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Automatic report

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Study ID: Saul\_A\_Cunningham\_Annona\_squamosa atemoya\_Australia\_2001

Contact: saul.cunningham@csiro.au

Credit: Rosalind Blanche, and Saul A. Cunningham

Publication: 10.1603/0022-0493-98.4.1193

Number of sites: 9 Year of sampling: 2001

Crop: Annona squamosa atemoya

Variety: There are missing varieties (given 0 out of 9).

Location: Full information.

Country: All reported countries are OK.

Field size: There are missing field sizes (given 0 out of 9).

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 9).

Visitation rate units: Insects per flower

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.