The triadic comparison of technology options data from XX on-farm experimental trials in YY countries

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# Abstract

The triadic comparison of technologies (tricot) is a citizen science approach for testing technology options in their target environments, which has been applied to on-farm testing of crop varieties. ‘Triadic’ refers to the sets of three technology options that are compared by each participant. In the approach, participants are invited to test a anonymous set of three technologies (out of a larger number, generally between 5 to 20) randomly assigned. […] Between 2011 and 2023 the tricot approach was applied in XX countries in Central America, Sub-Saharan Africa and Asia with YY crops.

# Background & Summary

700 words maximum The Background & Summary should provide an overview of the study design, the assay(s) performed, and the data generated, including any background information needed to put this study in the context of previous work and the literature, and should reference literature as needed. The section should also briefly outline the broader goals that motivated collection of the data, as well as their potential reuse value. We also encourage authors to include a figure that provides a schematic overview of the study and assay(s) design.

# Methods

The Methods should include detailed text describing any steps or procedures used in producing the data, including full descriptions of the experimental design, data acquisition assays, and any computational processing (e.g. normalization, image feature extraction). See the detailed section in our submission guidelines for advice on writing a transparent and reproducible methods section. Related methods should be grouped under corresponding subheadings where possible, and methods should be described in enough detail to allow other researchers to interpret and repeat, if required, the full study. Specific data outputs should be explicitly referenced via data citation (see Data Records and Citing Data, below). Authors should cite previous descriptions of the methods under use, but ideally the method descriptions should be complete enough for others to understand and reproduce the methods and processing steps without referring to associated publications. There is no limit to the length of the Methods section.

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Tables should be used to support the data records, and should clearly indicate the samples and subjects (study inputs), their provenance, and the experimental manipulations performed on each. They should also specify the data output resulting from each data-collection or analytical step, should these form part of the archived record.

# Technical Validation

The Technical Validation section should present any experiments or analyses that are needed to support the technical quality of the dataset. This section may be supported by figures and tables, as needed. This is a required section; authors must provide information to justify the reliability of their data. Possible content may include: - experiments that support or validate the data-collection procedure(s) (e.g. negative controls, or an analysis of standards to confirm measurement linearity) - statistical analyses of experimental error and variation - phenotypic or genotypic assessments of biological samples (e.g. confirming disease status, cell line identity, or the success of perturbations) - general discussions of any procedures used to ensure reliable and unbiased data production, such as blinding and randomization, sample tracking systems, etc. - any other information needed for assessment of technical rigour by the referees Generally, this should not include: - follow-up experiments aimed at testing or supporting an interpretation of the data - statistical hypothesis testing (e.g. tests of statistical significance, identifying differentially expressed genes, trend analysis, etc.) - exploratory computational analyses like clustering and annotation enrichment (e.g. GO analysis).

# Usage Notes

This section is optional The Usage Notes should contain brief instructions to assist other researchers with reuse of the data. This may include discussion of software packages that are suitable for analysing the assay data files, suggested downstream processing steps (e.g. normalization, etc.), or tips for integrating or comparing the data records with other datasets. Authors are encouraged to provide code, programs or data-processing workflows if they may help others understand or use the data. Please see our code availability policy for advice on supplying custom code alongside Data Descriptor manuscripts. For studies involving privacy or safety controls on public access to the data, this section should describe in detail these controls, including how authors can apply to access the data, what criteria will be used to determine who may access the data, and any limitations on data use. Code Availability For all studies using custom code in the generation or processing of datasets, a statement must be included under the subheading “Code availability”, indicating whether and how the code can be accessed, including any restrictions to access. This section should also include information on the versions of any software used, if relevant, and any specific variables or parameters used to generate, test, or process the current dataset.

# Acknowledgements

The Acknowledgements should contain text acknowledging non-author contributors. Acknowledgements should be brief, and should not include thanks to anonymous referees and editors or effusive comments. Grant or contribution numbers may be acknowledged.

# Author contributions

Each author’s contribution to the work should be described briefly, on a separate line, in the Author Contributions section.

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A competing interests statement is required for all papers accepted by and published in Scientific Data. If there is no conflict of interest, a statement declaring this must still be included in the manuscript.

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For initial submissions, authors may choose to supply a single PDF with embedded figures.

Authors are encouraged to consider creating a figure that outlines the experimental workflow(s) used to generate and analyse the data output(s).

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# References