Original Research Article

A Comparative study on Nutritional and Biochemical characterization of banana cultivars of Assam, India

Abstract

An experiment was conducted in the Department of Horticulture,Assam Agricultural University, Jorhatto evaluate the huge diversity among the different bananagermplasmin the state of Assam. The experiment comprised of 24 banana (*Musa* spp.) genotypes, of which the fruits were collected for precise biochemical characterizationof the variations present in the collection. This analysis had created a database of the biochemical characterization of the fruits of different indigenous banana genotypes of Assam from which, it can be concluded that, there exists great genotype diversity amongthe *Musa*germplasm of Assam considering the fruit biochemical aspects and considerable amount of genetic variations are present evenamong the closely related genotypes within the same genomic group.

Key words: genotype, diversity, biochemical,characterization, indigenous, banana.

Introduction

Banana(*Musa* spp.) is one of the most popular fruit crops of the entire world. And its largest diversity is found in Southern and South Eastern Asia, where banana is under cultivation before the prehistoric time. Therefore, generally, it is believed that all the bananas and plantains are indigenous to the warm, moist regions of tropical Asia comprising the countries of India, Burma, Thailand and the regions of Indo-china. (Shanmugavelu*et al.*, 1992).The genomic classification was designated as A and B for the two wild species acuminata and balbisiana, respectively with varying scores. The available world population of edible varieties of bananas was thus classified into diploid (AA), Triploid (AAA), Tetraploid (AAAA) arising from the species acuminata, diploid (BB) from species balbisiana, and hybrid diploids (AB), triploids (AAB & ABB) and tetraploid (AAAB and ABBB) developed from the outcrossing of both the species (Chattopadhyay, 2010).

Being a part of centre of origin of Banana, North-Eastern India shows a wide variation of *Musa* species and the interspecific hybrids including AAA, AAB, ABB and BB genomic groups (Bhattacharyya and Baruah, 2017). The existing diversity in the biochemical characters of the banana genotypes of Assam is of great importance considering the quality improvement and conservation of natural variability. But such informations in banana germplasmare very limited.With this background, the present experiment was carried out in the agro-climatic condition of Jorhat, Assam to evaluate some of the cultivars available in Assam along with some cultivars of national importance based on their nutritional cum biochemical characters as no systematic study has been conducted in the state for evaluation of local cultivars.

Materials and method:

The experimental materials comprised of 24 banana (Musa spp.) genotypes (Table 1)

Except for the culinary types (Kachkal white type and Kachkal Green type), for other cultivars, the fruits were harvested at full ripe stage and biochemical analysis of the banana fruits belonging to diversed genotypes were carried out. In case of culinary types, the fruits were harvested at the proper green stage at which these fruits become the best to be consumed as vegetables.

Result and discussion:

The mean performance of all the genotypes in case of fruit biochemical characters are presented in the Table 2 and the mean performances of the genomic groups are also shown in the Table 3.

A comparison of genotypes under study based on fruit biochemical characters revealed that the genotype “Chenichampa” recorded highest non-reducing sugar (11.99%), total sugar (20.35 %), sucrose content (11.99 %) and crude fibre content (0.49%) as compared to other genotypes. Regarding other genotypes, “Barjahaji” recorded highest ash content (5.0%) and Potassium content (1938.66 mg/100gm), “Kachkal (Green)” recorded highest in magnesium content (721.30 mg/100gm) and phosphoruscontent (9.61 mg/100gm). “BhatManohar” exhibited highest in nitrogen (0.20%) and protein content (1.25%), while highest calcium content (14.53 mg/100gm) and reducing sugar content (12.37%) were recorded in “BogiManohar”. Maximum value of TSS content (28.20 °B), titrable acidity (1.50%) and TSS:Acidity (128.25) were recorded in “Jatikal”, “Athiakal” and “SimaluManohar” respectively. Moisture content (75.66%) was recorded highest in “LasariManohar” and lowest in Jatikal (64.64%). Nutrition wise, LasariManohar was found to have least values of Magnessium (292.07mg/100g), Nitrogen (0.05%) as well as Protein (0.3%). As the name suggests, Amritsagar exhibited lowest acidity (0.21%). Doodhsagar banana was found with lowest calcium content (4.51mg/100g) and lowest crude fibre content (0.16%). With the fruits for culinary purpose both genotypes of Kachkal were found with lowest values of TSS, sucrose, reducing, non-reducing and total sugar. With the highest acidity in fruit pulp, the lowest value of TSS: acidity was found in case of Athiakal (14.49). Least contents of Phosphorus (2.9mg/100g) and Potassium (1006.44 mg/100g) were found in the fruits of Fesamanohar and SimaluManohar, respectively.

The comparison of genomic groups revealed that balbisiana diploids have shown highest average fruit moisture content (71.71%), higher amount of calcium (12.93mg/100g), magnesium (536.80mg/100g), phosphorus (7.75mg/100g), titrable acidity (0.89%) and high fibre content (0.37%). The lowest values of fruit moisture (69.12%), Ash content (3.26%), calcium (10.53mg/100g), phosphorus (5.40mg/100g), Potassium (1203.83 mg/100g), TSS (21˚B), Total sugar (12.72%) and fibre content (0.21%) content were recorded by ABB genomic group, and the lowest amount of magnesium (388.48mg/100g) and titrable acidity (0.33%) were found in case of AAA genomic group. Similarly, pure acuminata group (AAA) was also found to be associated with highest average ash content (3.93%), higher nitrogen (0.15%), protein (0.94%), potassium (1515.05mg/100g) and total sugar content (15.93%) of fruits. The increase in reducing sugar may be attributed to enzymatic conversion of starch to reducing sugar (Islam, 1998). TSS content was very low in the culinary banana genotypes and this was due to the fact that the sugar and the TSS content of fruits increase with maturity due to enzymatic conversion of starch to simpler sugars. A slow decrease in acidity, associated with increased TSS and total sugar content is a fundamental process during the ripening of fruits to impart the flavor, was also suggested by Kulkarni and Aradhya (2005).

The comparison of characters with regard to the extent of genetic variation could be better judged by the estimates of genotypic and phenotypic co-efficient of variances (GCV and PCV). For the present study, GCV and PCV were categorized as high, moderate and low according to measures given by Kavitha*et al.* (2008). Among the fruit biochemical characters estimated (Table 4), fruit acidity showed the highest values of GCV and PCV, followed by high

GCV and PCV in case of TSS to acidity ratio, percentage of reducing sugar, nitrogen and protein content of fruit, non-reducing sugar, sucrose, crude fibre, total sugar and phosphorus content of fruit and moderate values of GCV and PCV were found in case of Ca, Mg and K content and TSS of fruit. These results show adequate variation present among the genotypes under the study, whereas, low GCV was found in case of ash and moisture content of fruits.

The comparison of characters with regard to the extent of genetic variation could be better judged by the estimates of genotypic and phenotypic co-efficient of variances (GCV and PCV). For the present study, GCV and PCV were categorized as high, moderate and low according to measures given by Kavitha*et al*. (2008). Among the fruit biochemical characters estimated (Table 4), fruit acidity showed the highest values of GCV and PCV, followed by high GCV and PCV in case of TSS to acidity ratio, percentage of reducing sugar, nitrogen and protein content of fruit, non-reducing sugar, sucrose, crude fibre, total sugar and phosphorus content of fruit and moderate values of GCV and PCV were found in case of Ca, Mg and K content and TSS of fruit. These results show adequate variation present among the genotypes under the study, whereas, low GCV was found in case of ash and moisture content of fruits.

The estimates of heritability separate genetic variability from phenotypic variability and indicate possibility and the extent to which improvement can be brought about through proper selection. Characters possessing high heritability can be improved directly through selection, as, these are relatively less affected by environment. The magnitude of heritability indicates effectiveness of selection based on phenotypic performance (Johnson *et al*., 1955). In the present study (Table 4), almost all traits exhibited high heritability, except fruit moisture content (low heritability of 25.2%) indicating very low level of environmental influence. The heritability values alone are inadequate to be taken as a tool to calculate the amount of genetic progress achieved by selecting the best individual (Katiyar*et al*, 1974). Ramanujam and Thirumalachar (1967) opined that heritability estimates could be reliable if accompanied by a high genetic advance. Genetic advance as percentage of mean (GAM) is calculated on heritability estimates, phenotypic variation and selection differential at 5% selection intensity. In the present investigation, there was wide variation among characters for GAM. Genetic advance as per cent of mean, varied from 2.63% for fruit moisture content to 121.77% for fruit acidity. Fruit acidity recorded above 100% GAM. Swain (2017) also recorded more than 100% GAM for pulp to peel ratio and non-reducing sugar. High value of GAM and high heritability estimates for a particular character is a reliable measure to be considered for selection of any genotype for crop improvement (Rajamanickam and Rajmohan, 2010).

In the present study, high heritability and high GAM along with high level of GCV and PCV were observed for the characters such as nitrogen, phosphorus, protein, acidity, fibre and sugar contents of fruit. This indicated that these characters are predominantly controlled by additive gene action. Similar results were reported by Rosamma (1982) and Uma *et al.* (2000). This implies that selection of the above mentioned characters can bring about effective improvement, and may be exploited in breeding programmes. Genetic variability and variability components were estimated based on the performance of cultivars in one location. Therefore, results could be varied in another location due to significant location x accession interaction. However, the magnitude of variability components and character association of these banana cultivars provide valuable information for improving fruit quality parameters.

Conclusion:

On the basis of findings recorded from the biochemical analysis of various banana genotypes belonging to different genomic groups, it may be concluded that, the based on the characters under the study, the various genomic groups may be characterized with certain specifications. And certainly, there exists great genotype diversity among the *Musa*germplasm of Assam considering these characters. Considerable amount of genetic variationis present even among the closely related genotypes within the same genomic group. Based on the characters showing high potentiality for improvement, the superior genotypes can be selected for involving them as a parent in Banana improvement programs.

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Table. 1 Genotypes under the study

Genomic group	**Genotypes**	
AAA	1. Grand Naine (as standard)	4. Manjahaji
	2. Dwarf Cavendish	5. Amritsagar
	3. Barjahaji	6. Agnisagar
AAB	7. Assamese Malbhog	10. Doodhsagar
	8. Chenichampa	11. GobinTulsi
	9. Digjowa	12. Honda
ABB	13. Kachkal (Green)	18. BhatManohar
	14. Kachkal (White)	19. BogiManohar
	15. Jatikal	20. FesaManohar
	16. Ketchulepa	21. SimaluManohar
	17. Manohar	22. LasariManohar
BB	23. Bhimkal	24. Athiakal

Table 2: Mean performance of different genotypes of banana for fruit biochemical characters

Genotype	Genomic group	Moisture content (%)	Ash content (%)	Calcium content (mg/ 100g)	Magnesium content (mg/ 100g)	Nitrogen content (%)	Phosphorus content (mg/ 100g)	Potasium content (mg/ 100g)	Protein content (%)	TSS (°B)	Acidity (%)	Red Sugar content (%)	Non-reducing Sugar content (%)	Total sugar content (%)	TSS : Acidity	Sucrose content (%)	Crude fibre content (%)
Grand Naine	**AAA**	70.96	4.47	11.12	414.32	0.16	7.86	1358.11	1.02	21.50	0.38	7.12	9.68	16.80	56.48	9.68	0.38
Dwarf Cavendish	**AAA**	71.55	4.22	11.12	472.71	0.14	8.05	1458.53	0.87	19.54	0.37	6.23	9.39	15.63	53.05	9.39	0.22
Barjahaji	**AAA**	71.03	**5.00**	10.27	336.85	0.16	5.28	**1938.66**	0.98	20.38	0.38	7.57	9.86	17.42	54.21	9.86	0.24
Manjahaji	**AAA**	68.96	3.25	12.61	465.61	0.16	6.94	1557.86	0.98	23.62	0.41	7.17	8.29	15.47	57.85	8.29	0.38
Amritsagar	**AAA**	71.69	3.10	13.10	309.74	0.13	6.05	1397.07	0.80	21.58	**0.21**	8.19	9.10	17.29	108.11	9.10	0.41
Agnisagar	**AAA**	70.31	3.52	13.68	331.62	0.16	4.95	1380.04	0.97	22.92	0.22	5.29	7.67	12.96	103.89	7.67	0.30
Assamese malbhog	**AAB**	72.59	3.20	12.83	394.93	0.17	5.32	1359.19	1.03	24.22	0.47	6.57	9.51	16.08	52.12	9.51	0.19
Chenichampa	**AAB**	68.61	3.00	11.33	298.57	0.17	8.94	1226.74	1.06	26.26	0.44	8.36	**11.99**	**20.35**	60.01	**11.99**	**0.49**
Digjowa	**AAB**	70.92	3.23	11.76	338.01	0.16	8.74	1706.87	1.00	22.40	0.60	4.78	6.56	11.34	37.75	6.56	0.31
Doodhsagar	**AAB**	70.79	2.80	**4.51**	478.16	0.10	3.45	1205.18	0.64	23.02	0.56	7.31	7.81	15.12	41.03	7.81	**0.16**
GobinTulsi	**AAB**	70.68	3.69	14.10	316.59	0.16	4.55	1624.09	1.02	23.24	0.23	5.02	8.38	13.41	101.96	8.38	0.27
Honda	**AAB**	67.47	4.18	13.47	544.18	0.10	6.04	1723.43	0.64	21.50	0.33	7.55	10.66	18.21	66.72	10.66	0.35
Kachkal (Green)	**ABB**	66.90	4.46	12.83	**721.30**	0.10	**9.61**	1640.65	0.59	6.22	0.39	**0.49**	0.84	**1.33**	16.10	0.84	0.21
Kachkal (White)	**ABB**	69.65	4.29	12.40	617.47	0.09	9.47	1607.53	0.54	**5.72**	0.32	0.62	**0.77**	1.39	18.03	**0.77**	0.20
Jatikal	**ABB**	**64.64**	3.47	9.41	509.58	0.06	5.13	1210.18	0.36	**28.20**	0.55	6.00	8.31	14.31	51.75	8.31	0.28
Ketchulepa	**ABB**	70.26	**2.31**	9.66	402.49	0.12	3.11	1102.39	0.74	21.46	0.36	5.58	7.93	13.52	60.21	7.93	0.24
Manohar	**ABB**	70.91	3.17	8.29	511.11	0.18	4.61	1081.83	1.09	23.78	0.37	7.51	9.36	16.87	66.03	9.36	0.32
BhatManohar	**ABB**	68.73	2.39	10.35	490.66	**0.20**	4.41	1122.94	**1.25**	25.32	0.37	7.07	9.02	16.08	69.93	9.02	0.19
BogiManohar	**ABB**	69.02	3.62	**14.53**	358.63	0.10	4.47	1243.30	0.60	24.20	0.46	**12.37**	6.57	18.94	52.77	6.57	0.20
FesaManohar	**ABB**	68.22	3.12	10.27	325.02	**0.05**	**2.90**	1011.51	0.32	27.62	0.32	8.54	9.68	18.23	88.02	9.68	0.21
SimaluManohar	**ABB**	67.23	2.32	6.91	296.66	0.10	4.82	**1006.44**	0.60	27.60	0.22	5.88	8.30	14.18	**128.25**	8.30	0.23
LasariManohar	**ABB**	**75.66**	3.50	10.69	**292.07**	**0.05**	5.52	1011.51	**0.30**	19.88	0.33	6.52	5.84	12.36	60.28	5.84	0.21
Bhimkal	**BB**	71.69	3.69	13.89	524.63	0.11	7.94	1475.08	0.68	22.02	0.27	9.62	7.99	16.17	83.18	7.99	0.28
Athiakal	**BB**	71.73	3.13	11.97	548.98	0.08	7.57	1375.75	0.51	21.54	**1.50**	5.96	6.55	13.95	**14.49**	6.55	0.46
Gen. Mean		**70.01**	**3.46**	**11.30**	**429.16**	**0.12**	**6.07**	**1367.70**	**0.77**	**21.82**	**0.42**	**6.55**	**7.92**	**14.48**	**62.59**	**7.92**	**0.28**
S.E.D.		**1.94**	**0.20**	**0.87**	**25.59**	**0.01**	**0.27**	**69.60**	**0.08**	0.34	0.03	0.59	0.85	0.72	5.44	0.85	0.03
C.D. 5%		3.85	0.40	1.73	50.82	0.03	0.54	138.24	0.16	0.67	0.07	1.17	1.69	1.43	10.80	1.69	0.06

Table 3. Mean performance of genomic groups regarding fruit biochemical characters

Genomic group	**Moisture content (%)**	**Ash content (%)**	**Calcium content (mg/100g)**	**Magnesium content (mg/100g)**	**Nitrogen content (%)**	**Phosphorus content (mg/100g)**	**Potasium content (mg/100g)**	**Protein content (%)**	**TSS (°B)**	**Acidity (%)**	**Red Sugar content (%)**	**Non-reducing Sugar content (%)**	**Total sugar content (%)**	**TSS : Acidity**	**Sucrose content (%)**	**Crude fibre content (%)**
AAA	70.75	**3.93**	11.98	388.48	**0.15**	6.52	**1515.05**	**0.94**	21.59	0.33	6.93	9.00	**15.93**	72.27	9.00	0.32
AAB	70.18	3.35	11.33	395.07	0.14	6.18	1474.25	0.90	**23.44**	0.44	6.60	**9.15**	15.75	59.93	**9.15**	0.30
ABB	69.12	3.26	10.53	452.50	0.10	5.40	1203.83	0.64	21.00	0.37	6.06	6.66	12.72	**61.14**	6.66	0.23
BB	**71.71**	3.41	**12.93**	**536.80**	0.10	**7.75**	1425.41	0.59	21.78	**0.89**	**7.79**	7.27	15.06	48.84	7.27	**0.37**

Table 4. Estimates of variability parameters for different fruit biochemical characters of banana genotypes

Characters	**Genotypic coefficient of Variance(GCV)**	**Phenotypic coefficient of Variance(PCV)**	**Heritability Broad Sense (h²%)**	**Genetic Advance as % of Mean (5%)**
Moisture content	2.54	5.06	25.20	2.63
Ash content	19.85	21.90	82.10	37.04
Calcium content	20.42	23.77	73.80	36.15
Magnesium content	26.49	28.11	**88.80**	**51.40**
Nitrogen content	**33.90**	**37.70**	**80.80**	**62.78**
Phosphorus content	**33.11**	**33.85**	**95.60**	**66.70**
Potasium content	18.36	20.04	83.90	34.63
Protein content	**33.90**	**37.70**	**80.80**	**62.78**
TSS	24.84	24.96	**99.00**	**50.93**
Acidity	**60.42**	**61.76**	**95.70**	**121.77**
Red Sugar content	**36.94**	**39.57**	**87.10**	**71.02**
Non-reducing Sugar content	**31.92**	**36.14**	**78.00**	**58.09**
Total sugar content	**31.50**	**32.47**	**94.10**	**62.96**
TSS : Acidity	**45.38**	**47.41**	**91.60**	**89.48**
Sucrose content	**31.92**	**36.14**	**78.00**	**58.09**
Crude fibre content	**31.41**	**35.15**	**79.90**	**57.84**