were evaluated for the incidence of *A. dispersus* during years 2000 and 2001 at Indian Institute of Horticultural Research, Bangalore. Observations were recorded from three trees of about 10-year-old in each variety. Each tree was considered one replication. The population counts of nymphs, pupae and adults of whitefly were taken from 10 randomly selected shoots in each tree at monthly intervals during the peak season *i.e.* March-May. Besides pest population, the extent of incidence in terms of per cent shoot infestation was also calculated.

The data were subjected to statistical analysis. Based on the extent of shoot infestation guava varieties were grouped as– highly susceptible (>50%), susceptible (25-50%), moderately susceptible (10-25%) and least susceptible (<10%).

From the data presented in Table 2, it is evident that the germplasm collections of guava varied significantly in their reaction to *A. dispersus* incidence. In both the years under study, the variety Spear acid recorded the least incidence (0.00 in 2000 and 3.33 in 2001) while the varieties Portugal, Bangalore local and EC 147036 were the most preferred ones with more than 50% shoot infestation. In terms of population counts, higher total number of pupae and adult was recorded from Portugal and least from Spear acid and Allahabad Safeda. Among the popular cultivars, Allahabad Safeda, Arka Amulya and Arka Mridula were under least susceptible group (<10% shoot infestation) while Lucknow-49 was under moderately susceptible group (10-25%). There was a significant positive correlation (r = + 0.756) between population of whitefly and percent shoot infestation indicating the quick dispersed tendency of insect within a preferred variety. Detailed studies to correlate the incidence of *A. dispersus* with morphological and biochemical parameters of leaves in different varieties are in progress.

Table 2. Grouping of guava germplasm collections according to their reaction to spiralling whitefly

Group	Varieties/Lines
Least susceptible (<10%)	Allahabad Safeda, Arka Amulya, Arka Mridula, Banaras, Spear acid
Moderately susceptible (10.25%)	Florida, Hafsi, Karela, Lucknow-49, Nasik, Pear shaped, *P. guinense* Sindh, Smooth green, Superior sour lucidum
Susceptible (25-50%)	Behat coconut, Mirzapur seedling, Redflesh, Seedless whiteflesh EC 147034, EC 147039
Highly susceptible (>50%)	Bangalore local, Portugal, EC 147036

References

Mani M and A Krishnamurthy (1996) Spiralling whitely and its natural enemies on guava in Karnataka. *Insect Environment* **2:** 12.

Palaniswamy MS, KS Pillai, RR Nair and C Mohandas (1995) A new cassava pest in India. *Cassava Newslett.* **19:** 6-7.

Ranjith AM, DS Rao and J Thomas (1996) New host records of the mealy whitefly, *Aleurodicus dispersus* in Kerala. *Insect Environment* **2:** 35.

Characterisation and Intra-group Cluster Analysis of *Musa* Sub-group Pisang Awak (ABB)

S Uma, P Theriappan, M Dayarani, B Shyam and S Sathiamoorthy
National Research Centre for Banana, # 17, Ramalinganagar South Extension, Vayalur Road, Trichy-620017, Tamil Nadu

Key Words: Banana, Characterisation, *Musa acuminata*, *Musa balbisiana*

Bananas are the most important among food crops worldwide. They include diverse types such as dessert, cooking and roasting bananas. Bananas are also scientifically referred to by their genome groupings. The crop encompasses a range of diploids, triploids and tetraploids. These are categorised into different genomic groups on the basis of their ploidy levels and the genomes, which they contain. Simmonds and Shepherd (1955) suggested that the present day bananas originated from two wild and seedy species, *Musa acuminata* colla (2n=22) and *Musa balbisiana* colla (2n=22) which are native to South-East Asia, resulting in a series of diploid,

Indian J. Plant Genet. Resour. 14: 190-192 (2001)

triploid and tetraploid bananas. The resulting genomic groups were classified as AA, AB, AAA, AAB, ABB, AABB, AAAB, ABBB, BB with the letters A and B representing *Musa acuminata* and *M. balbisiana,* respectively.

India is endowed with rich agrobiodiversity, having 356 major and minor plant species and their wild relatives native to this country. The Indian sub-continent in the South-Asian region is believed to be the centre of origin and diversity for the genus *Musa*. Sustainable exploitation of these resources would require effective strategies for their identification and conservation (Singh *et al.* 2001).

The *Musa* germplasm collections have been studied to assess the complete representation of the range of diversity of bananas in the countries, to set priorities for further collection and to reduce duplication. Since there is no test for clonal identity, many clones have been collected several times under different names from various agro-ecological conditions of the country. Classification and identification have become further complicated by the fact that many morphological characters are greatly influenced by the growing conditions. Numerical taxonomic analysis (Simmonds and Shepherd, 1955; Silayoi and Chomchalow, 1987) utilising key morphological characters generates information on their genetic constitution. But this needs further characterization techniques for effective grouping and studying their performance details.

The present study is undertaken on Pisang Awak sub group a triploid with ABB as its genomic constituent. It is one of the major commercial clone of the country. Being hardy, it is widely adopted for cultivation by the marginal farmers across the country. Its wider distribution, under varying agro-climatic conditions resulted in greater diversity. At NRCB, Trichy, 48 accessions have been collected under this group.

The genus *Musa* comprises both cultivated and the wild taxa. The cultivated taxa have been spread by human agency far from their original centres. Keeping this in view, NRCB, Trichy has carried out exploration trips to various parts of the Indian sub-continent and collected different lines of *Musa* belonging to both wild and cultivated types. Further efforts were also made to collect exotic lines from all over the world through international organisations and agencies. In all, 907 accessions belonging to different genomic groups have been collected and are being maintained in our field genebank. Accessions have also been characterised morpho-taxonomically.

A character is a feature of an organism that can be measured, counted or otherwise assessed. Simple two-state qualitative characters for example colour of the compound tepal – cream or pink, were coded as binary *i.e.* by scoring 1 if that character is present and 0 if that character is absent. The data were computed and analysed using NTSYS package.

In the present study due to multivariate analysis of morphological variation among the *Musa* accessions, it is possible to classify the Pisang Awak (ABB) accessions into identifiable clone sets. The objective of this study was to assess phenotypic variation in (the genuinity) accurate classification within the groups. This is used to assess the relatedness and distance of sample characterized. A total of 18 qualitative parameters are found to differ among accessions. These accessions exhibit the traits over generations without visual modifications. The traits are: colour of the pseudostem, colour of the upper surface of leaves, nature of leaves, peduncle, position of bunch, appearance of bunch, rachis, colour of the male bract, colour of the compound tepal, colour of the free tepal, position of stamen, colour of pollen sac, position of fruits, length of fruits, colour of finger, fruit peel colour and apex of the fruit. In this communication, grouping of different accessions belonging to Pisang Awak subgroup is described.

The group includes members like Kostha Bontha, Pey Kunnan, Boodi Bale, Karpooravalli, Kanthali, Nukula Bontha *etc.* The group is characterised by robust, pink-pigmented pseudostem, droopy leaves and curved laminar edges. Bunch is pendulous, compact and cylindrical with geometrically cylindrical arrangement of hands around the peduncle. Variability among the members of this group is observed with respect to male flower and fruit parameters among others.

For this study, 48 accessions belonging to Pisang Awak (ABB) subgroup were considered. Morpho-taxonomic characterisation and Simmonds and Shepherd score card categorised these accessions under ABB while tentative key for classification developed at this centre enabled them under Pisang Awak subgroup. The characters most responsible for the variation pattern found in Pisang Awak and extent of similarity and dissimilarity was worked out.

According to the cluster analysis of matrix of distance co-efficients, two distinct groups were clear involving Bhurkel 1, 2., Karpooravalli 1, 2., Mas, Jammulapalm collection, Chinia and other involving Octoman, Bothi

Bale 1, 2, 3., Bhurkel 3, mas, Vellapalayankodan, Eni Komban and Amritapani. Of all the collections Shail Kela, Chinia 1, Poombidian and Kechulepa had distinct independent clustering. In many cases, the names and the actual accession did not go together due to wrong labelling at the secondary centres of collection.

Small clusters of three to four members were noticed varying especially for one or more traits. The genotypes included in a cluster have exhibited less variations within themselves where as genotypes of one main cluster had a wide variation between individuals of another cluster. Pisang Awak group being highly female fertile, produces ample seeds in open-pollinated conditions. The seed progenies thus developed have contributed greatly for the present variation. Molecular characterisation will further elucidate the genetic relatedness among the genotypes.

References

Silayoi B and N Chomchalow (1987) Cytotaxonomic and morphological studies of Thai banana cultivars. In: GJ Persley and EA De Langhe *Proceedings of Banana and Plantain Breeding Strategies* (ed.) 288p.

Simmonds NW and K Shepherd (1955) The Taxonomy and origin of the cultivated bananas. *J. Linn. Soc. Bot.* **55:** 302-312.

Singh HP, S Uma and S Sathiamoorthy (2001) A Tentative Key for Identification and Classification of Indian Bananas. 61p.

Estimates of Gene Effects for Grain Yield and its Components in Bread Wheat

RC Singh* and BP Singh
Department of Botany, SGN Khalsa College, Sri Ganganagar-335001, Rajasthan

Key Words: Epistatic, Additive, Dominance, Duplicate, Interaction and Components

Bread wheat is one of the important cereal crop of millions of people in the world and it is also being utilized as animal feed in some states of India. Therefore, genetic improvement of crop varieties is one of the tool to fulfil the future demand of wheat. Before initiation of any successful breeding program for improvement of grain yield and its components, it is essential to know precisely the genetic architecture of particular trait having economic value. Thus, estimation of relative magnitude of different gene effects, their interactions have immense value to the breeders as they provide useful information for choosing appropriate breeding procedures for future improvement of the traits.

The six generations [P_1, P_2, F_1, F_2, BC_1 and BC_2] of two crosses namely UP-301 x RAJ–3077 and CPAN–3004 x HD-2329 were planted under irrigated conditions with normal application of fertilizer (120 kg N and 40 kg P_2O_5/hectare) in RBD with 4 replications. Each plot consisted of 5 rows of P_1, P_2 and F_1, 10 rows of BC_1 and BC_2 and 15 rows of F_2 population. The rows were kept 20 cm apart from each other with 15 cm plant to plant distance. Border rows were also provided at the beginning as well as the end of experimental rows in each block.

At maturity the data on 10 randomly selected plants in P_1, P_2 and F_1 generations is 30. In F_2, BC_1 and BC2 for days to heading, days to maturity, plant height, effective tillers/plant, flat leaf area, spike length, spikelets/spike, 1000-grain weight, harvest index and grain yield/plant were recorded during *rabi*–1994-95. The data were subjected to individual scaling test (Mather, 1949) and joint scaling test (Cavalli, 1952) to detect the presence of gene interaction while weighted least square method was applied to estimate six genetic parameters. In case where three parameter mode was found inadequate, six parameter model suggested by Jinks and Jones (1958) was applied.

Statistical analysis of data of six generations of both the crosses revealed that additive (d) and dominance (h) had important role in the inheritance of characters under study with preponderance of dominance as reported earlier by Amawate and Behl (1995).

Results of individual (Mather, 1949) and joint scaling test (Cavalli, 1952) indicated that epistasis also had

---

* *Present Address: Agriculture Research Station, Fatehpur-Shekhawati, Dist. Sikar-332301, Rajasthan*

Indian J. Plant Genet. Resour. 14: 192-194 (2001)