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Genome classification of banana genetic resources of Manipur using morphological characters

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Abstract

Manipur, a northeastern state in India, harbours a rich diversity of both wild and cultivated bananas. The banana cultivars collected from all the districts were carried out for their taxonomic identification and genome group classification. A total of 27 cultivars were collected in the present study. Of all the cultivars, *Musa balbisiana* clone was represented by 3 cultivars; 8 cultivars were identified under *M. acuminata* clones. Majority of the cultivars (16) were identified as *Musa* species, hybrid of *M. balbisiana* and *M. acuminata.* Among these cultivars, 3 cultivars were classified under BB genome while 3 cultivars were classified under the AA genome group. The ABB genome group was represented by 13 cultivars. 5 non-seeded cultivars were classified under AAA genome group and the AAB group was also represented by 3 sweet smelling cultivars. The dendrogram constructed based on the 15 morphological characters showed the clustering of cultivars into 3 major groups, at a distance coefficient ranging from 0.60 to 0.50, corresponding to genome groups of the cultivars. The present findings provide the status of existing banana genetic resources from Manipur which could be utilized in improvement and conservation programs.

Key words: Banana; classification; genome group; identification; Manipur.

Introduction

Banana is giant herbaceous monocotyledonous plant and one of the most important food crops worldwide.[1,2] It belongs to the family Musaceae of order Zingeberales, which consists of two genera *Musa* and *Ensete*.[3] India is the largest producer of banana with a production of 27.01 million metric tonnes from an area of 0.765 million hectare contributing to 22.15% of global production, followed by Philippines (9.3%), China (9.2%), Ecuador (7.8%) and Brazil (7%).[4]

Southeast Asia is considered as centre of origin of *Musa* species, where numerous wild species occur in an area stretching from Papua New Guinea to India. Human interventions and movement brought *Musa acuminata* Colla into Indian sub-continent, where it introgressed with *M. balbisiana* Colla endemic to the northeastern

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region of India.[5] Majority of the *Musa* species are found in different agroclimatic condition and are widely distributed in northeast India,[6] which has been considered as the richest sources of natural banana diversity.[7] However, the correct identification and classification of banana cultivars in the region is hampered by the presence of different ethnic communities and languages. A variety is known by different names based on the dialects and the communities in different regions of the northeast India. Moreover, majority of the wild varieties are exposed to large-scale exploitation and destruction as a result of shifting cultivation by the local tribes, thereby wiping out *Musa* natural habitats.[8] This accentuates the need to collect, characterize and document germplasm before its extinction from these areas. Reliable identification and genetic information on the existing banana genetic resources will be useful for the effective breeding and conservation strategies.

Most of the edible bananas are derived from two wild species *viz. M. acuminata* (having AA genome) and *M. balbisiana* (having BB genome), through inter and intra specific hybridization, resulting the generation of many genome groups such as AA, AB, AAA, AAB, ABB, AABB, AAAB, and ABBB.[9] Conventionally, identification and classification of edible bananas and their wild relatives' genome has been based on morphological characters and their similarity to the two progenitor species, *M. acuminata* and *M. balbisiana*. In 1955, Simmonds and Shepherd[9] devised a new genome-based nomenclature system for the edible fruit bearing bananas based on their genotype. They have listed various features that were characteristic of *M. acuminata* and *M. balbisiana* and gave them arbitrary numerical values. They scored plants based on the visual assessment of these characters and assigned them with various genome groups. This system of classification has become a primarily referred for banana genotyping.

For crop improvement programs, germplasm collection and characterization are of fundamental importance because they provide plant breeders with a source of useful traits[10,11] and increase the knowledge on the genetic background of the crop.[12] Several qualitative and quantitative morphological characters including vegetative, inflorescence, male flowers and fruit characters are very useful for identification and classification of *Musa* species.[10,13] Recently, Lalrinfela and Thangjam[14] reported the genome classification of Mizoram banana varieties using morphological characters. Many other studies have also reported the genomic composition of different banana cultivars.[5,15,16] The present study is thus undertaken to carry out genomic classification of banana cultivars of Manipur using morphological characters.

Materials and Methods

Survey and collection of the samples

The distribution of banana varieties in different parts of Manipur was obtained from the consultation of the concerned officials of agriculture and horticulture departments of Manipur, and the regional farmers. As a result, all the banana cultivars were collected from all the 9 districts (Imphal West, Imphal East, Thoubal, Tamenglong, Bishnupur, Senapati, Chandel, Ukhrul, Churachandpur). The collected samples were planted and maintained in the field genebank of Department of Biotechnology, Manipur University, Imphal. Each of the collected cultivars was provided passport data and unique voucher numbers using International Plant Genetic Resources Institute (IPGRI) descriptors.[17]

Morphological identification and characterization

The taxonomical classification and identification of the collected banana samples were carried out by evaluating the habit, leaf, floral and fruit characteristics using the identification keys provided by Singh *et al.*[13] and Häkkinen[3] For genome classification, the morphological characters of vegetative, male and female inflorescence based on 15 characters suggested by Simmonds and Shepherd[9] were evaluated (see

Table 1. Morphological characters used for banana classification (Simmonds and Shepherd, 1955).

Sl. No	Characters	*Musa acuminata*	*Musa balbisiana*
1.	Pseudostem color	More or less heavily marked with brown or black blotches	Blotches slight or absent
2.	Petiolar canal	Margin erect or spreading,with scarious wings below,not clasping pseudostem	Margin enclosed, not winged below, clasping pseudostem
3.	Peduncle	Usually downy or hairy	Glabrous
4.	pedicel	Short	long
5.	Ovules	Two regular rows in each loculus	Four irregular rows in each loculus
6.	Bract shoulder	Usually high (ratio < 0.28)	Usually low (ratio > 0.30)
7.	Bract curling	Bract reflex and roll back after opening	Bracts lift but do not roll
8.	Bract shape	Lanceolate or narrowly ovate, tapering sharply from the shoulder	Broadly ovate ,not tapering sharpl
9.	Bract apex	Acute	Obtuse
10.	Bract color	Red, dull purple or yellow outside; pink, dull purple or yellow inside	Distinctive brownish-purple outside; bright crimson inside
11.	Color fading	fading Inside bract color fades to yellow towards the base	Inside bract color continuous to base
12.	Bract scars	Prominent	Scarcely prominent
13.	Free tepal of male flower	Variably corrugated below tip	Rarely corrugated
14.	Male flower color	Creamy white	Variably flushed with pink
15.	Stigma color	Orange or rich yellow	Cream, pale yellow or pale pink

Table 1) and a relative score was recorded.[9,18] For example, with respect to pseudostem colour, score of 1 is given, if the speudostem is heavily blotch with brown or black pigmentation. Similarly, a maximum score of 5 was given when blotches are completely absent and the pseudostem is more or less green. Intermediary scores from 1-5 depending on the extent of blotching and the score range from 1-75 (see Table 2).

Results and Discussion

A total of 27 different banana cultivars collected were evaluated for their taxonomic position as per the identification keys provided by Singh *et al.*[13] and Häkkinen[3]. The most important characters for their identification are the extent of pseudostem blotching, shape of leaf lamina base, leaf petiole canal and margins, sucker of orientation, peduncle hairness, prominence of bract scars in male axis, traits of male bracts (such as imbrications, external and internal color, persistence, behaviour, shape and

Table 2. Modified score card for assigning tentative genomic groups.

Genomes	Score card of	
	Simmonds and Shepherd (1955)	Singh & Uma (1996)
AA/AAA	15-23	15-25
AAB	24-46	26-45
AB	49	46-49
ABB	59-63	59-65
ABBB	67	66-69
BB/ BBB	-	70-75

apex), corrugation and texture of free tepal, color of male flower, fruit base insertion, fruit orientation and fruit apex. Among all the cultivars, 3 were identified as *M. balbisiana* clones (Luine, Changbi and Kharam laphu); 8 under *M. acuminata* clones (Korbot, Noneh laphu, Grand naine, Grand naine, Changbi mara chatpi, Des laphu, Chingchup and Mizoram laphu) and 16 under the *Musa* species (Ragunsen masung ahum naibi, Heijao angouba, Champa colla manbi, Champa colla angangbi, Teralaphoi, Champa colla, Morpi, Hei, Hangou, Masung ahum naibi, Meitei hei, Yensang chabi, Morshell, Nagunsen, Utteibi and Ngalai). Table 2 represent details of the cultivars on their taxonomic positions identified with the local names.

Based upon the scores of 15 morphological characters all the cultivars were classified into different genome groups (see Table 3). The 3 cultivars (Luine, Changbi and Kharam laphu) with the corresponding morphological score of 70, 71 and 71 respectively were classified under BB group. The 3 cultivars namely Korbot, Noneh laphu and Changbi mara chatpi having the same morphological score of 23, were classified under AA genome group. The ABB genome group was represented by majority of the cultivars studied, 13 cultivars (Ragunsen masung ahum naibi, Heijao angouba, Champa colla angangbi, Teralaphoi, Morpi, Hei, Hangou, Masung ahum naibi, Meitei hei, Yensang chabi, Morshell, Utteibi and Ngalai) with the morphological scores ranging from 54-63. The 5 non-seeded cultivars (Grand naine, Grand naine, Des laphu, Chingchup and Mizoram laphu) with the scoring range of 21-23 were classified under AAA genome group. The 3 sweet smelling cultivars (Champa colla manbi, Champa colla and Nagunsen) with the score of 33, 34 and 35 respectively were also classified under AAB group.

The score data from 15 morphological characters was also used for construction of dendrogram by Unweighted Pair Group Method with Arithmetic mean (UPGMA) based on SM correlation. The resulted dendrogram showed the clustering of cultivars into 3 major groups at a distance coefficient ranging from 0.60 to 0.50

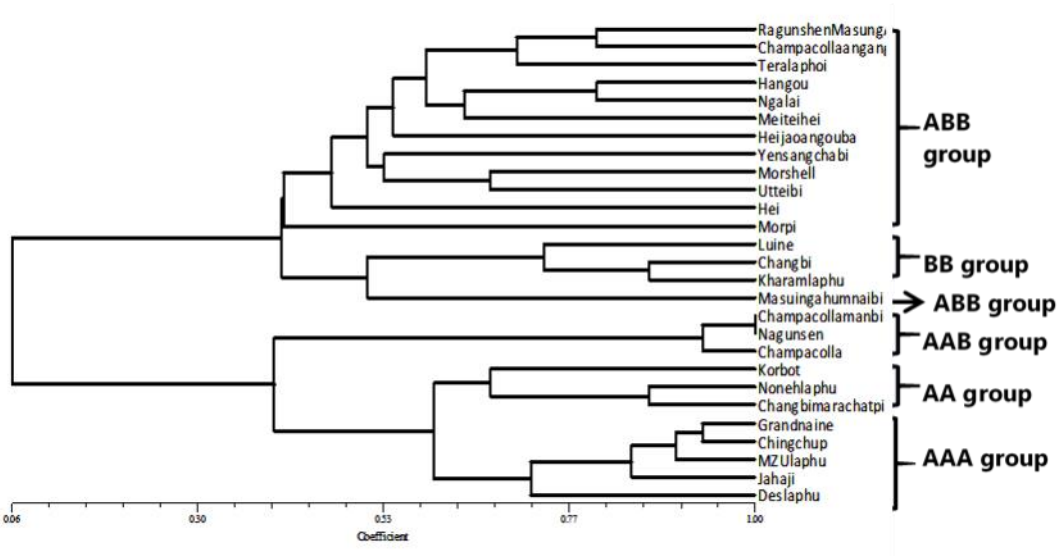

Figure 1. Dendrogram based on 15 morphological characters using SM coefficient of 27 different banana cultivars.

Table 3. List of banana cultivars and their genome group based on morphological characters.

Sl. no	Cultivars	Voucher no.	Scientific name	Morphological scores (Simmond and Shepherd, 1955)	Genome group
1	Ragunsen masung ahum	MUTRS-01	*Musa species*	60	ABB
2	Heijao angouba	MUTRS-02	*Musa* species	63	ABB
3	Champa colla manbi	MUTRS-03	*Musa* species	33	AAB
4	Champa colla angangbi	MUTRS-04	*Musa* species	63	ABB
5	Teralaphoi	MUTRS-05	*Musa* species	63	ABB
6	Luine	MUTRS-06	*Musa balbisiana*	70	BB
7	Champa colla	MUTRS-07	*Musa* species	34	AAB
8	Korbot	MUTRS-08	*Musa acuminata*	23	AA
9	Noneh laphu	MUTRS-09	*Musa acuminata*	23	AA
10	Morpi	MUTRS-10	*Musa* species	54	ABB
11	Hei	MUTRS-11	*Musa* species	62	ABB
12	Grand naine	MUTRS-12	*Musa acuminata*	23	AAA
13	Jahaji	MUTRS-13	*Musa acuminata*	23	AAA
14	Changbi mara chatpi	MUTRS-14	*Musa acuminata*	23	AA
15	Hangou	MUTRS-15	*Musa* species	63	ABB
16	Masung ahum naibi	MUTRS-16	*Musa* species	63	ABB
17	Meitei hei	MUTRS-17	*Musa* species	63	ABB
18	Des laphu	MUTRS-18	*Musa acuminata*	23	AAA
19	Yensang chabi	MUTRS-19	*Musa* species	61	ABB
20	Morshell	MUTRS-20	*Musa* species	59	ABB
21	Nagunsen	MUTRS-21	*Musa* species	35	AAB
22	Chingchup	MUTRS-22	*Musa acuminata*	22	AAA
23	Changbi	MUTRS-23	*Musa balbisiana*	71	BB
24	Mizoram laphu	MUTRS-24	*Musa acuminata*	21	AAA
25	Kharam laphu	MUTRS-25	*Musa balbisiana*	71	BB
26	Utteibi	MUTRS-26	*Musa* species	54	ABB
27	Ngalai	MUTRS-27	*Musa* species	63	ABB

(Fig. 1). The first group was further divided into three distinct sub-clusters corresponding to genome groups of the cultivars. The first sub-clusters comprise of 12 cultivars of ABB group (Ragunsen masung ahum naibi, Heijao angouba, Champa colla angangbi, Teralaphoi, Morpi, Hei, Hangou, Meitei hei, Yensang chabi, Morshell, Utteibi and Ngalai) while second sub-cluster was represented by 3 cultivars of BB group (Luine, Changbi and Kharam laphu). And the third sub-cluster is joined together by 3 cultivars of AA group (Korbot, Noneh laphu and Changbi mara chatpi). The second group is divided into two sub-clusters in which the first

sub-cluster consists of 3 cultivars of AAB genome group (Champa colla manbi, Champa colla and Nagunsen) and the second sub-cluster with 5 cultivars of AAA genome group (Grand naine, Grand naine, Des laphu, Chingchup and Mizoram laphu). The third major group was represented by Masung ahum Naibi, ABB group. Thus, cluster analysis showed the grouping of the cultivars based on their genome group except with the lone cultivar of Masung Ahum Naibi (ABB group). Table 2 shows details of grouping of the banana cultivars based on the cluster analysis.

To be of value, characterization descriptors must exhibit it polymorphism, either between or within taxa. Also they should be highly heritable, easy to visually score and consistently expressed in all environments. Manipur harbour a rich diversity of both wild and cultivated bananas. However, information on the banana genetic resources with long-established and introduced varieties was scanty. Collection and identification of cultivars in this region has always been a problem due to its hilly terrain where most of the bananas are found grown in the remote unexplored hills.[6] Moreover, Manipur is inhabited by various tribes speaking different languages and dialects which added more confusion to proper identification and documentation of banana. The same cultivar has different names like Changbi (Manipuri) is called Naachang in Paite, Zou, Gangte; and Mot in Kuki. Similar problems have been observed in East African Highland banana[19] and Mizoram banana.[14,16] The present study is thus very important for which the cultivars confusion would able to resolve among the farmers and for selection of the parent plant for breeding stock.

According to Sevile and Hole,[20] a proper germplasm evaluation according to morphological descriptors, determination of the agronomic value of germplasm and establishment of relationship with and between the species are always necessary for breeding programme and sustainable utilization. The present study will also be in support of Nwakanma *et al.*[21] that genetic studies and determination of genome composition at the early stage on *Musa* species, could effectively contribute the breeders in understanding the genetic resources of the plants, allowing them in the prediction of bunch characteristics. The identification of cultivars and classification of their genome groups will thus strengthen establishment of *Musa* improvement strategy in northeast India where valuable genetic resources are available.

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