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Similarity between banana genotypes of the prata subgroup tolerant to fusarium wilt

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Abstract

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As there is no effective chemical control for fusarium wilt, the use of resistant varieties becomes the main control tool for the disease. Lopes et al. (2014) carried out the selection of genotypes tolerant to fusarium wilt from plants collected in the irrigated perimeter of Jaíba, in the state of Minas Gerais. In this sense, the objective was to study the similarity of these silver banana genotypes tolerant to fusarium wilt with Prata-Anã and to define descriptors most associated with productivity through correlation analysis. Four banana genotypes classified as tolerant to fusarium wilt, selected by Lopes et al. (2014), and the cultivar Prata-Anã were evaluated based on ten quantitative descriptors, in four production cycles (mother, daughter, granddaughter, great-granddaughter). The data obtained were first analyzed by multivariate analysis of variance ($p \leq 0.05$). Subsequently, principal component analysis (PCA) was carried out, the dissimilarity matrix of treatments was determined using the Mahalanobis distance and a dendrogram was carried out using the UPGMA method. The characteristics that showed significant effects ($p \leq 0.05$) were analyzed using the Pearson correlation coefficient. The PCA and dendrogram results indicate three genotypes were similar to Prata-Anã, suggesting agronomic and commercial potential. The correlation analysis reports the productivity variable positively correlated with all the characteristics evaluated, with the most intense correlation established being with the weight of the stemless bunch. Knowledge of the magnitude of the association between agronomic traits allows us to know how the selection of one trait can cause changes in others.

Keywords: correlation analysis; *Fusarium oxysporum*; multivariate analysis; *Musa* spp.
Abbreviations: Foc. (*Fusarium oxysporum* f. sp. *cubense);* PCA (principal component analysis); Unimontes (State University of Montes Claros); UPGMA (Unweighted Pair Group Method with Arithmetic Mean)

Introduction

The banana (*Musa* spp.) is one of the main fruit crops in the world, belonging to the Musaceae family (Hinge et al., 2020). In Brazil, the crop holds significant prominence in both consumption and production, ranking as the fourth largest banana producer globally, with more than 450 thousand hectares of cultivated areas (FAO, 2021; Ibge, 2022).

However, issues related to diseases are compromising the productive sustainability of the sector.

Several diseases compromise banana cultivation, among them, fusarium wilt stands out, caused by the pathogen *Fusarium oxysporum* f. sp. *cubense* (Foc.), which has made various crops unviable in various parts of the world, as well as in the Brazilian territory, especially in the Northern region of Minas Gerais (Castricini et al., 2017). This region is responsible for over 40% of the entire state's production, with 401 618 tons harvested in 2021 (Seapa-MG, 2022), with the Prata-Anã cultivar being the predominant one.

There are several banana cultivars cultivated in Brazil, but there is a consumer preference for the Prata type, which, however, does not exhibit resistance to fusarium wilt (Nomura et al., 2016). Due to the lack of effective chemical control for fusarium wilt, the use of resistant varieties becomes the main tool for disease management (Boari et al., 2019). Therefore, there is a need to obtain new genotypes that possess some level of tolerance to the disease, which has been the focus of research efforts over the years.

The identification of sources of resistance is the first step towards the goal of developing cultivars tolerant to Foc. (Ribeiro et al., 2018). Lopes et al. (2014) conducted the selection of genotypes tolerant to fusarium wilt from plants collected in the irrigated perimeter of Jaíba, in the city of Jaíba-MG, located in the Northern region of Minas Gerais. The collected genotypes belong to the Prata-anã cultivar (AAB). According to Hu et al. (2015), banana cultivars containing the B genome exhibit greater tolerance to biotic stresses.

However, besides identifying genotypes resistant and/or tolerant to diseases, these should be evaluated for their agronomic performance and other morphological characteristics, preferably in diverse environments. Despite the genotypes selected by Lopes et al. (2014) as fusarium wilt tolerant having been agronomically evaluated during the selection, this process took place in an area contaminated by *Fusarium oxysporum* f. sp. *cubense*. This contamination could limit the identification of their maximum agronomic potential. Therefore, evaluating the productive capacity in areas free and/or with low incidence of fusariosis is a strategy to validate the selection of the obtained genotypes, allowing for a future commercial recommendation of the selected genotypes.

Knowledge of the similarity between genotypes is also important to determine those with greater commercial potential and better adaptation to crop management practices. For this purpose, multivariate analysis has been a relevant tool, frequently adopted in studies involving banana cultivation (Giuggioli et al., 2020; Villegas-Santa & Castañeda-Sánchez, 2020; Brisibe et al., 2021; Chetry et al., 2023). This type of analysis allows for assessing the similarity between treatments considering a set of characters, enabling the breeder to conduct a more comprehensive study of the characteristics of interest and their correlations (Cruz et al., 2012). In this context, the study of correlations is used to assess the effect of changes in one character on another, making it possible to determine the degree of association between phenotypic descriptors and their influences on productive aspects during the selection process (Donato et al., 2006).

In light of this, the objective was to study, using a multivariate approach, the similarity of Fusarium-tolerant Prata banana genotypes with Prata-Anã and to define descriptors more associated with productivity through correlation analysis.

Material and Methods

The experiment was conducted on a property located in the municipality of Porteirinha, in the state of Minas Gerais, at the latitude 43º15′49,89″, longitude 15º38′34″ and altitude de 530 m. The soil in this area was classified as Eutrophic Red Oxisol (EMBRAPA, 2013). The climate of the region is classified as type 'Aw,' characterized as hot tropical and featuring a dry winter (De Sá Júnior, 2012).

The area designated for the experiment was cultivated with sorghum prior to the experiment, and in the two years preceding the planting, it remained fallow with spontaneous vegetation. Samples of the soil were collected at a depth of 0–20 cm, analyzed, and presented the following results: pH (em água) = 6.3; P = 7.5 (mg dm^{-3}); K = 153 (mg dm^{-3}); Na = 0.1 (cmol$_c$ dm^{-3}); Ca^{+2} = 3.5 (cmol$_c$ dm^{-3}); Mg = 0.8 (cmol$_c$ dm^{-3}); Al^{+3} = 0.0 (cmol$_c$ dm^{-3}); H+Al = 1.5 (cmol$_c$ dm^{-3}); SB = 4.8 (cmol$_c$dm^{-3}); t = 4.8 (cmol$_c$ dm^{-3}); T = 6.3 (cmol$_c$ dm^{-3}); V = 77 %; m = 0%; B = 0.3 (mg dm^{-3}); Cu = 1.0 (mg dm^{-3}); Fe = 12.8 (mg dm^{-3}); Mn = 50.5 (mg dm^{-3}); Zn = 1.7 (mg dm^{-3}); CE = 0,4 dS m^{-1}; Sand = 58 (dag kg^{-1}); Silt = 27 (dag kg^{-1}); Clay = 15 (dag kg^{-1}); textural class = sandy loam.

The soil preparation involved subsoiling, plowing, harrowing, and furrowing. The planting was carried out using micropropagated seedlings obtained from the Micropropagation Laboratory of State University of Montes Claros (Unimontes), with a spacing of 3.0 x 1.9 meters. The irrigation system used was microsprinklers. The necessary fertilizations throughout the cycle were carried out following the recommendations of Donato et al. (2021).

The treatments included four banana genotypes selected by Lopes et al. (2014) and classified as Fusarium wilt-tolerant (Gen1, Gen7, Gen13, and Gen19), in addition to the Prata-Anã cultivar (Gen100). Four production cycles (mother, daughter, granddaughter, great-granddaughter) were evaluated, arranged in a split-plot design over time, in a randomized complete block design, with four replications. Each plot consisted of four rows of four plants, totaling 16 plants. The four central plants were considered as the useful ones.

For quantitative assessment, 10 descriptors were evaluated: plant height at bunch emergence (ALT); days between flowering and harvest (DFC); number of leaves at harvest (NF); leaf area index (LAI), estimated using the model device AccuPAR LP-80® PAR / LAI Ceptometer da Decagon Devices Inc., and assessed when 50% of the plants in each cycle had produced bunches, as described by Lena et al. (2016); productivity (PROD), determined by multiplying the weight of the hands by the number of plants per hectare, dividing the value by 1000 (expressed in tons); bunch weight with stalk (PENG), bunch weight without stalk (PCSE); total number of hands (NTP); total number of fruits (NTF), and the number of bunches per year (NCA).

The statistical analyses were conducted using the R software (R Core Team, 2018). The multivariate analysis of variance was performed using the ‘manova’ function, applying the Wilks’ test ($p \leq 0.05$) to assess the significance of factors and their interaction. The analysis through principal component analysis (PCA) was conducted using the assistance of the function “princomp”. Additionally, the dissimilarity matrix of treatments (genotype:cycle) was determined using the Mahalanobis distance, and a dendrogram was constructed using the method UPGMA (Unweighted Pair Group Method with Arithmetic Mean), with the assistance of the ‘dist’ and ‘hclust’ functions”. For characteristics that showed significant effects ($p \leq 0.05$), Pearson correlation coefficients between traits were estimated using the ‘cor’ function. The significant estimates by the t-test ($p \leq 0.05$) were graphically represented using the ‘qgraph’ function.

Results

The multivariate analysis of variance identified interaction between genotypes and cycles, a significant effect of cycles, but no influence of genotypes independently ($p > 0.05$) (Table 1). In this case, the significant effect of cycles observed indicates that there are differences in the agronomic performance of mother, daughter, granddaughter, and great-granddaughter plants in the evaluated genotypes.

Considering the correlations established among the variables, for the first principal component (PCA1), the plant height variable (ALT) was the only characteristic that showed a strong positive correlation with PCA1 (Table 2). The other characteristics, except for productivity (PROD), exhibited negative correlations.

Table 2. Correlation estimates of 10 descriptors with the first two Principal Components (PCA1 and PCA2), studied in four fusarium wilt-tolerant banana genotypes and ‘Prata-Anã’ across four production cycles. Unimontes, Porteirinha, MG

Descriptors[1]	Genotype		Interaction G × C	
	PCA1	PCA2	PCA1	PCA2
ALT	0.98	-0.16	0.78	0.49
DFC	-0.31	0.72	-0.24	0.64
NF	-0.94	0.11	0.86	0.15
IAF	-0.40	0.33	-0.73	-0.40
PROD	0.03	-0.98	0.88	-0.09
PENG	-0.87	-0.41	0.66	-0.62
PCSE	0.23	-0.93	0.87	-0.08
NTP	-0.98	-0.15	0.76	-0.35
NTF	-0.96	-0.23	0.83	-0.25
NCA	-0.94	-0.14	0.77	0.49

[1] Plant height at bunch emergence (ALT), number of leaves (NF), leaf area index (IAF), productivity (PROD), bunch weight with stalk (PENG), bunch weight without stalk (PCSE), total number of hands (NTP), total number of fruits (NTF), and number of bunches per year (NCA)

Regarding the correlations established with PCA2, the highest values were observed with the characteristics days from flowering to harvest (DFC), productivity (PROD), and bunch weight without stalk (PCSE) (Table 2). The highest associations occurred positively with DFC and negatively with bunch weight with stalk (PENG), indicating that the genotypes had a shorter period from flowering to harvest and higher bunch weight with stalk.

Table 1. Multivariate analysis of variance in the study of 10 quantitative descriptors evaluated in four fusarium wilt-tolerant banana genotypes and Prata-Anã across four production cycles. Unimontes, Porteirinha, MG

FV	GL	Wilks	F Aprox.	GL num.	GL den.	pValor
Blocks	3	0.040	0.630	30.000	9.482	0.838
Genotypes	4	0.001	1.952	40.000	13.231	0.094^{ns}
Residue A	12					
Cycles	3	0.000	46.570	30.000	106.340	≤0.01**
Genotypes × Cycles	12	0.032	1.372	120.000	294.130	0.017*
Residue B	45					

^{*,**,ns}Significant at 1% and 5%, and not significant, respectively, by the Wilks’ test at a 5% significance level

As bidimensional representations carried out with the first two Principal Components provided good explanations of the total variation, with values of 84.34% (Figure 1A) and 74.33% (Figure 1 B). When evaluating the bidimensional representation of the dispersion of genotypes (Figure 1A), three distinct groups were observed. The genotypes that comprised Group II (Gen1, Gen7, and Gen13) were closer to Gen100, showing greater similarity to Prata-Anã. However, these Fusarium wilt-tolerant genotypes exhibited lower productivity than Prata-Anã.

Gen19 showed greater dissimilarity in relation to all evaluated genotypes, demonstrating to be highly divergent from the model cultivar (Gen100). Thus, it can be affirmed that the genotype Gen19, due to its larger size, lower leaf quantity, lower bunch weight with stalk, fewer hands, fewer fruits, and fewer bunches per year, becomes the genotype of lesser agronomic interest among those evaluated.

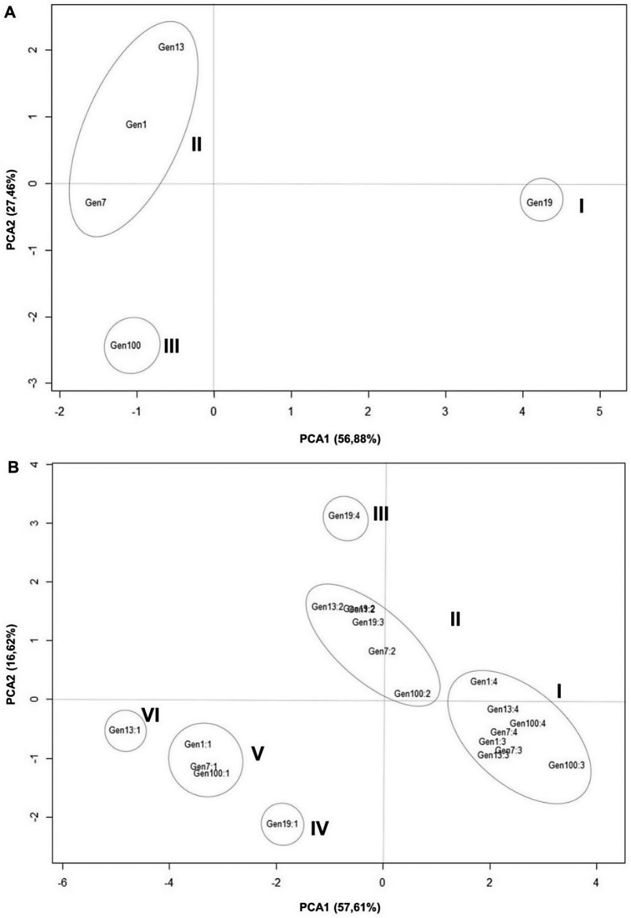

Fig. 1. Scatter plot of the first two Principal Components (PCA1 and PCA2) in the study of 10 quantitative descriptors evaluated in four Fusarium wilt-tolerant banana genotypes and Prata-Anã (Gen100) across four cultivation cycles. Unimontes, Porteirinha, MG. *Gen = refers to the genotype number evaluated in each cycle (:1; :2; :3 e :4)

Analyzing the dispersion of two scores considering genotypes and cycles, the formation of six groups was observed (I, II, III, IV, V e VI) (Figure 1B). Groups I and II, although distinct, were located close to each other. These two groups were composed of genotypes evaluated in cycles 2, 3, and 4.

The genotypes Gen1, Gen7, Gen13, and Gen100 in cycles 3 and 4 were the treatments that showed the highest results for the characteristics ALT, NF, PROD, PCSE, NTP, NTF, and NCA, but with lower values for IAF (Figure 1B). It is worth noting that, despite being superior to the other genotypes in cycle 1, genotype Gen19 was the only one that showed inferior performance in cycles 3 and 4. In the second cycle, it can be stated that the genotypes had similar performances.

On the other hand, groups IV, V, and VI were the most similar, characterized by being evaluated in cycle 1 (Figure 1B). Considering the correlations with the principal components within the genotype and cycle interaction (Table 2), group VI, formed by the genotype Gen13 in cycle 1, showed lower values for ALT, NF, PROD, PCSE, NTP, NTF, and NCA, and higher IAF. Meanwhile, genotype Gen19 in cycle 4 showed the shortest DFC and the highest PENG. Overall, it was observed that cycle 1 yielded the poorest agronomic results, except for the IAF characteristic.

In the UPGMA method, the results observed for the effects of genotypes corroborated with the results obtained by the principal component analysis (Figure 2A), that is, genotypes Gen1, Gen7, and Gen13 were grouped together with Prata-Anã. This similarity to Prata-Anã indicates that these genotypes, in addition to being fusarium wilt-tolerant, also have potential for future commercial recommendation. The method showed high cophenetic correlations (0.99/0.88), demonstrating reliability in the presented results.

When comparing the formation of clusters considering the interaction between genotypes and cycles, two groups were formed (Figure 2B). The cycles were the sources of variation that most contributed to the formation of clusters. Group I was formed by Fusarium wilt-tolerant genotypes and 'Prata-Anã' evaluated in cycle 1, while the other combinations of treatments (genotype:cycle) were grouped in the second group. It was also observed that, although not grouped into distinct clusters, genotype Gen19 tended to show greater separation from the other treatments, even within the group, especially in cycles 3 and 4.

When considering the interaction between genotypes and cycles, the results of the two multivariate methods were not

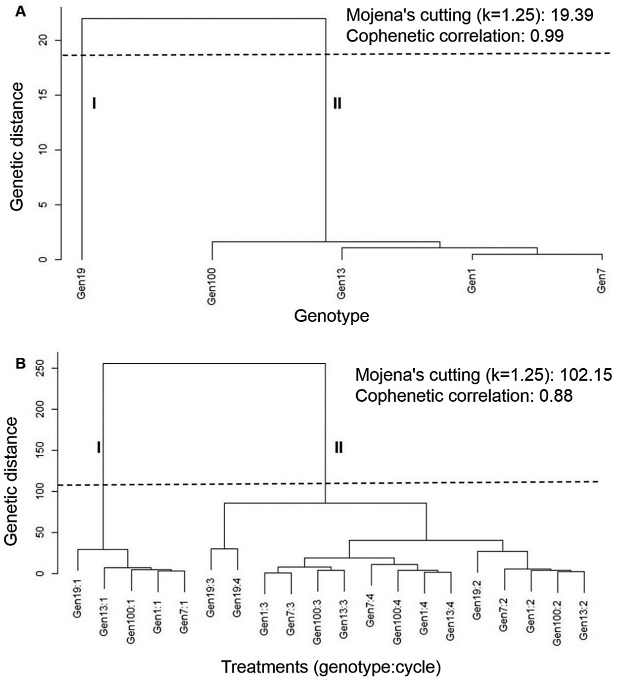

Fig. 2. Dendrogram obtained by the UPGMA algorithm from the Mahalanobis distance in the study of 10 quantitative characteristics evaluated in four fusarium wilt-tolerant banana genotypes and Prata-Anã (Gen100), across four cultivation cycles. Unimontes, Porteirinha, MG. *Gen= refers to the genotype number evaluated in each cycle (:1; :2; :3 e :4)

similar. The difference between the groups in the UPGMA method occurred only in relation to cycles, where the genotypes evaluated in cycle 1 were more dissimilar from the others (Figure 2B).

Gen19 was more influenced by the cycles, showing little variation in relation to PCA1 and high divergence in relation to PCA2. The other genotypes varied little in relation to PCA2 throughout the cycle, but there was a significant variation in PCA1. This is also observed in the dendrogram because the dispersion of these genotypes throughout the cycles is greater. It is further evidenced in the composition of the clusters, both by the principal components method (Figure 1A/B) and in the dendrograms by the UPGMA method (Figure 2B), where the cycles strongly influenced the formation.

Regarding the correlations between traits, performed by Pearson correlation, the leaf area index (IAF) was the only characteristic that showed significant negative correlations ($p \leq 0.05$). The leaf area index (IAF) showed a negative association of greater magnitude with the number of leaves (NF), moderate magnitude with plant height at bunch emergence (ALT), and lower magnitude with the number of bunches per year (NCA) (Figure 3).

As for the positive correlations established, those of greater magnitude occurred between bunch weight without stalk (PCSE) and productivity (PROD), and between total number of hands (NTP) and total number of fruits (NTF). Other relevant positive correlations, indicated by thicker lines, were between plant height at bunch emergence (ALT) and number of bunches per year (NCA) and ALT and number of leaves (NF). Positive correlations of lower magnitudes were observed for: bunch weight with stalk (PENG) and PROD, PENG and NTP, NF and NTF, NF and NTP, among others.

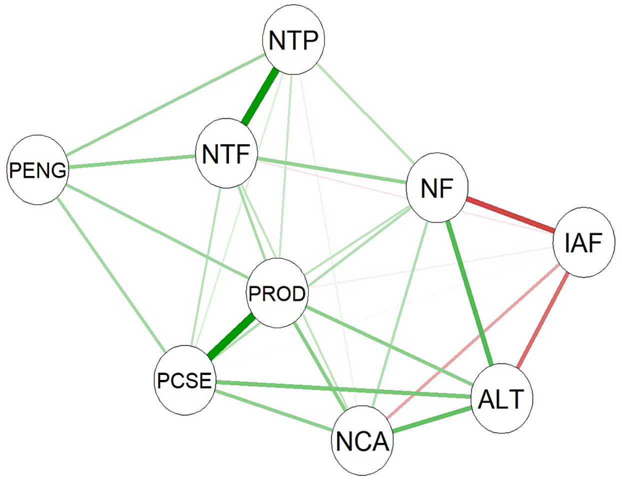

Fig. 3. Graphical scatter of the correlation matrix between the characteristics of plant height at bunch emission (ALT), number of leaves (NF), leaf area index (LAI), productivity (PROD), bunch weight with stem (PENG), weight stemless bunch (PCSE), total number of bunches (NTP), total number of fruits (NTF) and number of bunches per year (NCA), studied in four Fusarium wilt-tolerant banana genotypes and Prata-Anã, in four production cycles. Unimontes, Porteirinha, MG

The total number of fruits (NTF) established a significant correlation with all variables, except for plant height (ALT). This was observed for the number of bunches per year (NCA), which did not show a significant correlation ($p > 0.05$) only with bunch weight with stalk (PENG).

Productivity (PROD), the main agronomic characteristic evaluated, correlated positively and significantly ($p \leq 0.05$) with all the assessed characteristics. The strongest correlation was established with bunch weight without stalk

(PCSE), followed by the number of bunches per year (NCA), plant height (ALT), bunch weight with stalk (PENG) and total number of fruits (NTF) (Figure 3).

Discussion

Despite significant advancements in banana breeding in Brazil, especially regarding resistance to major diseases, the search for varietal ideotypes should be continuous and conducted across different cycles and growing environments (Arantes et al., 2017; Donato et al., 2018). This will ensure a more reliable selection of individuals with the most desirable traits. Due to the fact that cultivars of the 'Prata' subgroup are primarily generated by the selection of spontaneous mutations, theoretically, all material from the subgroup would have a standard morphology (Scherer et al., 2023). However, through statistical analyses, it becomes possible to observe and confirm the differences existing among materials of the same subgroup for certain characteristics.

The differentiated behavior of genotypes depending on the cycle, observed in the present study, is mainly associated with the degree of plant growth and vigor. In banana plants, the peak of productivity usually does not occur in the first cycle. It happens that the first two production cycles, cycles of the mother plant and the daughter plant, in general, are very contrasting regarding vegetative characteristics, with significant changes in plant height, vigor, fruit size, and consequently, productivity (Arantes et al., 2017; Marques et al., 2018; Siqueira et al., 2021). Typically, there is a gradual increase in these factors until the fourth cycle, when stabilization occurs. However, in the fourth cycle, results equal or less productive than in the third cycle may occur due to inadequate management or the action of other biotic or abiotic factors (Marques et al., 2018).

Principal component analysis (PCA) belongs to the family of dimension reduction methods and is particularly useful when the available data is large, with multiple variables or multiple observations per variable and with high correlation (Kherif & Latypova, 2020). The bidimensional representation is a good strategy in the study of dissimilarity between genotypes because it allows for better visualization of differences, even with many variables analyzed. According to Rencher (2002), for a good interpretation, it is necessary for two principal components to explain at least 70% of the total variance present in the dataset, a fact observed in this study.

The UPGMA is a hierarchical agglomerative method, indicated for composing clusters. In this method, the values of cophenetic correlation should be higher than 70% to represent the linear association between the dissimilarity matrix of the dendrogram and the matrix with the original distances (Silva & Dias, 2013), values found in the present study.

The results obtained from PCA analysis and the dendrogram show that the genotypes Gen1, Gen7, and Gen13 exhibited behavior similar to 'Prata-Anã,' one of the most cultivated varieties in Brazil (Salomão et al., 2020). It should be noted that the interest in cultivation by producers in Brazil for this variety is mainly due to its smaller size and good robustness, as this allows greater density, facilitates cultural treatments, is less susceptible to tipping over and facilitates harvesting (Arantes et al., 2017; Scherer et al., 2023).

Increasing plant density, especially in semi-arid regions, brings some advantages, such as improving water use efficiency, reducing damage caused by strong winds and excessive radiation, and, thinking about profitability, gross yield and liquid is greater for plantations with higher density compared to low density (Santos et al., 2019; Magalhães et al., 2020; Siqueira et al., 2021). Therefore, the observed similarity in this study indicates the agronomic and commercial potential existing in these genotypes, which also have the advantage of being tolerant to fusarium wilt (Lopes et al., 2014).

The correlation of productivity with production components (PENG, PCSE, NTF, and NCA) was expected, as these variables are directly associated, confirming the results obtained in other correlation studies (Uwimana et al., 2021; Assefa et al., 2023; Kalita et al., 2023). According to what was observed by Gichimu et al. (2020), growth variables, such as plant height, can be used as good production indicators, as they registered a significant positive correlation with bunch weight. Similar result can be observed in the present study, with a positively correlated moderate magnitude between the variable ALT and PROD and PCSE. Thus, the results suggest that improving these traits may contribute to an increase in crop productivity.

Kalita et al. (2023), evaluating 22 banana cultivars, observed the total number of leaves having a negative impact on productivity. Dos Santos (2019) observed that the correlation between the number of leaves and productivity was not significant. In the present study there was no negative effect, but a positive correlation of low magnitude.

The greater number of leaves contributes to an increase in leaf area (De Farias et al., 2013). In cases of negative correlation between NF and IAF, it is interpreted that the increase in the number of leaves caused a decrease in the leaf area index. In this case, the increase in the number of leaves may have resulted in the formation of leaves with smaller length and width, and, consequently, with a smaller leaf area. However, the positive correlations of NF with ALT and ALT with NCA, prove the importance of the number of leaves, since NF has a direct influence on bunch development (Soto Ballestero, 1992).

Dos Santos (2019) observed, evaluating banana cultivars ("BRS Princesa" and the 'Maçã' type), that the number of leaves at harvest had a positive and significant correlation with most productive characters, indicating that the greater the number of leaves at harvest, the greater the weight of the fruits, the weight of the bunches and the weight of the bunch. The greater or lesser number of live leaves at harvest may indicate a longer useful life of the leaf, since after floral differentiation the emission of this organ ceases (Moreira, 1987; Oliveira et al., 2007). The smaller the number of leaves at harvest, the lower the leaf photosynthetic efficiency, which reduces the availability of photoassimilates for the complete filling of the fruits, reducing their mass, the mass of the bunches and the mass of the bunch (Cavatte et al., 2012).

Knowledge of the magnitude of the association between agronomic traits is essential, as it allows us to know how the selection of one trait can cause changes in others (Castro et al., 2019). Thus, the significant correlations observed in this study can help in the prior recognition of more productive plots in commercial areas.

Conclusions

The fusariosis tolerant genotypes Gen1, Gen7 and Gen13 are the most similar to cv. Prata-Anã. The agronomic traits evaluated correlate positively with productivity.

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