Morphological and Molecular Analysis of Intravarietal Variability in Mango (*Mangifera indica* L.) cv. Dashehari in Lucknow region

ABSTRACT

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ABSTRACT

The present investigation entitled **"Morphological and Molecular Analysis of Intravarietal Variability in mango (*Mangifera indica* L.) cv. Dashehari in Lucknow region"** was conducted during the year 2016-2018 in Malihabad and Mal block of District Lucknow and Ph. D Horticultural Laboratory, Department of Horticulture, School of Agricultural Sciences and Technology, Babasaheb Bhimrao Ambedkar University, Lucknow with the following objective

1. survey the possibility of genetic diversity and variability in Dashehari mango in tow Blocks of district Lucknow i.e. Malihabad and Mall.
2. To evaluate the intravarietal variability in mango cv. Dashehari on the basis of vegetative characters.
3. To establish intravarietal variability in mango cv. Dashaheri on the basis of physico-chemical characters of the fruit.
4. Microscopy studies for exploring intravarietal variability in mango cv. Dashehari.
5. Molecular analysis of intravarietal variability in mango cv. Dashehari.

Data of 45 morphotypes were analyzed for exploring intravarietal variability in vegetative, floral, physico-chemical and stomatal characters and protein profiling. The experiment was laid out in Completely Randomized Design (CRD) with 15 treatments () and from each three replications (trees) were selected for the study. Standard methods and procedures were followed for recording various vegetative, floral, physico-chemicals and stomatal attributes and protein profiling. The salient findings are summarized below.

6.1 Vegetative parameters

Among 45 Dashehari morphotypes the morphotypes DM_{25} and DM_{14} was superior for trunk girth (cm) and number of secondary branches/per tree. However, the highest leaf length (cm) and petiole length was observed for morphotype DM_{38} while, maximum leaf width (cm) and leaf thickness was observed for morphotypes DM_5 and DM_9.

A statistically significant variability were found in floral parameters and the morphotype DM_{12} was better for panicle length (cm), panicle width (cm), number of florets per panicle, number of flowers per panicle, fruit set per panicle at mustard stage, fruit set per panicle at pea stage, final fruit set per panicle.

Variability analysis for vegetative and floral parameters in terms of phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), heritability (h^2 %), genetic advance (GA) and genetic advance as percent of mean (GAM %). The highest PCV, GCV and genetic advance as percent of mean was recorded for number of secondary branches while number of florets per panicle, fruit set at mustard stage, number of flowers per panicle and trunk girth (cm) showed narrow differences between PCV and GCV. However, the highest heritability and genetic advance was observed for number of flowers per panicle while, fruit set at mustard stage, trunk girth (cm), number of secondary branches per tree and number of florets per panicle showed reliable amount of heritability and genetic advance.

UPGMA dendrogram was prepared on the basis of tree and leaf data of 45 Dashehari morphotypes in order to establish their relatedness to each other. Samples were found to be very closely related and grouped into only three major clusters (cluster I, II and III) with additional sub-clusters.

6.2 Fruit physico-chemical traits

The significant variability was observed among the fruit physic-chemical attributes. The morphotype DM_{12} was superior for fruit length (cm), fruit weight (g), fruit volume (ml), fruit specific gravity, pulp weight (g), pulp:peel ratio, peel thickness (mm), pulp stone ratio and stone length while, morphotype DM_{38} was better for peel weight (g), stone weight (g) and stone volume (ml). However, morphotype DM_7 was best for stone width (cm) and stone thickness (cm). The morphotype DM_1, DM_2, DM_3, DM_{10}, DM_{24}, DM_{25}, DM_{27}, DM_{33}, DM_{40}, DM_{41} and DM_{44} was superior for TSS:acid ratio, total soluble solids (0Brix), non-reducing sugar (%), kernel width (cm), pH of the pulp, kernel thickness, titrable acidity (%), reducing sugar (%), total sugar (%), fruit length (cm) and kernel length.

Analysis of Phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), heritability (h^2), genetic advance (GA) and genetic advance as

percent of mean (GAM %). The highest PCV and GCV was found for kernel width (cm), kernel thickness (cm), TSS:acid ratio, reducing sugar (%) and total soluble solids. However, the highest heritability (%), genetic advance (%) and genetic advance as percent of mean (%) were observed for TSS:acid ratio, total soluble solids, reducing sugar (%) and kernel width.

6.3 Microscopy studies of different Dashehari morphotypes

Stomatal traits found highly variable among the different Dashehari morphotypes. The morphotypes DM_{28} better for stomatal length (µm), stomatal pore length (µm) and stomatal pore width (µm) while, morphotype DM_5 best for stomatal width (µm). However, morphotype DM_1 and DM_{30} was superior for trichome length (µm) and trichome width (µm). Morphotype DM16 was better for stomatal density (μm^{-2}).

Variability analysis for stomatal traits in terms of phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), heritability (h^2 %), genetic advance (GA) and genetic advance as percent of mean (GAM %). All stomatal traits showed narrow differences between PCV and GCV. The highest PCV and GCV were observed for stomatal pore width (µm). However, the highest heritability and genetic advance were observed for trichome length (µm), trichome width (µm) and stomatal density (μm^{-1}) while, genetic advance as percent of mean was observed for stomatal pore width (µm)and stomatal length (µm).

A UPGMA dendrogram was prepared on the basis of stomatal characteristics of 45 Dashehari morphotypes in order to establish their relatedness to each other. The 45 Dashehari morphotypes under study were found to be very closely related and grouped into only two major clusters (cluster I and II) with additional sub-clusters, differentiating the morphotypes collected from different areas. Cluster-I consisted of 43 morphotypes which further divided into five sub-groups (cluster IA, IB, IC, ID and IE) while cluster-II comprised two morphotypes which was divided into two sub-groups (cluster IIA and IIB).

6.4 Protein profiling of different Dashehari morphotypes

The protein profiling showed distinct polymorphism in electrophoretic banding patterns and led to the detection of total of 10 bands**.** The maximum number of

bands (10 bands) was reported for morphotype DM_{21} and DM_{41} followed by DM_6, DM_{13}, DM_{21}, DM_{23} and DM_{40} (9 bands), respectively.

In the initial screening the molecular weight of the 10 bands obtained ranged from 242 kDa to 8 kDa. The morphotype DM_4 and DM_{11} having maximum (242 kDa) band size.

The value of similarity index (SI) is presented in Table 4.15. 0.8% similarity was observed for morphotype DM_1 with DM_6, DM_{12} with DM_{16} and DM_{17} and DM_{38} with DM_{40} showed 0.8% similarity.

The UPGMA dendrogram of the protein profile obtained using hierarchical genetic distance based clustering revealed two main clusters (Plate 12). Cluster-II contained only one morphotypes (DM_{24}). Cluster-I was further divided into four sub-clusters (IA, IB, IC and ID).

CONCLUSION

Statistically significant intravarietal variation was recorded in the fruit morphology of 45 Dashehari morphotypes of mango under the study which could be substantiated with variations observed in the stomatal characteristics.

Estimates of genetic components for vegetative, floral characters, fruit morphology, fruit chemical parameters and stomatal characters. Among them the number of secondary branches, flowers per panicle, kernel parameters, reducing sugar , TSS:acid ratio, stomatal pore size and stomatal density are inherent characters and helpful for breeding program for further crop improvement.

The UPGMA dendrogram was prepared on the basis of stomatal and molecular data and the sample population was grouped into two main clusters which subdivided into further sub-groups.

Intravarietal variation in the population could be because of the lack of availability of true-to-type planting material at the time of establishment of these orchards. It could also be an expression of the adaptations of trees to variable microenvironment and edaphic factors of the orchards under study or of the stionic effect in the plants since they are all propagated on seedling rootstocks through approach grafting.

On the basis of present study using SDS-PAGE in mango a usable protein band polymorphism has been observed which can be exploited to study intravarietal variability of the morphotypes as per clustering in the morphotypes with similar band patterns.

However, this clearly indicated that morphological, stomatal, biochemical and molecular methods of morphotype characterization of mango are not alternative methods, but they are complimentary to each other.