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## SOP20:

### Standard Operating Procedure (SOP) for Phenotypic Field data collection and management for hybrids evaluation



	<b>Crop:</b> Banana <b>Function:</b> Phenotypic Field data collection and management for hybrids evaluation	<b>SOP #</b>	20
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<b>SOP Owner</b>	Stanley Bayo and Ronald Kivumbi	<b>Approval Date</b>	8 <sup>th</sup> April 2025

## • **Standard Operating Procedure (SOP) for Data Collection, Analysis and Statistical Design in Banana Breeding**

### • **Authors & Contributors**

S. Bayo\*, R. Kivumbi ([R.Kivumbi@cgiar.org](mailto:R.Kivumbi@cgiar.org)), R. Swennen ([R.Swennen@cgiar.org](mailto:R.Swennen@cgiar.org)), M. Batte ([M.Batte@cgiar.org](mailto:M.Batte@cgiar.org)), M. Nyine ([M.Nyine@cgiar.org](mailto:M.Nyine@cgiar.org)), A. Brown ([A.Brown@cgiar.org](mailto:A.Brown@cgiar.org))

\*Correspondence: [s.bayo@cgiar.org](mailto:s.bayo@cgiar.org)

### • **1. Introduction**

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Data *management* in breeding operations is of paramount importance. Decisions taken at every stage of the breeding cycle need to be accurate and fast but become complex when large amounts of data are generated. Inaccuracies with data is likely when established methods for data collection and management are not followed. Mistakes will slow the speed to boost genetic benefits for smallholder farmers. In order to guarantee that all required breeding data for bananas are accurately collected and made easily available, this document outlines standard operating procedures for data collection and management in banana breeding. This document will be updated when new knowledge is generated.

### • **2. Purpose**

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This SOP provides detailed procedures for data collection, analysis, and statistical design for hybrid evaluations in the banana breeding program. It ensures data quality, consistency, and the application of appropriate statistical methodologies.

### • **3. Scope**

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This procedure applies to all personnel involved in data collection and management in banana breeding trials, including data collectors, field technicians, data managers, and statistics consultants.

### • **4. Responsibilities**

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#### 4.1 Data Collectors

- Collect daily data from assigned trial
- Submit weekly data to the Data Manager
- Ensure proper labelling and handling of samples

#### 4.2 Field Technicians

- Assist data collectors with the setup and organization of trials
- Maintain equipment and ensure tools are functioning properly

#### 4.2 Data Manager

- Review submitted data for completeness and quality
- Conduct field validation if data quality is subpar
- Perform data analysis using statistical models
- Upload validated data to Musabase (<https://www.musabase.org/>)

#### 4.3 Statistics Consultant

- Provides guidance on the choice of appropriate statistical models
- Assist in generating and interpreting statistical analyses

### • **5. Data Collection Tools**

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- Tablets: Equipped with the Field book app for data entry
- QR Codes: Fixed on every plant for easy identification and data tracking
- Tape Measure: For measuring plant height and circumference
- Weight Balance: For weighing bunches and fingers
- Meter Rule: For additional measurement accuracy

### • **6. Data Collection Procedure**

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#### 6.1 Generation of trial layouts

- Trial layouts are generated in Musabase (<https://www.musabase.org/>)
- Barcodes for each genotype are generated and printed
- The barcodes are attached to the corresponding plants in the field
- Trial layout is exported to Field book
- All traits to be measured are entered in Fieldbook App

All traits to be measured are activated in field book before starting to collect data

#### 6.2 Assignment of Trials

- Each data collector is assigned specific trials based on expertise and familiarity
- Assignments are communicated clearly, along with the location and specifics of the trial

#### 6.3 Daily Data Collection

Data collectors must follow the schedule for data collection:

- Frequency: Daily
- Timing: Collect data in the morning (the coolest part of the day) to minimize stress on plants and ensure accurate measurements

#### 6.4 Data Submission

- Data must be submitted weekly to the Data Manager
- Format: Data should be submitted via email or a shared drive in a predefined template

- Deadline: Submissions are due every Friday by 5 PM

## 6.5 Data Entry Guidelines

- Ensure all data is entered accurately into the Fieldbook App
- Double-check entries against physical measurements to prevent errors

## • **7. Traits to be collected**

s/n	Trait list	Description
1	Bunch orientation 1-5  cycle 1 main plant  at harvesting  COMP:0000466	Observe the angle of the bunch with the pseudostem and choose the most similar option from the 5 schematic drawings of descriptor 6.4.6 in the reference material, 1 = hanging vertically; 2 = slightly angled; 3 = hanging at a 45-degree angle; 4 = horizontal; 5 = erect
2	Bunch orientation 1-5  cycle 2 main plant  at harvesting  COMP:0000473	
3	Bunch orientation 1-5  cycle 3 main plant  at harvesting  COMP:0001057	
4	Bunch weight in kg  cycle 1  at harvesting  COMP:0000453	Harvest the bunch by cutting the peduncle 10 cm above the first ridge above the most proximal hand and immediately below the most distal hand and weigh the bunch (including the rachis), using scales. In kg
5	Bunch weight in kg  cycle 2  at harvesting  COMP:0000455	
6	Bunch weight in kg  cycle 3  at harvesting  COMP:0000456	
8	Plant height in cm  cycle 1 main plant  at flowering  COMP:0000824	Measure the distance from the collar, or from the pseudostem base at the ground if the collar is not visible, to the intersection of the petioles of the two youngest leaves (leaf ranks 1 and 2), using a measuring pole or sliding ruler. In cm
9	Plant height in cm  cycle 1 tallest sucker  at harvesting  COMP:0000934	
10	Plant height in cm  cycle 2 main plant  at flowering  COMP:0000840	
11	Plant height in cm  cycle 2 tallest sucker  at harvesting  COMP:0000769	
12	Plant height in cm  cycle 3 main plant  at flowering  COMP:0000888	
13	Plant height in cm  cycle 3 tallest sucker  at harvesting  COMP:0000782	Measure the circumference of the pseudostem of the plant at 1 m from the collar, or from the pseudostem base at the ground if the collar is not visible, using a tape measure. In cm
14	Plant circumference at 100 cm from the collar  cycle 1  at flowering  COMP:0001091	
16	Plant circumference at 100 cm from the collar  cycle 2  at flowering  COMP:0001093	
18	Plant circumference at 100 cm from the collar  cycle 3  at flowering  COMP:0001095	Count number of all types of suckers of the mat.
20	Number of suckers: count  cycle 1  "shooting"  COMP:0000088	
21	Number of suckers: count  cycle 1  "harvesting"  COMP:0000087	

22	Number of suckers: count  cycle 2  "shooting"  COMP:0000090	
23	Number of suckers: count  cycle 2  "harvesting"  COMP:0000089	Count number of all types of suckers of the mat.
24	Number of suckers: count  cycle 3  "shooting"  COMP:0000092	
25	Number of suckers: count  cycle 3  "harvesting"  COMP:0000091	
26	Number of functional leaves: count  cycle 1  "shooting"  COMP:0000051	Count number of functional leaves (leaves that have 50% or more of their surface as green, healthy, photosynthetic tissue)
27	Number of functional leaves: count  cycle 1  "harvesting"  COMP:0000050	
28	Number of functional leaves: count  cycle 2  "shooting"  COMP:0000053	
29	Number of functional leaves: count  cycle 2  "harvesting"  COMP:0000052	
30	Number of functional leaves: count  cycle 3  "shooting"  COMP:0000055	
31	Number of functional leaves: count  cycle 3  "harvesting"  COMP:0000054	
32	Number of hands in bunch: count  cycle 1  COMP:0000093	Count number of hands in the bunch
33	Number of hands in bunch: count  cycle 2  COMP:0000094	
34	Number of hands in bunch: count  cycle 3  COMP:0000095	
35	Number of fingers in bunch: count  cycle 1  COMP:0000008	Count number of fingers in multiple hands
36	Number of fingers in bunch: count  cycle 2  COMP:0000009	
37	Number of fingers in bunch: count  cycle 3  COMP:0000010	
38	Finger weight in g  cycle 1  COMP:0000081	Weigh a finger, using scales. Associate the data with the Hand rank. Collect this data from six fingers in total - three fingers in the middle of the outer whorl from the second hand and from the second-most distal hand. In g
39	Finger weight in g  cycle 2  COMP:0000082	
40	Finger weight in g  cycle 3  COMP:0000083	
41	Finger external length in cm  cycle 1  COMP:0000096	Measure the length of a finger that is at the 'ready to eat' stage, along the external (dorsal) arc, excluding the pedicel and the fruit tip, using a tape measure  Associate the data with the Hand rank and the Number of fingers measured. Collect this data from six fingers in total - three fingers in the middle of the outer whorl from the second hand and from the second-most distal hand. In cm
42	Finger external length in cm  cycle 2  COMP:0000097	
43	Finger external length in cm  cycle 3  COMP:0000098	
44	Finger circumference in cm  cycle 1  COMP:0000105	Measure the circumference of a finger at its widest point, using a tape measure and record the data in cm.  Associate the data with the Hand rank. Collect this data from six fingers in total - three fingers in the middle of the outer whorl from the second hand and from the second-most distal hand.
45	Finger circumference in cm  cycle 2  COMP:0000106	
46	Finger circumference in cm  cycle 3  COMP:0000107	



47	Planting  date of plant  COMP:0000976	Record the date of planting following DD/MM/YYYY format
48	Flowering of the plant  cycle 1  date of  COMP:0000364	Record the date of flowering/shooting following DD/MM/YYYY format
49	Flowering of the plant  cycle 2  date of  COMP:0000365	
50	Flowering of the plant  cycle 3  date of  COMP:0000366	
51	Harvesting  cycle 1  date of  COMP:0000461	Record the date of bunch harvesting following DD/MM/YYYY format
52	Harvesting  cycle 2  date of  COMP:0000462	
53	Harvesting  cycle 3  date of  COMP:0000463	
54	Fruit parthenocarp  cycle 1  COMP:0001045	Parthenocarpic (1) - ovary of all fruits on a bunch enlarged to form fruit filled with pulp mostly without seed; Not parthenocarpic (0) - ovary of some or all fruits remain small and lack pulp or are fully enlarged but have more seed than pulp
55	Fruit parthenocarp  cycle 2  COMP:0001046	
56	Fruit parthenocarp  cycle 3  COMP:0001047	
67	Youngest leaf spotted rank  cycle 1  at flowering  COMP:0000373	Record the rank (order) of the youngest leaf spotted (the first fully unfurled leaf or 50 % unfurled for pathology trials) with at least 10 discrete, mature, necrotic lesions or one large necrotic area with 10 light-coloured dry centres), counting the rank by starting with the youngest completely unrolled leaf as 1 and moving downwards, associating the data with the date of data collection
58	Youngest leaf spotted rank  cycle 1  at harvesting  COMP:0000379	
59	Youngest leaf spotted rank  cycle 2  at flowering  COMP:0000374	
60	Youngest leaf spotted rank  cycle 2  at harvesting  COMP:0000380	
61	Youngest leaf spotted rank  cycle 3  at flowering  COMP:0000375	
62	Youngest leaf spotted rank  cycle 3  at harvesting  COMP:0000381	
63	Fruit fill 1-2  cycle 1 main plant  at harvesting  COMP:0000465	Visual estimation of a fruit filling for Early Evaluation Trial stage only, 1 = filled; 2 = not filled
64	Fruit fill 1-2  cycle 2 main plant  at harvesting  COMP:0000472	
65	Raw pulp colour visual estimation 1-3  cycle 1  COMP:0001042	A quick field evaluation of the raw pulp to determine acceptability based on yellow colour using Mbwarzirume (Matooke) as a standard control. Scale: 1 = White colour; 2 = Yellow colour slightly lighter than that of Mbwarzirume; 3 = Deep yellow pulp colour same as that of Mbwarzirume
66	Raw pulp colour visual estimation 1-3  cycle 2  COMP:0001043	
67	Raw pulp colour visual estimation 1-3  cycle 3  COMP:0001044	
68	Sap amount estimation 1-3  cycle 1  COMP:0001039	Quickly determine the amount of sap in the raw pulp on a mature bunch in the EET field. 1= a lot of sap; 2 = a little sap; 3 = no sap.
69	Sap amount estimation 1-3  cycle 2  COMP:0001040	
70	Sap amount estimation 1-3  cycle 3  COMP:0001041	

## • **8. *Statistical Design for Hybrid Evaluations***

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### 8.1 Early Evaluation Trial for Mchare Breeding

Design: Randomized Complete Block Design (RCBD)

Replications: 3 blocks

Copies per genotype: 6 copies per genotype

### 8.2 Layout

- Each block will consist of 2 randomized copies of each genotype
- Checks will be planted throughout the field after every two mats of the experimental unit to ensure uniformity and facilitate comparative evaluation

Example Layout:

Block 1: [Genotype A1] [Genotype A2] [Check] [Genotype B1] [Genotype B2] [Check]

Block 2: [Genotype A1] [Genotype B2] [Check] [Genotype A2] [Genotype B1] [Check]

Block 3: [Genotype B1] [Genotype B2] [Check] [Genotype A1] [Genotype A2] [Check]

### 8.3 Full Sib Family Evaluation

- Design: Randomized Complete Block Design (RCBD)
- Replications: Randomly replicated within blocks
- Family configuration: Each family will have 16 sibs planted together in a block
- Layout: Families should be distributed across multiple blocks to minimize environmental bias

Example Layout:

Block 1: [Family 1] [Family 2] [Family 3] [Family 4]

Block 2: [Family 3] [Family 1] [Family 4] [Family 2]

Block 3: [Family 2] [Family 4] [Family 1] [Family 3]

## • **9. *Statistical Design for Hybrid Evaluations***

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### 9.1 Initial Quality Check

- The Data Manager will review the submitted data for completeness, consistency, and accuracy
- Use a checklist to ensure all required traits have been recorded

### 9.2 Field Validation

- If the data quality is inadequate, the Data Manager will return to the field to cross-verify data with the physical plants
- Discuss any discrepancies with data collectors

### 9.3 Upload

- Upon confirming data quality, the Data Manager will upload validated data to Musabase
- Ensure the data is formatted correctly, and all necessary metadata is included

## • **10. Data Analysis Procedure**

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### 10.1 Statistics Analysis Overview

- Data Managers and statistical consultants will perform the following analyses: Descriptive statistics (mean, median, standard deviation) for all traits, Analysis of variance (ANOVA) to evaluate differences among genotypes and families, Regression analysis to identify relationships between traits and environmental factors, Mixed models to account for both fixed and random effects, especially in multi-environment trials.

### 10.2 Statistical Models

Statistical models will be simplified and made accessible for easy use by team members. Key models to be used include:

- Fixed Effects Model: to analyse main effects of genotype, environment, and treatments
- Random Effects Model: to handle variability among blocks and random replicates
- Mixed Effects Model: to incorporate both fixed and random factors, allowing for better predictions and insights

### 10.3 Software for Analysis

- GenStat: Used for general statistical analysis and ANOVA
- R Studio: Utilized for advanced statistical modelling and graphical representation of data
- Code snippets will be provided for common analyses to ensure ease of use

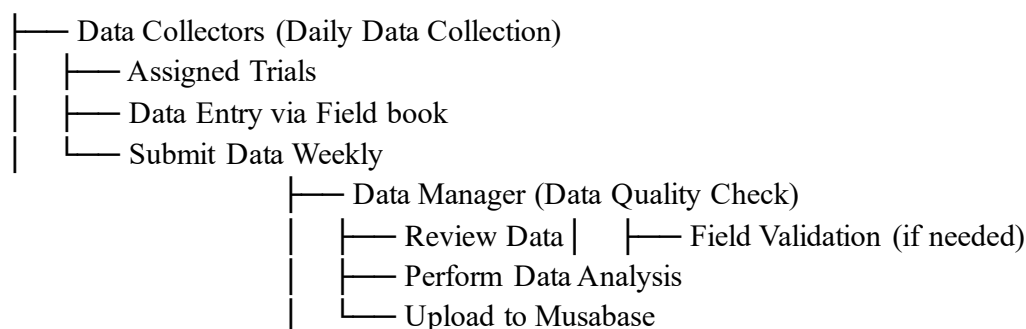
### 10.4 Availability of Models

- All statistical models and analysis scripts will be documented and available on a shared drive
- Training sessions will be held quarterly to familiarize team members with the analysis tools and models

## • **11. Data Flow Dendrogram**

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### Data Collection



## • **12. Record Keeping**

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- All collected data should be backed up electronically and stored securely.



- Maintain logs of daily activities and observations, including any issues encountered during data collection.

- ***13. Review and Revision***

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This SOP will be reviewed annually and revised as necessary to incorporate improvements or changes in protocols.

- ***14. Training and Compliance***

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- All personnel involved in data collection and management must undergo training on this SOP
- Compliance with this SOP is mandatory and will be monitored regularly

- ***15. Conclusion***

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This SOP establishes a standardized framework for data collection, analysis, and statistical design in the banana breeding program. By ensuring data quality, consistency, and appropriate statistical methodologies, it supports reliable hybrid evaluations. The outlined procedures apply to all personnel involved in data management, fostering efficiency and accuracy across breeding trials. Adherence to this SOP will enhance the integrity of research outcomes, ultimately contributing to the development of improved banana hybrids.

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**International Address:**

Suite 32  
5th Floor, AMP House  
Dingwall Road  
Croydon  
CR0 2LX, UK

**Registered Office:**

PMB 5320, Oyo Road  
Ibadan, Oyo State

**Headquarters**

PMB 5320, Oyo Road, Idi-Oshe  
Ibadan, Nigeria  
Tel.: +1 201 6336094  
+234 700 800 4482  
Fax.: +44 (208) 711 3786 (via UK)

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