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Selection of the parental combinations through multivariate analysis in dessert banana genotypes for hybridization programme

Saudamini Swain[1], Partha Sarathi Munsi[2], Swarnalata Das[*3] and Prabhu Charan Lenka[1]

[1]Department of Fruit Science, OUAT, Bhubaneswar, Odisha, India
[2]Department of Horticulture, Visva-Bharati, West Bengal, India
[3]Department of Plant breeding & Genetics, OUAT, Bhubaneswar, Odisha, India

*Corresponding author e-mail: swarnalata1967@rediffmail.com

Abstract

In the present investigation 22 dessert banana genotypes were evaluated under coastal plain zone of Odisha during the year 2013-14 and 2104-15 in a randomized block design with three replications. Observations were recorded on growth parameters and yield attributing traits. Analysis of variance indicated significant differences among the genotypes in respect of all the growth parameters and yield attributing traits. The PCV and GCV (phenotypic and genotypic coefficient variation) were higher for finger weight, bunch weight and number of fingers. Bunch girth and finger weight had very high broad sense heritability (h^2). Finger weight recorded the highest genetic advance followed by bunch weight. All the genotypes, on the basis of total variability were grouped into twelve distinct clusters. Maximum number of cultivars was accommodated in Cluster 1 followed by Cluster 7. Inter cluster distance was the highest between cluster 12 and cluster 7. Bunch girth made the maximum contribution to divergence (45.02 %) followed by finger weight (39.83 %).

Highlights

- Improvement of banana genotypes in respect of number of hands/bunch, number of fingers/bunch, finger length, finger weight and bunch weight would be rewarding as these traits had high GCV and PCV along with high heritability and high genetic advance.
- Maximum inter cluster distance was observed between cluster 12 and cluster 9.
- Grand Naine of cluster 12 may be crossed with genotypes of cluster 9 through somatic hybridisation/ sexual hybridization to develop superior transgressive segregants or heterotic hybrids.

Keywords: Banana, PCV, GCV, heritability, genetic advance, PCA, D^2 analysis

Banana (*Musa* spp.), is the 2nd most important fruit crop in India next to mango. World banana production is around 103 million tonnes annually, of which bananas cultivation for the export trade account for only 10% (Aurore *et al.* 2009). India is the largest producer of banana in the world producing about 30.0 million metric tonnes from 8.3 lakh hectares (NHB, 2010). Hence, fruit harvested from bananas are important components of food security in the tropical world and provide income to the farming community through local and international trade. Banana is a very popular fruit due to its low price and high nutritive value. It is a rich source of carbohydrate and rich in vitamins particularly vitamin B. It is also a good source of potassium, phosphorus, calcium and magnesium. The fruit is easy to digest, free from fat and cholesterol. Banana plants also provide useful by-products, such as fiber, vegetables, beer, wine and vinegar (Aurore *et al.* 2009).

Banana cultivation is an important source of income to the farming community of Odisha. But Banana

production in Odisha is very low, contributing only 2% to the total banana production in the country (NHM year book). The low production could be alleviated by developing high yielding genotypes which indirectly demands evaluation and selection of elite genotypes. Selection on the other hand depends upon the genetic variability present in the base population. For the success of any breeding programme the basic requirement is the variability found within the members of the population. It is this variation which if heritable could be used for cultivar improvement, as improved cultivars are the backbone of any orchard system (Sharma *et al.* 2013).

Use of Mahalanobis D^2 statistics to estimate or evaluate the net/total divergence in breeding for crop improvement has been indicated by number of workers in different fruit crops. Rai and Mishra (2005) followed D^2 analysis to study genetic divergence in a set of 17 genotypes of bael. Hernandez-Delgado *et al.* (2007) studied genetic diversity in Mexicana guava germplasm. Jagadeesh *et al.* (2007) studied genetic variability for fruit quality in jackfruit. Saran *et al.* (2007) studied genetic diversity in Indian jujube for powdery mildew and other traits. Rajan *et al.* (2007) followed multivariate analysis to assess genetic diversity in guava. Chipojola *et al.* (2009) studied the genetic diversity and relationship among 40 accessions of cashew. The use of genetically divergent parents in hybridization under transgressive breeding programme is dependent upon categorization of breeding material on the basis of appropriate criteria (Santos *et al.* 2011).

Apart from providing requisite assistance or help in selection of divergent parents in hybridization, D^2 statistics also adequately assists in the measurement of diversification and the contribution of the relative proportion of each component trait towards the total genetic divergence or variation. While studying the clonal variability in mango, Manchekar *et al.* (2011) reported substantial variation after applying D^2 statistics. Jana *et al.* (2015) studied genetic divergence in guava. Kabita *et al.* (2016) followed D^2 analysis for identification of elite cashew hybrids. Ghaderi-Ghahfarokhi *et al.* (2016) studied geographical discrimination of 24 pomogranate cultivars using chromatographic analyses and multivariate statistical methods.

Quantitative classification offers a divergence value among individuals and thus enables breeders to understand the racial affinities and evolutionary pattern in various species of cultivated plants. Furthermore, it also helps in making decisions in selection of the best parental combinations in hybridization programme. It serves as a sound basis of grouping any two or more genotypes based on minimum divergence or resemblance between them.

Therefore, prior to initiation of any breeding programme the extent of variability present must be adequately assessed so that the breeding programme could yield the desired results. To use or exploit the available variability present in the genetic material in the form of some specific groups or classes, the divergence studies based upon some desirable/suitable parameters is of very essential and of utmost significance. Keeping in view the above the genetic variation and cluster analysis using D^2 statistics was undertaken with the objectives to assess the variability present among the twenty two banana genotypes and potential use of this variability for further crop improvement through hybridization.

Materials and methods

The experiment was conducted in a randomised block design with three replications under All India Coordinated Research Project on Fruits at Central Research Station, OUAT, Bhubaneswar (East and SE Coastal Plain Zone, $20°15'$N latitude and $85°52'$ E longitude) in the year 2013-14 and 2014-15. The experimental material comprised of 22 banana genotypes of which 11 were national released cultivars and 11 were local landraces of Odisha (as given in Table 2).

Healthy sword suckers of uniform size (weighing 11.5 kg) and age (23 months old) were used as planting materials. Suckers were dipped in 0.2% carbendazim (2g/litre of water) and 0.25% triazophos (2.5ml/litre) solutions for about 30 minutes as a prophylactic measure against fusarium wilt disease, nematode and corm weevil infestation. Treated suckers were kept under shade for about 24 h before planting. Pits with dimension of 45 cm × 45 cm × 45 cm were made by post hole digger at a spacing of 2 m × 2 m. In each treatment 10 pits were prepared. A spacing of 1m was left in between replications to provide demarcation. The suckers were planted in the centre of the pit and the soil was pressed

firmly around the suckers. Planting was done on 5th August 2013. Irrigation was applied as and when necessary. Fertiliser was applied to the banana plants @ 200:50:200 g N:P:K/plant in four split doses i.e., at the time of planting, at 3rd, 5th and 7th months after planting. Five plants were selected at random in each plot to record observations on height of the pseudostem, girth of the pseudostem, number of leaves, length of leaf, width of leaf, days to shooting, days to harvest, length of bunch, girth of bunch, number of hands, number of fingers, length of finger, girth of finger, finger weight and bunch weight. The mean performance was evaluated by averaging the mean of plant crop and 1st ratoon crop. Genetic parameters and divergence study was done taking the mean data of all observations by using SAS software (9.0 version).

Results and discussion

The mean squares from analysis of variance for dessert banana cultivars with respect to fifteen traits are presented in Table 1. The results revealed the presence of significant (P < 0.01) differences among the traits studied. The overall result showed the presence of genetic variability among the tested dessert banana cultivars.

Table 1: Mean sum of square in respect of 22 characters

Character	Mean sum of square
1. Height of the pseudostem at shooting	1330.17**
2.Girth of the pseudostem at shooting	71.27**
3.Number of leaves	2.47**
4. Leaf length(cm) at shooting	241.41**
5. Width of leaf	47.10**
6. Days to shooting	3322.40**
7. Days to harvest	3205.95**
8. Bunch length	84.79**
9. Bunch girth	173.66**
10. Number of hands/bunch	5.52**
11. Number. of fingers	2988.50**
12. Finger length	23.64**
13. Finger girth	3.09**
14. Finger weight	1827.04**
15. Bunch weight (yield/plant)	28.68**

Mean performance of banana cultivars in

respect of growth parameters

From Table 2, it was observed that the national released variety BCB-1 recorded the highest plant height (271.95 cm). BCB-1 was statistically at par with the national released cultivars Martman, Ney Poovan, Red Banana and the local cultivars Ganga Tulsi, Champa Patia, Sakhigopal Patkapura, Red Green Banana and Harianta Chini Champa. The minimum plant height was recorded in Grand Naine (178.75 cm) and other national released and local cultivars were significantly taller than Grand Naine except Robusta (182.83 cm). Red Banana had maximum girth of 69.15 cm followed by BCB-1(66.12 cm) and it was statistically at par with Red Green banana, Chini Champa, Martman, Ganga Tulsi, Harianta Chini Champa, Sakhigopal Patkapura, Satasankha Patkapura, Chakrakeli and Robusta. The minimum pseudostem girth was recorded in Manjeri Nendran (48.35 cm) and it was at par with Grand Naine, H-531, Balipatna Champa, Ney Poovan, Deshi Patkapura, Amrutpani, Champa, Champa Patia and Chandanpur Patkapura. Chandanpur Patkapura had the maximum leaf length of 144.25 cm followed by H-531 and BCB-1 which were statistically at par but significantly superior to rest of the cultivars. Red Green Banana was found statistically at par with BCB-1, Champa, Champa Patia and Chakrakeli and found significantly superior to rest of the cultivars. Leaf width varied significantly in the cultivars (Table 2).

Maximum leaf width was observed in Red Green Banana (60.5 cm) and Chini Champa recorded the lowest width. Two local cultivars Red Green Banana and Balipatna Champa had produced significantly higher width as compared to the national check Grand Naine. Number of leaves per plant at the time of shooting varied from 10.47 to 14.70. BCB-1 ranked first having 14.70 number of leaves/plant, Chandanpur Patkapura ranked 2nd and Harianta Chini Champa had 3rd rank. The national cultivar H-531 produced the lowest number of leaves (10.47). In pooled mean data leaf area was minimum in Robusta (0.36 m²) and the maximum in Red Green Banana (0.68 m²). Red Green Banana recorded significantly higher area than the check cultivar Grand Naine (0.41 m²) and all other cultivars were at par with the check. Number of days taken from planting to shooting was found significant among the cultivars (Table 2). The national cultivars

Table 2: Mean Performance of 22 desert banana cultivars in respect of vegetative characters

Genotype	Pseudostem height	Pseudostem girth	No. of leaves at shooting	Leaf length(cm)	Leaf width(cm)	Leaf area (m²)	Days to Shooting from Planting
V_1-Champa	234.55	54.00	12.15	121.375	56.35	0.55	311.75
V_2- H-531	214.35	50.52	10.47	108.2	47.03	0.41	172.85
V3- Grand Naine	178.75	50.15	11.53	100.6	51.1	0.41	286.4
V_4 – Chini Champa	235.25	64.25	13.73	116.2	43.93	0.41	347.5
V_5- Robusta	182.83	60.47	11.70	96.15	46.58	0.36	291.63
V_6- Deshi Patkapura	230.88	53.92	12.17	106.5	44.92	0.38	313.45
V_7- Red Banana	262.48	69.15	10.72	109.7	51.17	0.45	374.48
V_8-Ranital Patkapura	245.20	59.47	12.17	111.075	46.85	0.41	319.68
V_9-Chandanpur Patkapura	230.45	56.60	14.12	144.25	51.65	0.60	320.33
V_{10}-Chakrakeli	244.80	60.72	12.97	118.375	53.77	0.51	308.75
V_{11}- Red Green Banana	255.73	65.92	10.52	135.325	63.22	0.68	365.90
V_{12}-BCB-1	271.95	66.12	14.70	129.375	54.1	0.56	378.80
V_{13}- Satasankha Patkapura	226.30	61.10	12.22	113.825	51.55	0.47	308.48
V_{14}-Balipatna Champa	244.05	51.40	12.12	107.025	59.27	0.51	295.50
V_{15}-Ney Poovan	262.88	52.00	12.52	110.3	48.42	0.43	291.90
V_{16}-Sakhigopal Patkapura	259.55	61.35	13.20	113.6	47.70	0.44	331.50
V_{17}-Martaman	264.98	64.00	12.77	110.275	51.30	0.45	315.48
V_{18}-Amrutpani	241.38	53.97	11.90	108.175	53.60	0.47	328.85
V_{19}-Champa Patia	269.15	55.40	13.10	119.5	55.60	0.53	333.55
V_{20}-Ganga Tulasi	271.13	63.10	11.82	104.575	44.42	0.37	319.45
V_{21}- Manjeri Nendran	214.65	48.35	12.40	116.65	51.95	0.49	302.18
V_{22}-Harianta Chini Champa	246.70	61.52	13.90	113.25	50.00	0.45	312.15
SE±(m)	12.91	1.87	0.48	4.70	1.00		
CD 5%	38.86	5.50	1.41	13.84	2.95		

BCB-1 and H-531 scored first rank and last rank respectively. BCB-1, Red Banana and Red Green Banana were late in shooting whereas Balipatna Champa, Ney Poovan, Robusta, Grand Naine and H-531 were earlier in shooting.

Mean performance of banana cultivars in respect of yield and yield attributing characters

Mean data reflected (Table 3) earliness of H-531 (264.43 days) and lateness of BCB-1 (466.25 days), Red Banana (465.23 days) and Red Green Banana (457.40 days). The local cultivars Ganga Tulsi, Satsankha Patkapura, Ranital Patkapura, Harianta Chini Champa and Balipatna Champa were found to be at par with the check variety Grand Naine (376.38 days). Pooled mean revealed that Grand Naine was unique amongst all, having the highest bunch length (66.83 cm) and none of the local and national cultivar was at par with it. The lowest bunch length was recorded in Manjeri Nendran (36.93 cm) and it was statistically at par with the cultivars Harianta Chini Champa and Amrutpani. The local cultivar Satsankha Patkapura attained the highest bunch girth of 95.90 cm and it was at par with Red Green Banana (94.33 cm) and Chandanpur Patkapura (91.05 cm). Ney Poovan recorded the highest number of hands/bunch (10.18) followed by Grand Naine (9.93) and the lowest was recorded

in Red Banana (4.95). The local cultivar Champa Patia having the highest number of fingers (191.50) significantly exceeded the check Grand Naine (135.75). The cultivars Ney Poovan, BCB-1, Robusta, Champa and Balipatna Champa had more number of fingers than the check. Manjeri Nendran recorded the highest finger length (23.08) followed by check Grand Naine. Ranital Patkapura was found to be at par with the check and all other cultivars had

significantly short finger length. Red Banana had the highest girth (14.68 cm) and Champa Patia had the lowest girth (9.38 cm). None of the local cultivars recorded significantly higher girth than the check cultivar. Red Banana had the highest finger weight (136.68 g) and it was at par with Manjeri Nendran (127.0 g), Robusta (126.33 g), Red Green Banana (125.25 g) and Grand Naine (122.75 g). The lowest finger weight was recorded in Ney Poovan (37.10

Table 3: Mean Performance of 22 desert banana cultivars in respect of yield characters

Genotype	Days to harvesting from Planting	Bunch length (cm)	Bunch girth (cm)	No. of Hands/ bunch	No.of Fingers/ bunch	Length of finger (cm)	Girth of finger (cm)	Finger weight (g)	Bunch weight (kg)/plant
V_1-Champa	409.08	54.5	68.63	9.1	146.75	13.45	12.03	70.75	12.01
V_2- H-531	264.43	47.3	73.13	5.88	99.75	13.05	12.20	62.75	8.55
V3- Grand Naine	376.38	66.83	69.53	9.93	135.75	22.15	12.00	122.75	20.61
V_4 - ChiniChampa	438.58	49.20	66.05	7.35	108.50	12.28	11.93	62.40	8.71
V_5- Robusta	383.88	56.43	84.25	9.80	150.25	17.55	12.48	126.33	21.34
V_6- Deshi Patkapura	404.70	49.53	78.80	6.55	81.75	15.90	12.20	89.48	9.32
V_7- Red Banana	465.23	47.98	81.00	4.95	62.50	15.90	14.68	136.68	10.83
V_8-Ranital Patkapura	404.83	47.10	85.25	5.83	86.50	18.05	12.25	101.95	10.34
V_9-Chandanpur Patkapura	419.88	56.83	91.05	6.30	88.00	16.75	12.23	100.25	12.25
V_{10}-Chakrakeli	403.45	54.25	80.20	6.23	98.75	13.18	12.20	101.58	12.55
V_{11}- Red Green Banana	457.40	48.15	94.33	5.08	66.25	16.10	14.10	125.25	10.81
V_{12}-BCB-1	466.25	51.08	83.88	8.30	151.50	14.30	10.55	61.65	11.99
V_{13}- Satasankha Patkapura	405.85	58.25	95.90	6.08	79.75	14.53	12.58	109.95	10.05
V_{14}-Balipatna Champa	389.43	53.23	77.75	8.55	144.25	12.60	11.35	58.25	9.64
V_{15}-Ney Poovan	388.95	59.03	79.48	10.18	185.00	11.65	9.88	37.10	8.59
V_{16}-Sakhigopal Patkapura	420.25	45.28	67.30	7.00	89.75	15.98	12.43	95.88	10.31
V_{17}-Martaman	408.53	49.13	83.45	8.00	105.75	15.43	12.63	82.50	10.81
V_{18}-Amrutpani	419.85	43.73	64.13	7.48	92.75	10.50	10.08	64.98	7.48
V_{19}-Champa Patia	403.10	53.28	76.60	9.80	191.50	9.05	9.38	45.15	11.20
V_{20}-Ganga Tulasi	412.20	48.55	65.80	7.00	81.00	11.85	11.73	59.50	6.85
V_{21}- Manjeri Nendran	392.43	36.93	82.68	5.10	47.75	23.08	12.60	127.00	6.38
V_{22}-Harianta Chini Champa	404.08	41.93	68.63	8.05	109.75	11.85	10.73	52.45	6.25
SE±(m)	13.64	2.55	3.18	0.67	17.06	1.51	0.52	11.96	1.58
CD 5%	40.12	7.49	9.36	1.97	50.18	4.45	1.55	35.17	4.66

g). Robusta recorded the highest bunch weight (21.34kg) and at par with the check Grand Naine (20.61kg). But the national check Grand Naine significantly gave higher yield as compared to other cultivars. Chandanpur Patakapura was the highest yielder and Harianta Chini Champa was the lowest yielder among local cultivars.

Genetic parameters (GCV, PCV, heritability, genetic advance)

Mean, range, genotypic co-efficient of variability (GCV %), phenotypic co-efficient of variability (PCV%), heritability (broad sense; H) and genetic advance as % of mean (GA) are presented in Table 4. The grand mean for pseudo stem height was 240.36 cm. The estimates of GCV and PCV were low. Broad sense heritability was found to be moderate (58.4%) with low GA (14.50) indicating that selection for this trait would not be effective.

Though the genotypic co-efficient of variability (9.72) and phenotypic co-efficient of variability (10.72) were low in case of pseudostem girth but they were close to each other indicating that the effect of environment in expression of this trait was negligible. High heritability (82.1%) and low genetic gain (18.14) in respect of pseudostem girth indicates that improvement in pseudo stem girth through selection would be less effective. The

genotypic co-efficient of variability was the lowest (8.09) indicating that less variation is present in the population for number of leaves. Phenotypic co-efficient of variability was also low (9.77).

Moderate degree of heritability (68.5 %) was accompanied with low genetic advance (13.8) indicating that improvement in number of leaves through selection would be less effective. The mean leaf length was 114.28 cm and the range was very high. The genotypic co-efficient of variability was low (8.69) indicating that less variation is present in the population for leaf length. Phenotypic co-efficient of variability was also low (10.46). Moderate degree of heritability (68.5 %) accompanied with low genetic advance (13.8) indicated that improvement in length of leaves through selection would be less effective. The genotypic co-efficient of variability for leaf width was 9.29 % whereas phenotypic co-efficient of variability was 9.69 % and these two parameters were almost equal. So environment has no role in expression of leaf width. This trait was highly heritable (91.8 %) with low genetic advance (18.34).

Days to shooting ranged from 172.85 to 378.80 days with the mean of 315.02 days. The genotypic co-efficient of variability was 12.71% whereas phenotypic co-efficient of variability was 13.16 %. Heritability was too high (93.2 %) and GA was low

Table 4: Genetic parameters of 22 banana cultivars

Character	Mean	Range	GCV (%)	PCV (%)	Heritability (broad sense)	GA (%) of Mean
1. Height of the pseudostem at shooting (cm)	240.36	178.75-271.95	9.21	12.06	0.584	14.50
2. Girth of the pseudostem at shooting (cm)	58.34	48.35-69.15	9.72	10.72	0.821	18.14
3. Number of leaves	12.41	10.47-14.70	8.09	9.77	0.685	13.80
4. Leaf length(cm) at shooting	114.28	96.15-144.25	8.69	10.46	0.689	14.86
5. Width of leaf (cm)	51.11	43.92-63.23	9.29	9.69	0.918	18.34
6. Days to shooting	315.02	172.85-378.80	12.71	13.16	0.932	25.29
7. Days to harvest	406.31	264.42-466.25	9.62	10.09	0.908	18.88
8. Length of bunch (cm)	50.84	36.92-66.83	12.36	13.24	0.872	23.78
9. Girth of bunch (cm)	78.08	64.13-95.90	11.92	11.94	0.996	24.51
10. No. of. hands	7.39	4.95-10.17	22.06	23.04	0.916	43.51
11. No. of fingers	109.25	47.75-191.50	34.24	36.49	0.880	66.18
12. Length of finger (cm)	14.78	9.05-23.07	22.85	23.66	0.933	45.48
13. Girth of finger (cm)	11.92	9.37-14.67	10.33	10.53	0.963	20.90
14. Finger weight (g)	86.12	37.10-136.68	35.02	35.18	0.991	71.82
15. Bunch weight (kg)	10.76	6.25-21.33	34.58	35.78	0.934	68.85

(25.29) and this may be due to non additive gene actions. Days to harvest ranged from 264.42 to 466.25 days with the mean of 406.31 days indicating that some cultivars were early type and some were late type. The genotypic co-efficient of variability was 9.62% whereas phenotypic co-efficient of variability was 10.09 %. Heritability was high (90.8 %) and GA was low (18.88) and this may be due to non additive type of gene actions.

The mean bunch length was 50.84 cm and the range was high (36.92- 66.83). The genotypic co-efficient of variability was 12.36 indicating that less variation is present in the population for bunch length. Phenotypic co-efficient of variability was 13.24. High degree of heritability (87.2 %) accompanied with low genetic advance (23.78) indicated non additive type of gene actions. The genotypic co-efficient of variability was 11.92 and phenotypic co-efficient of variability was 11.94 in case of bunch girth. High degree of heritability (99.6 %) accompanied with low genetic advance (24.51) indicated non additive type of gene actions.

The genotypic and phenotypic co-efficient of variability were 22.06 and 23.04. Heritability was very high (91.6 %) for number of hands/bunch and genetic advance was medium (43.51). So selection could be followed for further improvement of this trait. The average number of fingers/bunch was 109.25 across the cultivars and it ranged from 47.75 to 191.50. The genotypic and phenotypic co-efficient of variability were moderate (34.24 and 36.49). This indicated that the present population retained variability for further selection. High heritability (88.0 %) with high genetic advance (66.18) indicated positive response to selection. The mean finger length was found to be 14.78 cm and the range was 9.05 to 23.07 cm. The estimates of genotypic (22.85) and phenotypic co-efficient of variability (23.66) were close to each other. Though the genetic variability had been depleted to a larger extent still then some amount of variability is present in the population for further selection. High heritability (93.3 %) with moderate genetic advance (43.51) indicated positive response to selection.

The average girth of finger was 11.92 cm and it ranged from 9.37 to 14.67. The estimates of genotypic (10.33) and phenotypic co-efficient of variability (10.53) were very low indicating that genetic variability had been fully exploited for improvement of finger girth and further selection would not be beneficial. It showed high heritability (96.3 %) with low genetic advance (20.90) indicating that finger girth is governed by non additive type of genes.

The average finger weight was 86.12 g and the minimum finger weight recorded was 37.10 g and the maximum was 136.68 g. The genotypic (42.89) and phenotypic co-efficient of variability (42.91) were very high. Finger weight exhibited high heritability (99.1 %) with high genetic advance (71.82) indicating additive type of gene action and selection for this trait would go in positive direction. The mean bunch weight across the cultivars was 10.76 kg and the range was 6.25 to 21.33 kg. This

Table 5: Inter and intra cluster distances

	Cl.1	Cl. 2	Cl. 3	Cl. 4	Cl.5	Cl.6	Cl.7	Cl.8	Cl.9	Cl.10	Cl.11	Cl.12
Cl.1	**307.30**	538.44	727.65	988.71	1364.87	946.76	914.05	771.29	495.42	545.96	1088.82	788.49
Cl.2	538.44	**0.00**	78.37	121.48	297.00	212.69	387.07	314.94	456.92	733.94	515.72	1235.18
Cl.3	727.65	78.37	0.00	78.86	190.15	124.49	530.15	151.27	588.14	717.44	391.33	1201.56
Cl.4	988.71	121.48	78.86	0.00	92.51	154.38	557.79	338.85	763.27	1026.11	487.56	1608.01
Cl.5	**1364.87**	297.00	190.15	92.51	0.00	205.28	705.73	478.20	888.02	1290.32	476.55	1824.56
Cl.6	946.76	212.69	124.49	154.38	205.28	0.00	757.62	218.53	776.40	708.04	571.61	1464.42
Cl.7	914.05	387.07	530.15	557.79	705.73	757.62	**258.50**	1002.02	820.37	1650.84	1069.83	1830.25
Cl.8	771.29	314.94	151.27	338.85	478.20	218.53	1002.02	**0.00**	691.89	462.28	495.79	963.11
Cl.9	495.42	456.92	588.14	763.27	888.02	776.40	820.37	691.89	0.00	737.86	775.41	818.12
Cl.10	545.96	733.94	717.44	1026.11	1290.32	708.04	1650.84	462.28	737.86	0.00	793.87	488.65
Cl.11	1088.82	515.72	391.33	487.56	476.55	571.61	1069.83	495.79	775.41	793.87	0.00	692.28
Cl.12	788.49	1235.18	1201.56	1608.01	1824.56	1464.42	1830.25	963.11	818.12	488.65	692.28	0.00

Table 6: Cluster means (Tocher Method)

	Ch.1	Ch. 2	Ch. 3	Ch. 4	Ch.5	Ch.6	Ch.7	Ch.8	Ch.9	Ch.10	Ch.11	Ch.12	Ch.13	Ch.14	Ch.15
Cl.1	245.53	59.11	12.73	112.76	49.34	321.68	414.02	48.37	69.94	7.34	101.13	13.12	11.66	74.63	9.18
Cl.2	264.98	64.00	12.78	110.28	51.30	315.48	408.53	49.13	83.45	8.00	105.75	15.43	12.63	82.50	10.81
Cl.3	245.20	59.48	12.18	111.08	46.85	319.68	404.83	47.10	85.25	5.83	86.50	18.05	12.25	101.95	10.34
Cl.4	230.45	56.60	14.13	144.25	51.65	320.33	419.88	56.83	91.05	6.30	88.00	16.75	12.23	100.25	12.25
Cl.5	226.30	61.10	12.23	113.83	51.55	308.48	405.85	58.25	95.90	6.08	79.75	14.53	12.58	109.95	10.05
Cl.6	255.73	65.93	10.53	135.33	63.23	365.90	457.40	48.15	94.33	5.08	66.25	16.10	14.10	125.25	10.81
Cl.7	262.01	56.23	13.11	116.55	54.35	324.94	411.93	54.15	79.43	9.21	168.06	11.90	10.29	50.54	10.35
Cl.8	214.65	48.35	12.40	116.65	51.95	302.18	392.43	36.93	82.68	5.10	47.75	23.08	12.60	127.00	6.38
Cl.9	214.35	50.53	10.48	108.20	47.03	172.85	264.43	47.30	73.13	5.88	99.75	13.05	12.20	62.75	8.55
Cl.10	262.48	69.15	10.73	109.70	51.18	374.48	465.23	47.98	81.00	4.95	62.50	15.90	14.68	136.68	10.83
Cl.11	182.83	60.48	11.70	96.15	46.58	291.63	383.88	56.43	84.25	9.80	150.25	17.55	12.48	126.33	21.34
Cl.12	178.75	50.15	11.53	100.60	51.10	286.40	376.38	66.83	69.53	9.93	135.75	22.15	12.00	122.75	20.61

result clearly revealed that most of the cultivars had low bunch weight. The genotypic and phenotypic co-efficient of variability were moderate (34.58 and 35.78). This indicated that the present population retained enough variability for further selection. High degree of heritability (93.4 %) accompanied with high genetic advance (68.85) indicated additive gene action and there is ample scope for improvement of bunch weight.

D^2 analysis and PCA (Canonical roots)

Genetic diversity analysis is generally used to identify diverse genotypes for hybridization purpose. The genotypes grouped together in a cluster are less divergent than the ones which fall into different clusters. From the results of D^2 analysis it was observed that twenty two cultivars were grouped into 12 numbers of clusters (Fig. 1) of which ten clusters were monotypic. Cluster 1 comprised of 8 genotypes such as Champa (V1), Chini Champa (V4), Deshi Patkapura (V6), Chakrakeli (V10), Sakhigopal Patkapura (V16), Amrutpani (V18), Ganga Tulasi (V20) and Harianta Chini Champa (V22); cluster 7 comprised of four genotypes namely BCB-1 (V12), Balipatna Champa (V14), Ney Poovan (V15) and Champa Patia (V19); cluster 2 was a mono cluster containing the variety Martaman (V17); cluster 3- Ranital Patkapura (V8), cluster 4- Chandanpur Patkapura (V9), cluster 5- Satasankha Patkapura (V13), cluster 6- Red Green Banana (V11), cluster 8- Manjeri Nendran (V21), cluster 9- H-531 (V2), cluster 10- Red Banana (V7), cluster 11- Robusta (V5) & cluster 12- Grand Naine

(V3) respectively (Fig. 1).

From the 3 D plot (Fig. 2) it was observed that the twenty two genotypes were grouped into 12 numbers of clusters. The genotypes present in each cell represented one cluster like Tocher's method but the composition of cluster was different. Here.

The maximum inter-cluster D^2 values were observed between clusters IV and V indicating wide genetic diversity between the genotypes. Since, these clusters have more inter-cluster distances among themselves, selection of parents from such clusters for hybridization programme would help to evolve novel hybrids. The number of genotypes falling in these two clusters was 6 and 1. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Inter-cluster distance was found to be minimum in cluster II indicating close relationship and similarity for most traits in the genotypes of this cluster. Hence, selection of parents from this cluster is to be avoided. Similar studies conducted on other crops by Singh *et al.* (5) in pomegranate, and Rai and Misra (3) in bael have suggested selection of distant parents based on D2 analysis.

The intra (diagonal value) and inter cluster distances were presented in Table 5. The maximum intra cluster distance was 307.30 and minimum was 0.0. The longest inter cluster distance (1830.25) was observed between cluster 7 and cluster 12. Since, these clusters have more inter-cluster distances among themselves, selection of parents from such
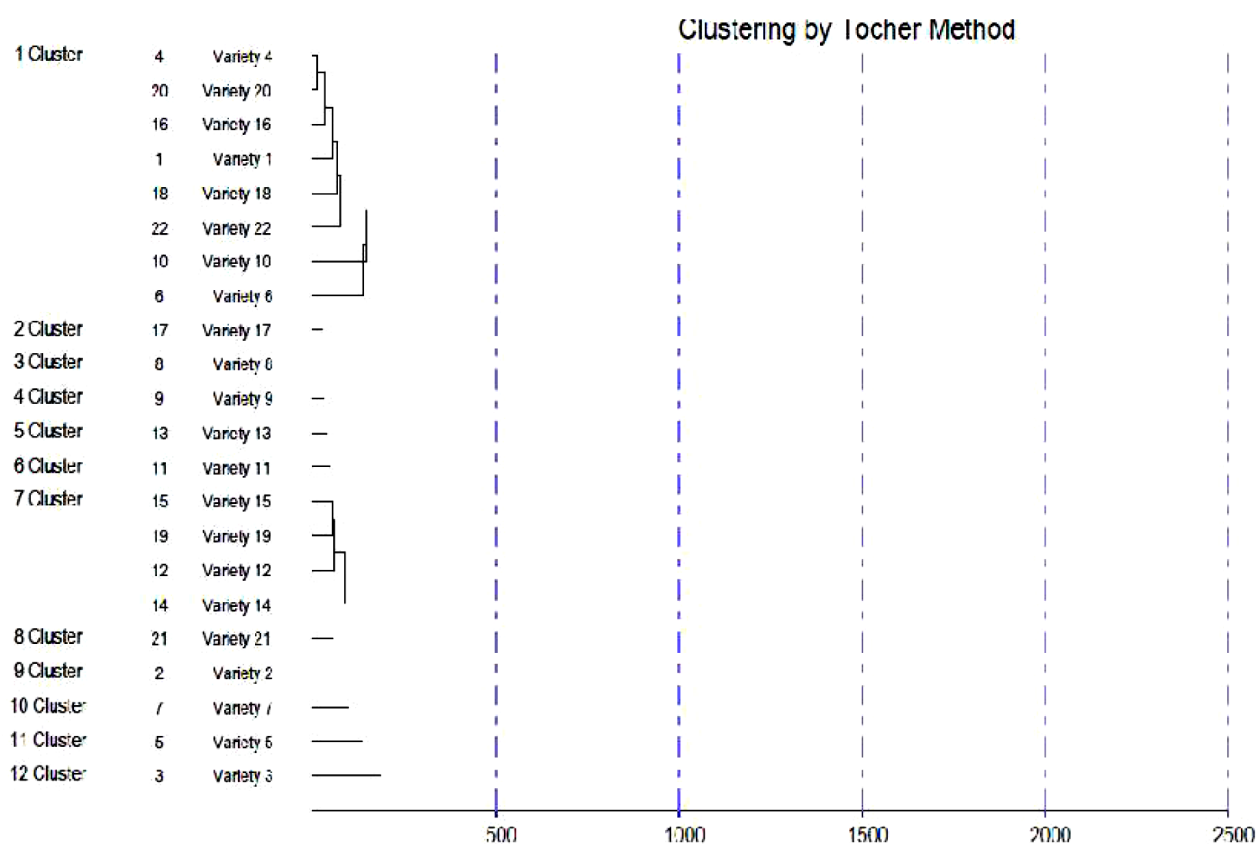
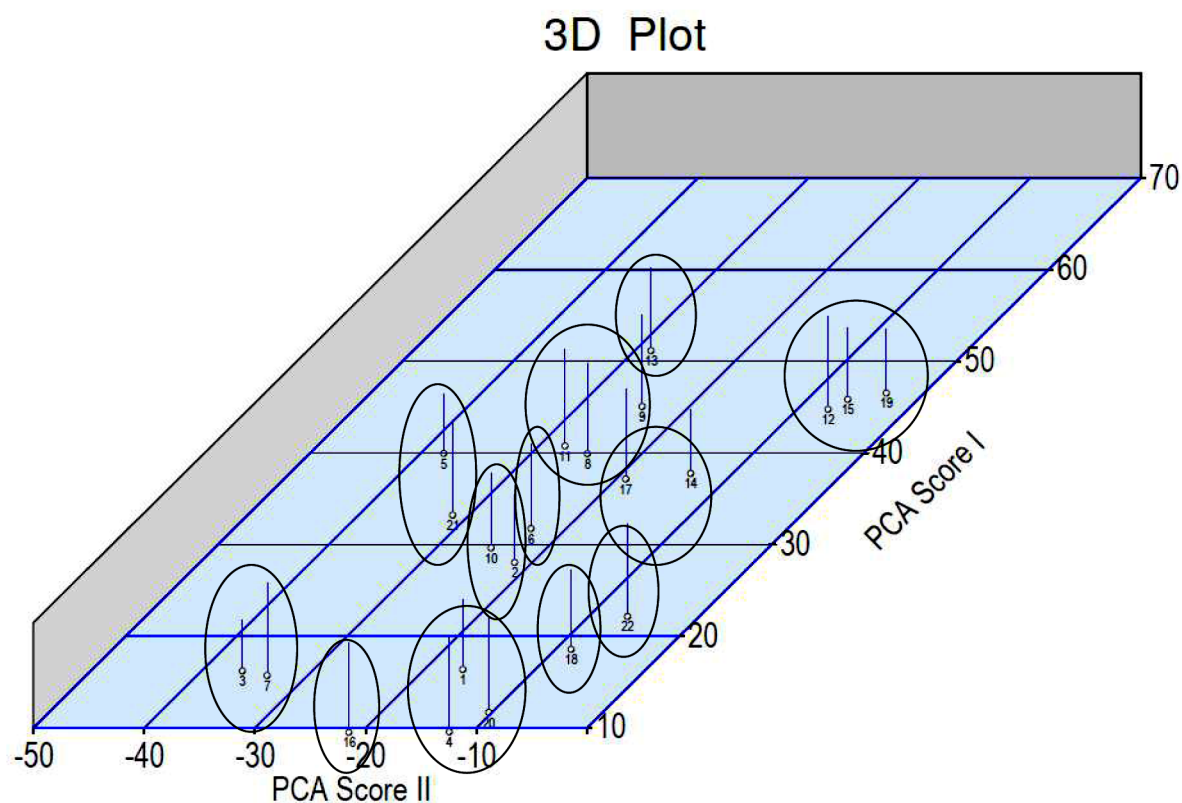Fig. 1: Clustering of the cultivars by Tocher's method

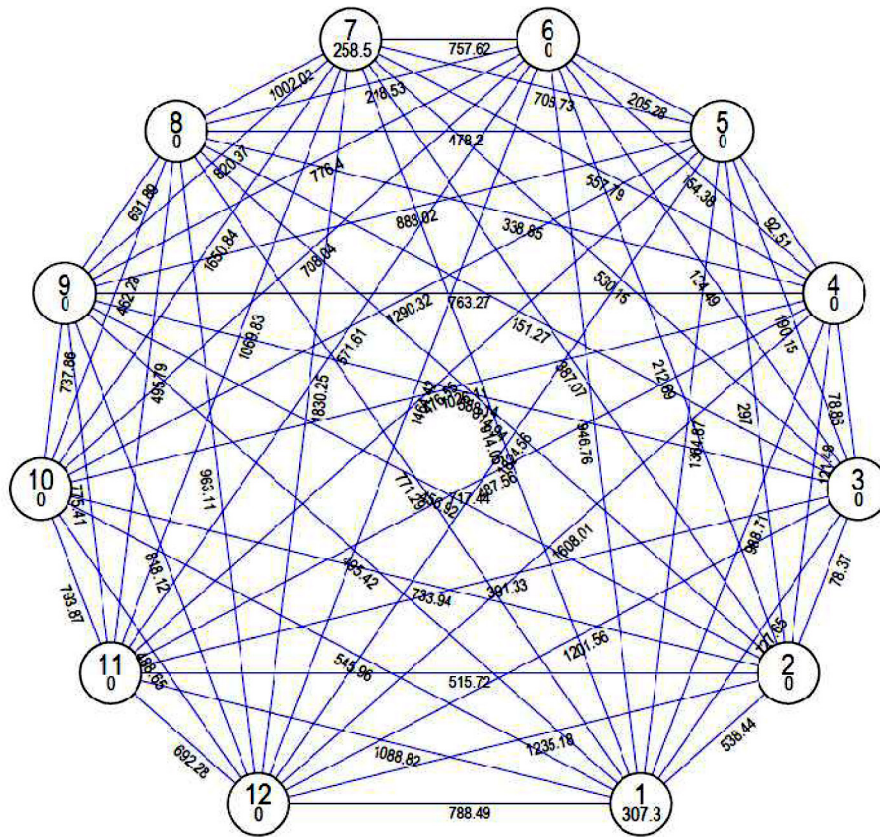Fig. 2: Three dimensional plots for clustering using PCA scores

Fig. 3: Inter and intra cluster distances

clusters for hybridization programme would help to evolve novel hybrids. Cluster 1 was farthest from cluster 5 (1364.87) and nearest to cluster 9 (495.42). Cluster 2 was farthest from cluster 12 (1235.18) and nearest to cluster 3 (78.37). Cluster 3 was farthest from cluster 12(1201.56) and nearest to cluster 2 (78.37). Cluster 4 was farthest from cluster 12(1608.01) and nearest to cluster 3 (78.86). Cluster 5 was far away from cluster 12(1824.56) and nearest to cluster 4 (92.51). Cluster 6 was farthest from cluster 12(1464.42) and nearest to cluster 3 (124.49). Cluster 7 was farthest from cluster 12(1830.25) and nearest to cluster 2 (387.07). Cluster 8 was farthest from cluster 7 (1002.02) and closest to cluster 3 (78.86). Cluster 9 was farthest from cluster 5 (888.02) and closest to cluster 2 (456.92). Cluster 10 was farthest from cluster 7 (1650.84) and closest to cluster 8 (462.28). Cluster 11 was farthest from cluster 1 (1088.82) and closest to cluster 3 (391.33). This inter and intra cluster distances indicated some uniqueness of cluster 12.

Cluster means for the 15 characters is presented in Table 6. For pseudo stem height cluster 12 recorded the lowest mean of 178.75 cm and cluster 2 had the highest mean. Cluster 10 showed the highest mean for pseudo stem girth. Cluster 4 showed the highest mean for number of leaves (14.13) and leaf length (144.25). The highest mean for leaf width (63.23) was exhibited by cluster 6. Cluster 9 was characterized by early in shooting time (172.85) and harvesting time (264.43). The highest mean for bunch length (66.83) was exhibited by cluster 12 and the highest mean for bunch girth (95.90) was exhibited by cluster 5. The highest mean for number of hands (9.93) was exhibited by cluster 12 and the highest mean for number of fingers (168.06) was recorded by cluster 7. The highest mean for finger length (23.08) was presented by cluster 8. Cluster 10 was characterized by the highest mean for finger girth (14.68) and finger weight (136.68). Cluster 11 recorded the highest mean for bunch weight (21.34) followed by cluster 12 (20.61). Bunch girth made

Photos on Banana Genotypes
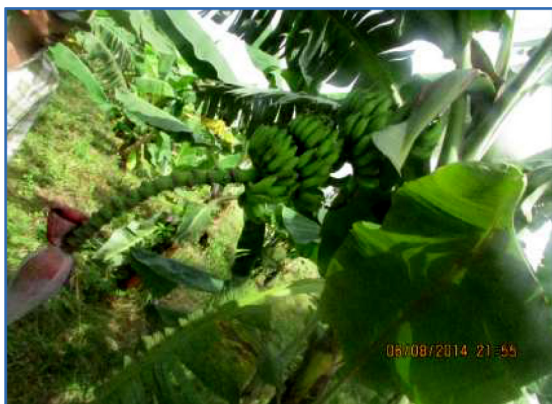
Champa bunch with male flower

H - 531 with male flower

Grand Naine with male flower

Chini Champa with male flower

Robusta bunch with male flower

Deshi Patkapura with male flower

Red banana bunch in plant

Ranital Patkapura bunch with male flower

Chandanpur Patkapura with male flower	**Chakrakeli bunch with male flower**
Red green banana bunch with male flower	**BCB-1 bunch with male flower**
Satsankha patkapura bunch with male flow(2)	**Balipatna champa with male flower**
Neypoovan bunch with male flower	**Sakhigopal Patkapura bunch with male flower**
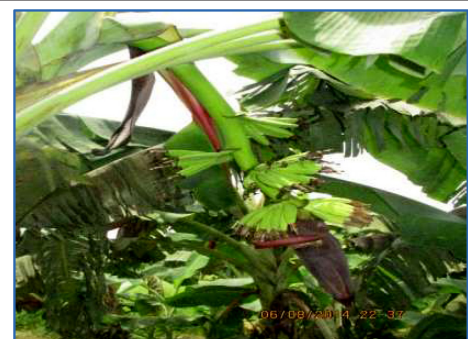
Martaman bunch with male flower (2)

Amritpani bunch with male flower (2)

Champapatia bunch with male flower

Ganga Tulasi with male flower

the maximum contribution to divergence (45.02 %) followed by finger weight (39.83 %). Grand Naine was found to be the best genotype.

In the present investigation phenotypic variance was relatively higher than the genotypic variance for all the traits. However, the magnitude of difference for most of the traits indicates that there was lesser influence of environment on these characters. This reveals that selection based on any traits would definitely reflect on bunch weight. High genotypic and phenotypic co-efficient of variation was recorded for number of fingers, bunch weight and finger weight while moderate GCV and PCV was observed in number of hands/bunch and finger length. This was further supported by the higher magnitude of heritability coupled with higher magnitude of genetic advance registered for most morphological traits especially for bunch weight, number of fruits/hand, number of fingers, and finger weight and number of hands/bunch. The genetic

co-efficient of variability estimate would furnish the most reliable information on the amount of advance expected from the selection.

The low PCV and GCV estimated in the present study may be either due to the occurrence of low spontaneous mutation rates or to the small population size or to both reasons. Out of the fifteen characters on which genetic analysis was done, only bunch weight, leaf length and average fruit weight had moderate heritability and expected genetic advance showing promise for genetic improvement. Higher heritability and expected genetic advance were observed for bunch weight and average fruit weight which may be due to wide genetic variability of the germplasm belonging to different genomic groups. It has also been reported that heritability estimates would be reliable if accompanied by a high expected genetic advance. For any crop improvement programme presence of genetic variability in the population is quite indispensable. In the present investigation genetic

variability present in the population was studied. Sirisena *et al.* (2000) estimated variability parameters within `Mysore' banana clones and their implication for crop improvement. Lenka *et al.* (2004) reported variation among nine varieties of plantain. They also observed high heritability in respect of bunch weight and number of fingers/bunch. Mohammed *et al.* (2013) evaluated 11 cooking banana (*Musa* sp.) clones of East Africa origin for study on genetic variability and distance. Kavitha *et al.* (2008) studied genetic variability like genetic variance, heritability and genetic advance in 19 banana hybrids in order to identify desirable genotypes for crop improvement programme. Crouch *et al.* (2000) made comparative analysis of phenotypic and genotypic diversity among 76 plantain landraces (*Musa* spp. AAB group). Although significant progress has been made over the past two decades, only a few hybrid-bred cultivars (mostly tetraploids) are grown in significant acreages by banana farmers. As noted by Ortiz *et al.* (2011), the focus of Musa breeding needs to gradually shift from addressing existing constraints to assessing the risk potential of emerging threats and preparing to respond to them, particularly under a changing climate that may increase both abiotic and biotic stress incidences and severity in this crop.

For an efficient breeding program, selection of genetically divergence and superior genotypes is important. Therefore, making crosses between genotypes which would ensure the exploitation of heterosis and development of transgressive segregants. For estimation of maximum heterotic effects, selection of parents belonging to different clusters would be profitable (Jana *et al.* 2015). In this case the maximum inter-cluster D^2 values were observed between clusters 12 and 7 indicating wide genetic diversity between the genotypes. Since, these clusters have more inter-cluster distances among themselves, selection of parents from such clusters for hybridization programme would help to evolve novel hybrids. The number of genotypes falling in these two clusters was 1 and 4. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Singh *et al.* (5) in pomegranate, and Rai and Misra (3) in bael have suggested selection of distant parents based on D^2 analysis.

Conclusion

The present investigation indicated that number of hands/bunch, number of fingers/bunch, finger length, finger weight and bunch weight had high GCV and PCV along with high heritability and high genetic advance. Hence selection for these yield attributing traits would be rewarding. Grand Naine present in cluster 12 may be crossed with parents of cluster 9 through somatic hybridisation/sexual hybridization to develop superior transgressive segregants or heterotic hybrids.

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