Crop Improvement in *Musa* – Evaluation of Germplasm for Male and Female Fertility

S Uma, S Sathiamoorthy, HP Singh[2] and M Dayarani[1]
[1]*National Research Centre for Banana, Tiruchirapalli-620 017 (Tamil Nadu)*
[2]*Horticulture Commissioner, Krishi Bhavan, New Delhi-110 011*

A total of 450 accessions of *Musa* (bananas and plantains) at National Research Centre for Banana, Tiruchirapalli, (NRCB) field genebank were screened for their male and female fertility. Male fertility was screened with respect to pollen production, pollen fertility and pollen germination. Apart from AA members, ABB genomes namely Pisang Awak, Monthan and Bluggoe were found to be better pollen parents, with the exception of Peyan subgroup. Screening for female fertility revealed that subgroups Mysore and Pome (AAB) and Pisang Awak and Bluggoe (ABB) were potential female parents of use in *Musa* improvement programme. Though seed characters varied greatly with respect to pollen and female parent combinations, variability was noticed with respect to number of seeds/fruit, seed distribution, colour, shape and weight.

Key Words: Banana, Crop Improvement, Germplasm, Female Fertility, Fertility, Male Fertility, *Musa*, Seed Fertility

India is the largest producer of banana in the world with 14 million tonnes of production annually. It contributes to 31.7% of total fruit production and ranks as the number one fruit crop in the country (Singh and Uma 1996). India is believed to be one of the major centres of *Musa* origin, exhibiting great diversity for bispecific clones like AB, AAB and ABB. Three major species *M. acuminata, M. balbisiana* and *M. schizocarpa* are thought to be the original species responsible for evolution of present day cultivars (Horry 1993). In India diversity is observed mainly in *acuminata* and *balbisiana.*

Banana cultivars are characterized by male and female sterility, with a range from moderate to absolute sterility and parthenocarpy. But parthenocarpic expression is dependent on various factors like cultivar and congenial pollen parents. Hence, in the present study, efforts were made to recognize potential pollen parents with desirable traits and cultivars of commerce requiring improvement with respect to one or two traits and 450 *Musa* accessions were evaluated for this purpose.

Material and Methods

A total of 450 *Musa* accessions belonging to various groups and subgroups (Table 1) were evaluated for male and female fertility during 1995-98. Male fertility was evaluated in terms of pollen production and pollen fertility. Anther sacs for each accession were scored in 3 replicates for pollen count. Each anther sac was cut into four equal pieces and each quadrant was squashed and observed under microscope. Numbers of pollen grains produced per quadrant were counted and total pollen grain produced per sac was estimated (Sathiamoorthy, 1973). According to the count, accessions were classified as nil, scanty (<1,000), medium (1,000-10,000) and polleniferous (>10,000). Pollen fertility was assessed by *in vitro* germination of the pollen grains in 0.5% sucrose medium for 30 min. The per cent of fertile pollen was estimated for accessions and rated as highly fertile with >90% pollen germinating, 40-50% germination was rated as fertile, 20-40% germination was rated as medium 5.0-20.0% was rated poor and <5% as very poor (Sathiamoorthy, 1973).

Female fertility was assessed by selecting polleniferous male parents and hand pollinating during early morning hours (6-8 am). Mature anthers were slit vertically using a needle and pollen grains were extracted. These were collected on a camel hair brush and pollinated on to the flowers opened on the same day. The accessions setting seeds even under open-pollinated conditions were also considered to be female fertile. Data on seed in terms of colour, shape, size, 100-seed weight, seed position in fruit and seed bearing hands in a bunch were also collected.

Results and Discussion

Pollen fertility studies are shown in Table 1 which revealed that most of the *acuminata* (diploids and tetraploids) and *balbisiana* clones were highly polleniferous along with Monthan and Bluggoe subgroups. Subgroups Peyan, members of Monthan, Bluggoe and Pisang Awak exhibited medium polleniferous nature. Pome, Mysore, Nendra Padathi, Cavendish and AB subgroups exhibited very

Table 1. Pollen fertility details in *Musa* accessions

Genomic Group (rating)	Subgroup	Pollen production (rating)	Pollen fertility (rating)	Pollen germination (%)
AA	–	Profuse	74.8	+++
AAA	Robusta	Nil-scanty	2.8	+
	Dwarf Cavendish Thella Chakkarakeli	Nil-scanty	0.0	+
AB	Kunnan	Nil		–
	Ney Poovan	Nil		–
AAB	Silk	Scanty	3.6	+
	Mysore	Nil-scanty	8.4	+
	Plantain	Non-polleniferous	–	–
	Pome	Nil-scanty	6.9	+
	Nendra Padathi	Nil-scanty	10.7	+
ABB	Pisang Awak	Medium	66.3	+++
	Peyan	Medium	24.5	+++
	Monthan	Medium-profuse	61.4	++
	Bluggoe	Medium-profuse	78.6	+++
BB/BBB	–	Profuse	72.4	+++
Tetraploids		Profuse	88.9	+++

scanty pollen, while plantains, selected members of Pome, Mysore and Nendra Padathi produced no pollen at all. Most of the members of Pome group exhibited degenerating pollen sacs with the development of female phase.

Study on female fertility revealed that 46 female fertile accessions belonging to various genomic groups and subgroups were female fertile with an average seed set ranging from 1-250 seeds/fruit (Table 2). *Balbisiana* clones recorded the highest seeds of 150-250 seeds/fruit followed by Pisang Awak subgroup of ABB genome. Results show that a lot of variability exists in the *Musa* germplasm with respect to number of hands with seeds, fruits with seeds, number of seeds/fruit. Seed exhibited variability with respect to size, shape, colour, wrinkleness of seed coat and germinability (Table 2).

Table 2. Variability among *Musa* accessions with respect to open-pollinated seed characters

Genomic group	Subgroup	Average no. of seeds/fruit	Position in the fruit	Seed colour	Seed shape	100-seed wt. (g)
AA		2-10	Terminal	Black	Spherical	46.2-48.5
AAA		–	–	–	–	–
AB		–	–	–	–	–
AAB	Mysore	3-12	Random	Black	Flattenned	62.5-88.9
	Pome	5-12	Random	Black	Flattenned	48.3-77.8
	Silk	–	–	–	–	–
	Plantain	1-2	Distal end	Black	Round	56.3-72.8
	Nendra Padathi	–	–	–	–	–
ABB	Pisang Awak	5-30	Terminal & through out Black	Black to Pitch	Angular	74.0-115.6
	Bluggoe	1-35	Random	Black	Irregular Round Angular	48.6-85.3
	Monthan	1-3	Distal end	Black	Round	65.3-85.3
	Peyan	2-4	Random	Brown Black	Irregular	40.9-62.3
BB/BBB	*Balbisiana* clones non seeded	10-15	Random	Black	Flattenned	60.2-68.3
	Seeded	125-250	Throughout	Brown Brown-Black Black	Round Angular Flattenned	51.2-92.3

The study also revealed the potential female parents under each genomic group and subgroup easily set seeds when grown along with polleniferous varieties. Cavendish among AAA genome, Neypoovan and Kunnan among bispecific AB origin, Silk, Nendra Padathi of AAB failed to set seeds even under artificial, protected pollination. Though, Mysore and Pome subgroups of AAB exhibited good seed setting efficiency, Poovan (Mysore) had seasonal restrictions, which set seeds only during September-February months. Among ABB genome, all the four subgroups exhibited female fertility and the highest with Bluggoe subgroup. Position of the seed varied from terminal, distal, random and throughout the fruit length. But most subgroups exhibited affinity for random seed set while only Plantain (AAB) and Monthan (ABB) favoured seed set at distal end. Some members of Pisang Awak subgroups like Chinia set 25-30 seeds distributed throughout the pulp uniformly.

Seed colour and surface had little variability with brown to black and smooth to rough. Different seed shapes and embryo in the genus *Musa* were studied and described by Humphrey (1986) and Chin (1995). In the present study among the cultivated varieties, seed shape varied from round, irregular to flattened. In general, size of all seeds ranged from 4-6 mm. Hundred seed weight ranged from 40.9 g in Peyan subgroups (ABB) to 115.6 g in Pisang Awak (ABB) subgroup (Table 2). Germination percentage varied with genome and subgroups. The highest was recorded in Pisang Awak (54.8%) after *balbisiana* clones (68.9%) and least recorded among plantains with 1.8%. The reasons for varied germination and congenial conditions for germination needs to be worked out for different genome groups.

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