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RESEARCH ARTICLE

Unravelling the genetic variability and trait interrelationships in Banana (*Musa spp.*)

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Abstract

Banana (*Musa spp.*) is a vital fruit crop contributing significantly to food security and global economy. Understanding the relationships between various traits, quality and yield is crucial for improving yield and fruit quality through targeted breeding programs. This study investigates the genetic variability, correlation and path analysis of key traits in banana to unravel their direct and indirect effects on yield. A diverse set of 47 banana accessions was evaluated for eleven traits. The pseudo stem girth, bunch length, number of hands, finger length, number of fingers per bunch and suckering capacity recorded higher estimates of Genotypic Coefficient of Variance (GCV) and Phenotypic Coefficient of Variation (PCV). Among the eleven traits, 10 traits showed high heritability and Genetic Advance as Percent of Mean (GAM) whereas the leaf length showed high heritability and moderate GAM. The number of fingers per bunch exhibited positive correlation with the number of leaves, bunch length, number of hands and pseudo stem girth indicating their contribution in yield determination. Path coefficient analysis further demonstrated that the number of hands per bunch had the highest positive direct effect on number of fingers per bunch, followed by pseudo stem girth, number of leaves and leaf length, highlighting their potential as selection criteria for yield improvement. Conversely, the traits bunch length showed indirect effect on yield through other traits indicating their complex role in banana productivity. These findings provide valuable insights into trait interrelationships and offer a framework for developing high-yielding banana varieties through innovative and conventional breeding strategies.

Keywords: banana; GCV; number of hands; path analysis

Introduction

Banana (*Musa spp.;* Family: Musaceae) is one of the oldest cultivated crops in the world, with its cultivation dating back to around 600 BC (1). It serves as a key staple fruit in tropical and subtropical regions. It is cherished not only for its nutritional value but also for its global popularity and economic importance. Banana is the second most important fruit crop in India (2). Most cultivated bananas are diploids (2n=2x=22), triploids (2n=3x=33) or tetraploids (2n=4x=44), which have originated from inter and intraspecific crosses between *M. acuminata* Colla. and *M. balbisiana* Colla., the two wild diploid species, in the *Eumusa* section of the *Musa* genus (3), which contributes the A and B genomes, respectively.

Bananas are of great cultural and economic significance in Southern Tamil Nadu. This region is renowned for growing diverse banana varieties, including the widely appreciated "Nendran" and "Rasthali," known for their exceptional flavour and nutritional value. These bananas are dietary staple, commonly featured in cooking traditional dishes and even in festive or religious ceremonies. Bananas are an excellent source of carbohydrates and essential vitamins, especially vitamin B (4). Banana is a key source of livelihood for many farmers in the region, contributing to the local economy. The banana, with its countless uses, is often called "Kalpataru", a plant of great worth. Farmers of Southern Tamil Nadu face challenges in banana cultivation due to unpredictable weather patterns, such as droughts and floods, which affect crop yield and quality. Identifying a suitable climate resilient variety tailored to the specific climate, soil and water conditions in Southern Tamil Nadu would help farmers achieve better yield, reduce crop loss and enhance resilience to environmental stress, ultimately improving their income and sustainability.

Crop improvement primary aim is to quantify the genetic parameters of the crop and understand the extent to which traits are heritable (5). Characterizing the existing germplasm is necessary step in the development of new cultivars. Calculating the genetic coefficient of variation alongside heritability provides a clear understanding of the potential progress that can be achieved through selection (6).

Furthermore, analysing these genetic correlations could aid in the development of more efficient and sustainable banana cultivation practices, potentially leading to increased yields and better economic outcomes for farmers and industries reliant on this adaptable crop. Taking all these factors into consideration, this study presents a comprehensive analysis of biometric data on eleven traits from 47 banana accessions, comprising six diploid, 40 triploid and one tetraploid clone of *Musa spp*.

Materials and Methods

The study encompassed forty-seven distinct banana accessions sourced from multiple locations of India (Table 1). The accessions collected were maintained at the genetic conservatory of Banana Research Station, VOC Agricultural College and Research Institute campus, Killikulam, Thoothukudi district, Tamil Nadu, where the field study took place during the year 2023-24 and 2024-25 in *kharif* season. The diploid banana accessions include 6 accessions, three having AA genome and three with AB genome. Triploid accessions include 40 accessions comprising four with AAA genome, 19 with AAB genome and 17 with ABB genome. A single tetraploid germplasm with ABBB genome has also been utilized for the study (Table 1).

The farm is located at 8.73° latitude and 77.87° longitude. The crop was spaced at 1.8 X 1.8 m with three replications in Random Block Design (RBD). Standard agricultural practices were abided to raise a good crop. Each replication of each accession had three randomly chosen plants for observation of 11 morphological parameters namely plant height (cm), number of leaves, suckering capacity, leaf length (cm), leaf width (cm), pseudostem girth (cm), bunch length (cm), number of hands per bunch, number of fingers per bunch, finger length (cm) and finger girth (cm).

Table 1. List of accessions used for the research

S.No.	Accession	Genome	S.No.	Accession	Genome
1.	Manoranjitham	AAA		Chengalikoden	ABB
2.	Co-3	AAB		Jahaji	AAA
3.	Poovan	AAB		Alpon	AAB
4.	Rajavazhai	AAA		Nendran	AAB
5.	Martaman	AAB		Krishna Vazhai	AAB
6.	Boothibale	ABB		Garomoina	AAB
7.	Udhayam	ABB		Jwari bale	AAB
8.	Kaveri kalki	ABB		Chingan	AAB
9.	Kachkel	ABB		Chenichampa	AAB
10.	Lamby	ABB		Hybrid Sawai	ABBB
11.	Peykunnan	ABB		Numaran	AAB
12.	Karimbontha	ABB		Pisang lilin	AA
13.	Bainsa	ABB		Kanai bansi	AA
14.	Kaitkhullung	ABB		Thella chakkarakeli	AAA
15.	Nutepong	ABB		Rasakadali	AB
16.	Ashy Batheesa	ABB		Laden	AAB
17.	Pacha Bontha Batheesa	ABB		Kariyanan	AA
18.	Birbutia	ABB		Ney Poovan	AB
19.	Kaveri saba	ABB		Malaikeli	AAB
20.	Pagar Banana	ABB		Padali moongli	AAB
21.	Laden Pointed	AAB		Kodappanila Kunnan	AB
22.	H1	AAB		Desikadali	ABB
23.	Sirumalai	AAB			
24.	Karpura chakkarakeli	AAB			
25.	H2	AAB			

Various biometric methods were then used to estimate the Genotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variation (PCV), broad-sense heritability (7) and genetic advance (8). These genetic parameters, correlation and path coefficient analyses were performed using R software, version 3.4.3. (9).

Results and Discussion

The heterogeneity of accessions was studied which aimed to improve the yield of banana. The assessment of genetic variability, broad-sense heritability (h^2b), Genetic Advance as Percent of Mean (GAM) and genotypic and phenotypic coefficients of variation were analysed for eleven morphological traits of 47 banana accessions.

Analysis of Variance (ANOVA)

The analysis of variance found to be significant at 1 % level with respect to the parameters *viz.,* plant height (cm), number of leaves, suckering capacity, leaf length (cm), leaf width (cm), pseudostem girth (cm), bunch length (cm), number of hands per bunch, number of fingers per bunch, finger length (cm) and finger girth (cm), indicating the presence of great amount of variability among the accessions (Table 2)

Genotypic and phenotypic coefficient of variation

The results are shown in Table 3, where PCV was only slightly higher than GCV for each trait, suggesting that the environment had less effect on the phenotypic expression. The number of fingers per bunch (52.22 %), pseudostem girth (48.39 %), number of hands (46.87 %), suckering capacity (35.04 %), finger length (30.47 %), bunch length (29.06 %) and plant height (20.37 %) reported maximum PCV. The number of fingers per bunch (51.92 %), pseudostem girth (48.17 %), the number of hands (46.65 %), suckering capacity (34.60 %), finger length (29.94 %) and bunch length (28.53 %) reported maximum GCV. Higher GCV and PCV for bunch weight, hand weight, pseudostem girth and suckering capacity in six accessions of

Table 2. Analysis of variance for morphological characters of Banana

S. No	Characters	Mean sum of squares		
		Replication	Treatment	Error
1	Plant Height	0.1328	4.6748	0.1027
2	Number of leaves	0.5299	9.0446	0.3931
3	Suckering capacity	0.0658	1557.8629	0.1300
4	Leaf length	39.2499	4750.0751	50.3467
5	Leaf width	2.0943	516.8702	7.4284
6	Pseudo stem girth	5.9999	1500.1215	6.7153
7	Bunch length	57.9738	2798.6809	27.1033
8	Number of Hands	0.2261	29.2313	0.1523
9	Number of Fingers	3.7910	4443.8464	14.6100
10	Finger length	0.8808	61.5317	0.7707
11	Finger girth	0.1475	13.4234	0.3616

Table 3. Genetic estimates of Banana morphological traits

Trait	GCV	PCV	Heritability	GA as % of Mean
PH	19.7789	20.3794	94.19	39.54
NL	15.3365	16.1133	90.59	30.07
SC	34.6033	35.0456	97.49	70.38
LL	10.2422	11.4680	79.77	18.84
LW	13.8502	14.5696	90.37	27.12
PG	48.1746	48.3986	99.08	98.78
BL	28.5328	29.0635	96.38	57.70
NH	46.6555	46.8719	99.08	95.66
NF	51.9260	52.2224	98.87	106.36
FL	29.9442	30.4701	96.58	60.62
FG	18.5321	19.2597	92.59	36.73

banana were reported in previous research work (10). Moderate GCV and PCV were recorded for fruit width (18.53 % and 19.25 %), number of leaves per plant (15.33 % and 16.11 %), leaf width (13.85 % and 14.56 %) and leaf length (10.24 % and 11.46 %) respectively. For plant height, pseudo stem girth, number of leaves per plant, leaf length, leaf width, suckering capacity, the number of hands, the number of fingers per bunch, finger length and finger girth, there was no significant difference between the phenotypic and genotypic coefficients of variation, indicating that these characteristics were less influenced by the environment. It shows that these variations have genetic base and selection can be exercised.

Heritability and genetic advance as percent mean

Heritability in a broad sense reveals the amount of heritable aspect of a trait. Heritability estimations differentiate between genetic and phenotypic variability and show whether and to what degree appropriate selection can lead to improvement (9). Parameters with high heritability can be enhanced directly through selection, as they are comparatively less influenced by the environment. The extent of heritability reflects the efficiency of selection in phenotypic performance (8). In the present study, all the traits exhibited high heritability, which ranged from 79.77 for leaf length to 99.08 % in pseudostem girth and number of hands with 99.08 %. It is followed by number of fingers per bunch (98.87 %), suckering capacity (97.49 %), finger length (96.58 %), bunch length (96.38 %), plant height (94.19 %), finger girth (92.59 %), number of leaves per plant (90.59 %), leaf width (90.37 %) and leaf length (79.77 %) (Table 3). Comparatively higher values of heritability for these traits indicate that a large proportion of the phenotypic coefficient of variance was attributable to the genotypic coefficient variance. Similar findings were already reported in earlier scientific investigation (11).

In this experiment, there was wide variation among 11 traits of banana for genetic advance (Table 3). Genetic advance as percent of mean, varied from 18.84 to 106.36. Nine traits *viz.,* plant height (39.54), pseudostem girth (30.07), suckering capacity (70.38), leaf width (27.12), bunch length (57.70), number of hands (95.66), number of fingers per bunch (106.36), finger length (60.62) and finger girth (36.73) showed higher genetic advance, along with high heritability. This indicates that these traits are mainly governed by additive type of gene action as reported by previous studies (8).

The hypothesis reported in earlier experiments (12), suggested that traits with high heritability and GA are controlled by additive gene effects. This indicated that choosing the more number of fingers per bunch, increased pseudostem girth, more number of hands, high suckering ability, length of fingers and lengthier bunch can lead to significant enhancements and may be utilized in breeding programs.

Further, high value of PCV, GCV and heritability, coupled with genetic advance, was exhibited by six traits *viz.,* number of fingers per bunch, pseudostem girth, number of hands, suckering capacity, finger length and bunch length which revealed that these are the ideal targets for selection-based breeding programs.

Correlation

In any breeding program, enhancing yield is primary goal however, yield is complex trait influenced by various factors making direct selection for yield ineffective. The traits that are less affected by the environment may help to enhance the fruit yield, if they are correlated. It is widely accepted that the relationship among various traits indicates the coordination of physiological processes typically achieved through gene linkage (13). In breeding program development, understanding the magnitude and strength of the associations between traits is a main prerequisite (14), as this knowledge allows for the genetic enhancement of one trait through the selection of another. The character association analysis via correlation coefficient for eleven traits is presented in Fig. 1 and Table 4. The interrelationships between the eleven characteristics varied significantly. In accordance with the scale in Fig. 1, the significant or nonsignificant differences are shown with green and red squares, which represent positive and negative correlations, respectively.

Plant height has highly significant positive correlation with pseudo stem girth (0.49) and bunch length (0.34). The number of leaves showed a highly significant positive correlation with pseudostem girth (0.58), bunch length (0.52), number of hands (0.34), number of fingers per bunch (0.42) and finger length (0.32). The result recorded with present investigation was on the line of results recorded by earlier experiments (11). Pseudostem girth showed positive correlation with plant height (0.49), number of leaves per plant (0.58), bunch length (0.66), number of hands (0.33), number of fingers per bunch (0.47) and finger length (0.42). It means that increase in pseudo-stem girth also increased the plant height, number of leaves per plant, bunch length, number of hands per bunch, number of fingers per bunch and finger length. Similar results were observed in previous studies (15) those reported that the pseudostem girth showed positive correlation with number of hands per bunch and number of fingers per bunch.

Bunch length showed significant positive correlation with plant height (0.34), number of leaves per plant (0.52), pseudostem girth (0.66), number of hands (0.47), number of fingers per bunch (0.40), finger length (0.71) and finger girth (0.52). The number of hands showed positive correlation with the number of leaves (0.34), pseudostem girth (0.33), bunch length (0.47) and number of fingers per bunch. The number of fingers per bunch showed significant positive correlation with the number of leaves (0.42), pseudostem girth (0.47), bunch length (0.40) and number of hands (0.87). The number of hands per bunch was positively correlated with pseudostem girth (0.60) and number of fingers per bunch (0.97) in previous studies (15). Number of fingers per bunch showed significant positive correlation with pseudostem girth (0.60). Finger length registered a significant positive correlation with the number of leaves (0.32), pseudostem girth (0.42), bunch length (0.71) and finger girth (0.67). Finger girth showed a positive correlation with bunch length (0.52) and finger length (0.67). Similarly, the correlation studies in various banana cultivars were also reported in earlier scientific investigations (11, 16, 17).

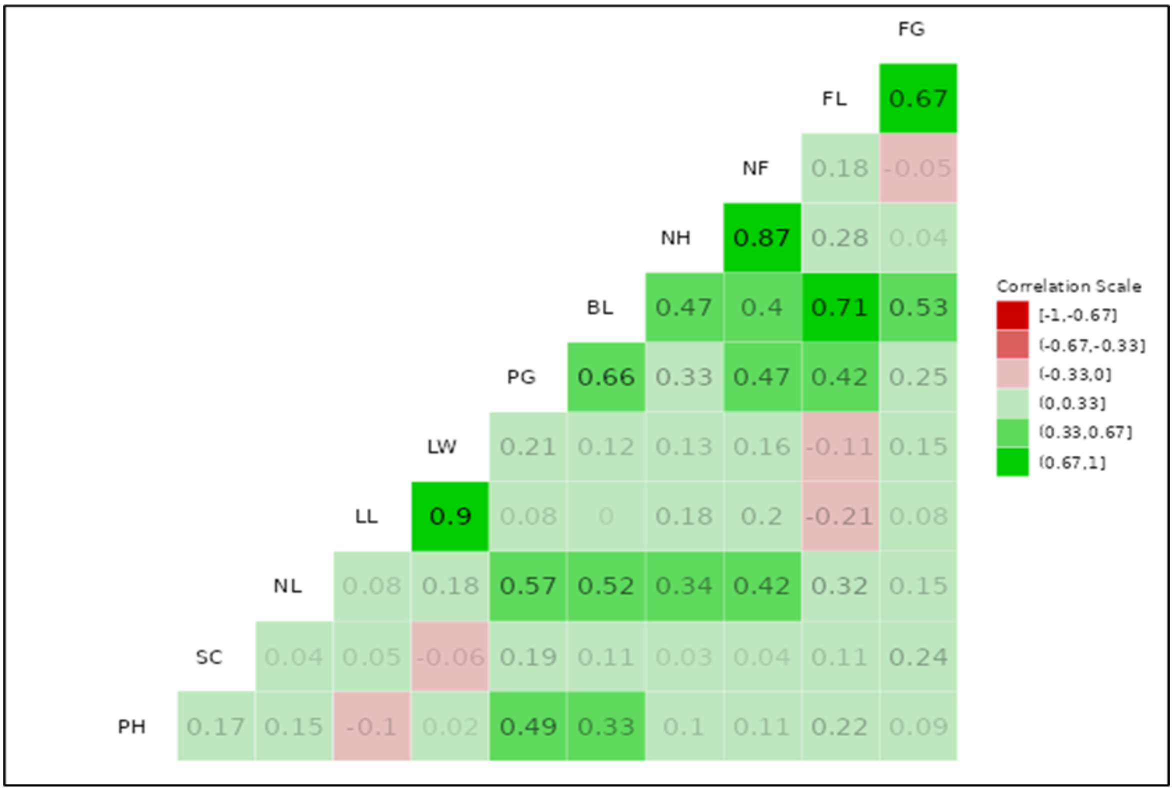

Fig. 1. Correlation plot for 11 growth and yield components of Banana.

Table 4. Simple correlation among the various biometric traits in Banana

Traits	PH	NL	SC	LL	LW	PG	BL	BW	NH	NF	FL
NL	0.14										
SC	0.17	0.04									
LL	-0.10	0.08	0.05								
LW	0.02	0.18	-0.06	0.90****							
PG	0.49***	0.58****	0.19	0.08	0.21						
BL	0.34*	0.52***	0.11	0.00	0.12	0.66****					
BW	0.15	-0.23	0.12	-0.14	0.23	0.35	0.56**				
NH	0.10	0.34*	0.03	0.18	0.13	0.33*	0.47***	0.59			
NF	0.11	0.42**	0.04	0.20	0.16	0.47***	0.40**	0.65**	0.87****		
FL	0.22	0.32*	0.11	-0.22	-0.11	0.42**	0.71****	0.23	0.28	0.18	
FG	0.09	0.15	0.24	0.08	0.15	0.25	0.52***	0.15	0.04	-0.05	0.67****

Significance levels: $p < .0001$ ****; $p < .001$ ***, $p < .01$ **, $p < .05$ *

PH:Plant height
NL:Number of leaves
SC:Suckering capacity
LL:Leaf length
LW:Leaf width
PG:Pseudostem girth
BL:Bunch length
NH:Number of hands per bunch
FL:Finger length
FG:Finger girth
NF:Number of fingers per bunch

Path analysis

It was utilized to structure the relationship between the dependent and the independent traits. To gain a better insight into the direct and indirect effect of each trait on yield and the use of selection pressure for yield enhancement, it is crucial to partition the correlation coefficient into direct and indirect effects via path coefficient analysis. The path coefficient data is presented in Table 5 and Fig. 2. In present investigation, number of hands (0.833) exhibited positive and high direct effect on the number of fingers per bunch followed by pseudostem girth (0.348), leaf length (0.061) and number of leaves per plant (0.06). The bunch length had a positive high

Table 5. Direct and indirect effects for eleven yield components of Palmyrah genotypes

Traits	PH	NL	SC	LL	LW	PG	BL	NH	FL	FG
PH	-0.074	0.009	-0.003	-0.006	-0.002	0.171	-0.049	0.08	-0.012	-0.005
NL	-0.011	0.06	-0.001	0.005	-0.013	0.200	-0.076	0.279	-0.018	-0.007
SC	-0.012	0.003	-0.015	0.003	0.004	0.067	-0.016	0.028	-0.006	-0.012
LL	0.008	0.005	-0.001	0.061	-0.063	0.028	0.00	0.15	0.012	-0.004
LW	-0.002	0.011	0.001	0.055	-0.070	0.074	-0.018	0.109	0.006	-0.008
PG	-0.036	0.034	-0.003	0.005	-0.015	0.348	-0.098	0.272	-0.023	-0.012
BL	-0.025	0.031	-0.002	0.000	-0.009	0.231	-0.147	0.390	-0.039	-0.026
NH	-0.007	0.02	-0.001	0.011	-0.009	0.114	-0.069	0.833	-0.015	-0.002
FL	-0.016	0.019	-0.002	-0.013	0.008	0.146	-0.105	0.230	-0.055	-0.034
FG	-0.007	0.009	-0.004	0.005	-0.01	0.087	-0.077	0.035	-0.037	-0.050

Residual effect: 0.158

PH:Plant height
NL:Number of leaves
SC:Suckering capacity
LL:Leaf length
LW:Leaf width
PG:Pseudostem girth
BL:Bunch length
NH:Number of hands per bunch
FL:Finger length
FG:Finger girth
NF:Number of fingers per bunch

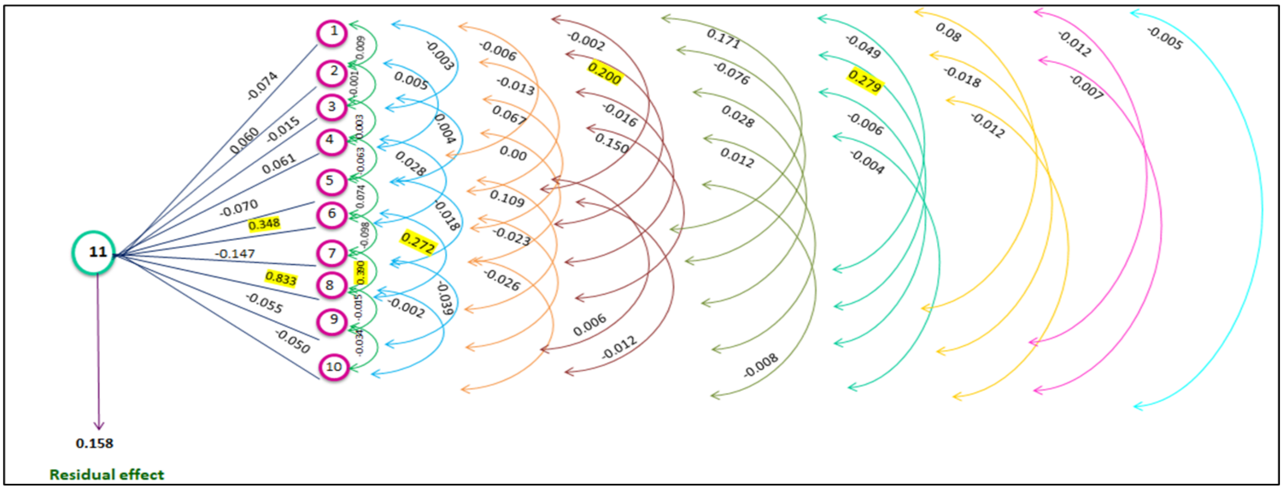

Fig. 2. Path diagram of the Banana morphological characters.

1.Plant height
2.Number of leaves
3.Suckering capacity
4.Leaf length
5.Leaf width
6.Pseudostem girth
7.Bunch length
8.Number of hands per bunch
9.Finger length
10.Finger girth
11.Number of fingers per bunch

indirect effect through the number of hands (0.390) and pseudostem girth (0.231) on the number of fingers per bunch. Pseudostem girth has high indirect positive effect through number of hands (0.272) on the number of fingers per bunch. Finger length had a high indirect positive effect through the number of hands per bunch (0.230) on number of fingers per bunch. These characters also showed a positive correlation with the number of fingers per bunch. Suckering capacity (-0.015), finger girth (-0.050), finger length (-0.055), plant height (-0.074), leaf width (-0.070) and bunch length (-0.147) showed direct negative effects on number of fingers per bunch. Analysis of path coefficient depicted that high direct and indirect contribution of number of fingers per bunch was manifested by number of hands per bunch and pseudostem girth. The selection based on these traits would significantly influence the yield of banana.

Conclusion

This study concluded that a significant genetic variability existed among the 47 banana accessions, offers promising opportunities for trait improvement through selection. High heritability and genetic advance were observed for key traits like pseudostem girth, number of hands and number of fingers per bunch, indicating their potential for enhancement. Correlation and path analysis underscored the importance of traits such as pseudostem girth and number of hands in improving banana yield. These traits are largely influenced by additive genetic effects, making them ideal candidates for breeding programs. The insights gained from this research can guide future efforts in banana crop improvement, aiming to increase productivity and sustainability. Ultimately, selecting traits based on their direct and indirect effects will be crucial in optimizing banana yields.

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Authors' contributions

SPR carried out the genetic studies, participated in the design of the study and drafted the manuscript. PA and ARA participated in the data collection, statistical analysis and edited the manuscript. MMI involved in collection of germplasm and supervision of experiment. APM, MMI, JM and TM involved in conducting and expertly supervised the entire experiment.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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