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# Rank-based data synthesis of heterogeneous trials to identify the effects of climatic factors on the reaction of *Musa* genotypes to black leaf streak disease

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## Abstract

Synthesis of crop trial data can generate insights that are not available from the analysis of individual studies, but such synthesis is often constrained by the heterogeneity of data among studies. Rank-based data synthesis provides the flexibility to combine data of heterogeneous types and from different sources. We demonstrate the application of rank-based data synthesis of heterogeneous trial data to assess the effect of climatic factors on the reaction of several *Musa* genotypes to black leaf streak disease (BLSD; caused by *Pseudocercospora fijiensis* [sexual morph: *Mycosphaerella fijiensis*]). We aggregated data from the main public repositories of *Musa* trial data. We applied model-based recursive partitioning with the Plackett–Luce model, using climatic data as covariates. The model identified the maximum length of the dry spell as the main variable influencing differences in genotypic response to BLSD, dividing the aggregated trial dataset into humid and dry environments. We found differences in the reaction of genotypes to BLSD between these environments. In humid environments, NARITA 8 was found to be the most resistant genotype, while in dry environments FHIA-01 was the best performing improved genotype. We also

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**Abbreviations:** BLSD, black leaf streak disease; DDT, disease development time; DII, disease infection index; NFL, number of functional leaves; NSL, number of standing leaves; YLS, youngest leaf spotted.

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assessed reliability, which is the probability of outperforming the reference genotype (Calcutta 4). In humid environments, NARITA 2, NARITA 8, and FHIA-01 had the highest reliability, while in dry environments only the landrace Saba surpassed 50% reliability. The information generated by our data synthesis approach supports selecting *Musa* genotypes for further evaluations at new locations.

# 1 | INTRODUCTION

Crop variety trial data are essential for producing relevant information to support critical decision making in agronomy and crop science. These data are expensive to obtain, since field trials require a significant investment of time and resources. Research synthesis of heterogeneous studies can help to generalize conclusions and to better account for environmental variability, compared to the analysis of individual studies (Makowski, 2021). Furthermore, appropriate data synthesis methodologies can add value to existing crop trial data, by (1) integrating results from trials with different types of data and from different sources, (2) comparing a higher number of genotypes than would be feasible in individual field experiments, and (3) adding environmental data that were not available at the time at which each individual trial was conducted, providing new insights on the effect of environmental factors (genotype × environment interaction).

Current data synthesis methods often encounter obstacles related to poor data standardization (Eagle et al., 2017). Combining data from multiple trials with different experimental designs, measurement scales and data quality pose problems for data management and for subsequent statistical analysis (Simko & Pechenick, 2010). Simko and Pechenick (2010) proposed the use of rank-aggregation methods to allow for the combination of heterogeneous plant breeding data from different experiments. By converting diverse numerical measurements into rankings, trial data can be aggregated in one dataset and analyzed with appropriate statistical methods. Brown et al. (2020) suggested that the rank-aggregation approach could be extended to analyze heterogeneous data from crop trial evaluations under different environmental conditions by using climatic data to account for effects of abiotic stress on genotypic performance. van Etten, de Sousa et al. (2019) analyzed farmer-participatory crop experiments in which field data were collected by farmers as rankings, following the "tricot" approach (van Etten, Beza et al., 2019), and then combined with environmental data. Brown et al. (2022) demonstrate that data synthesis of tricot trial data of common bean (*Phaseolus vulgaris* L.) genotypes in Central America provides new insights to climate adaptation by predicting the performance of varieties beyond the locations in which they were tested.

Black leaf streak disease (BLSD), also known as black Sigatoka, is a fungal disease that affects banana leaves, causing necrotic lesions which gradually reduce the plant's photosynthetic capacity (Churchill, 2011). BLSD is caused by the fungus *Pseudocercospora fijiensis* (sexual morph: *Mycosphaerella fijiensis*) (Guzman et al., 2018). It is the most destructive leaf disease of bananas and is considered to be among the 10 most destructive diseases in global agriculture (Pennisi, 2010). BLSD both reduces yields and fruit quality and affects the wider environment because its control currently relies heavily on frequent applications of chemical fungicides (De Lapeyre de Bellaire et al., 2010). The cultivation of BLSD-resistant varieties is considered to be the most sustainable disease control method. Thus, the selection and release of such BLSD-resistant varieties have become crucial for banana producers. Location-specific information on how different genotypes perform under different climatic conditions can support decision making that considers genotype by environment interactions (G × E) and is useful for *Musa* breeding programs.

Here, we apply the data synthesis approach (Brown et al., 2020) to a combination of data from various evaluations of *Musa* genotype reactions to BLSD and climatic data that are used as model covariates. To the best of our knowledge, this is the first application of such an approach to BLSD data originally collected in a non-ranking format. Multi-environment trials of *Musa* genotypes are complex to conduct because of their intricate requirements of space and time (Tenkouano et al., 2012). Our main objective is to demonstrate application of the data synthesis approach to unveil the effect of climatic factors on the reaction of several *Musa* genotypes to BLSD. Our interest is to explain rather than to predict a genotype's reaction to BLSD; the models are fitted and validated accordingly. The specific objectives are to: (1) aggregate heterogeneous trial data previously deemed incompatible, (2) assess the effect of climatic variables and indices on the reaction of several genotypes to BLSD, and (3) identify the best performing genotypes across different locations.

## 2 | MATERIAL AND METHODS

### 2.1 | Musa trial data

We retrieved data from the three main public data repositories currently storing field evaluation data on *Musa* genotypes: AgTrials, MusaBase, and the *Musa* Germplasm Information System (MGIS) (Bauchet et al., 2018; Hyman et al., 2017; Ruas et al., 2017). From each repository, we selected data that fulfilled the following criteria:

1. Contains evaluations of *Musa* genotype reactions to BLSD
2. Contains geographic coordinates of trial locations
3. Contains the start and end dates of the evaluation period (i.e., planting date, and either shooting or harvesting date)
4. Genotypes evaluated at least partially overlap among trials (see connectivity in Section 2.5)

Table 1 presents the studies and projects in which the selected data were originally produced, the number of evaluated genotypes, number of locations, temporal extent, and the data repository from which we retrieved the data.

Figure 1 shows the 22 unique locations of the trials. To provide a general description of the climatic conditions at the trial locations, Table 2 presents the yearly mean temperature, precipitation, and relative humidity, averaged from monthly climatologies for the reference period 1991–2020 (Hersbach et al., 2018), which roughly covers the time span of the aggregated dataset (1990–2019, Table 1).

### 2.2 | Converting data to rankings

To analyze the data using the Plackett–Luce model (Luce, 1959; Plackett, 1975), the data were transformed from numerical BLSD measurements to a ranking format. Five different metrics for BLSD evaluation were used in the original trial data (Table 3). The scores for these metrics were used to rank the genotypes within each trial, where the order of the ranking depended on the metric used in a trial. For instance, in evaluations where the youngest leaf spotted (YLS) was reported, genotypes with the highest values were ranked first. Conversely, for rating scales such as disease infection index (DII), representing the diseased surface per plant, genotypes with the lowest values were ranked first. If multiple measurements were made in the same evaluation, we selected the metric for which the most data were available and which resulted in a more homogeneous aggregated dataset (i.e., higher possible number of rankings are derived from the same metric). In the final aggregated dataset, 33 of the rankings were derived from the underlying variable YLS, 3 from disease development time (DDT), 41 from DII, 24 from the number of standing

**Core Ideas**

- Data synthesis generated new insights by bringing together heterogeneous *Musa* crop trial data.
- The novel method converts disease scores to ranks and uses environmental data.
- *Musa* genotypes react differently to black leaf streak disease with different dry spell lengths.

leaves (NSL), and 9 from the number of functional leaves (NFL).

If the trial data were reported at plant or block level, we treated each block as an individual experiment and the summarized results at the block level generated a ranking. On the contrary, where trial data were available only as summarized results, the ranking was constructed using the averaged values. Each evaluation cycle generated a separate ranking. For example, trials evaluating over two cycles (i.e., mother and first ratoon) produced two separate rankings. The evaluation also depends on decisions made when the trial was designed. For instance, YLS is usually registered at shooting, but in some cases, it may have been registered only at harvest or at both. These differences were considered in order to define the period for which climatic data were obtained for modeling (see Section 2.3). In the aggregated dataset, the evaluation period for all YLS, DDT, and NFL and for one DII was from planting to shooting. For the rest of the data, where the BLSD metric was DII and NSL, the evaluation period was from planting to harvest.

To convert the data from numerical measurements to ranks, we used the function *rank_numeric()* from the R package *gosset* (de Sousa, Brown et al., 2023). The rankings were constructed separately for each evaluation and then aggregated into a sparse matrix, where the columns are the evaluated genotypes, and the rows correspond to the evaluations. After aggregating all the evaluations, the number of rankings was 110, with 62 genotypes evaluated. Information about the evaluated genotypes is presented in Table 4. There are three types of genotype: (1) a crop wild relative, (2) landraces, and (3) improved genotypes either through breeding (hybrids) or selection of somaclonal variants.

Guzman et al. (2018) described two types of reactions and three types of interactions of *Musa* genotypes to and with BLSD:

1. Incompatible interaction characterized by high resistance (HR) or hypersensitivity (phenotype 1). This expression of high resistance is characterized by the blockage of disease development at an early stage and YLS is not observed.
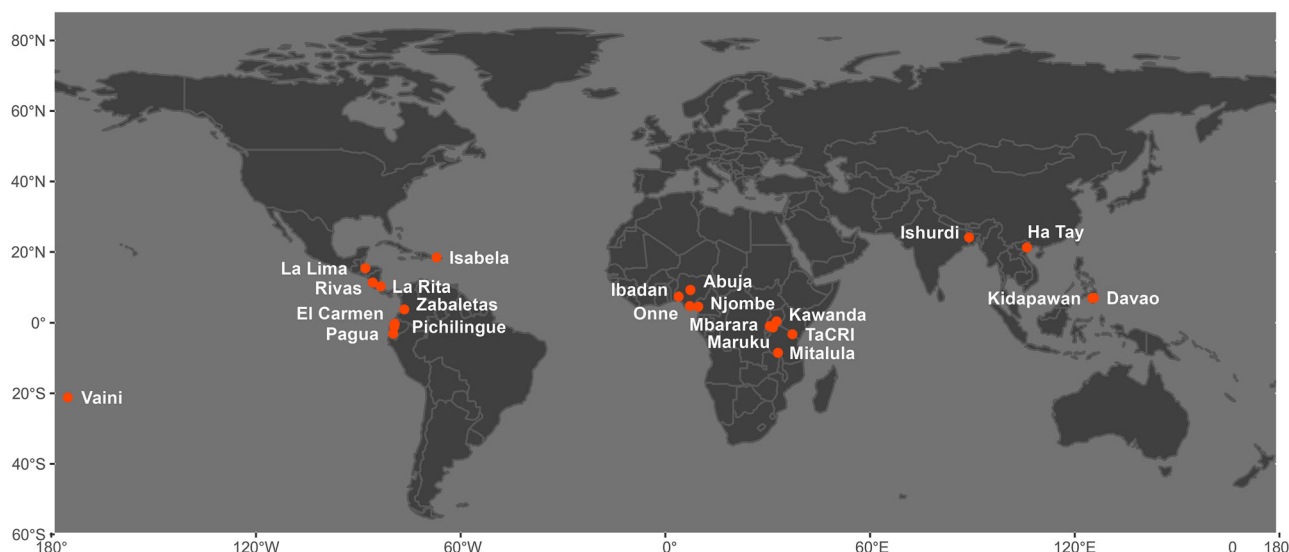2. Compatible interaction with two types of reaction:

**FIGURE 1** Unique locations of trials included in the aggregated data set.

2.1 Partial resistance (phenotype 2) expressed by slow disease evolution (from first streak symptoms to spots) and a reduction in pathogen reproduction. The YLS is high. There is a large progression of response with phenotype 2 from resistance to almost complete susceptibility.

2.2 Susceptibility (phenotype 3) expressed by rapid disease evolution; YLS is low.

The BLSD reactions indicated in Table 4 follow the types of reaction described above. The classification of any genotype into one of the three phenotypes results from evaluating the host reaction under field conditions in comparison with references of known resistance phenotypes. We used Calcutta 4 as the reference in our analysis; it is frequently used as a highly resistant reference in BLSD evaluations.

## 2.3 | Climatic data

To account for climatic effects on the plant host reaction to BLSD, we used climatic data retrieved from the AgERA5 database (Boogaard & van der Grijn, 2020; Copernicus Climate Change Service, 2020). We downloaded the following variables: daytime maximum temperature, nighttime minimum temperature, daily precipitation flux, and relative humidity at 6:00 a.m., 9:00 a.m., 12:00 p.m., 3:00 p.m., and 6:00 p.m. The initial set of climatic covariates (temperature, precipitation, and relative humidity) were chosen based on guidelines for *Musa* disease evaluation (Orjeda, 1998) and previous studies relating BLSD to climatic factors (Churchill, 2011; Jacome & Schuh, 1992; Yonow et al., 2019). The climatic data were extracted for the period of each evaluation that generated a ranking. This corresponds to either the time from

planting to shooting or from planting to harvest, depending on what was reported in each evaluation. If more than one cycle was reported, the start time for the ratoon cycle was computed as the end time of the previous crop cycle. For example, for a second cycle in which YLS at shooting is reported, the evaluation period of the mother is from planting to shooting, whereas for the first ratoon cycle, the evaluation time is from the shooting of the mother to the shooting of the first ratoon cycle. All relative humidity variables were averaged over the evaluation period of each trial (i.e., either planting to shooting or planting to harvest). Precipitation and temperature variables were used as inputs with R package *climatrends* (de Sousa, van Etten et al., 2023) to compute climatic indices (Table 5).

## 2.4 | Plackett–Luce trees

The Plackett–Luce model (Luce, 1959; Plackett, 1975) is a statistical model for ranking data. Its implementation in the R package *PlackettLuce* (Turner et al., 2020) is an extension of the original model that allows ties and partial rankings, although ties of order four or higher are difficult to analyze. Given a set S of J items S = $\{i_1, i_2, \ldots, i_j\}$, the probability of selecting an item $i_j$ from S is represented by:

$$P\left(i_j \mid S\right) = \frac{\alpha_{i_j}}{\sum_{i \varepsilon S} i}$$

where $\alpha_i \geq 0$ is the worth of item $i$ (Turner et al., 2020). An item with a higher worth value is more likely to be selected (Turner et al., 2020). To account for context-specific differences among rankings, the *PlackettLuce* package is coupled with the model-based recursive partitioning framework of the R package *partykit* (Hothorn & Zeileis, 2015; Zeileis

**TABLE 1** Description of the trials included in the data synthesis.

| Study/Project | Data repository | Number of locations[a] | Experimental design | Number of blocks | Number of cycles | Number of genotypes | Temporal extent | Number of generated rankings |
|---|---|---|---|---|---|---|---|---|
| IMTP-1 | AgTrials | 6 | Observation plots without replication | | 2 | 17 | 1990–1992 | 4 |
| IMTP-2 | AgTrials | 8 | RCBD | 5 | 1 | 19 | 1995–1997 | 13 |
| IMTP-3 | AgTrials | 7 | RCBD | 3–5[b] | | 40 | 1999–2003 | 26 |
| Orlando Narváez (2004) | AgTrials | 3 | CRD | | 1 | 13 | 2003–2004 | 3 |
| Irish et al. (2013) | MGIS | 1 | RCBD | 4 | 2 | 19 | 2008–2009 | 2 |
| Irish et al. (2019) | MGIS | 1 | RCBD | 4 | 2 | 15 | 2014–2016 | 2 |
| WP4-BBB-Project | MusaBase | 5 | RCBD | 4 | 3 | 32 | 2016–2019 | 60 |

Abbreviations: CRD, completely randomized design; IMTP, International Musa Testing Program; MGIS, *Musa* Germplasm Information System (currently does not store trial data, but provides a curated selection of literature on phenotypic evaluations of *Musa* genotypes); RCBD, randomized complete block design; WP4-BBB, Working Package 4 Breeding Better Bananas Project.

[a]Some locations are repeated across studies; unique locations are presented in Figure 1.

[b]Varies among trials within the same study; information corresponds to the original design but not all data were available for data synthesis (e.g., one cycle missing).

et al., 2008). The combination of the recursive partitioning algorithm (Zeileis et al., 2008) and the Plackett–Luce model (Turner et al., 2020) produce a Plackett–Luce tree. Accordingly to Zeileis et al. (2008) and (Turner et al., 2020), the algorithm proceeds as follows:

1. The Plackett–Luce model is fitted to the entire dataset.
2. The influence of each covariate on the stability of worth parameters is assessed.
3. If instability exceeds a given minimum threshold, the dataset is split into two partitions (also referred to as "nodes"). The split is generated by selecting a split value of a certain covariate with the strongest parameter instability. Samples above and below this value are assigned to different partitions (categorical variables can also be used to create partitions). To each partition, a Plackett–Luce model is fitted separately.
4. The algorithm stops either when no significant instabilities are detected or when the resulting partitions are smaller than a pre-specified minimum size. Otherwise, steps 1–3 are repeated, analyzing stability for each of the data partitions separately, and splitting them further.

The threshold in step 3 is specified by the $\alpha$ parameter in the Plackett–Luce tree model function, which defines the threshold significance level at which to admit a split (Zeileis et al., 2008). We used a Bonferroni-corrected $\alpha$ value of 0.05. In step 4, the threshold refers to the minimum number of observations required in a node. In our case, we set the minimum node size as 35% of the aggregated dataset. In predictive mode, this threshold might be considered as too conservative. However, we are modeling in explanatory mode and very small nodes might be uninformative. Furthermore, the model requires some level of connectivity among compared items, which might not be feasible with very few observations per node. Further details about connectivity are provided in Section 2.5.

## 2.5 | Network connectivity

To compute finite maximum likelihood estimates (MLE) and standard errors with *PlackettLuce*, the network of items should be strongly connected, which means that a win–lose relationship should exist between each pair of items included in the rankings (Hunter, 2004; Turner et al., 2020). From the initial aggregated dataset, we removed genotypes that were weakly connected to others. To guarantee the representativeness of genotypes among trials and avoid extremely biased comparisons, we only kept genotypes that were present in at least 5% of the trials. This threshold was defined through an iterative search of the minimum amount of data that guarantees model convergence and minimizes data loss. It resulted in

**TABLE 2** Location name, geographic coordinates, and yearly mean climatic data (temperature, annual precipitation, and relative humidity) for the period 1991–2020 at unique trial locations.

| Country | Location | Longitude (°) | Latitude (°) | Temperature (°C) | Precipitation (mm) | Relative humidity (%) |
|---|---|---|---|---|---|---|
| Bangladesh | Ishurdi | 89.033 | 24.133 | 25.57 | 1,996.97 | 77.04 |
| Cameroon | Njombe | 9.650 | 4.583 | 25.83 | 4,889.37 | 87.46 |
| Colombia | Zabaletas | −76.517 | 3.817 | 19.40 | 2,607.82 | 88.99 |
| Costa Rica | La Rita | −83.450 | 10.267 | 25.01 | 3,311.83 | 85.91 |
| Ecuador | Pichilingue | −79.483 | −1.100 | 23.84 | 1,608.95 | 90.27 |
| Ecuador | El Carmen | −79.317 | −0.233 | 23.32 | 3,019.01 | 87.61 |
| Ecuador | Pagua | −79.769 | −3.074 | 22.04 | 1,436.69 | 89.27 |
| Honduras | La Lima | −87.933 | 15.417 | 24.42 | 1,769.74 | 86.89 |
| Nicaragua | Rivas | −85.799 | 11.356 | 26.35 | 1,707.09 | 80.97 |
| Nigeria | Abuja | 7.333 | 9.267 | 26.45 | 1,756.53 | 64.04 |
| Nigeria | Onne | 7.167 | 4.767 | 26.20 | 1,471.82 | 87.43 |
| Nigeria | Ibadan | 3.900 | 7.433 | 26.09 | 2,874.01 | 80.79 |
| Philippines | Davao | 125.600 | 7.083 | 26.65 | 1,888.76 | 80.27 |
| Philippines | Kidapawan | 125.154 | 7.014 | 25.27 | 6,103.88 | 83.60 |
| Puerto Rico | Isabela | −67.051 | 18.472 | 25.75 | 2,789.3 | 80.92 |
| Tanzania | Mitalula | 33.000 | −8.500 | 24.57 | 6,581.55 | 55.59 |
| Tanzania | Maruku | 31.500 | −1.333 | 20.93 | 1,125.93 | 82.07 |
| Tanzania | TaCRI | 37.246 | −3.244 | 17.41 | 1,805.36 | 79.42 |
| Tonga | Vaini | −175.167 | −21.167 | 24.14 | 851.55 | 76.80 |
| Uganda | Kawanda | 32.600 | 0.417 | 21.08 | 614.2 | 86.99 |
| Uganda | Mbarara | 30.617 | −0.933 | 20.91 | 1,095.14 | 72.74 |
| Vietnam | Ha Tay | 105.983 | 21.300 | 24.20 | 2,406.38 | 78.95 |

*Source*: Climatic data from Hersbach et al. (2018).

**TABLE 3** Description of metrics commonly used for black leaf streak disease (BLSD) evaluations.

| Metric | Description |
|---|---|
| Disease development time (DDT) | Number of days from infection (occurring at the appearance of the unfolded leaf) to the appearance of 10 or more necrotic mature lesions. |
| Disease infection index (DII) | $DII = \frac{\sum nb}{(N-1)T} 100$<br>$N$ = number of grades in the scale<br>$n$ = number of leaves in each grade<br>$b$ = grade<br>$T$ = total number of leaves scored |
| Number of functional leaves (NFL) | Total number of leaves per plant with more than 50% green area. |
| Number of standing leaves (NSL) | Total number of standing leaves per plant, starting from the highest unfolded leaf, regardless of infection status. |
| Youngest leaf spotted (YLS) | The first (from top to bottom) fully unfolded leaf with 10 or more necrotic lesions. |

*Source*: Adapted from Bauchet et al. (2018), Jones & Tézenas du Montcel (1994), and Orjeda (1998).

37% of the genotypes being discarded. When a Plackett–Luce tree is fitted, a network that is initially strongly connected might become weakly connected if the dataset is divided by the recursive partitioning algorithm. The *PlackettLuce* package provides a solution for networks that are not strongly connected, through the inclusion of pseudo-rankings (Turner et al., 2020). These are symmetric wins and losses between an artificial item and each of the real items, which make the network strongly connected. Even though our initial network was strongly connected (Figure 2) after removing the weakly connected genotypes, we used the pseudo-rankings mechanism to guarantee the connectivity of the network after partitioning

**TABLE 4** Main characteristics of Musa genotypes included in the data synthesis.

| Name | Status | BLSD reaction | Genome | Subgroup/Type | Breeding program | Information source |
|---|---|---|---|---|---|---|
| Agbagba | Landrace | S | AAB | Plantain | *NA* | (Ferris et al., 1999) |
| BITA-2 | Hybrid | PR | ABBB | Plantain | IITA | (Ning et al., 2007); (Noupadja & Tomekpé, 2001) |
| BITA-3 | Hybrid | PR | AAAB | Plantain | IITA | (Bakry et al., 2009); (Ortiz & Vuylsteke, 1998) |
| Burro Cemsa | Landrace | PR | ABB | Bluggoe | *NA* | (Alvarez, 1997) |
| Cachaco | Landrace | PR | ABB | Bluggoe | *NA* | (Guzman et al., 2018) |
| Calcutta 4 | Wild | HR | AAw | *M. acuminata* subsp. *burmannicoides* | *NA* | (Guzman et al., 2018) |
| CRBP-39 | Hybrid | PR | AAAB | Plantain | CARBAP | (Cohan et al., 2003) |
| EMB 403 | Hybrid | PR | AAAB | | EMBRAPA | (Hernández Núñez, 1995) |
| FHIA-01 | Hybrid | PR | AAAB | Pome | FHIA | (Irish et al., 2013) |
| FHIA-02 | Hybrid | PR | AAAA | | FHIA | (Karamura et al., 2012) |
| FHIA-03 | Hybrid | PR | AABB | | FHIA | (Karamura et al., 2012) |
| FHIA-17 | Hybrid | PR | AAAA | | FHIA | (Irish et al., 2013) |
| FHIA-18 | Hybrid | PR | AAAB | Pome | FHIA | (Irish et al., 2013) |
| FHIA-20 | Hybrid | PR | AAAB | Plantain | FHIA | (Sakyi-Dawson et al., 2008) |
| FHIA-21 | Hybrid | PR | AAAB | Plantain | FHIA | (Irish et al., 2013) |
| FHIA-23 | Hybrid | PR | AAAA | | FHIA | (Orjeda, 2000) |
| FHIA-25 | Hybrid | PR | AAB | | FHIA | (Njukwe et al., 2010) |
| French Sombre | Landrace | S | AAB | Plantain | *NA* | (Guzman et al., 2018) |
| Grande Naine | Landrace | S | AAA | Cavendish | *NA* | (Guzman et al., 2018) |
| Gros Michel | Landrace | S | AAA | Gros Michel | *NA* | (Guzman et al., 2018) |
| Kisansa | Landrace | S | AAA | EAHB | *NA* | (Kimunye, Were et al., 2021); (Nyombi et al., 2009) |
| Lakatan | Landrace | U | AA | | *NA* | IMTP-2 data |
| Mbwazirume | Landrace | S | AAA | EAHB | *NA* | (Kimunye, Were, et al., 2021) |
| Nakitembe | Landrace | S | AAA | EAHB | *NA* | (Karamura & Karamura, 1994); (Kimunye, Were et al., 2021) |
| NARITA 2 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021) |
| NARITA 4 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021) |
| NARITA 6 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021) |
| NARITA 7 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 8 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |

(Continues)

**TABLE 4** (Continued)

| Name | Status | BLSD reaction | Genome | Subgroup/Type | Breeding program | Information source |
|---|---|---|---|---|---|---|
| NARITA 9 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 10 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 11 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 12 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 13 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 14 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 15 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 16 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 18 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 19 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 20 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 21 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 22 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 23 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 24 | Hybrid | S | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021; Tushemereirwe et al., 2015) |
| NARITA 25 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |
| NARITA 26 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Tushemereirwe et al., 2015) |

(Continues)

**TABLE 4** (Continued)

| Name | Status | BLSD reaction | Genome | Subgroup/Type | Breeding program | Information source |
|------|--------|---------------|--------|---------------|------------------|---------------------|
| NARITA 27 | Hybrid | PR | AAA | EAHB | NARO-IITA | (Kimunye, Jomanga, et al., 2021) |
| Ndizi Uganda | Landrace | S | AAA | EAHB | *NA* | (Karamura et al., 2012); (Kimunye, Were et al., 2021) |
| Niyarma Yik | Landrace | S | AA | | *NA* | (Guzman et al., 2018) |
| PA 03-22 | Hybrid | S | AAAB | Pome | EMBRAPA | (Irish et al., 2013) |
| Pisang Berlin | Landrace | S | AA | Inarnibal | *NA* | (Guzman et al., 2018) |
| Pisang Ceylan | Landrace | PR | AAB | Mysore | *NA* | (Guzman et al., 2018) |
| Pisang Jari Buaya | Landrace | S | AA | Pisang Jari Buaya | *NA* | (Kimunye, Were et al., 2021) |
| PITA-16 | Hybrid | S | AAB | Plantain | IITA | (Irish et al., 2013) |
| PV 03-44 | Hybrid | PR | AAAB | Pome | EMBRAPA | (Irish et al., 2013) |
| Rose | Landrace | PR | AA | *M. acuminata* subsp. *malaccensis* | *NA* | (Kimunye, Were et al., 2021) |
| Saba | Landrace | PR | ABB | Monthan | *NA* | (Guzman et al., 2018) |
| SH-3436-9 | Somaclonal variant | PR | AAAA | Highgate | INIVIT | (Orjeda, 2000) |
| SH-3640 | Hybrid | S | AAAB | | FHIA | (Irish et al., 2013) |
| Valery | Landrace | S | AAA | Cavendish | *NA* | (Guzman et al., 2018) |
| Williams | Landrace | S | AAA | Cavendish | *NA* | (Guzman et al., 2018) |
| Yangambi Km5 | Landrace | HR | AAA | Ibota Bota | *NA* | (Guzman et al., 2018) |

*Note*: EAHB landraces were assumed to be susceptible. NARITAs were assumed to be partially resistant following Tushemereirwe et al. (2015), except those indicated as susceptible by Kimunye, Jomanga et al. (2021).

Abbreviations: BLSD, black leaf streak disease; CARBAP, Rural Associations' Confederation of Buenos Aires and La Pampa; EMBRAPA, Brazilian Agricultural Research Corporation; FHIA, Fundación Hondureña de Investigación Agrícola; HR, highly resistant; IITA, International Institute of Tropical Agriculture; INIVIT, Instituto de Ingestigaciones de Viandas Tropicales; *NA*, not applicable; NARO, National Agricultural Research Organization; PR, partially resistant; S, susceptible; U, unknown.

splits. The use of pseudo-rankings also reduces the variance and bias of the worth parameter estimators (Turner et al., 2020). The number of pseudo-rankings to the artificial item is set by the *npseudo* parameter in the Plackett–Luce model; we set *npseudo* = 2. Network connectivity is also important to guarantee tree stability, as detailed in Section 2.7. Cultivars Williams and Gros Michel are commonly used as susceptible references in BLSD evaluations. Pisang Ceylan is often used as a partially resistant reference. Figure 2 shows how these reference genotypes enabled the comparison of genotypes, which were not compared to each other in the same trial. For instance, the FHIAs and NARITAs were not compared directly in any of the aggregated trials.

## 2.6 | Handling tied ranks

In the present analysis, we found many cases in which the evaluated genotypes were tied, especially in lower rank positions. The Plackett–Luce model implemented in the R package *PlackettLuce* can handle ties up to an order of four (Turner et al., 2020). Unfortunately, the large number of ties

in our data prevented model convergence. Therefore, from the subset of tied genotypes in a single rank, we removed all except one of the tied genotypes. For instance, if six items are tied in the low part of a single ranking, we remove five genotypes and keep one from the tied subset. To avoid bias, the genotype to be retained was randomly selected. We found that changing which genotype was retained had a negligible influence on the overall results.

## 2.7 | Stability assessment of the Plackett–Luce tree

A well-known limitation of recursive partitioning as used in Plackett–Luce trees is model instability, which means that a small change in the input data can cause large changes in the output (Breiman, 1996; Philipp et al., 2018; Strobl et al., 2009). Stability is fundamental in the explanatory models to guarantee that similar model results (i.e., semantic similarity of the learned predictor–response relationship) are obtained using the same algorithm on a different random sample from the same data generation process (Philipp et al., 2018). We

**TABLE 5** Climatic variables and indices used as model covariates. Indices were calculated for the evaluation period of each trial (e.g., planting to shooting).

| Variable | Description | Unit |
|---|---|---|
| MLDS | Maximum length of dry spell (consecutive days with precipitation <1 mm) | day |
| MLWS | Maximum length of wet spell (consecutive days with precipitation ≥1 mm) | day |
| r10mm | Number of heavy precipitation days (10≤ rain <20 mm) | day |
| r20mm | Number of very heavy precipitation days (rain ≥20 mm) | day |
| R95p | Total precipitation when rain >95th percentile | mm |
| R99p | Total precipitation when rain >99th percentile | mm |
| Rtotal | Total precipitation (mm) on wet days (rain ≥1 mm) | mm |
| Rx1day | Maximum 1-day precipitation | mm |
| Rx5day | Maximum 5-day precipitation | mm |
| SDII | Simple daily intensity index (total precipitation divided by the number of wet days) | mm/day |
| rhum_06h | Daily relative humidity at 6:00 a.m., averaged over the evaluation period | % |
| rhum_09h | Daily relative humidity at 9:00 a.m., averaged over the evaluation period | % |
| rhum_12h | Daily relative humidity at 12:00 p.m., averaged over the evaluation period | % |
| rhum_15h | Daily relative humidity at 3:00 p.m., averaged over the evaluation period | % |
| rhum_18h | Daily relative humidity at 6:00 p.m., averaged over the evaluation period | % |
| CSDI | Cold spell duration index (maximum consecutive nights with temperature <10th percentile) | day |
| DTR | Diurnal temperature range (mean difference between daily maximum temperature and daily minimum temperature) | ˚C |
| maxDT | Maximum daytime temperature | ˚C |
| maxNT | Maximum nighttime temperature | ˚C |
| minDT | Minimum daytime temperature | ˚C |
| minNT | Minimum nighttime temperature | ˚C |
| SU | Summer days (number of days with maximum temperature > 30˚C) | ˚C |
| T10p | 10th percentile of night temperature | ˚C |
| T90p | 90th percentile of day temperature | ˚C |
| TR[a] | Tropical nights (number of nights with maximum temperature >25˚C) | ˚C |
| WSDI | Warm spell duration index (maximum consecutive days with temperature >90th percentile) | day |

[a]Removed from the model because it has near zero variability.

assessed stability through data sampling using the framework proposed by Philipp et al. (2018) and implemented in the R package *stablelearner* (Philipp et al., 2016). The method consists of fitting an ensemble of trees, each with a resampled instance of the original dataset, and counting the number of times each variable generates a split (Philipp et al., 2016). If the variables selected for splitting in the original tree are consistently selected across the ensemble of trees, then the original tree is considered stable (Philipp et al., 2016). We created 1000 subsamples, each using 80% of the original data (sampling without replacement). We selected this sampling method to generate sufficiently large learning samples and to ensure strong network connectivity (see Section 2.5). We fitted a Plackett–Luce tree to each of the 1000 subsamples and recorded for each variable how many times it was used to generate a split. To facilitate interpretation, we report the relative frequencies per variable using a histogram.

## 2.8 | Supporting software

We used the following R (R Core Team, 2022) packages for data management and preparation: *readr*, *readxl, janitor, dplyr, gosset*, and *caret* (de Sousa, Brown et al., 2023; Firke, 2021; Kuhn, 2022; Wickham & Bryan, 2022; Wickham, François et al., 2022, 2022). Climatic variables were obtained using the packages *ag5Tools* and *climatrends* (Brown et al., 2023; de Sousa, van Etten et al., 2023). The statistical modeling was performed with the packages *PlackettLuce, stablelearner, gosset*, and *qvcalc* (de Sousa, Brown et al., 2023; Firth, 2020; Philipp et al., 2016; Turner et al., 2020). The figures were made with packages *ggplot2*, *ggparty, patchwork*, *GGally, and tmap* (Borkovec & Madin, 2019; Pedersen, 2020; Schloerke et al., 2021; Tennekes, 2018; Wickham, 2016). The geospatial data were handled with packages *sf* and *terra* (Hijmans, 2021; Pebesma, 2018).
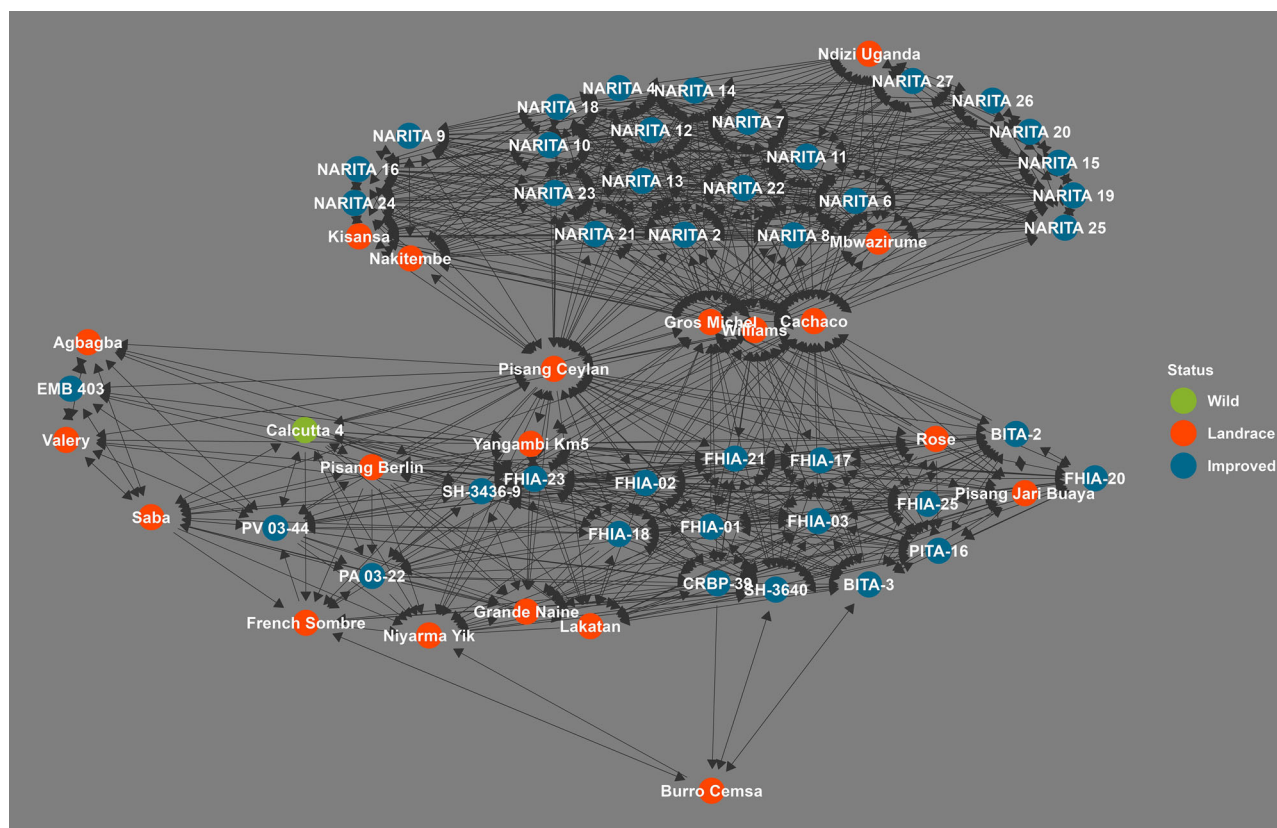
**FIGURE 2** Network of win (outgoing arrows) and lose (incoming arrows) relationships between each pair of evaluated *Musa* genotypes. Incoming and outgoing arrows between the same pair indicate different outcomes at independent evaluations.

# 3 | RESULTS

## 3.1 | Plackett–Luce tree

The model selected the variable (maximum length of dry spell [MLDS], consecutive days with precipitation < 1 mm) as the best splitting variable, partitioning the dataset in two. While MLDS is a rainfall-derived index, it is only very weakly correlated with rainfall indices such as Rtotal ($r = -0.06$) and r10mm ($r = -0.03$). However, MLDS has a strong negative correlation with rhum_09 ($r = -0.75$). Figure 3 shows how the environments of the two nodes selected by the model differ in terms of length of dry spell and relative humidity, expressed by the variables MLDS and rhum_09. There are no major differences between the environments in terms of rainfall variables such as r10mm and Rtotal. Therefore, the Plackett–Luce model discriminated two main environmental conditions, humid environments (node 2) and dry environments (node 3).

The Plackett–Luce tree model that resulted from fitting the aggregated data is presented in Figure 4.

Figure 5 presents a visualization of the Plackett–Luce tree model that is complementary to Figure 4. While some genotypes seem to outperform the reference (Calcutta 4), only

NARITA 8 does so in humid environments with statistical significance (Tables 6 and 7). However, there are statistically significant differences among genotypes.

The horizontal black bars in Figure 4 represent quasi-standard errors (Firth & De Menezes, 2004) and reflect the unbalanced distribution of genotype evaluations across the environments identified by the Plackett–Luce tree model (humid and dry) (Figure 6).

The (log) worth estimates for the Plackett–Luce tree model are presented in Table 6 for node 2 (humid environments) and in Table 7 for node 3 (dry environments). In addition to the difference in estimated worth values, we calculated reliability, which is the probability of each genotype outperforming the check or reference genotype (Eskridge & Mumm, 1992). The reliability estimates are conservative because of the shrinkage effect of using pseudo-rankings (Section 2.5).

## 3.2 | Stability assessment

The results of fitting 1000 Plackett–Luce trees by subsampling 80% of the data are presented in Figure 7. In 855 of the 1000 Plackett–Luce trees, the splitting variable was MLDS, as shown in the case of the single tree presented in Figure 4. Therefore, the original tree can be considered stable.
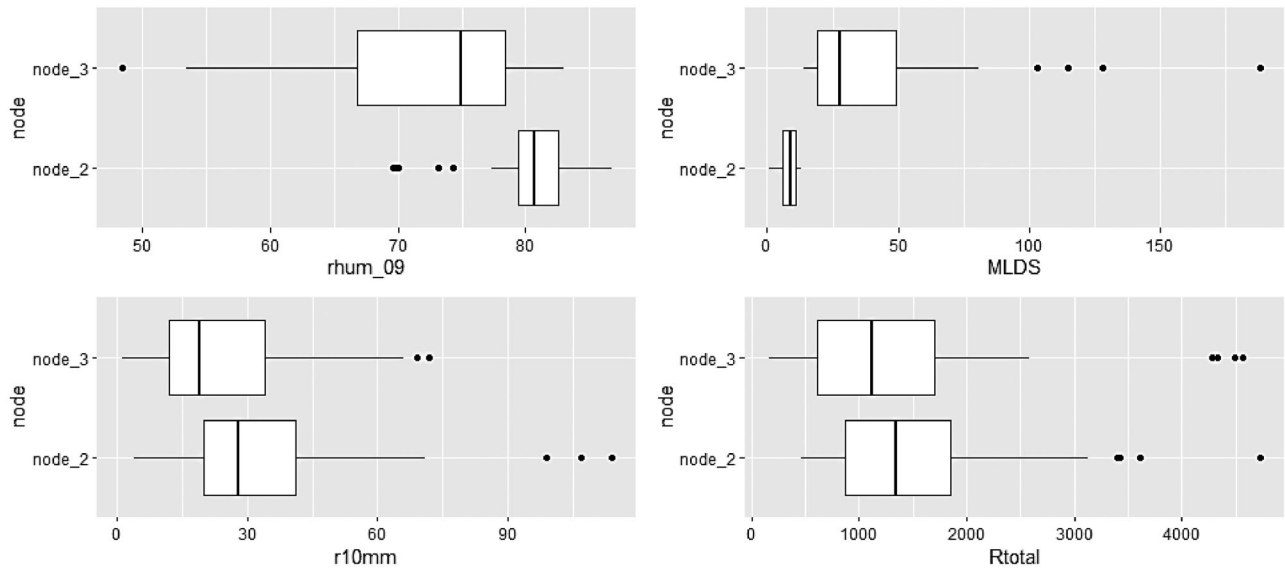
**FIGURE 3** Differences between the two nodes resulting from the Plackett–Luce tree model, in terms of relative daily humidity at 09:00 (rhum_09), maximum length of dry spell (MLDS), number of days with heavy precipitation (r10mm), and total precipitation on wet days (Rtotal).

**TABLE 6** Worth estimates and reliability for the top 10 ranked genotypes in humid environments (node 2). The worth estimates are presented in the logarithmic scale. The worth of genotype Calcutta 4 is zero as it serves as the reference.

| Genotype | Estimate | Std. error | z value | Pr(> |z|) | quasiSE | quasiVar | Reliability | relSE |
|---|---|---|---|---|---|---|---|---|
| NARITA 8 | 1.496 | 0.810 | 1.848 | 0.065 | 0.415 | 0.172 | 0.817 | 0.070 |
| FHIA-01 | 1.193 | 0.800 | 1.492 | 0.136 | 0.511 | 0.262 | 0.767 | 0.103 |
| NARITA 2 | 0.956 | 0.851 | 1.123 | 0.261 | 0.489 | 0.240 | 0.722 | 0.108 |
| EMB 403 | 0.314 | 1.140 | 0.275 | 0.783 | 0.959 | 0.920 | 0.578 | 0.234 |
| NARITA 14 | 0.309 | 0.785 | 0.394 | 0.693 | 0.365 | 0.133 | 0.577 | 0.091 |
| NARITA 23 | 0.201 | 0.786 | 0.256 | 0.798 | 0.364 | 0.133 | 0.550 | 0.091 |
| Calcutta 4 | 0.000 | 0.000 | NA | NA | 0.657 | 0.432 | NA | 0.159 |
| FHIA-25 | −0.148 | 0.738 | −0.200 | 0.841 | 0.377 | 0.142 | 0.463 | 0.091 |
| NARITA 9 | −0.216 | 0.865 | −0.249 | 0.803 | 0.514 | 0.265 | 0.446 | 0.121 |
| Pisang Ceylan | −0.225 | 0.679 | −0.332 | 0.740 | 0.222 | 0.049 | 0.444 | 0.054 |

Significance levels ***, 0.001; **, 0.01; *, 0.05; relSE, standard error of reliability.

**TABLE 7** Worth estimates and reliability for the top ten ranked genotypes in dry environments (node 3). The worth estimates are presented in the logarithmic scale. The worth of genotype Calcutta 4 is zero as it serves as the reference.

| Genotype | Estimate | Std. error | z value | Pr(> |z|) | quasiSE | quasiVar | Reliability | relSE |
|---|---|---|---|---|---|---|---|---|
| Saba | 0.036 | 1.394 | 0.026 | 0.979 | 0.677 | 0.458 | 0.509 | 0.164 |
| Calcutta 4 | 0.000 | 0.000 | NA | NA | 1.285 | 1.651 | NA | 0.283 |
| FHIA-03 | −0.060 | 1.586 | −0.038 | 0.970 | 0.964 | 0.929 | 0.485 | 0.221 |
| NARITA 24 | −0.117 | 1.350 | −0.087 | 0.931 | 0.341 | 0.116 | 0.471 | 0.083 |
| FHIA-01 | −0.294 | 1.455 | −0.202 | 0.840 | 0.729 | 0.531 | 0.427 | 0.163 |
| FHIA-02 | −0.322 | 1.705 | −0.189 | 0.850 | 1.146 | 1.313 | 0.420 | 0.233 |
| FHIA-21 | −0.325 | 1.413 | −0.230 | 0.818 | 0.705 | 0.497 | 0.419 | 0.156 |
| FHIA-18 | −0.411 | 1.496 | −0.275 | 0.783 | 0.813 | 0.661 | 0.399 | 0.171 |
| Rose | −0.680 | 1.589 | −0.428 | 0.669 | 0.962 | 0.925 | 0.336 | 0.174 |
| Pisang Ceylan | −0.685 | 1.299 | −0.527 | 0.598 | 0.258 | 0.066 | 0.335 | 0.055 |

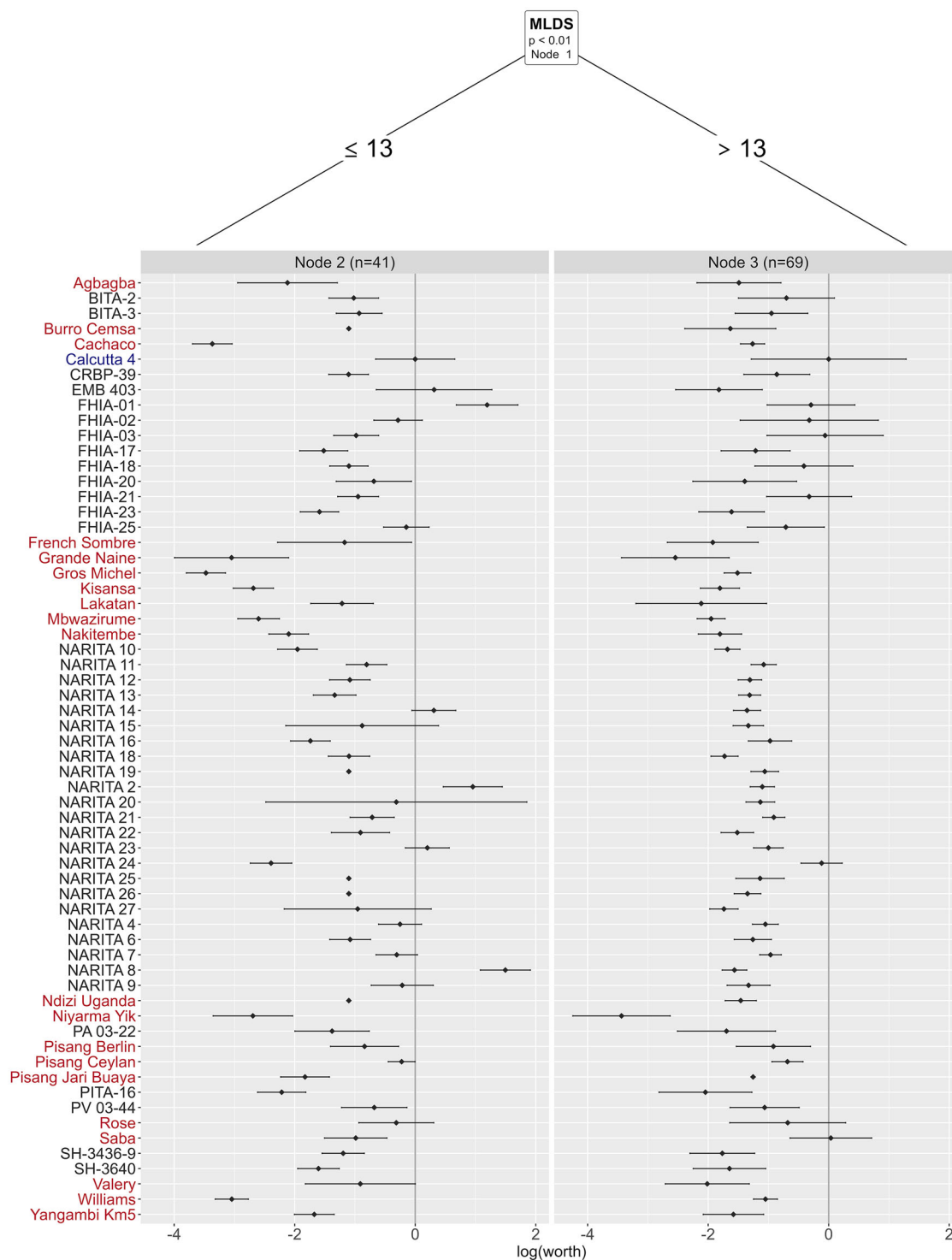Significance levels ***, 0.001; **, 0.01; *, 0.05; relSE, standard error of reliability.

**FIGURE 4** Plackett–Luce tree of *Musa* genotypes split into two nodes by variable maximum length of dry spell (MLDS) during the Black leaf streak disease (BLSD) evaluation period. The worth estimates of each genotype are presented on the *x*-axis on a logarithmic scale. The worth estimate for Calcutta 4 is set to zero as it served as the BLSD-resistant reference. The vertical gray lines show the zero intercept. Horizontal black bars represent quasi-standard errors of each estimated worth. The *y*-axis shows genotype names, with color indicating genotype status (blue, wild; red, landrace; gray, improved genotype). Node 2 = humid environments; node 3 = dry environments.
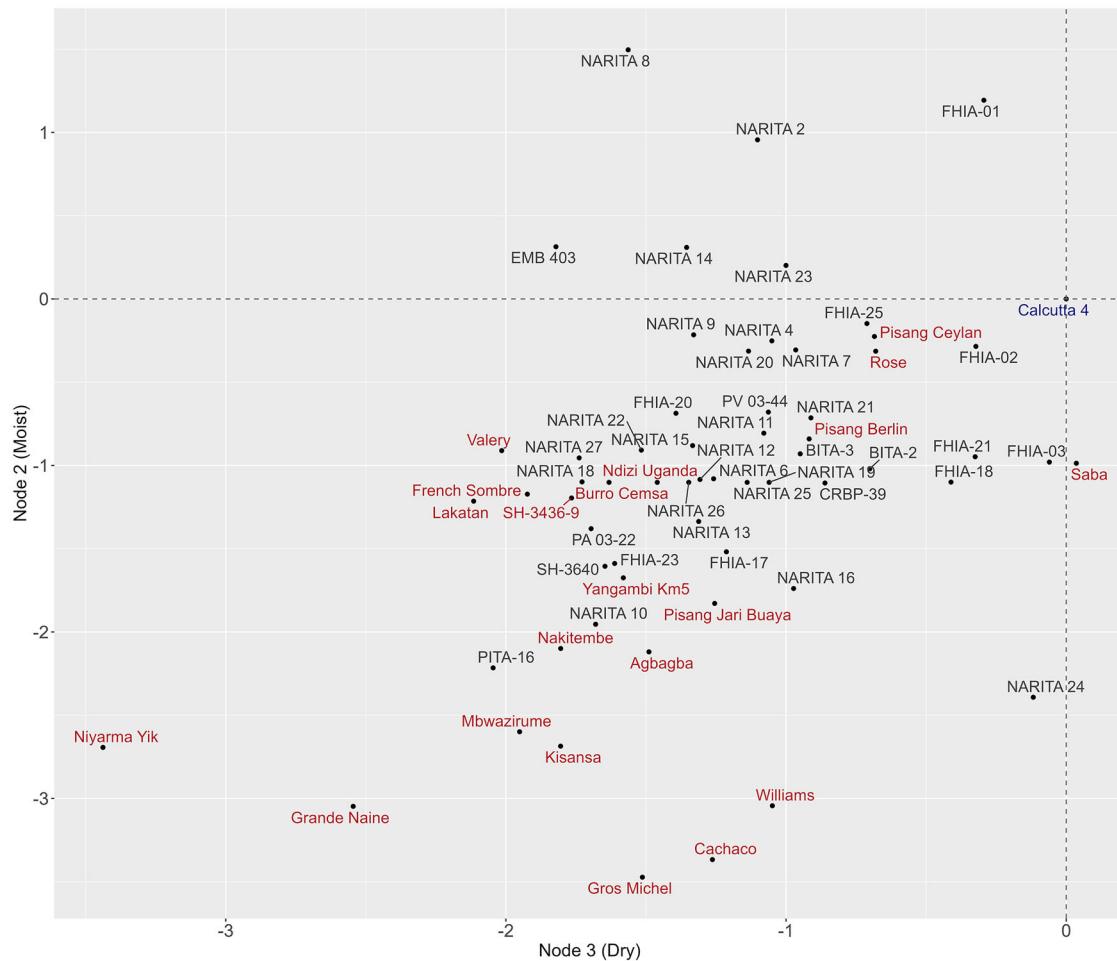
**FIGURE 5**　Worth estimates (on logarithmic scale) of each genotype in each of the nodes from the Plackett–Luce tree model. Color indicates genotype status (blue, wild; red, landrace; gray, improved genotype).

# 4 │ DISCUSSION

The Plackett–Luce tree model (Figure 4) identified the MLDS as the most important climatic variable determining *Musa* genotypes' reactions to BLSD. MLDS is a rainfall-derived climatic index, expressed as the number of days with precipitation less than 1 mm. While it is derived from rainfall, it is strongly negatively correlated with relative humidity ($r = -0.75$). The Plackett–Luce model partitioned the aggregated dataset into two contrasting environments: humid environments (node 2) in which the dry spell is less than or equal to 13 days, and dry environments (node 3) with a dry spell of more than 13 days. Humid environments (node 2) are assumed to be more favorable than dry environments (node 3) to BLSD development (Churchill, 2011; Guzman et al., 2018). Humidity is indeed required during various steps in the BLSD infection cycle, such as for infection efficacy (spore penetration in stomates), lesion growth on leaves, and fungus sporulation (Guzman et al., 2018). Therefore, humid environments (node 2) are considered appropriate climatic conditions in which to evaluate differences in BLSD (Perez-Vicente et al.,

2021). However, dry environments cannot be considered to be disease-free, as differences were found among genotypes. Environmental conditions act on both the host (banana plant) and the pathogen (*P. fijiensis*). From our results, it is not possible to discriminate between the two but only to formulate plausible hypotheses to be further investigated or considered in future research.

From the Plackett–Luce tree, we identified a contrasting reaction of genotypes across environments. For example, NARITAs 8 and 24 have relatively extreme and opposite responses to BLSD in humid (node 2) and dry (node 3) environments. In these cases, it might be that the genetic component of resistance in these genotypes has a different expression in different environments (Craenen & Ortiz, 1997) or at a particular stage (e.g., sporulation) of the disease cycle (Abadie et al., 2003). In the case of NARITA 8, its seems that its resistance component is expressed in humid (node 2) but not in dry (node 3) environments. On the other hand, NARITA 24 appeared susceptible in humid environments (node 2), while in dry environments (node 3), its performance did not differ from that of the reference,
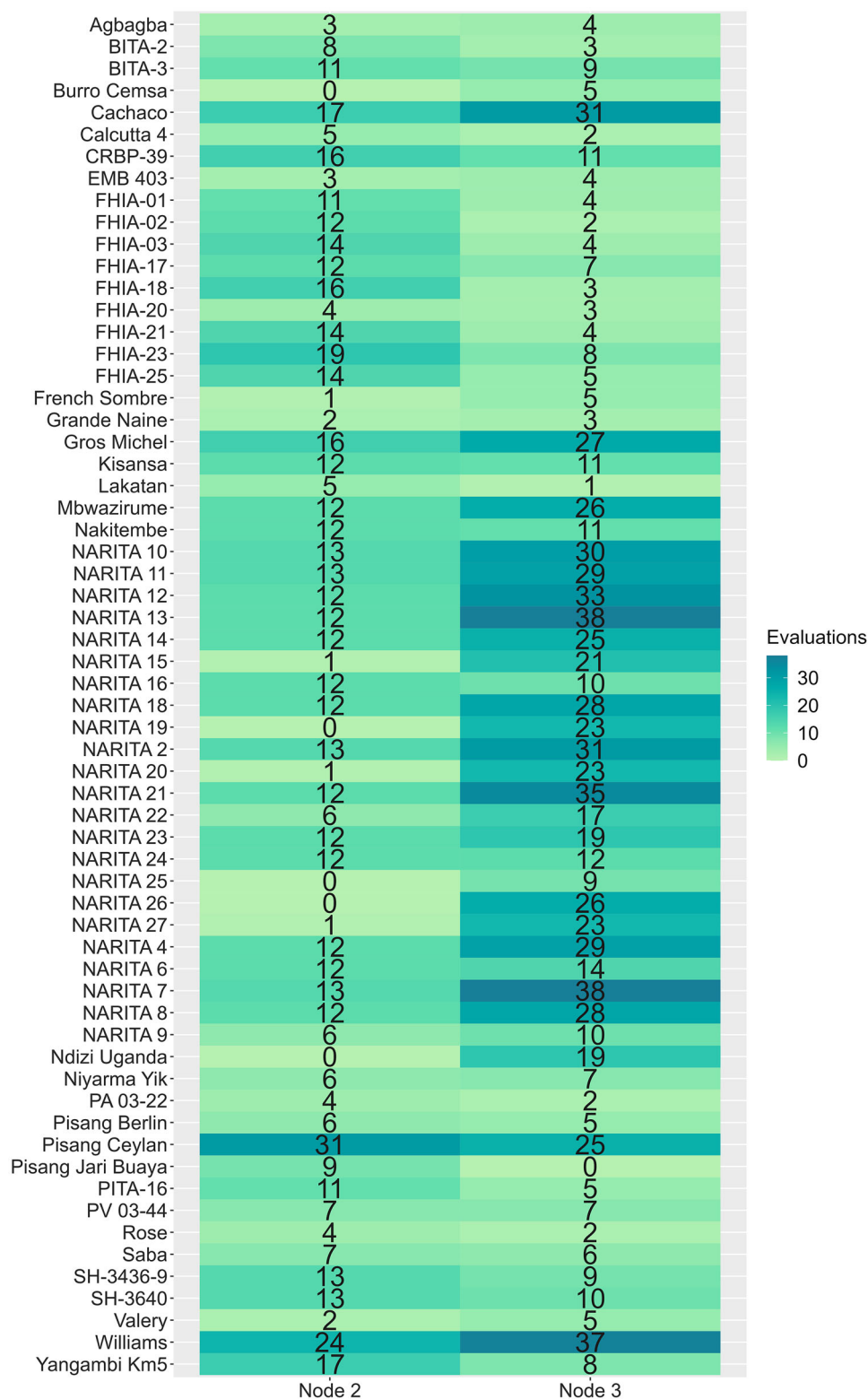
FIGURE 6    Number of times that each genotype has been evaluated in each environment (node 2 = humid; node 3 = dry).
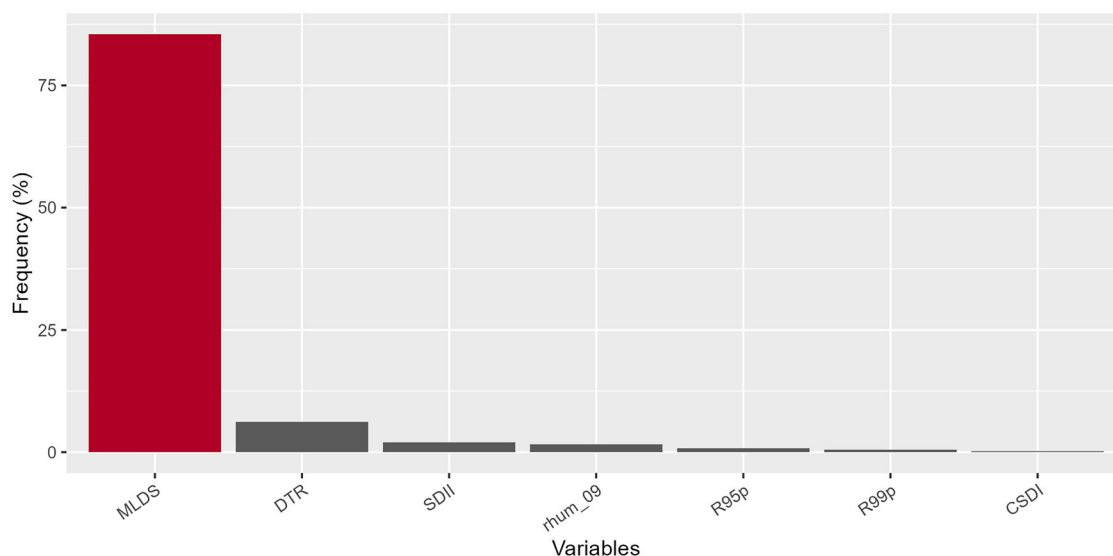
**FIGURE 7** Relative frequencies with which a variable is selected for a split in each of the 1,000 runs of the ensemble of trees. The red bar indicates the variable selected in the original tree. Only variables that were selected at least once are shown. See Table 5 for variables' descriptions. CDSI, cold spell duration index; DTR, diurnal temperature range; MLDS, maximum length of dry spell; R95p, R99p, total precipitation when rain >95th and >99th percentiles, respectively; rhum_09h, daily relative humidity at 9:00 a.m.; SDII, simple daily intensity index.

Calcutta 4. Our results might help to explain the contradictory results among previous studies in which NARITA 24 was evaluated. For instance, in evaluations of NARITAs by Tushemereirwe et al. (2015), NARITA 24 was among the best performing genotypes with respect to BLSD reaction. In contrast, it performed poorly in two locations in Uganda in evaluations conducted by Kimunye, Jomanga et al. (2021). Another contrasting result between environments is FHIA-03, which performed better in dry environments than in humid environments. We concur with Kimunye, Were et al. (2021) that the effect of environmental factors on the reaction of genotypes to BLSD should be further investigated at different locations.

While Calcutta 4 was used as the highly resistant reference, failure of a genotype to outperform Calcutta 4 cannot be considered poor performance. Calcutta 4 has qualitative resistance, which blocks disease development at an early stage (Guzman et al., 2018). In contrast, quantitative resistance allows disease development but seems to be more durable than qualitative resistance (Guzman et al., 2018). Therefore, we advise against interpreting our results through dichotomization of whether or not a genotype outperforms the resistant reference. In dry environments (node 3), differences between the reference, Calcutta 4, and each of the genotypes included in the top 10 are not statistically significant (Table 7). Hence, we cannot say that the top 10 genotypes performed differently from the reference, but they did perform better than the rest of the genotypes.

Water is a major limiting abiotic factor for banana growth (Turner, 1995). We hypothesize that plant growth could be negatively affected in dry conditions (node 3), as banana plants react very early to water deficit (Eyland et al., 2022) and require constant rainfall for normal development (Turner et al., 2007). The genotype FHIA-01 performed well in both humid and dry environments, which is in agreement with both its partial resistance to BLSD and its tolerance of extended periods of deficient rainfall (Rowe & Rosales, 1993). Furthermore, of the top 10 best performing genotypes in dry environments, 6 contain the *Musa balbisiana* (B) genome, which has been identified to contribute to drought tolerance (Thomas et al., 1998; van Wesemael et al., 2019; Vanhove et al., 2012). Abiotic stresses can affect plant reaction to diseases (Bostock et al., 2014). In the case of *Musa*, there is evidence that nutritional deficiencies and poor soil conditions predispose BLSD infection (Guzman et al., 2018). Our results suggest that predisposition to BLSD caused by drought should be further explored.

Evaluation metrics based on leaf number (e.g., YLS) strongly depend on plant growth (Guzman et al., 2018). Slower plant growth in dry environments could induce some bias in rankings in which the disease variable is linked to leaf number, such as YLS, NFL, and NSL. In spite of this potential bias, the Plackett–Luce tree model seems to adequately detect the different reactions of genotypes with partial resistance among environments (G × E), while it is also consistent with the expected performance of susceptible genotypes, such as Grand Naine, Gros Michel, and Niyarma Yik.

Our results could help to select genotypes of interest to breeders for further testing. For example, NARITA 8, FHIA-01, and NARITA 2 were not only the best performing genotypes in humid environments, but also the most reliable in outperforming the reference Calcutta 4 (Table 6). This

can provide impetus for breeding programs to include certain genotypes in new evaluations, based on their overall reliability in addition to their worth (ranking probability). In humid environments, only genotypes EMB 403, FHIA-01, and NAR-ITAs 2, 8, 14, 20, and 23 have more than 50% reliability, while in dry environments, only the landrace Saba marginally surpassed 50% reliability. Reliability is especially relevant given the lengthy process of developing and releasing a *Musa* genotype. For instance, FHIA-21 took 30 years from crossing to release (Tenkouano et al., 2019). Our results support the use of both ranking-probabilities and reliability as criteria for selecting genotypes for further testing in new locations, minimizing the risk of investment.

# 5 | CONCLUSIONS

Our work presents the first application of the data synthesis approach in combining heterogeneous trial data and using climatic data as model covariates to discover *Musa* genotypes' reactions to BLSD. We aggregated data from 110 evaluations in 31 heterogeneous trials evaluating *Musa* genotypes for reaction to BLSD. The rank-based data synthesis methodology enabled the comparison of 62 genotypes, aggregated from trials established at 22 unique locations, with a temporal range from 1990 to 2019. The large number of banana genotypes analyzed in our study would typically be challenging to compare in a single advanced multi-location testing trial. We have demonstrated how field trial environmental conditions can be reconstructed using publicly available climate datasets even where locally sensed weather data are lacking. In our work, the large temporal range for which the AgERA5 data is available (1979 to present) allowed the addition of climatic data as model covariates for all the data selected for the study. The MLDS, a precipitation-derived climatic index, was found to be the best splitting variable in the Plackett–Luce tree model. We found that humidity is the main climatic factor driving differential reactions of genotypes to BLSD. Our results support previous evidence that genetic components of resistance to BLSD are triggered under different environmental conditions, leading to different genotypic response patterns. We have provided insights to support the use of reliability in selecting genotypes for further evaluation.

One limitation of our study is the inherent information loss from the transformation of metric data to rankings. In the present case, information loss is reduced by the documented knowledge about different reactions of genotypes to BLSD. This supports the importance of considering expert knowledge in the implementation of the data synthesis approach (Brown et al., 2020).

Another limitation of our study is that despite the aggregation of several trials, the sample size of the aggregated dataset is still relatively small, due to the relative scarcity of *Musa*

evaluation data in public repositories. Increased availability of trial data in public repositories is therefore required for further applications of the data synthesis approach to efficiently (re)use crop trial data. We expect our findings to motivate plant breeding programs to share their data in public repositories, to enable future reanalysis with extended versions of the dataset used in our study.

# AUTHOR CONTRIBUTIONS

**David Brown**: Conceptualization; data curation; formal analysis; investigation; methodology; software; visualization; writing—original draft; writing—review and editing. **Sytze de Bruin**: Conceptualization; formal analysis; methodology; supervision; writing—review and editing. **Kauê de Sousa**: Data curation; formal analysis; methodology; software; writing—review and editing. **Catherine Abadie**: Formal analysis; investigation; writing—review and editing. **Sebastien Carpentier**: Formal analysis; investigation; writing—review and editing. **Lewis Machida**: Data curation; formal analysis; investigation; writing—review and editing. **Jacob van Etten**: Conceptualization; data curation; formal analysis; funding acquisition; investigation; methodology; software; supervision; visualization; writing—review and editing.

# CONFLICT OF INTEREST STATEMENT
The authors declare no conflict of interest.

# DATA AVAILABILITY STATEMENT
All the R code and data required to reproduce the analysis are publicly available in the public repository https://github.com/AgrDataSci/Data_Synthesis_Musa_Trials_BLSD

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