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Diversity assessment of synthetic hybrids of banana developed through hybridization based on morphological and yield characters

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Abstract

Banana is one of the most important fruit crops cultivated extensively in the tropical and sub-tropical regions of the world. Among these, India emerges as the foremost in banana production globally, however, it is also accompanied by numerous challenges especially in terms of biotic and abiotic stresses. These rising threats make the breeding programme focus on increasing the gene base of banana to guide informed crosses or breeding programmes for the development of new and improved cultivars. Therefore, the present study was undertaken to evaluate 27 synthetic banana hybrids developed through hybridization along with 18 parents utilized in developing these hybrids to explore the diversity and assess the effectiveness of characters influencing yield and morphological diversity. The result revealed high genetic variability, as indicated by significant GCV and PCV levels, suggests potential for further improvement. The tetraploid hybrids - H-916 produced the highest bunch weight of 25.86 kg while H-02-25 and H-02-34 showed better morphological vigour. Correlations between bunch weight and plant characteristics showed strong positive associations but the number of suckers demonstrated a negative association. Hierarchical cluster analysis grouped the genotypes into four distinct clusters which revealed differences between and within the ploidy levels. The growth characteristics of diploids and tetraploids displayed greater variability than those of triploids. The multivariate matrix demonstrated how different traits relate to each other and overall, the research demonstrates how these hybrids present promising breeding potential and proves genetic improvement to be the most sustainable approach to breed hybrids with good yield potential as well as increase the gene bank which can help identifying elite lines for specific banana improvement programmes. However, the findings require multi location and multi season validation for its stability prior to cultivar recommendation.

Key words: Banana, synthetic banana hybrids, genetic diversity, cluster analysis, ploidy

Introduction

Banana (*Musa* spp.; Musaceae) is one of the globally important fruit crops and a significant contributor to the global food commodity after rice, wheat and milk (Horry, 2000). Banana being non-seasonal, produces fruits throughout the year and contributes to the livelihood and food security to millions of people across the globe (Debnath *et al*., 2019; Lescot, 2020). With an estimated global production of 151.34 million metric tonnes, banana is the leading fruit crop. The top five countries namely, India, China, Indonesia, Nigeria, and Ecuador make 54.08 percent of the total banana production in the world. Among them, India is the largest producer of bananas in the global scenario accounting for an annual production of 37.61 million metric tonnes, which is equivalent to 24.85 percent of total world banana production (FAOSTAT, 2023). In India, Maharashtra is the largest producing state with an annual production of 6.53 million MT followed by Andhra Pradesh (5.83 million MT), Tamil Nadu (4.72 million MT), Uttar Pradesh (4.19 million MT) and Gujarat (4.01 million MT) (MoA&FW, 2023-24). However, recognition goes to India on becoming the largest producer of bananas in the world, but this achievement has not come easy as several challenges pertain to it, the most critical one being several pests and diseases that affect banana crops during the entire growth period, while nematodes, and *Fusarium* wilt identified as particularly destructive. Addressing these challenges, breeders are in a continuous process of developing new banana hybrids with desirable traits. Thus, breeding of cultivars to develop resistant or tolerant varieties is probably the most sustainable way of health management in banana crops. Increasingly, banana breeding is reliant on the development of hybrids from crossing wild species of bananas to cultivated banana types. Such hybrids are believed to produce superior lines with a higher level of genetic variation than their parents, exploiting desirable traits found in wild and cultivated species. Phenotypic evaluation and yield attributing characters would provide an important tool of understanding the morphological diversity and possibly the productivity potential of different banana hybrids, thereby assisting in identifying elite lines with desirable traits contributing to diversification and improvement of banana cultivars.

In agronomic evaluation studies, it is a common practice to measure quantitative descriptors such as phenotypic vegetative cycle and yield, which are easy to quantify (Ortiz, 1997). The present study focuses on these specific phenotypic traits as they are indicative of growth, earliness and productivity, all of which are vital for the identification and selection of superior individuals/hybrids. Such synthetic banana hybrids can also contribute to the conservation and enhancement of banana germplasm. By crossing wild bananas with cultivated one is another means by which researchers can broaden the existing genetic base, and conserve genetic diversity. This conserves genetic resources and develops a basis for studying and utilizing the different genetic traits demonstrated by the diverse banana species. These hybrids can further be evaluated and selected for their agronomic performance, disease resistance, marketability, and consumer preferences. Successful hybrids can then be released as new varieties, offering greater diversity in banana types available to farmers and consumers.

Taking into account all of the aforementioned factors, a study was undertaken with a primary objective to explore the diversity of twenty-seven banana hybrids developed using nineteen different cross combinations along with eighteen parents utilized in developing these hybrids.

Materials and methods

Plant materials and location: The present study was undertaken at College Orchard, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu state, India during the year 2021-2022. It involved evaluation of 27 synthetic hybrids of banana, comprising 10 diploids, 7 triploids and 10 tetraploids in addition to the 18 parents (Table 1). The study covered a total of 45 genotypes, and the experiment was laid out in randomized complete block design (RCBD) having five replications with 3 plants per replication planted at a spacing of 1.8 x 1.8 m. Fertilizers were applied as per the recommended dose (110:35:330 g of NPK/plant) used by the farmers of Tamil Nadu. Regular irrigation was applied using drip irrigation system in order to avoid water stress particularly during hot dry weather condition and critical crop growth stages. The physico-chemical properties of soils showed that the soil was clayey loam in texture, alkaline (pH - 8.28) and NPK content were 272:23:811 kg/ha. Geographically, Coimbatore lies around 426.72 m asl, at a place between 11°N latitude and 77°E longitude. The temperature ranged between 21.90 to 31.11 °C with 85.17% and 49.30% relative humidity in the morning and noon, respectively. Total rainfall in the year summed up to 697.96 mm.

Morphological and yield attributing characters: The characters related to plant (pseudostem height, pseudostem girth, number of functional leaves, leaf length, leaf girth, phyllochron and number of suckers) and bunch (bunch weight, number of hands per bunch, number of fingers in second hand, total fingers per bunch, finger length, finger girth, finger weight, pulp weight and peel weight) were thoroughly assessed to obtain comprehensive information necessary for discerning phenotypic and presumably genetic diversity among all the genotypes. The observations on plant characters were recorded at shooting and bunch traits at harvest. The data pertaining to morphological and bunch characteristics were gathered in accordance with the standardized descriptors for Banana (*Musa* spp.) (IPGRI-INIBAP/CIRAD, 1996). Crop duration was also recorded and expressed in days.

Statistical analysis: The differences among the hybrids and parents were evaluated by submitting the different characters to one-way ANOVA followed by Tukey at 5% level of significance for mean comparison. Correlation between the traits were determined using the Pearson correlation coefficients. All the aforementioned statistical analysis were performed using a web-application - KAU-GRAPES$_{1.0.0}$ (General R-shiny based Analysis Platform Empowered by Statistics). Several parameters, such as minimum value, maximum value, mean, skewness, heritability (h^2), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance as percent of mean (GA), standard deviations (SD), standard error of difference [SE(d)], and coefficient of variation (CV) were evaluated for the variables. CV was used as an indicator of variability. One way ANOVA and DMRT (P<0.05) analysis for ploidy wise dataset was performed using SPSS (version 26). Hierarchical cluster

Table 1. Cross combinations of the synthetic hybrids (H) and their parents (P) taken up for the study along with their ploidy status

Hybrids	Symbol	Parentage	Ploidy Status
H-531	H1	Poovan x Pisang Lilin	AAB
H-902	H2	Poovan x Rose	AAB
H-906	H3	Poovan x Pisang Lilin	AAAB
H-912	H4	H-516 x Rose	AAB
H-914	H5	Poovan x Ambalakadali	AAB
H-915	H6	Poovan x Ambalakadali	AAAB
H-916	H7	Poovan x Erachivazhai	AAAB
H-923	H8	Poovan x H-516	AAAB
H-926	H9	H-201 x Anaikomban	AAB
H-943	H10	Rose x H-516	AA
H-02-25	H11	Karpooravalli x Red Banana	AABB
H-02-34	H12	Karpooravalli x Red Banana	AABB
H-11-03	H13	Anaikomban x Pisang Lilin	AA
H-11-06	H14	Anaikomban x Pisang Lilin	AA
H-11-08	H15	Ambalakadali x Rose	AA
H-11-09	H16	Ambalakadali x Rose	AA
H-11-18	H17	Erachivazhai x Pisang Lilin	AA
H-11-21	H18	Tongat x Pisang Lilin	AAA
H-11-23	H19	Tongat x Pisang Lilin	AAAB
H-11-36	H20	H-911 x YKM-5	AA
H-11-37	H21	H-911 x YKM-5	AA
H-11-41	H22	H-940 x YKM-5	AA
H-11-44	H23	NPH-02-01 x Rose	AAAB
H-11-69	H24	H-201 x FHIA-1	AAAB
H-11-70	H25	H-201 x FHIA-1	AAAB
H-11-71	H26	H-201 x Rose	AAB
H-11-113	H27	Sanna Chenkadali x PA-03-44	AA
Parents			
FHIA-1	P1	-	AAAB
YKM-5	P2	-	AAA
Karpooravalli	P3	-	ABB
Tongat	P4	-	AA
Poovan	P5	-	AAB
Erachivazhai	P6	-	AA
Ambadakadali	P7	-	AA
Anaikomban	P8	-	AA
Pisang Lilin	P9	-	AA
Rose	P10	-	AA
Sanna chenkadali	P11	-	AA
Red Banana	P12	-	AAA
PA-03-44	P13	-	AAAB
NPH-02-01	P14	H-201 x Anaikomban	AAB
H-201	P15	(Bareli Chinia x Pisang Lilin) x Robusta	AB
H-516	P16	Anaikomban x Pisang Lilin	AAA
H-911	P17	H-516 x Rose	AA
H-940	P18	H-201 x H-516	AA

analysis (HCA) was performed by subjecting the variables to the libraries "dendextend", "circlize", "factoextra" and "cluster" to generate robust hierarchical clustering using RStudio (v 4.1.1). Prior to cluster analysis, all data were standardized to eliminate the influence of differences in measurement scales and units among variables. Hierarchical clustering was performed using Ward's minimum variance method based on Euclidean distance. Additionally, a multivariate matrix consisting of scatter plot along with histograms and correlations of important variables were performed using JMP® Pro 17.0.0 software to identify relationships between multiple variables and gain insights into the underlying patterns and trends in the data.

Results and discussion

Variability and morphological description: A total of 45 genotypes were included in the study (27 hybrids and 18 parents), and an analysis of variance revealed highly significant mean squares for all morphological and yield-related traits (Table 2). It was evident that there was considerable natural variation in all the traits, which shows the existence of enough genetic diversity among the genotypes that can further be enhanced with various breeding strategies. The extent of variability elucidated in this study hold significant importance due to their focus on morphological traits, which possess a high degree of heritability. High level of GCV and PCV were recorded for peel weight (64.67%, 65.94%), bunch weight (57.14%, 57.84%), pulp weight (53.35%, 53.51%) and finger weight (52.64%, 52.75%) respectively, indicating adequate genetic variability and these traits are important for further improvement (Table 3). Such high values of the GCV and PCV indicate that the genetic component contributes significantly to the variations as seen by several descriptors. The close proximity between GCV and PCV values for select traits suggests that these characteristics are predominantly influenced by genetic factors rather than environmental fluctuation. Mathukmi *et al*. (2022) reported high estimates of GCV and PCV for bunch weight (52.58 %, 53.05%), pulp weight (50.07%, 50.20%), peel weight (48.66%, 48.83%) and fruit weight (46.42%, 46.45%) respectively among 20 banana genotypes. Likewise, Rajamanickam and Rajmohan, (2020) obtained high estimates of GCV and PCV for number of fingers per bunch (64.80%, 65.22%), fruit weight (52.23%, 52.35%) and pulp weight (50.56%, 50.68%) respectively among 23 triploid banana ecotypes. Heritability estimates play a crucial role in predicting the reliability of phenotypic values and its estimates ranged from 46.07% (number of leaves) to 99.60% (fruit weight). Additionally, genetic advance serves as an indicator of the progress that can be expected through the implementation of selection strategies within the relevant population and in the present study, genetic advance as percent of mean varied from 12.87% (number of leaves) to 130.67% (Peel weight) (Table 3). Heritability alone indicates effectiveness based on phenotypic performance and high broad-sense heritability with high genetic advance suggests strong genetic control and potential selection

Table 2. Mean square for morphological and yield attributing characters in banana genotypes

Source of variation	df	PH (cm)	PG (cm)	NOL	LL (cm)	LW (cm)	LA (m^2)	PLC (Days)	NOS	PTH (Days)
Genotypes	44	20607.46**	1098.47**	9.30**	3871.86**	599.38**	39.61**	3.39**	61.66**	11939.42**
Replication	4	0.92	2.75	2.18	8.44	5.99	2.09	0.32	1.32	15.30
Error	176	22.21	10.78	1.76	20.45	12.13	1.81	0.24	2.38	13.35
Source of variation		BW (kg)	NOH	NOF	TFB	FL (cm)	FG (cm)	FW (g)	PuW (g)	PeW (g)
Genotypes	44	176.13**	15.67**	16.24**	6632.83**	67.57**	39.00**	10213.89**	4889.37**	1563.62**
Replication	4	2.25	1.75	4.16	82.83	0.73	0.28	2.04	19.89	19.03
Error	176	0.88	0.48	1.48	15.29	0.35	0.35	8.20	5.89	12.26

** Significant at $P< 0.01$. Please refer to Table 3 for abbreviation

Table 3. Descriptive statistics for the morphological and yield attributing characters in synthetic hybrids and parents

Character	Abbreviation	Unit	Min.	Max.	Mean	Skewness	h^2 (%)	GCV (%)	PCV (%)	GA mean (%)	SD	SE (d)	CV (%)
Pseudostem Height	PH	cm	114.80	381.60	237.09	0.217	99.46	27.06	27.14	55.60	64.20	2.94	27.08
Pseudostem Girth	PG	cm	26.00	82.20	57.28	-0.224	95.28	25.75	26.38	51.78	14.82	2.05	25.88
Number of leaves per plant	NOL	Number	10.80	17.40	13.34	0.693	46.07	9.20	13.56	12.87	1.36	0.84	10.22
Leaf length	LL	cm	117.40	231.62	169.41	0.037	97.41	16.38	16.60	33.31	27.83	2.84	16.43
Leaf width	LW	cm	41.00	86.46	64.07	-0.363	90.64	16.92	17.77	33.17	10.95	2.20	17.09
Leaf area	LA	cm^2	3.29	17.04	8.04	0.544	80.61	34.21	38.11	63.28	2.81	0.85	35.03
Phyllochron	PLC	Days	6.80	10.80	7.78	1.352	72.83	10.22	11.98	17.97	0.82	0.30	10.59
Number of suckers	NOS	Number	2.80	19.60	6.75	1.580	83.31	51.00	55.88	95.90	3.51	0.97	52.01
Planting to Shooting	PTS	Days	166.80	381.20	250.10	0.911	99.53	15.79	15.82	32.44	39.50	1.70	15.79
Shooting to Harvest	STH	Days	87.60	157.20	120.39	0.699	97.02	13.45	13.65	27.28	16.24	1.80	13.49
Planting to Harvest	PTH	Days	270.80	533.60	370.49	0.882	99.44	13.18	13.22	27.08	48.87	2.31	13.19
Bunch Weight	BW	kg	1.47	25.86	10.36	0.253	97.56	57.14	57.85	116.26	5.94	0.60	57.28
Number of hands	NOH	Number	4.20	12.00	7.59	0.220	86.46	22.97	24.70	43.99	1.77	0.44	23.32
Number of fingers in 2nd hand	NOF	Number	11.00	18.80	15.40	-0.302	66.55	11.15	13.67	18.75	1.80	0.78	11.70
Total fingers per bunch	TFB	Number	49.80	183.00	110.10	0.226	98.86	33.04	33.23	67.68	36.42	2.59	33.08
Finger length	FL	cm	6.58	24.02	13.84	0.124	97.48	26.49	26.83	53.88	3.68	0.37	26.56
Finger girth	FG	cm	4.60	15.70	10.67	-0.646	95.64	26.06	26.64	52.49	2.79	0.37	26.17
Finger weight	FW	g	14.78	192.06	85.82	0.342	99.60	52.65	52.75	108.23	45.20	1.79	52.67
Pulp weight	PuW	g	7.40	128.20	58.58	0.137	99.40	53.35	53.51	109.57	31.27	1.57	53.38
Peel weight	PeW	g	5.32	79.56	27.24	1.323	96.20	64.67	65.94	130.67	17.68	2.22	64.93
Pulp peel ratio	PPR	-	0.67	5.88	2.35	1.137	78.32	47.72	53.92	87.00	1.14	0.38	48.26

response. Therefore, combined heritability and genetic advance enhance selection prediction. In the present study, high heritability coupled with high genetic advance as percent mean was recorded for bunch weight, finger weight, pulp weight and peel weight. Hence, it can be deduced that these traits may be influenced by additive genetic factors, indicating that phenotypic selection would be advantageous for their enhancement**.**

The coefficient of variation for the characters related to the banana plant ranged from 10.22 % to 64.93%**.** However**,** peel weight exhibited the highest CV (64.93%) followed by bunch weight (CV = 57.28%) and pulp weight (CV 53.38%), which showed significant variation in pulp and peel weight of the fruits that greatly influence the bunch weight. Furthermore, the lowest CV (10.22%) was observed in the number of leaves per plant followed by Phyllochron (CV = 10.59%) (Table 3).

The analysis of synthetic banana hybrids revealed that the hybrid H-02-25 exhibited the greatest morphological characteristics followed by H-02-34. Among the parents, Red Banana and Karpooravalli exhibited better growth and the hybrids H-02-25 and H-02-34 had Karpooravalli x Red Banana as their parental combination, indicating their close relationship.

The banana is herbaceous but can carry large bunches of fruit. Leaf characteristics are important to the growth and development of fruit. The variability of leaf trait was moderate to high with CV values ranged from 10.22 to 35.03%. The highest number of functional leaves per plant (17.40) and leaf area per plant (17.04 m^2) was found in H-02-25. Phyllochron ranged from 7.00 to 10.80 days, whereas suckers per mat ranged from 3.00 in H-531 to 19.60 in H-11-37. The total crop duration was found to be in the range of 270.80 (H-201) to 533.60 days (Red Banana) in the case of synthetic hybrids, whereas it was in the range of 275.60 (H-11-36) to 460.40 days (H-02-34) (Fig. 1).

Wide variations were seen for yield and bunch related traits with CV values ranging from 11.70% for number of fingers in second hand to 64.93% for peel weight (Table 3). The highest bunch weight was observed in H-916 (25.86 kg), the number of hands per bunch in H-11-23 (10.40) and total fingers per bunch in H-914 (167.40). Maximum fruit weight was recorded in H-11-21 (192.06 g) followed by H-916 (190.12 g) while minimum bunch weight (1.46kg) and fruit weight (15.72 g) were recorded in H-11-03. The large variation seen in the genotypes indicates wide genetic diversity which can be used for selection and heterosis breeding.

In addition to the response of the hybrids, we further categorized the hybrids based on their ploidy level and the result revealed significant variation among different ploidy groups. In this context, DMRT ($P<0.05$) was performed to indicate the difference between different ploidy level (Table 4) and compared the distribution of morphological variables and bunch traits among different ploidy level. It revealed higher variability in diploids and tetraploids as compared to triploids in terms of pseudostem height and girth but for bunch traits, the variability was higher in diploids as compared to triploids and tetraploids. The elevated plant height and girth noticed in tetraploids can be attributed to the dosage complementation that arises from their ploidy (Sankar, 2013). Hybrids with shorter plant height was obtained, particularly when Pisang Lilin, Rose and H-516 were involved as a male parent. These findings suggest that the parental traits related to dwarfism can be inherited by offspring. These observations imply that segregation for plant height can allow the breeder to select comparatively semi tall or dwarf plant. An increase in ploidy level resulted in a decrease in sucker production (Bhende and Kurien, 2016) and same behaviour was reported in this study. Blomme *et al*. (2000) reported that diploid bananas have an unregulated suckering behaviour, which means all suckers grow vigorously. On the other hand, triploids and tetraploids have regulated or inhibited suckering, where only 2 or 3 suckers grow vigorously or no sucker grows vigorously, respectively. The economic value of good bunch weight cannot be overstated in *Musa* breeding programs. Significant variations in bunch weight were recorded. The tetraploid hybrids - H-916 depicted highest bunch weight, followed by H-11-23 and H-02-25. The higher bunch weight of tetraploid hybrids corresponded with a greater number of leaves, finger length, girth and weight, rather than the total number of hands and fingers. It is thus plausible that higher order epistatic interactions play a key role in determining the actual performance of hybrids. The result is in line with previous findings by different authors (Goncalves *et al*., 2018; Kamira *et al*., 2016 and Sagar *et al*., 2017) who identified varietal differences in bunch weight across various banana genotypes. Banana bunch weight was found to be influenced by the number of fruits per bunch and the weight of individual fruits (Lédo *et al*., 2008).

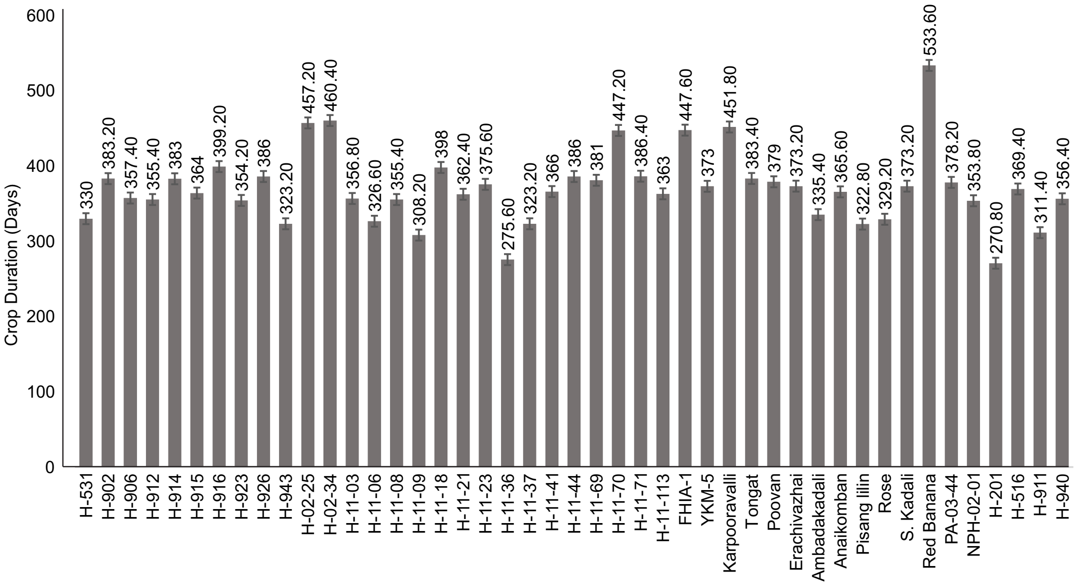

Fig. 1. Crop duration of synthetic hybrids of banana and their parents

Multivariate matrix: The multivariate analysis for important traits was conducted, exhibiting the scatter plot, phenotypic frequency distribution and correlation (Fig. 2). The scatter plots depicted a linear trend for most of the variables, while the histogram presented the phenotypic frequency distribution of each variable, emphasizing the overall similarities in their growth habits. Pearson correlation analysis was carried out to assess the strength of the relationship between the traits examined. Pseudostem height

Table 4. DMRT analysis of growth and bunch characters among different ploidy levels of 27 synthetic hybrids of banana

Ploidy	PH	PG	NOL	LL	LW	LA	PLC	NOS	PTS	STH	PTH
Diploid	205.16^{a}	46.92^{a}	13.42a	160.88^{a}	57.24^{a}	6.84^{a}	7.48^{a}	10.92^{a}	231.00^{a}	108.60^{a}	339.60^{a}
Triploid	241.92^{a}	61.97^{b}	13.26a	176.40^{ab}	65.83^{b}	8.41^{ab}	7.77^{ab}	5.80^{a}	242.86^{ab}	126.63^{b}	369.49^{ab}
Tetraploid	301.24^{b}	70.71^{b}	13.50a	196.36^{b}	73.53^{c}	10.61^{b}	8.56^{b}	4.84^{b}	269.96^{b}	128.26^{b}	398.22^{a}
SD	58.52	59.63	1.56	26.97	65.50	2.89	0.91	3.95	34.22	15.14	42.24
SEm	11.26	14.21	0.30	5.19	9.88	0.56	0.17	0.76	6.58	2.91	8.13
Ploidy	BW	NOH	NOF	TFB	FL	FG	FW	PuW	PeW	PPR	
Diploid	6.27^{a}	6.84^{a}	15.10^{a}	90.42^{a}	12.50^{a}	8.03^{a}	50.07^{a}	32.53^{a}	17.54^{a}	1.80^{a}	
Triploid	12.43^{b}	7.91^{ab}	15.71^{a}	110.89^{ab}	15.71^{a}	12.37^{b}	115.60^{b}	76.08^{b}	39.52^{b}	2.25^{a}	
Tetraploid	14.70^{b}	8.60^{b}	15.72^{a}	128.20^{b}	13.60^{a}	12.18^{b}	110.97^{b}	74.48^{b}	36.49^{b}	2.43^{a}	
SD	5.99	1.56	1.81	35.01	3.78	2.74	48.45	31.74	19.50	1.02	
SE	1.15	0.30	0.35	6.74	0.73	0.53	9.32	6.10	3.75	0.19	

depicted strong positive correlation (SPC) with pseudostem girth (r = 0.89), leaf area (r = 0.79) and bunch weight (r = 0.63). Number of suckers showed generally weak associations and was negatively associated with most yield related traits, including bunch weight. However, bunch weight decides the productivity of overall banana plantation and understanding its correlation with growth characteristics and bunch traits will give a greater understanding on the important factors that can be considered for obtaining an adequate bunch weight in the breeding programme. The results depicted significant positive correlation with pseudostem height (r = 0.63), pseudostem girth (r = 0.71), leaf area (r = 0.70) and number of hands (r = 0.73), while negatively correlated with number of suckers (r = - 0.17). All the bunch traits such as number of hands per bunch (NOH), total fingers per

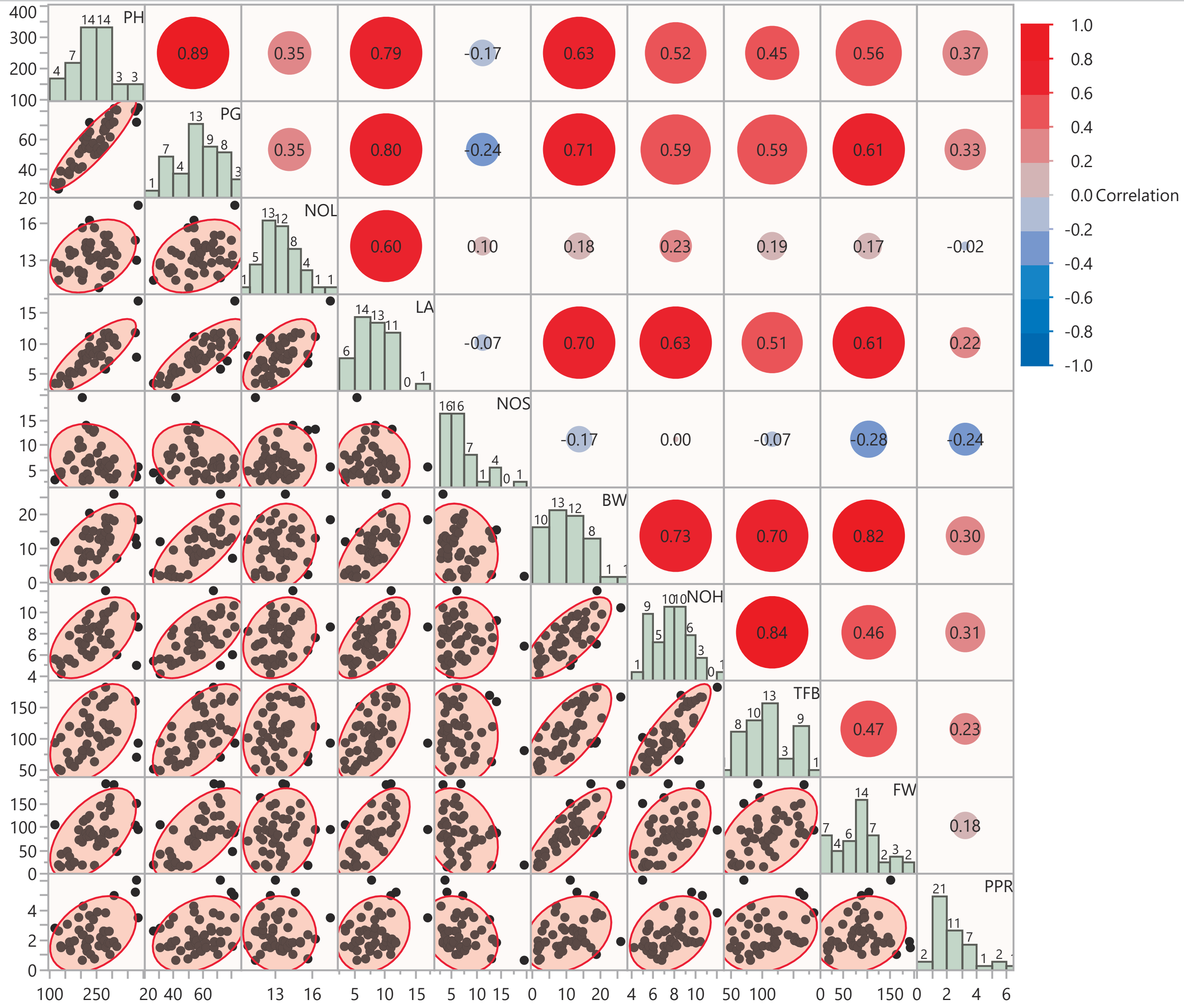

Fig. 2. Multivariate analysis consisting of scatter plot matrix, phenotypic frequency distribution and correlation coefficient matrix displaying the relationship between the variables. The bivariate scatter plots with a trend line are shown and each variable's distribution is displayed diagonally. Correlation between the variables is given in a circle colour chart

bunch (TFB), fruit weight (FW) and pulp peel ratio (PPR) showed significant positive correlation with bunch weight. The present findings are in agreement with those of Mahdi *et al*. (2014), who reported reduction in bunch weight with increased number of suckers. This can be attributed to the fact that suckers compete with the mother plant for nutrients, water, and sunlight, which can lead to stunted growth and reduced productivity (Benson, 2013). Therefore, it is important to manage the number of suckers and remove excess ones to ensure optimal growth and yield in banana cultivation. Pseudostem height, girth, leaf area, finger size and finger weight highly influence the bunch weight and was positively correlated. Similar results were obtained by Soares *et al*. (2012), where they reported significant and positive relation between bunch weight, pseudostem height and finger weight, however, the correlation between bunch weight and pseudostem girth was not significant. Lima Neto *et al*. (2003) also reported significant and positive correlation for almost all genotypes. The number of leaves depicted low but positive correlation with bunch weight states that higher leaf area is more important than number of leaves as it increased the area of photosynthesis. In improvement programs, the strength of the correlation among traits is a crucial consideration. If there is a significantly strong correlation among the traits being studied, it indicates potential for successful breeding (Tancred *et al*. 1995).

Cluster analysis: Circular hierarchical cluster was generated using the Ward method, taking into account all the variables measured, provided a comprehensive view of the similarities and dissimilarities among the genotypes in 4 distinct clusters (Fig. 3). Clustering technique was employed to study the similarity pattern of 45 genotypes based on the corresponding means of all the traits. The first cluster (Cluster I), comprised of six genotypes (2 synthetic hybrids and 4 parents). Two hybrids in this cluster namely, H-02-25 and H-02-34, exhibited exceptionally high pseudostem height and were tetraploid in their genomic constitution, along with 4 parents (3 triploids -Karpooravalli, Red Banana, Poovan and 1 tetraploid - FHIA). Interestingly, these hybrids were observed to be positioned in the same cluster to their respective parents *i.e* ., Red banana and Karpooravalli, indicating their genetic relatedness. Cluster II stands out for its 7 genotypes (6 synthetic hybrids and 1 parent) that display a favourable growth habit, high bunch weight and yield attributing characters. This cluster comprises 1 diploid (Tongat), 2 triploids (H-914 and H-11-21) and 4 tetraploids (H-906, H-916, H-923 and H-11-23). On the other hand, Cluster III comprises 22 genotypes (14 synthetic hybrids and 8 parents) including 10 diploids (H-11-06, H-11-08, H-11-18, H-11-41, H-11-113, H-516, Ambalakadali, Anaikomban, Erachivazhai and Sanna chenkadali), 7 triploids (H-531, H-902, H-912, H-926, H-11-71, YKM-5 and NPH-02-01) and 5 tetraploids (H-915, H-11-44, H-11-69, H-11-70 and PA-03-44) and they are characterized by moderate growth habits. Lastly, Cluster IV comprises of 10 genotypes which are solely diploids namely, Pisang Lilin, Rose, H-201, H-911, H-940, H-943, H-11-03, H-11-09, H-11-36 and

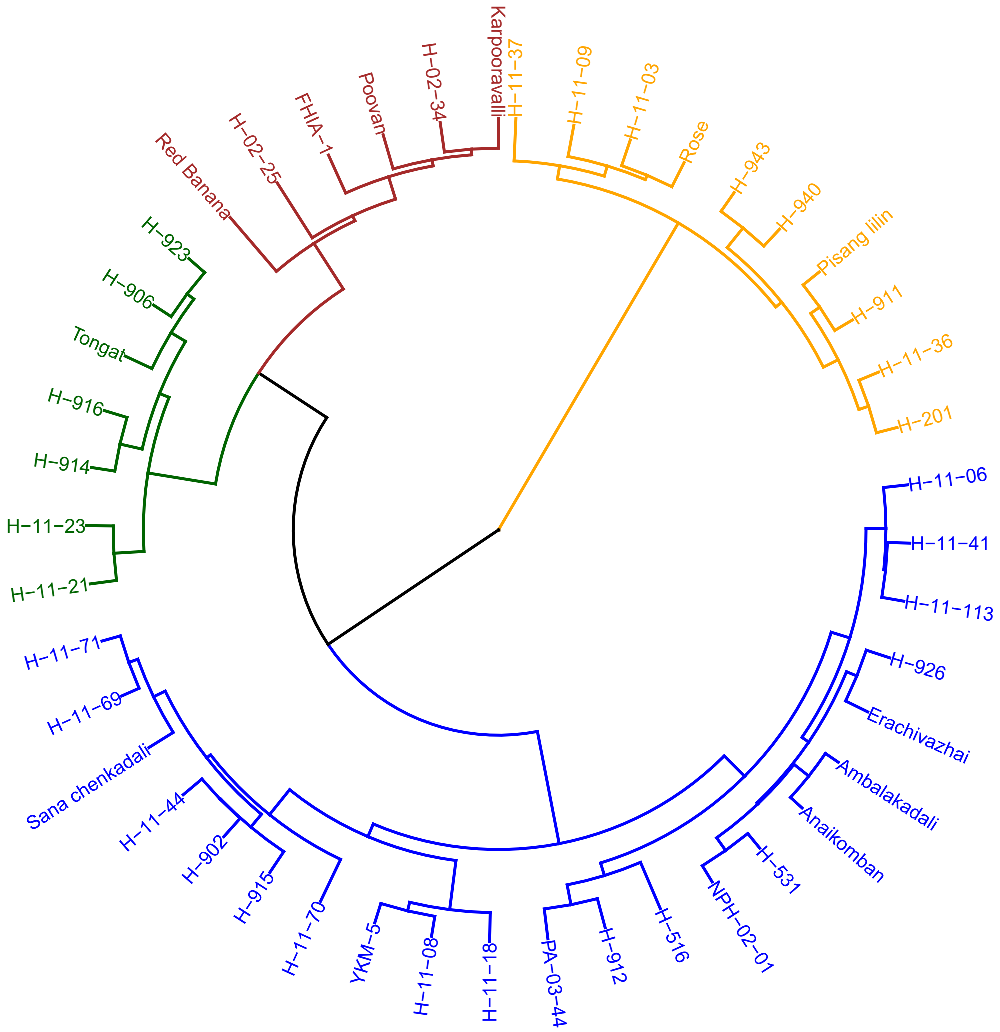

Fig. 3 Circular hierarchical clustering analysis based on morphological and bunch characters of 27 synthetic hybrids and 18 parents

H-11-37 exhibited a suboptimal growth habit, least bunch and finger weight compared to other clusters. Among all the clusters, Cluster I was distinguished by good growth habit and bunch weight, whereas cluster II was characterized by high bunch weight and yield attributing characters, in addition to favourable growth habit. Cluster III displayed moderate growth habits and Cluster IV comprised solely of diploid genotypes displayed inadequate growth habit and low bunch weight. Notably, cluster I and II had the most significance, as it exhibited desirable traits such as high bunch weight and good growth. The parents falling under these clusters are Red banana, Karpooravalli, Tongat, Poovan and FHIA-1 which are important banana cultivars and can be utilized in banana improvement programmes. Therefore, hybridization between genotypes falling in different clusters may provide ample scope for development of desirable lines. Cluster IV being diploid in nature can be utilized as an important male parent in hybridization programmes. The results of the present study suggested that hybridization of genotypes in cluster I and II with cluster IV could produce a diverse range of traits in the subsequent generation. This could potentially lead to the identification of elite lines (Devarajan *et al*., 2021).

Morphological and yield attributing characters play an important role in the conduct of breeding programmes, diversity studies and genetic mapping. The results of this study provided an important insight and revealed significant phenotypic variation for physical and yield-related traits among 27 synthetic banana hybrids and their parents. Hybrids such as H-02-25 and H-02-34 showed good vegetative vigor but H-916 proved to be a promising high yielding tetraploid hybrid. Traits like bunch weight, finger weight, pulp weight and peel weight indicated high variation which can be used as useful criteria in selection for improvement of bananas. However, before these hybrids can be recommended for wide cultivation or breeding application, they need to be evaluated and screened for tolerance to biotic and abiotic stress in multi-location and multi-season trials.

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