full information.

Yield units: NA

Yield: NA

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+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 area of each field [in hectares].

- 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.

- According to our raw data, there is not enough taxonomic resolution to estimate richness. 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.