

Genetic diversity study and characterization of the DNA fingerprinting pattern of Banana (*Musa* sp.) genotypes of Assam

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ABSTRACT

The Plantains and bananas are native to tropical Asia, which includes India, Burma, Thailand, and Indo-china. And being a part of this area, Assam has huge banana diversity. The 24 genotypes of bananas (*Musa* spp.) from four distinct genetic groups (AAA, AAB, ABB and BB) were collected from various parts of Assam to study the genetic diversity present among the genotypes. In order to analyze the DNA fingerprint pattern of 24 genotypes, 52 randomly chosen SSR markers were used and 197 bands were scored, out of which 170 bands were found to be polymorphic. Maximum numbers of polymorphic bands were amplified by SSR8. Average number of total bands and polymorphic bands per marker were 6.16 and 5.31, respectively. While comparing every single pair of genotypes, for 276 combinations, the Jaccard's coefficient of similarity was computed based and UPGMA cluster analysis was carried out, which shows the genetic relationships between the genotypes visually and identified two large genotype clusters of genotypes. During the investigation, specific bands or molecular identities for some genotypes were found from the banding profile of SSR markers. This study demonstrated that there is a significant degree of genetic variation present even among closely related genotypes within the same genomic group and that there is a substantial deal of genotype diversity within the *Musa* germplasm of Assam.

Key words: banana, Genotype, Diversity, Assam, DNA, Fingerprint, Cluster analysis.

Introduction

Banana is a monocot, perennial, herbaceous plant, domesticated by selection from several wild species of the genus *Musa* of Musaceae family. In Southeast Asia, it has been cultivated before the prehistoric time and hence the World's largest Banana diversity is found there. The bananas and plantains are indigenous to the tropical Asia comprising of the regions

of India, Burma, Thailand and Indo-china. Most of the present day edible banana varieties have originated from the two species of section Eumusa under genus *Musa*, namely *Musa acuminata* and *Musa balbisiana*. It had been observed that the edible varieties developed not only through natural outcrossing, but also through natural mutation and polyploidy. Thus, in nature there are several genomic groups under *Musa*. 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). Broadly, 4 centers of Banana species diversity are there: (1) north east India, north Myanmar, southeast China; (2) peninsular Malaysia, west Indonesia; (3) Philippines; and (4) New Guinea and adjacent islands. But till date all the banana prevailing regions of south East Asia have not been surveyed properly (Nayar 2010). Early studies have suggested that parthenocarpy originated in the Malayasian sub species of *M. acuminata* ssp. *Malaccensis* from which arose the range of cultivated AA and AAA bananas. Then those were carried by towards northeast India, where wild *M. balbisiana* was there in wild condition, resulting in AB, AAB, and ABB genomic groups of banana (Nayar, 2010).

Being a part of South-east Asia 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). Cultivar diversity of North-eastern states of India has also shown a large variation with cultivars belonging to various genomic groups (Bhattacharyya and Baruah, 2017). The state of Assam has rich biodiversity of a large number of Banana types belonging to both *acuminata* and *balbisiana* genomes. With this background and keeping in view the large variations present within *Musa* spp. in the state of Assam, the present study was undertaken to carry out characterization of the DNA fingerprinting pattern of Banana germplasm of Assam using SSR markers.

Materials and Methods

The experimental materials comprised of 24 banana (*Musa* spp.) genotypes collected from different parts of Assam belonging to four different genomic groups (Table 1).

The total genomic DNA from each genotype included in the present study was extracted following the protocol of Murray and Thompson (1980) with slight modification. DNA was extracted from young unfurling leaves of 5-pooled individuals per geno-

Table 1. Genotypes under the study

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

type to ensure better representation of the genotype. Quality and quantity of genomic DNA was estimated based on agarose gel electrophoresis and spectral analysis. Fifty two SSR markers were selected from published literature at random which produced a minimum amplification product size of 100bp and above for analyzing the DNA fingerprint pattern of 24 genotypes (Table 2).

The molecular weight of the PCR products, obtained for each primer from SSR analysis, was designated, based on a ladder of known molecular weight. The molecular data were scored on the basis of presence or absence of an amplified particular DNA fragment. Only unambiguous and reproducible bands were scored in binary format as '1' = band present; '0' = band absent and '9' = missing data. SSR data were analyzed by using the software package, NTSYS-pc Version 2.1 (Rohlf, 2000). The binary data generated by SSR analysis were used to calculate percent polymorphism and Polymorphism information content (PIC) was evaluated by using the formula by Anderson *et al.* (1993).

Genetic relatedness among the genotypes was computed by using the Jaccard's coefficient of similarity using SIMQUAL module of NTSYS-pc. The

Table 2. List of primers (SSR markers) used for screening of genotypes

Primers	Forward Primer	Reverse Primer	Annealing Temperature (°C)	Reference	
SSR 1	TTTGCTGGTTGGGCTGA	CCCCCTTTCCTCTTTTGC	62	Onyango <i>et al.</i> 2010	
SSR 2	CCCGTCCCATTCTCA	TTCGTTGTCATGGAATCAT	58		
SSR 3	GCACGAAGAGGCATCAC	GGCCAAATTGATGGACT	58	Ge <i>et al.</i> 2005	
SSR 4	TCGCCTCTCTTAGCTCTG	TGTTGGAGGATCTGAGATTG	58		
SSR 5	AGAACGTTTFGCTGTTGGAG	GCTTCTGTCATCGTTTTGTC	58		
SSR 6	ACTGCTGCTCTCCACCTCAAC	GTCCCCCAAGAACCATATGATT	62		
SSR 7	AAGAAGGCACGAGGGTAG	CGAACCAAGTGAAATAGCG	63.5		
SSR 8	GGAAAACGCGAATGTGTG	AGCCATATAACCGAGCACTTG	60		
SSR 9	CGTCACAGAAGAAAGCACTTG	CCTCTCCATCGTCATCAATC	61		
SSR 10	GAGCCCATTAAGCTGAACA	CCGACAGTCAACATACAATACA	63		
SSR 11	TGAATCCCAAGTTTGGTCAAG	CAAAACACTGTCCCCATCTC	60		Mattos <i>et al.</i> 2010
SSR 12	TGATGCATTGGATGATCTCG	AAAACACACCAACTCCATCCC	55		
SSR 13	CCCTGACAGATCCTTTGTGG	GGAGACTTCCACCTTTTCCG	54		
SSR 14	CCTTCATCATCATCACGGC	ACCACGACCTCCTCCTCTC	54		
SSR 15	CACATCACACGCTCTGCTTC	TTTTTCGGCTGATCCAATTC	54		
SSR 16	CAAAGTTTGAAAGGGAGGGG	CTCGGACCACTAGCTTCCTG	58		
SSR 17	GGGATGGCGCACTTCTTC	AATCCGGGTGTAAGGAACC	54		
SSR 18	CATCGAGGATGCACATCAAG	CCAAAAGAGCCACGATTGAG	54		
SSR 19	TGCTGCGATTCTACTCATCG	TGCCCTCCTTGTCTGTATC	56		
SSR 20	TGTGTGACTACTCCCGTTTC	GTCTGCTGTATCCCGAG	56		
SSR 21	GTGTTGAGAGCTTTCAGCC	AGAACAATCAAGCCAGCAGC	54		
SSR 22	CCTCGCACATCAACCCTTAC	CATGATCACCATTTCCTCCC	56		
SSR 23	TGAACTCTTGCTACCCAGC	TTAGTGGCTTCTGTCCCAGG	55		
SSR 24	AGGGCACAAAGCGCTCAAG	CAATGAACGCATCACAGTCC	56		
SSR 25	CGGAGGATGTTGTTCTCGTC	CACGGGCTGTATTTGGTAGG	56		
SSR 26	TGGAGATGAAGAAGATCGCC	TCATCAAGTGCGTTGCATTC	55		
SSR 27	TCGTCTGATCATTTCCTTC	ACGCACGAGTAAGTTGTCCC	58		
SSR 28	TTCTTTTCTCTCTCCCACC	TAGGGTTTTAGATCGACGC	54		
SSR 29	AGCGGAAGAGGGTAGAGAGC	ATCTTCTGCTGGTTCATGGC	56		
SSR 30	GAGCCGTGGCTGTCACTAAG	TATACTCTCGATCACCGGGC	54		
SSR 31	TCGCAAGAATCTCACCTTCC	TGGTCTTCAGGTTCCGTTTC	56		
SSR 32	TCAGCAGACAATGCAAGAGC	GCAGTCCAACCTGGCCTTATG	55		
SSR 33	GCTGCTCTCGTTGTTATCC	GCTGCTCTCGTTGTTATCC	56		
SSR 34	AAACCCTCCACCAACACCTC	GTTTGGTGCTCATTGCTGTG	55		
SSR 35	GTCAATTCCTAGCGAGAGCG	AAATTGAGCTCCACAGGGTG	55		
SSR 36	AGAAGGGCTGGAAAGAGAGC	AATCCTGCAATTATGGCTGC	56		
SSR 37	GCGTCAGGTTGTCATTTTCG	CGGCATATCTATCCACCACC	56		
SSR 38	GGAACACAAACACGATGCAG	TTTGCACCTTTGTTCAAGGCAG	56		
SSR 39	AACATGCAGAGGGAGTGGTC	ATTGCTGATGGAGATGGAGG	56		
SSR 40	TATCAAGCCTAATCGGCCAC	TGCATCAAAAATTTCCAGCTC	52		
SSR 41	TGAAATCTGAACCCTGGTGG	ACGCACACACACACAATG	56		
SSR 42	TGATGCTCTTAACCCTTGCC	CGGTCCGATCAATATCGTC	56		
SSR 43	CGGAAGTGGCAGGGTAGAGA	CCCAACAACCTATGGCGGAGA	60	Buhariwalla <i>et al.</i> 2005	
SSR 44	CTACAACAATAATCCAGGGCAA	GGTCATCACGGCGTTCTCCA	61		
SSR 45	CCAGCGATAACCCTTCATGACCA	CTGATTAGGATTTGAAAGGGCAA	63		
SSR 46	GTTACATGAAGACCGGGCAA	CTCTCGATGGGTTTCCCAAGGA	60		
SSR 47	CTGCCTCTCCTTCTCCTTGGA	TCGGTGATGGCTCTGACTCA	55		
SSR 48	AGGTGCCACACAGTTCAGACA	CAACCCAAACCTGTTCCGACCAA	54		
SSR 49	ATGCCAAAGAAGGGAAGGGAA	TAATGCCGGAGGATCAGTGTGA	54		
SSR 50	AGATTCGGTTTCCGTTGCTA	AGTTTATTCGGTGGACGTTAACGA	54		
SSR 51	AGTGAGTGCCCCAAACGTGA	AAAATGTGCAAATGGGCGTGGA	56		
SSR 52	TCACATACCGAACAGAGAGAG TCA	CCGACCGTGAACCTCTTTTCCA	55		

pair wise genetic similarity index was calculated as per Jaccard's coefficient of similarity (Jaccard, 1908) is given below:

$$F = N_{AB1} / (N_T - N_{AB0})$$

Where,

F = Similarity index

N_{AB1} = Number of bands present (scored 1) in both accessions A and B

N_{AB0} = Number of bands present in all test entries but not present in accessions A and B.

N_T = Total number of bands scored in the study.

The degree of genetic relationship among the studied banana genotypes as revealed by Jaccard's coefficient of similarity was represented through cluster analysis using algorithm of "Unweighted Pair Group Method with Arithmetic Average" (UPGMA), by feeding similarity matrix as input data. In UPGMA, averaging of distance is based on the total number of taxa in the clusters. The graphical representation of genetic relationship among the genotypes was done in the form of dendrogram.

Results and Discussion

Amplification profile analysis of SSR primers

Out of 52 primers tested initially, 32 polymorphic primers that gave clear banding pattern were used in the present study (Table 3). A total of 197 bands were scored from 24 banana genotypes under the study, out of which 170 were found to be polymorphic. Maximum number of polymorphic bands were amplified by SSR8, whereas, least number of polymorphic bands was produced by SSR33 and SSR50. Average number of total bands and polymorphic bands per marker were 6.16 and 5.31, respectively. All amplified fragment were polymorphic in 15 SSR primers- SSR8, SSR9, SSR16, SSR17, SSR18, SSR25, SSR30, SSR34, SSR35, SSR40, SSR42, SSR44, SSR46, SSR48 and SSR50; and the average polymorphism per primer was 84.95%. Polymorphism information content (PIC) ranged from 0.913 (SSR41) to 0.061 (SSR23) with an average value of 0.436. The highest PIC value of SSR41 showed that this primer had a better discriminatory power of this primer to reveal higher level of genetic diversity among the genotypes.

Molecular identity of banana genotypes

Table 4 represents some of the specific bands representing a few of the banana genotypes under the

Table 3. Polymorphism analysis of the SSR marker

Marker name	Total band amplified	Number of polymorphic band	polymorphism %	PIC
SSR 3	3	2	66.67	0.163
SSR 8	14	14	100.00	0.91
SSR 9	3	3	100.00	0.759
SSR 13	7	6	85.71	0.677
SSR 15	5	4	80.00	0.273
SSR 16	6	6	100.00	0.347
SSR 17	5	5	100.00	0.369
SSR 18	9	9	100.00	0.415
SSR 21	8	4	50.00	0.382
SSR 22	4	3	75.00	0.72
SSR 23	4	2	50.00	0.061
SSR 24	8	6	75.00	0.09
SSR 25	5	5	100.00	0.378
SSR 26	5	3	60.00	0.203
SSR 27	8	6	75.00	0.392
SSR 28	6	3	50.00	0.135
SSR 30	4	4	100.00	0.538
SSR 31	4	3	75.00	0.134
SSR 32	6	5	83.33	0.252
SSR 33	2	1	50.00	0.75
SSR 34	7	7	100.00	0.273
SSR 35	3	3	100.00	0.552
SSR 39	13	11	84.62	0.269
SSR 40	6	6	100.00	0.776
SSR 41	9	8	88.89	0.913
SSR 42	11	11	100.00	0.488
SSR 44	4	4	100.00	0.149
SSR 46	8	8	100.00	0.752
SSR 48	6	6	100.00	0.829
SSR 49	6	5	83.33	0.079
SSR 50	1	1	100.00	0.826
SSR 51	7	6	85.71	0.13
TOTAL	197	170		
Average	6.16	5.31	84.95	0.437

study. These bands were identified as molecular IDs for the genotypes based on their reproducibility. A single band of 400bp was identified for Digjowa with SSR27 (Plate 2). Another band of 250bp size was identified for both the red bananas (Agnisagar and Gobin Tulsi) in case of SSR22 (Plate 4).

Marker mediated inter accession genetic variation

Pairwise Jaccard's coefficient of similarity was calculated for 276 combinations (Table 5). The UPGMA cluster analysis graphically representing the genetic relationship among the genotypes (Fig. 1 Dendrogram) revealed that two major clusters of genotypes i.e. cluster 1 and cluster 2 (Table 6).

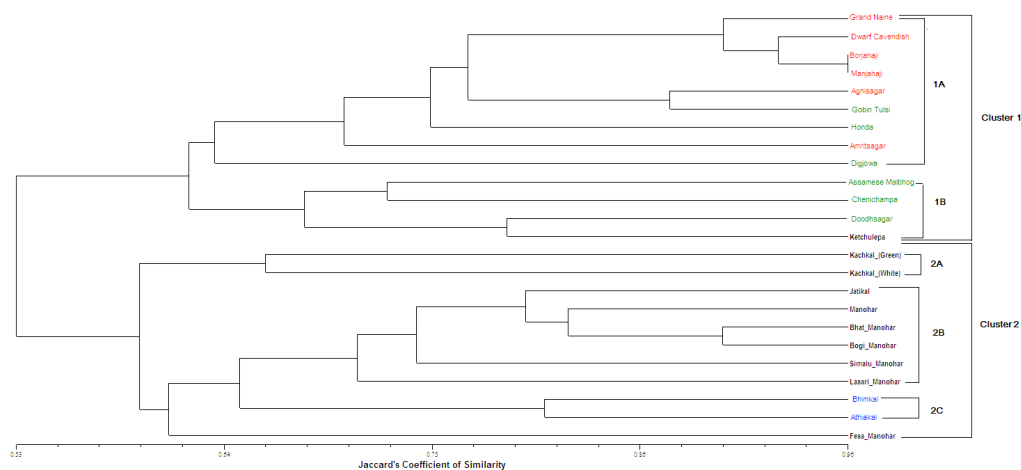


Fig. 1. Dendrogram showing relationships among banana genotypes based on SSR markers

Diversity analysis with the use of molecular markers determines the degree of relatedness and help in accurate grouping of genotypes to identify ancestors and to detect the duplication. Molecular marker based genetic diversity analysis has potential for assessing changes in genetic diversity over time and space (Duwick, 1984). The average Jaccard's similarity index based on 32 SSR markers was calculated to be 0.552, which suggested that the genotypes under the study had significant differences. Among the banana genotypes, genetic similarity index ranged from 0.378 to 0.965. Among the genotypes, the maximum similarity (0.965) was observed between Barjahaji and Manjahaji, followed by 0.938 between Manjahaji and Dwarf Cavendish, 0.918 between Barjahaji and Dwarf Cavendish, 0.895 between Manjahaji and Grand Naine and 0.876 between Barjahaji and Grand Naine. All these four genotypes belong to the Cavendish group of bananas under the genomic group AAA. Despite of having morphological and agronomical differences, the molecular studies had confirmed their close relationship based on their genomic constituents.. A

high similarity index of 0.899 was obtained between Bhat Manohar and Bogi Manohar bananas, as well as, between both the red pigmented bananas taken under the study (Agnisagar and Gobin Tulsi), *i.e.* 0.872. Between the two genotypes (Bhimkal and Athiakal) of banana belonging to diploid *balbisiana* genomic group (BB), the similarity index was found to be 0.806, which indicated presence of differences between the two genotypes at genetic level based on this marker based study. The minimum similarity (0.378) was exhibited between Bhimkal and Amritsagar, followed by 0.400 between Athiakal and Amritsagar, indicating diverse nature of those

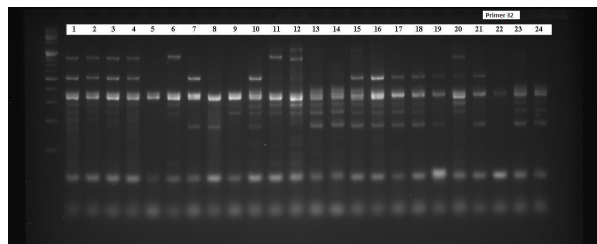


Plate 1. Polymorphic banding pattern of 24 banana genotypes produced by SSR32

Table 4. Molecular ID's of banana genotypes

SSR Primer	Size (bp)	Genotypes
SSR27	400	Digjowa
SSR8	180	Ketchulepa, Manohar
SSR22	250	Agnisagar, Gobin Tulsi
SSR34	470	Grand Naine, Kachikal (Green)
SSR9	1250	Bogi Manohar, Fesa Manohar, Bhimkal
SSR39	250, 180	Malbhog, Doodhsagar, Ketchulepa
SSR51	195	Amritsagar, Agnisagar, Gobin Tulsi

Table 5. Jaccard's coefficient of similarity among the banana genotypes using SSR marker

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19	V20	V21	V22	V23	
V2	0.928																							
V3	0.876	0.918																						
V4	0.895	0.938	0.965																					
V5	0.660	0.674	0.746	0.715																				
V6	0.739	0.750	0.803	0.787	0.803																			
V7	0.600	0.616	0.629	0.617	0.592	0.639																		
V8	0.675	0.663	0.688	0.696	0.615	0.677	0.724																	
V9	0.634	0.641	0.634	0.632	0.558	0.634	0.588	0.617																
V10	0.611	0.599	0.582	0.591	0.528	0.630	0.740	0.667	0.581															
V11	0.779	0.758	0.764	0.750	0.702	0.872	0.617	0.665	0.654	0.659														
V12	0.747	0.758	0.720	0.739	0.612	0.731	0.617	0.675	0.687	0.679	0.783													
V13	0.503	0.488	0.479	0.497	0.468	0.515	0.567	0.525	0.477	0.541	0.471	0.533												
V14	0.426	0.430	0.449	0.439	0.467	0.470	0.521	0.438	0.447	0.481	0.429	0.436	0.661											
V15	0.629	0.598	0.600	0.599	0.510	0.572	0.616	0.623	0.560	0.690	0.563	0.608	0.664	0.543										
V16	0.616	0.622	0.596	0.614	0.493	0.615	0.697	0.620	0.596	0.787	0.624	0.614	0.547	0.489	0.694									
V17	0.599	0.577	0.579	0.587	0.457	0.561	0.564	0.572	0.557	0.616	0.534	0.569	0.673	0.539	0.787	0.681								
V18	0.612	0.582	0.584	0.592	0.480	0.566	0.599	0.606	0.515	0.630	0.556	0.565	0.667	0.496	0.801	0.665	0.837							
V19	0.654	0.633	0.626	0.625	0.510	0.581	0.614	0.602	0.524	0.635	0.571	0.589	0.671	0.507	0.801	0.699	0.800	0.899						
V20	0.588	0.584	0.576	0.565	0.536	0.528	0.526	0.535	0.541	0.544	0.527	0.585	0.596	0.548	0.647	0.521	0.623	0.649	0.709					
V21	0.525	0.520	0.521	0.520	0.414	0.494	0.561	0.550	0.484	0.556	0.494	0.538	0.664	0.556	0.678	0.600	0.757	0.772	0.750	0.596				
V22	0.503	0.479	0.497	0.479	0.431	0.497	0.566	0.533	0.466	0.584	0.488	0.525	0.621	0.504	0.710	0.539	0.683	0.750	0.692	0.579	0.708			
V23	0.510	0.487	0.497	0.487	0.378	0.454	0.522	0.479	0.449	0.490	0.455	0.455	0.667	0.557	0.640	0.535	0.692	0.689	0.676	0.537	0.711	0.712		
V24	0.453	0.436	0.444	0.435	0.400	0.437	0.500	0.462	0.455	0.507	0.429	0.426	0.615	0.619	0.580	0.507	0.612	0.583	0.590	0.543	0.650	0.629	0.806	

(V1: Grand Naine, V2: Dwarf Cavendish, V3: Barjahaj, V4: Manjahaj, V5: Amritsagar, V6: Agnisagar, V7: Assamese Malbhog, V8: Chenichampa, V9: Digjowa, V10: Doodhsagar, V11: Gobin Tuli, V12: Honda, V13: Kachkal (Green), V14: Kachkal (White), V15: Jatikal, V16: Ketchulepa, V17: Manohar, V18: Bhat Manohar, V19: Bogi Manohar, V20: Fesa Manohar, V21: Simalu Manohar, V22: Lasari Manohar, V23: Bhimkal, V24: Athiaka) Table 6. Clusters based on Jaccard's coefficient of similarity

genotypes. This concludes that higher the similarity index more is the similarity between the genotypes in comparison. And even though there is similarity among closely related genotypes, there exists considerable variation at their genomic level.

Two major clusters were observed in the dendrogram based on Jaccard's coefficient of similarity. Cluster 1 could be subdivided into 1A and 1B, whereas cluster 2 could be subdivided into sub-cluster 2A, 2B and 2C. Sub-cluster 1A was the largest with 9 genotypes that originally belong to AAA and AAB genomic groups based on scoring technique of banana classification. The sub-cluster 1B consisted of Assamese Malbhog, Chenichampa, Doodhsagar and Ketchulepa. The first three genotypes come under AAB genomic group based on scoring technique of *Musa* classification, whereas, Ketchulepa comes under ABB genomic group. Therefore, much diversity could be seen in this sub-cluster. Both the culinary genotypes Kachkal Green and Kachkal White consisted the sub-cluster 2A, giving rise to distinct difference with any other genotype. The sub-cluster 2B comprised of all the Manohar genotypes and Jatikal, among which Bogi Manohar and Bhat Manohar were the closest

Clusters	Sub-clusters	Genotypes
1	1A	Grand Naine, Dwarf Cavendish, Barjahaji, Manjahaji, Agnisagar, Gobin Tulsi, Honda, Amritsagar, Digjowa
	1B	Assamese Malbhog, Chenichampa, Doodhsagar, Ketchulepa
2	2A	Kachkal (Green), Kachkal (White)
	2B	Jatikal, Manohar, Bhat Manohar, Bogi Manohar, Simalu Manohar, Lasari Manohar
	2C	Bhimkal, Athiakal
	-	Fesa Manohar

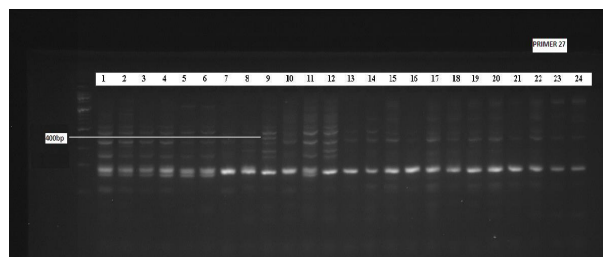


Plate 2. Polymorphic banding pattern of 24 banana genotypes produced by SSR27 showing 400bp band in Genotype 9, *i.e.* Digjowa

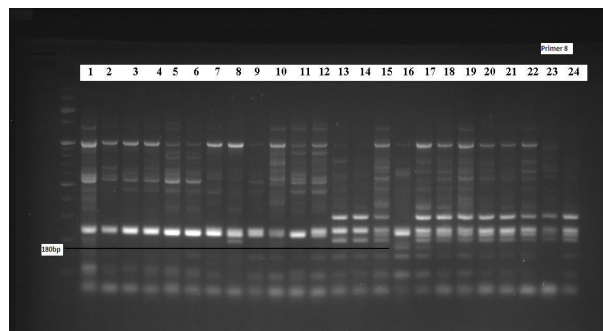


Plate 3. Polymorphic banding pattern of 24 banana genotypes produced by SSR8 showing 180bp band in Genotype 16 and Genotype 17, *i.e.* Ketchulepa and Manohar

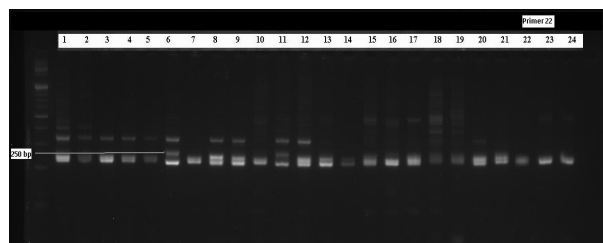


Plate 4. Polymorphic banding pattern of 24 banana genotypes produced by SSR22 showing 250bp band in Genotype 6 and Genotype 11, *i.e.* Agnisagar and Gobin Tulsi

relatives. In this clustering process, Bhimkal and Athiakal were placed in a single group, representing their close relation with each other and at the same time their distant relationship with other genotypes.

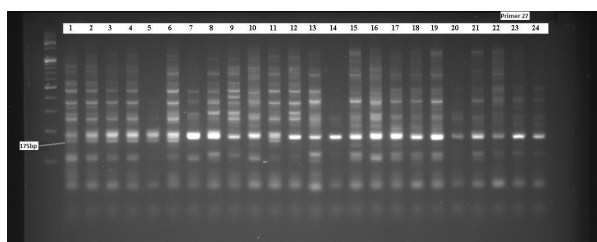


Plate 5. Polymorphic banding pattern of 24 banana genotypes produced by SSR27 showing 175bp band in Genotypes 1-6 and Genotype 11, *i.e.* Grand Naine, Dwarf Cavendish, Barjahaji, Manjahaji, Amritsagar, Agnisagar and Gobin Tulsi

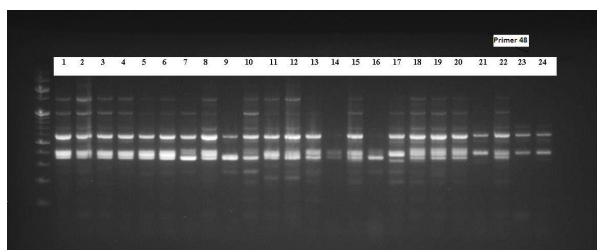


Plate 6. Polymorphic banding pattern of 24 banana genotypes produced by SSR48

From the banding profile of SSR markers, specific bands for some specific genotypes were identified during the study, which could be considered as molecular identities for these specific genotypes. This study showed existence of great genotype diversity among the *Musa* germplasm of Assam and considerable amount of genetic variations are present even among the closely related genotypes within the same genomic group.

Conflict of Interest- None

References

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