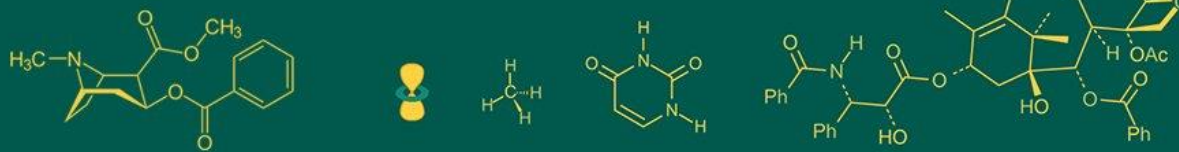


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Genetic variability, diversity and character association in quantitative traits of mango (*Mangifera indica* L)

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Abstract

Studies were conducted at ICAR-Indian Agricultural Research Institute, New Delhi during 2021 to 2022. Seventy mango hybrids and parents were studied for their genetic variability, heritability, and character association between yield and quality traits to estimate the contribution of traits towards yield. High genotypic (GCV) and phenotypic coefficient of variation (PCV) were recorded for number of hermaphrodite flowers per panicle, number of male flowers per panicle, fruit retention, fresh bark to wood ratio, total number of panicles and number of fruits per panicle which provide wide scope of improvement through selection. Moreover, high heritability and genetic advance were also observed in fruit retention, number of panicles, number of hermaphrodite flowers per panicle and fruit weight. Genetic divergence was assessed in 70 mango hybrids with their parents grouped into nine clusters indicating the presence of diversity for difference traits the cluster I had maximum number of hybrids. While cluster IX had highest mean for fruit yield per tree. Number of panicles, fruit diameter, tree girth, number of fruits per panicle at marble stage, tree height, exhibited significant positive correlation with fruit yield per tree. Path analysis revealed that number of panicles, number of female flowers, number of fruits per panicle, stomatal density and internodal width had maximum direct effect on fruit yield per tree.

Keywords: Genetics, variability, diversity, quantitative traits, mango

Introduction

Mango (*Mangifera indica* L.) is a significant fruit crop in tropical and subtropical regions of India, renowned for its wide range of genetic diversity and consumer preference. The primary method of propagating mango is through sexual reproduction, resulting in a diverse genetic pool. Despite the existence of mango breeding programs in agricultural research institutes, there is still potential for further enhancing mango quality through breeding efforts. To achieve this, it is crucial to have a comprehensive understanding of the genetic characteristics involved, which aids in assessing the progress of breeding programs and developing effective strategies (Rajan *et al.*, 2021) [34].

In plant breeding, having comprehensive knowledge of the relationship between yield and its contributing traits is essential. Exploiting the genetic variability present in specific traits and understanding their interrelationships are key factors in enhancing a crop. The level and nature of variability within a population are influenced by both genetic and non-genetic factors (Bhandari *et al.*, 2017) [17]. Assessing the extent of variability is vital for crop improvement, as genetic advancements rely on the availability of genetic variability (Govindaraj *et al.*, 2015) [17]. Parameters such as heritability, genotypic coefficient of variation, and phenotypic coefficient of variation play significant roles in evaluating the inheritance pattern of traits. Additionally, correlation coefficients and path analysis are crucial tools for trait selection and the formulation of breeding programs.

The mango cultivation in the subtropical region of India is known to possess substantial genetic diversity; however, a systematic investigation of this diversity has not been undertaken. Hence, the primary objective of this study is to assess the genetic variability, correlations, and conduct path analysis to determine the key contributing characters influencing mango yield (Dinesh *et al.*, 2015) [13].

This comprehensive analysis aims to facilitate the identification and selection of superior mango varieties with desirable traits for improved agricultural practices (Usman *et al.*, 2001) [45].

To design an effective breeding program, it is crucial to consider the genetic diversity present in the available germplasm. Genetic diversity plays a pivotal role in selecting appropriate parental lines for establishing new breeding populations and ensuring long-term selection gains (Swarup *et al.*, 2021) [44]. Additionally, understanding the genetic diversity or similarity among crop species aids in their efficient utilization and conservation. When parents with high genetic diversity are chosen, they are more likely to contribute desirable traits to their progeny, resulting in the production of high heterotic crosses and a broad range of variability in subsequent generations. In recent years, researchers have been focusing on studying the genetic diversity of various crop species, including mango, to enhance their utilization and conservation efforts. The greater the genetic diversity within a crop species, the higher the probability of obtaining highly heterotic F₁ hybrids and a wide array of variability in subsequent generations. Understanding and effectively utilizing the genetic diversity present in mango germplasm is of utmost importance for successful breeding programs and sustainable crop improvement. Therefore, the current investigation was conducted to estimate variability, diversity, and associations among different mango hybrids, aiming to further enhance our understanding and utilization of the genetic potential within the mango population.

In mango breeding programs, Mahalanobis D² analysis is a

valuable tool for evaluating the diversity and relationships among different mango genotypes. By computing the Mahalanobis distances using phenotypic traits, breeders can gain valuable insights into the genetic structure and relatedness within the mango population. This analysis enables breeders to identify genotypes that are genetically distinct and diverse, making them suitable candidates for hybridization. By selecting diverse parents for crossing, breeders can enhance the chances of developing improved mango varieties with desired traits. Utilizing Mahalanobis D² analysis empowers breeders to make informed decisions and optimize their mango breeding programs for the successful development of superior mango cultivars (Indian *et al.*, 2019) [20].

Materials and Methods

The current investigation was conducted on mango hybrids of the Amrapali x Sensation, which were maintained in the hybrid's evaluation block of the Division of Fruits and Horticultural Technology at the Indian Agricultural Research Institute in New Delhi from 2021 to 2022. The research location is situated at 28.40° N latitude and 77.10° E longitude, at an altitude of 228.16 m above sea level. The area experiences a semi-arid, subtropical climate with an average annual rainfall of 40cm.

The experiment was carried out using a Randomized Block Design (RBD) with three replications. The research material consisted of 70 mango hybrids (Amrapali x Sensation) and their respective two parent varieties. The list of hybrids and parents presented in Table 1 with their corresponding age groups.

Table 1: List of Parents and hand pollinated hybrids

Sl. No.	Hybrids	Age group	Sl. No.	Hybrids	Age group	Sl. No.	Parent/hybrid	Age group
1	H-1-16	7 to 10 years	26	H-3-6	11 to 20 years	51	H-1-13	21-30 years
2	H-7-9	7 to 10 years	27	H-3-9	11 to 20 years	52	H-1-14	21-30 years
3	H-1-9	7 to 10 years	28	H-3-8	11 to 20 years	53	H-3-7	21-30 years
4	H-7-2	7 to 10 years	29	H-11-2	11 to 20 years	54	H-3-11	21-30 years
5	H-9-5	7 to 10 years	30	H-11-4	11 to 20 years	55	H-3-14	21-30 years
6	H-16-1	11 to 20 years	31	H-11-5	11 to 20 years	56	H-1-8	21-30 years
7	H-16-3	11 to 20 years	32	H-12-3	11 to 20 years	57	H-1-3	21-30 years
8	H-22-1	11 to 20 years	33	H-12-4	11 to 20 years	58	H-1-5	21-30 years
9	H-18-4	11 to 20 years	34	H-4-8	11 to 20 years	59	H-3-3	21-30 years
10	H-7-1	11 to 20 years	35	H-11-1	11 to 20 years	60	H-3-4	21-30 years
11	H-16-2	11 to 20 years	36	H-11-6	11 to 20 years	61	H-4-2	21-30 years
12	H-22-2	11 to 20 years	37	H-12-1	11 to 20 years	62	H-4-3	21-30 years
13	H-6-9	11 to 20 years	38	H-12-5	11 to 20 years	63	H-1-6	21-30 years
14	H-6-10	11 to 20 years	39	H-12-6	11 to 20 years	64	H-4-1	21-30 years
15	H-17-1	11 to 20 years	40	H-12-8	11 to 20 years	65	H-7-4	21-30 years
16	H-17-3	11 to 20 years	41	H-12-10	11 to 20 years	66	H-3-2	21-30 years
17	H-17-4	11 to 20 years	42	H-12-11	11 to 20 years	67	H-1-1	>30 years
18	H-18-2	11 to 20 years	43	H-4-7	11 to 20 years	68	H-13-1	>30 years
19	H-18-3	11 to 20 years	44	H-6-2	11 to 20 years	69	H-13-4	>30 years
20	H-19-1	11 to 20 years	45	H-9-4	11 to 20 years	70	H-13-5	>30 years
21	H-4-6	11 to 20 years	46	H-9-1	11 to 20 years	71	Amrapali (P1)	25 to 26 years
22	H-3-12	11 to 20 years	47	H-9-8	21-30 years	72	Sensation (P2)	30 to 31 years
23	H-19-2	11 to 20 years	48	H-4-9	21-30 years			
24	H-15-1	11 to 20 years	49	H-1-11	21-30 years			
25	H-1-2	11 to 20 years	50	H-1-12	21-30 years			

Tree height was measured using a standard wooden scale, starting from the base of the tree near the soil surface and extending to the highest point of the crown. Stem girth was measured at a height of 30 cm from the ground using a measuring tape. The tree spread was recorded by measuring

the canopy spread in the East-West (E-W) and North-South (N-S) directions with a measuring tape. Tree volume (m³) was calculated according to Castle's method (1983). The first three internodes of each bearing shoot were measured, and the average internode length of five bearing shoots was recorded

in centimeters. Panicle emergence on bearing shoots was rated based on the criteria suggested by Rathore (2005). The intensity of anthocyanin pigmentation in newly emerged inflorescences was rated using a scale of 3 to 7 provided in the 'Mango Descriptor' published by IPGRI (2006). The sex ratio was calculated by dividing the number of hermaphrodite flowers by the number of male flowers. Inflorescence shape was observed following the descriptor for mango by the International Plant Genetic Resources Institute, Rome, Italy. Floral malformation percentage was calculated by dividing the number of malformed panicles per tree by the total number of panicles per tree. The number of fruits was counted on 10 panicles in all four directions, and the fruit set per panicle was expressed as a percentage. Fruit set and fruit retention (%) of the progeny and parent trees were observed on ten panicles in all four directions at 20, 40, 60, and 80 days after flowering. The maturity of fruits was determined using the water displacement method, and ratings were given accordingly. Individual fruit weight was measured using an electric balance. Total yield (kg) per tree was calculated by multiplying the number of fruits per tree by the average fruit weight. Yield efficiency was calculated by dividing the yield by the canopy volume (kg/m³).

Stomatal length, stomatal width, pore length, pore width, and stomatal density of the progeny and parent trees were estimated on the abaxial surface of leaves using an electron microscope with magnifications of 10x and 40x. The estimation followed the procedure described by Cahyanto at the PG lab, IARI, New Delhi. The focus was on the leaf epidermis, specifically the lower surface (abaxial), and the number of stomata in a defined area of the leaf surface was manually counted by visually scanning the microscope field or by capturing digital images. Stomatal density was calculated by dividing the number of stomata on the abaxial side of each hybrid and their parents by the surface area of their leaves, which was triplicated under the electron microscope.

To estimate the Bark-Wood ratio, fully matured strong vegetative shoots from the main branches of the progeny and parent trees were selected. Three replications of each sample shoot were measured according to the procedure described by Damour and Normand (2009) [11]. Fresh bark-wood weight, fresh bark weight, and fresh wood weight were measured using a weighing balance, and then the samples were dried at 90 °C for 72 hours. The weight of the oven-dried bark-wood samples was measured, while the thickness and diameter of the fresh and dried bark-wood were measured using digital vernier calipers, expressed in millimeters.

Total phenol estimation was carried out using the terminal buds of fresh emerging panicles from the progeny and parent trees. The total phenolic content (mg/g FW basis) of the hybrids and their parents was estimated using the Folin-Ciocalteu method (Singleton & Rossi, 1965) [41] with terminal buds.

The recorded observations were analyzed using Windostat 9.30 ver. software, following the Randomized Block Design (RBD) methodology. A total of sixteen characteristics were analyzed through analysis of variance to determine the significance of differences between the means.

Mean

The mean value of each character was worked out by dividing the totals by the corresponding number of observations.

Arithmetic mean (\bar{X}) = $\Sigma X / N$

Where,

ΣX = Sum of all the observations for each character in replication

N = Corresponding number of observations

Genotypic and phenotypic variances

The genotypic and phenotypic coefficients of variation were calculated using the formula introduced by Burton and De Vane in 1953. The genetic advance in percentage of mean was determined using the method developed by Comstock and Robinson in 1952.

$$\text{Genotypic variance } \sigma_g^2 = \frac{M_2 - M_3}{r}$$

$$\text{Phenotypic variance } \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_g^2 = Genotypic variance (GV)

σ_p^2 = Phenotypic variance (PV)

σ_e^2 = Environmental variance (EV)

M_2 = Treatment mean sum of squares

M_3 = Error mean sum of squares

r = replication

Standard error of mean

Standard error of mean was calculated by following formula

$$\text{SEm} = \frac{\sqrt{2\text{EMS}}}{r}$$

Critical difference

$$\text{CD} = \sqrt{2\text{EMS}} \times t - \text{value} / r$$

Critical difference was calculated by following formula

Where,

EMS = error mean sum of squares

t value = table value of error difference at 5% level of significance

r = number of replications

Significant "F" value indicates that, there is significant difference among the treatments/genotypes. But to compare with any two particular treatments, it is tested against CD value.

Coefficient of variation

Genotypic and phenotypic coefficients of variation were computed according to Burton (1953) based on the estimate of genotypic and phenotypic variances as follows.

$$\text{GCV} = \frac{\sqrt{\text{GV}}}{\bar{X}} \times 100$$

$$\text{PCV} = \frac{\sqrt{\text{PV}}}{\bar{X}} \times 100$$

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GV = Genotypic variance

PV = Phenotypic variance

\bar{X} = General mean of character

Heritability

Heritability in broad sense refers to the proportion of genetic variance to the total observed variance in the population. It has been estimated as per the formula given by Lush (1940).

$$h^2 (bs) = \frac{\text{Genotypic variance } (\sigma^2g)}{\text{Phenotypic variance } (\sigma^2p)} \times 100$$

Where, $\sigma^2 g$ and $\sigma^2 p$ are the genotypic and phenotypic variances. Further, the range of heritability in broad sense was classified as suggested by Johnson *et al.* (1955)^[23].

Estimated heritability (broad sense) was classified as low (< 30%), medium (30 - 60%) and high (> 60%) and the range of genetic advance as a percentage of mean was classified as low (< 10%), moderate (10 - 20%) and high (> 20%) as suggested by Johnson *et al.* (1955)^[23].

Genetic Advance (GA)

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al.* (1955)^[23].

$$GA = k \times \frac{(\sigma^2 g)}{\sqrt{(\sigma^2 p)}}$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

k = Selection differential at 5 per cent selection intensity i.e. 2.06

Genetic Advance as per cent Mean (GAM)

Genetic advance as per cent mean was worked out for each character adopting the formula given by Johnson *et al.* (1955)^[23].

$$GAM = GA \times \frac{100}{X}$$

GA = Genetic advance

X = General mean

Correlation Genotypic (r_g) and phenotypic (r_p) coefficients of correlation were estimated as suggested by Al- Jibourie *et al.*, (1958)^[2].

$$\text{Genotypic correlation} = \frac{C_o V_{xy} (G)}{\sqrt{V_x (G) \times V_y (G)}}$$

$$\text{Phenotypic correlation} = \frac{C_o V_{xy} (P)}{\sqrt{V_x (P) \times V_y (P)}}$$

Where,

$C_o V_{xy} (G)$ = Genotypic covariance between x and y

$C_o V_{xy} (P)$ = Phenotypic covariance between x and y

$V_x (G)$ = Genotypic variance of character x

$V_x (P)$ = Phenotypic variance of character x

$V_y (G)$ = Genotypic variance of character y

$V_y (P)$ = Phenotypic variance of character y

Test of significance of correlation was tested by comparing the 'r' value with obtained value.

To establish a cause and effect relationship, the first step used was to partition genotypic and phenotypic correlation

coefficient into direct and indirect effects by path analysis suggested by Dewey and Lu (1959)^[12] and developed by Wright (1921)^[47].

The genetic diversity was estimated utilizing Mahalanobis D²-statistics, initially proposed by Mahalanobis (1936)^[27] and extended by Rao (1952)^[35]. Group constellation was determined using Tocher's method. Additionally, canonical variate analysis, as per Rao (1964)^[36], was performed to validate the results obtained from the cluster and D² analyses.

Results and Discussion

The analysis of variance revealed significant differences among the crosses and parents for all twelve traits studied, indicating the presence of substantial variation within the experimental material. This finding suggests that the studied population exhibits a considerable genetic variation, providing a strong basis for further analysis and the selection of desirable traits (Table 2).

In the current study, the phenotypic coefficient of variation (PCV) was found to be greater than the corresponding genotypic coefficient of variation (GCV) for all the characters examined. This observation indicates the significant influence of the environment on the expression of these traits. However, the differences between the GCV and PCV values were relatively small, suggesting that the traits studied were less influenced by environmental factors. To classify the range of PCV and GCV values, the criteria proposed by Sivasubramanian and Madhavamenon in 1973 were followed. Accordingly, values ranging from 0% to 10% were considered as low, values between 10% and 20% were classified as moderate, and values exceeding 20% were regarded as high.

Higher estimates of GCV was observed for number of hermaphrodite flowers per panicle, number of male flowers per panicle, fruit retention, fresh bark to wood ratio, total number of panicles and number of fruits per panicle at marble stage, (Table 3). Highest estimates of PCV was observed for fruit retention, number of hermaphrodite flowers per panicle, number of male flowers per panicle, Number of fruits per panicle (Marble Stage), fresh bark to wood ratio and total number of panicles. The differences between values of PCV and GCV were less for tree girth, tree height, fruit yield per tree, fresh bark wood to bark ratio and number of male flowers per panicle indicating that these characters were largely under genetic control and environment had least influence on the expression of these traits. Similar results conformity with Kevadiya (2006)^[24], Rathod (2007)^[37] and Majumder (2012)^[28], Nayak *et al.*, (2013)^[31], Patel *et al.*, (2016)^[32], Himabindu *et al.*, (2016)^[19] and Galal *et al.*, (2017)^[17] findings in mango.

Singh and Kumar (2010)^[39] studied phenotypic and genotypic coefficient of variability for growth, yield and yield attributes and showed higher PCV than the GCV for all the characters under consideration, indicating high degree of environmental influence. The PCV ranged from 9.28 for plant girth to 44.0 for fruit yield and GCV ranged from 5.95 for plant girth to 42.26 for fruit yield. However, the genotypic coefficient of variance does not provide full scope for estimating the variation which is heritable in nature and thus it would be necessary to estimate its heritability.

Dwivedi *et al.*, (1995)^[14] also observed that selection based on characters having higher PCV would be more effective in papaya. According to Burton (1952) a character having high value of GCV with high heritability would be more valuable

in selection programme. Accordingly, fruit yield, fruit weight and fruiting length were having high estimate of GCV and heritability which indicates direct selection for these characters would be effective.

The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it is used as a predictive role in selection procedures. High heritability was recorded for majority of the characters viz., tree girth (98.70), tree height (94.80), number of male flowers per panicle (91.70), fresh bark weight to wood ratio (91.40), Number of hermaphrodite flowers per panicle (90.60), fruit yield per tree (88.20) and total number of panicles (85.90). High heritability generally indicate that the environment effect was very low and enables the breeder to select plants on the basis of the phenotypic expression.

Genetic advance as per cent of mean were high for fruit retention (97.44%) followed by number of panicles (90.51), number of hermaphrodite flowers per panicle (85.32%), tree girth (82.81%), number of male flowers per panicle (80.12%), fruit weight (77.00%), number of fruits per panicle at marble stage (70.14), number of fruits per panicle at harvest (61.85%), stomatal density (57.33%), tree height (57.18%), fresh bark weight to wood ratio (55.00%) and fruit yield per tree (51.68%). Similar results were obtained by Patel *et al.*, (2016)^[32], Shridher and Galal *et al.*, (2017)^[17].

Rathod (2007)^[37] found high heritability coupled with genetic advance in mango for the traits like fruit length, fruit weight, sugars, acidity ascorbic acid, peel percentage and stone percentage indicating importance of these traits for crop improvement programme. Bhowmick *et al.*, (2008)^[8] conducted an experiment to study heritability and genetic advance for different physico-chemical traits among nine mango genotypes. They found high heritability coupled with genetic advance for most of physico-chemical traits. Islam *et al.*, (2010)^[22] in mango reported high heritability along with high degree of genetic advance (GA) for yield per plant (95.38% and 93.38), number of fruits per plant (89.90% and 49.63), fruit weight (99.35% and 114.31), fruit breadth (90.14% and 49.70), stone weight (99.05% and 90.82), stone length (98.34% and 51.83) and pulp: stone ratio (98.74% and 66.34).

Clustering of genotypes under study is presented in (Figure 1 & table 4). Based on the D^2 values all the genotypes were grouped into nine clusters, signaling the presence of diversity for different traits. The cluster I had the highest number of genotypes (48) followed by cluster II (14) and cluster III (4). The cluster IV, V, VI, VIII, VIII and IX were solitary clusters. The diversity among 72 hybrids and parents was measured by adopting D^2 analysis. The contribution of each character towards total genetic diversity is presented in Table 5. The characters like fruit yield per tree (15.22%), number of hermaphrodite flowers per panicle (13.58%), fruit bark wood to weight ratio (12.54%), number of fruits per panicle at marble stage (11.45%), tree girth (7.75%), fruit retention (7.50%), number of male flowers per panicle (6.85%), number of panicles (6.49%), fruit bark to wood weight (4.85%) and number of fruits at panicle during harvest (4.54%).

The cluster means for 16 various characters under study revealed considerable differences between the groups (Table 6). Cluster II was characterized with minimum tree height (4.61 m) and maximum tree height reported by cluster VII (10.11). The minimum tree girth (39.87 cm), number of panicles (74.36), inflorescence length (23.52), fruits per

panicle at marble stage (4.59), fruit yield per tree (9.39 kg) was observed in cluster II. The maximum number of panicles (283.50), inflorescence length (27.75),

The intra and inter cluster D^2 values among 72 accessions presented in Table 7 and Fig. 2 revealed that cluster II and IX showed minimum intra-cluster D^2 value (0) followed by cluster I (498.91), whereas, maximum intra-cluster D^2 value (723.06) was shown by cluster III followed by cluster II (579.90), indicating considerable genetic divergence among the accessions of this cluster and was due to both natural and artificial selection forces among the hybrids and parents. Minimum inter-cluster D^2 value was observed between the cluster VII and VI (205.97) followed by cluster VIII and VI (300.81) indicated close relationship among the accessions. The selection of parents from genetically close clusters may be due to narrow genetic base and inbreeding depression. Maximum inter-cluster D^2 value was observed between the cluster II and IX (4182.05) followed by cluster I and IX (2957.82), cluster III and IX (2866.95), cluster IV and IX (2525.95) indicated that the accessions belonging to these groups were genetically most diverse and can be used as a parent in hybridization programme. This type of hybridization would be useful for obtaining transgressive segregants. The result of the present study was in line with the findings of Barhate *et al.*, (2012)^[5], Barholia & Yadav (2014)^[6] and Indian *et al.*, (2019)^[20].

The yield being a complex trait, it is difficult to exploit various yield contributing traits through the knowledge of correlation only, therefore, it is important to carry out other analysis including path coefficient that provides a clear indication for selection criterion (McGiffen *et al.*, 1994)^[30]. This allows the partitioning of the correlations among studies traits and their components into direct and indirect effects. The data for all the studied traits were averaged and fruit yield per yield was taken as dependent variable and all the other traits were considered as casual/ independent variables

Correlation measures the degree and direction of relationship between two or more variables. The study of character association helps breeder in fixing a selection criterion for fruit yield in parental lines such as selection will be effective in isolation than correlating the correlation of phenotypic values and subjected to change in the environment.

Gupta *et al.*, (1996)^[18] studied correlation in mango indicate that fruit diameter had significant positive correlation with fruit weight, stone weight, stone width, seed weight and seed width, whereas, negative correlation with stone thickness as well as petiole length. The fruit weight was significant positive correlation with stone length, stone width, stone weight and seed width and seed length but negatively correlated with seed weight. Azevedo *et al.*, (1998)^[4] studied the phenotypic and genotypic correlations among plant height and crown direction. Leaf blade length was highly significantly correlated with leaf blade width; and petiole length significantly correlated with crown north-south direction. Rathod (2007)^[37] studied genotypic and phenotypic correlation among fruit traits of mango and found that the genotypic correlation was higher than their corresponding phenotypic correlations for all the traits and also reported stone weight was highly significantly correlated with seed length, seed width and seed weight. However, it was negatively correlated with leaf blade width and TSS: acidity ratio. Wright *et al.*, (2007)^[47] noticed that genotypic correlation coefficient was higher than that of phenotypic correlation coefficient for most of fruit traits. Islam *et al.*, (2010)^[22] reported in mango that yield per plant was strongly

and positively correlated with fruit weight, fruit breadth, stone weight, fruit length and pulp-stone ratio. Barhate *et al.*, (2012) [5] studied phenotypic and genotypic correlation coefficient between number of fruits per tree and yield and found significant positive correlation of yield with number of fruits per tree, plant height, tree spread and tree girth. Vasugi *et al.*, (2013) [46] noticed higher genotypic correlation than phenotypic correlation in mango and found that fruit weight was most closely associated with pulp percent, total sugar, non-reducing sugar, reducing sugar and stone weight. Bhowmick *et al.*, (2008) [8] studied genotypic and phenotypic correlation among fruit traits of mango and found that genotypic correlation coefficient was higher than phenotypic correlation coefficient for most of characters.

Total soluble solids in juice showed significant positive correlation with total sugars (0.88) and reducing sugars (0.62) and negative correlation with juice acid content (- 0.47). Akhter *et al.*, (2013) [1] reported that fruit diameter, rind thickness, length of segment and number of segments had positive and highly significant phenotypic association with fruit weight and also genotypic positive association. The percent fruit set had negative genotypic and phenotypic association with fruit weight.

Correlation analysis for growth, yield and yield related traits was presented (Table 7). The fruit yield per tree was found to have significant positive correlation with traits like number of panicles (0.602), tree girth (0.474), number of fruits per panicle at marble stage (0.427), tree height (0.379), number of fruits at panicle at harvest (0.173). Similarly, non-significant positive correlation was observed with traits like internodal width, number of hermaphrodite flowers, fruit weight and stomatal density were positive. Fruit weight was found to have significant positive correlation with number of male flowers per panicle (0.417), number of hermaphrodite flowers (0.317), tree girth (0.277), internodal length (0.258) and number of panicles (0.208) and negatively significant association with fruit retention percent (-0.195). Similar

results obtained by Galal *et al.*, (2017) [17].

The path analysis furnishes a method for partitioning the correlation coefficients into direct and indirect effects and measures the relative importance of the causal factors involved. Path analysis was carried out for fifteen traits on fruit yield per tree (Table 8). The path coefficient analysis directed that number of panicles (0.433) demonstrated utmost positive direct effect on fruit yield per tree followed by number of female flowers (0.440), number of fruits per panicle at marble stage (0.216), stomatal density (0.214) and internodal width (0.157). Hence, these traits may be directly attributed for the improvement of fruit yield per tree and important in the selection of better hybrid in mango. The residual effect was not high (36.50%) and most of the variability (63.50%) in fruit yield per tree was well accounted for by the variables.

Based on the results it can be concluded that in general the traits distribution pattern was similar among the hybrid populations. However, considering the overall quantitative characteristics of the full-sib hybrids some differences were noted between parental genotypes, which gave rise to progenies that differ amongst each other. Wide variation in terms of morphological, flowering, fruiting and yield observed among hybrids. It was also evident that for a particular trait, the maternal effect was pronounced, however for some traits paternal effect was prominent. In addition, some traits showed non-specific trends. On the basis of overall assessment of 70 hybrids, twelve, namely, H-1-8, H-1-5, H-12-8, H-1-3, H-22-1, H-15-1, H-13-4, H-19-1, H-13-5, H-4-9, H-3-6 and H-12-6 and were identified as better performing hybrids. Of these, H-1-8, H-1-5, H-12-8 and H-2-6 though released, need to deserve a place in mango varietal trial under different agro-climatic regions of the country. Results suggested that the quantification of traits could help to understand the potential of hybrids and in selection of desirable hybrids for domestic and export markets as well for selection of potential parents for future utilization in improvement programmes.

Sl. No.	Short Names	Full Names
1	TH	Tree height (m)
2	TG	Tree Girth (cm)
3	TNP	Total number of panicles
4	IL	Inflorescence length (cm)
5	IW	Inflorescence Width (cm)
6	NHF	Number of Hermaphrodite flowers per panicle
7	NMFPT	Number of Male flowers per panicle
8	NFFPT	Number of fruits per panicle (Marble Stage)
9	NFP	Number of fruits at panicle (Harvest)
10	FR	Fruit Retention (%)
11	FW	Fruit weight
12	SD	Stomatal Density (stomata/mm ²)
13	PC	Phenol Content (mg/g)
14	FBWW/DBWW	Fresh Bark wood weight/Dry bark wood weight
15	FBW/FWW	Fresh bark weight/fresh wood weight
16	FYPT	Fruit yield per tree

Legend

Sl. No.	Genotypes	TH	TG	TNP	IL	IW	NHF	NMFPT	NFFPT
1	H-1-16	3.25	45.27	43.00	21.98	20.00	241.90	808.55	4.36
2	H-7-9	3.18	39.31	93.00	27.25	24.25	59.00	649.33	5.00
3	H-1-9	2.57	33.67	115.50	25.60	22.80	176.23	367.55	7.80
4	H-7-2	2.94	28.72	76.00	25.40	22.25	116.93	429.61	4.65
5	H-9-5	2.79	16.77	20.00	9.25	7.25	25.00	63.80	2.85
6	H-16-1	2.88	23.55	10.00	13.25	12.25	36.15	67.70	1.50
7	H-16-3	3.00	28.53	94.00	26.75	23.25	303.68	416.78	6.95

8	H-22-1	4.35	40.70	32.50	24.00	21.30	101.05	217.80	2.80
9	H-18-4	5.96	42.99	84.00	18.95	18.25	117.57	157.80	5.05
10	H-7-1	5.01	29.48	81.50	19.81	19.00	113.78	467.90	5.80
11	H-16-2	3.66	30.55	108.00	19.60	18.75	152.50	298.90	6.22
12	H-22-2	4.12	31.55	94.50	26.50	23.00	105.87	268.55	7.00
13	H-6-9	5.04	35.30	64.00	28.15	21.25	77.95	130.95	2.15
14	H-6-10	6.00	46.30	102.50	26.40	22.25	85.08	173.00	5.40
15	H-17-1	3.50	34.87	101.00	26.75	24.25	72.98	182.30	5.70
16	H-17-3	5.43	41.64	44.00	27.00	23.75	67.92	325.50	3.71
17	H-17-4	5.38	39.32	44.00	13.50	11.75	45.34	62.90	2.40
18	H-18-2	6.35	53.17	101.50	25.50	22.00	355.93	1163.25	7.00
19	H-18-3	6.88	49.21	126.50	23.50	20.00	299.03	935.18	6.80
20	H-19-1	3.70	41.50	105.00	25.85	23.50	91.15	404.35	8.10
21	H-4-6	3.66	38.35	112.50	19.20	17.75	64.25	141.25	4.30
22	H-3-12	4.55	46.46	97.50	27.25	23.25	48.20	261.70	6.60
23	H-19-2	4.25	74.92	122.50	29.25	19.25	195.53	856.18	6.90
24	H-15-1	6.55	61.41	100.00	27.50	25.75	54.85	345.43	7.80
25	H-1-2	6.11	55.37	58.50	25.40	24.25	98.55	404.10	4.02
26	H-3-6	7.10	64.41	81.50	25.50	24.00	69.30	238.40	2.78
27	H-3-9	5.82	39.96	81.50	26.85	25.25	117.68	234.55	4.25
28	H-3-8	6.85	51.56	74.50	24.25	20.00	60.45	568.55	14.30
29	H-11-2	8.16	55.68	39.00	25.75	21.75	44.95	412.90	6.40
30	H-11-4	6.57	49.36	46.50	25.00	23.25	45.95	564.00	5.90
31	H-11-5	7.02	58.27	77.00	24.00	18.25	98.93	384.88	5.60
32	H-12-3	7.14	57.36	136.50	23.50	17.75	87.95	548.40	5.75
33	H-12-4	6.88	54.85	31.00	24.00	15.75	141.50	813.95	3.32
34	H-4-8	10.12	78.29	72.50	27.25	16.50	87.97	291.08	3.05
35	H-11-1	8.88	71.33	88.50	25.25	16.50	72.27	128.20	2.55
36	H-11-6	7.12	50.40	126.00	24.25	14.50	47.05	264.33	1.85
37	H-12-1	7.14	79.41	87.50	25.25	18.75	74.15	492.25	5.95
38	H-12-5	6.57	71.38	109.50	26.00	17.25	44.93	411.55	4.60
39	H-12-6	7.67	89.54	205.00	26.50	20.50	99.55	991.00	6.70
40	H-12-8	6.33	76.66	227.50	27.25	17.75	97.38	949.40	6.15
41	H-12-10	7.27	73.46	152.00	27.25	19.50	46.85	278.00	5.45
42	H-12-11	7.22	81.61	268.50	27.25	18.75	46.05	267.10	5.40
43	H-4-7	8.58	95.34	99.00	12.75	9.50	35.30	128.00	3.65
44	H-6-2	6.35	69.60	151.50	26.25	19.25	69.00	410.45	6.15
45	H-9-4	7.19	88.96	111.50	26.25	16.75	190.25	1012.10	9.50
46	H-9-1	7.35	81.77	186.75	26.69	18.69	56.39	405.63	5.16
47	H-9-8	8.15	91.32	232.00	27.50	20.50	78.63	241.64	7.15
48	H-4-9	7.79	89.38	180.00	25.75	20.75	67.15	462.20	6.75
49	H-1-11	8.79	94.18	202.50	24.25	20.25	50.05	350.20	13.00
50	H-1-12	7.16	85.73	195.50	24.75	20.75	48.60	226.45	17.50
51	H-1-13	8.69	97.18	75.50	24.25	17.25	72.90	354.15	11.50
52	H-1-14	7.24	91.22	145.50	26.25	18.75	136.13	678.03	8.60
53	H-3-7	7.69	96.48	234.50	27.00	25.00	196.80	854.35	5.50
54	H-3-11	7.57	88.79	125.00	13.50	9.75	90.15	293.65	3.50
55	H-3-14	8.06	78.89	194.00	27.25	17.75	117.18	211.35	5.50
56	H-1-8	7.84	99.46	283.50	27.75	19.25	254.18	356.72	24.65
57	H-1-3	8.89	116.22	271.50	24.25	18.25	48.25	255.60	11.50
58	H-1-5	7.59	89.54	123.50	26.25	21.50	252.60	356.72	9.25
59	H-3-3	6.89	79.84	142.00	25.00	17.50	62.75	295.34	11.60
60	H-3-4	6.77	76.71	27.50	11.25	8.50	35.13	154.20	5.85
61	H-4-2	7.20	81.45	232.00	26.50	12.25	74.79	411.65	10.85
62	H-4-3	6.99	83.53	212.50	26.00	11.75	63.55	531.10	8.80
63	H-1-6	8.89	132.21	188.50	25.25	17.25	163.50	680.30	8.05
64	H-4-1	7.55	96.48	234.50	27.00	25.00	196.80	854.35	5.50
65	H-7-4	6.73	124.46	139.00	31.75	25.50	267.50	601.80	8.95
66	H-3-2	7.54	109.17	193.63	27.50	19.88	172.84	666.89	7.83
67	H-1-1	8.17	104.30	130.50	26.50	25.00	269.70	430.45	17.50
68	H-13-1	8.13	91.63	77.50	21.55	16.75	64.35	362.05	4.80
69	H-13-4	7.96	89.65	158.00	27.50	18.25	131.07	307.90	11.80
70	H-13-5	10.11	121.38	198.00	27.50	22.00	59.98	332.00	12.95
71	Amrapali	6.13	53.32	112.50	26.50	24.25	86.23	942.80	5.85
72	Sensation	9.04	121.22	252.50	25.50	21.75	90.93	171.90	10.45
	Mean	6.50	68.50	125.64	24.51	19.40	109.61	427.48	6.95
	C.V.	6.68	4.73	21.42	16.15	17.06	21.78	18.21	25.61
	S.E.	0.18	1.32	10.99	1.62	1.35	9.75	31.78	0.73
	C.D. 5%	0.49	3.68	30.56	4.49	3.76	27.11	88.37	2.02

Sl. No.	Genotypes	NFP	FR	FW	SD	PC	FBWW/DBWW	FBW/FWW	FYPT
1	H-1-16	0.90	23.44	187.20	771.15	6.55	3.15	0.92	8.31
2	H-7-9	1.15	23.00	223.48	719.30	6.56	2.46	0.59	15.02
3	H-1-9	1.15	14.79	102.33	796.95	7.55	3.16	0.92	5.68
4	H-7-2	0.90	19.62	117.98	755.15	6.64	2.37	1.00	5.37
5	H-9-5	0.65	11.41	66.33	757.50	7.05	2.10	0.42	2.80
6	H-16-1	0.60	20.00	57.81	664.50	7.97	2.23	0.59	2.17
7	H-16-3	1.15	16.47	207.07	664.25	7.18	2.32	0.95	8.28
8	H-22-1	0.65	22.72	177.87	591.50	5.07	1.04	0.62	21.19
9	H-18-4	1.20	25.90	160.92	621.10	7.30	0.88	0.37	11.94
10	H-7-1	1.20	20.84	157.09	578.45	8.47	2.16	0.59	5.85
11	H-16-2	1.25	20.25	170.65	593.50	5.80	1.16	0.50	7.08
12	H-22-2	1.50	21.49	114.22	682.05	6.40	1.49	0.60	8.63
13	H-6-9	0.95	45.87	142.79	588.80	5.87	2.09	0.82	17.95
14	H-6-10	1.55	36.76	170.90	634.40	6.56	2.48	0.61	13.00
15	H-17-1	2.10	37.08	80.60	694.55	8.00	1.35	0.54	15.58
16	H-17-3	0.35	9.74	138.44	645.70	6.33	1.89	1.00	2.63
17	H-17-4	0.50	10.43	72.68	601.60	6.76	1.41	0.63	3.26
18	H-18-2	1.55	21.92	207.07	675.15	8.05	1.52	0.63	10.39
19	H-18-3	1.20	17.92	181.38	638.00	6.37	1.03	0.31	9.42
20	H-19-1	1.50	18.51	232.99	625.20	7.07	0.96	0.63	12.66
21	H-4-6	1.30	31.72	199.11	594.75	6.11	1.12	0.50	7.22
22	H-3-12	1.15	17.47	187.00	610.90	8.54	1.04	0.52	9.95
23	H-19-2	2.20	31.87	168.28	615.95	6.59	1.09	0.50	13.35
24	H-15-1	0.53	6.79	232.50	616.95	8.44	0.96	0.63	6.21
25	H-1-2	0.38	9.24	193.38	625.90	7.05	0.64	0.35	10.00
26	H-3-6	0.25	8.95	198.24	696.65	6.75	1.13	0.43	18.92
27	H-3-9	0.43	10.04	84.40	676.60	6.97	1.26	0.96	11.21
28	H-3-8	1.05	7.49	148.87	707.50	5.76	1.45	0.68	7.29
29	H-11-2	1.00	14.94	128.73	717.65	6.40	1.79	0.68	6.59
30	H-11-4	2.51	48.97	119.02	693.70	7.26	2.15	0.70	7.82
31	H-11-5	0.65	12.15	157.20	702.75	7.73	1.82	0.94	5.38
32	H-12-3	1.15	21.09	164.81	659.20	8.46	1.23	0.59	12.04
33	H-12-4	1.70	49.63	190.53	674.95	5.79	0.90	0.83	1.35
34	H-4-8	1.20	38.58	143.59	743.50	5.42	1.14	0.63	10.35
35	H-11-1	1.30	50.00	130.75	653.00	6.31	1.51	0.54	11.75
36	H-11-6	1.25	62.06	102.79	678.15	6.82	1.01	0.61	11.48
37	H-12-1	1.10	19.74	158.17	660.95	5.56	1.13	0.76	16.81
38	H-12-5	1.20	24.40	132.26	677.30	6.79	1.24	0.65	10.85
39	H-12-6	1.55	22.69	225.18	642.89	4.78	0.55	0.96	13.09
40	H-12-8	1.50	23.07	230.00	627.37	5.11	0.83	0.98	22.61
41	H-12-10	1.30	22.13	184.23	627.14	5.27	0.92	0.64	18.22
42	H-12-11	1.00	19.23	156.58	629.93	5.88	0.95	0.65	16.47
43	H-4-7	0.50	6.85	62.75	663.29	4.68	1.25	0.65	10.43
44	H-6-2	0.90	16.23	174.69	562.20	4.94	0.39	1.02	13.08
45	H-9-4	1.20	12.66	209.52	676.30	4.95	1.24	0.65	14.15
46	H-9-1	1.08	20.01	158.39	588.65	5.24	0.56	0.55	16.93
47	H-9-8	1.00	13.87	133.79	541.45	4.21	0.58	0.36	13.84
48	H-4-9	0.35	5.16	241.11	548.40	4.81	0.98	0.65	18.80
49	H-1-11	0.50	3.68	89.40	643.85	4.63	0.65	0.39	14.75
50	H-1-12	0.95	5.42	131.62	588.95	5.61	0.67	0.95	12.40
51	H-1-13	1.40	11.67	156.64	698.85	4.44	0.70	0.42	17.92
52	H-1-14	1.60	18.05	194.48	593.65	4.34	0.98	0.65	17.20
53	H-3-7	1.25	22.19	184.20	564.10	5.46	0.59	0.68	15.98
54	H-3-11	1.00	14.26	81.70	638.00	5.76	1.04	0.71	8.01
55	H-3-14	1.30	23.34	145.57	616.05	5.10	0.49	0.69	17.42
56	H-1-8	2.00	8.21	175.51	581.70	5.06	0.92	0.72	42.96

57	H-1-3	0.80	6.51	189.62	607.85	3.63	0.85	0.69	20.78
58	H-1-5	0.80	9.69	317.32	590.10	6.05	0.92	0.68	10.00
59	H-3-3	1.20	11.31	139.40	536.10	5.59	0.58	0.92	13.47
60	H-3-4	0.50	4.26	75.12	555.00	4.83	0.50	1.02	4.15
61	H-4-2	1.30	13.91	209.75	605.90	3.40	0.49	0.70	9.63
62	H-4-3	1.15	17.26	208.08	658.55	3.93	1.13	0.59	8.05
63	H-1-6	1.10	16.69	221.53	480.10	3.47	0.54	0.39	8.12
64	H-4-1	1.25	22.17	184.20	550.10	5.06	1.10	0.68	15.97
65	H-7-4	1.50	19.25	184.64	530.20	5.90	0.42	0.44	9.82
66	H-3-2	1.25	17.70	199.61	570.50	4.59	0.41	0.77	10.49
67	H-1-1	1.80	10.35	198.09	519.45	4.03	0.37	0.96	8.89
68	H-13-1	0.70	14.87	169.83	551.35	3.91	0.41	0.77	7.71
69	H-13-4	1.55	13.22	150.19	600.75	3.79	0.76	0.68	21.32
70	H-13-5	1.60	12.58	280.85	447.45	4.00	0.70	0.61	22.45
71	Amrapali	0.90	15.34	184.59	755.00	7.41	0.83	0.69	13.35
72	Sensation	1.10	10.57	99.58	1125.00	4.18	0.70	0.69	30.00
	Mean	1.13	19.27	163.29	639.18	5.89	1.18	0.67	12.28
	C.V.	29.28	41.42	15.17	11.44	7.48	16.72	9.78	23.25
	S.E.	0.13	3.26	10.11	29.86	0.18	0.08	0.03	1.17
	C.D. 5%	0.38	9.06	28.12	83.04	0.50	0.22	0.07	3.24

Table 2: ANOVA Summary for various growth and yield traits in mango hybrids and parents

Source	Replication	Treatment	Error
Degrees of freedom	2	71	142
IL	3.6610	56.089**	1.764
IW	1.1490	53.547**	1.577
NHF	146.2920	16730.468**	57.001
NMFPT	3080.943*	202625.633**	653.334
NFFPT	0.1090	47.205**	0.216
NFP	0.0010	0.602**	0.006
FR	0.5410	407.831**	1.986
FW	25.2860	7987.654**	96.054
SD	2225.5740	23973.299**	1753.076
PC	0.2310	5.393**	0.162
FBWW/DBWW	0.0010	1.258**	0.01
FBW/FWW	0.0010	0.099**	0.002

Table 3: Estimation of genetic parameters for various growth and yield traits in mango hybrids and parents

Sl. No.	Genetic Parameters	GCV	PCV	h ² (BS)	GA	GAM (%)
1	Plant height (m)	28.51	29.28	94.80	3.72	57.18
2	Tree Girth (cm)	40.47	40.75	98.70	56.72	82.81
3	Total number of panicles	52.77	56.96	85.90	92.14	90.51
4	Inflorescence length (cm)	16.36	22.99	50.70	5.88	23.99
5	Inflorescence Width (cm)	20.63	26.77	59.40	6.36	32.76
6	Number of Hermaphrodite flowers per panicle	67.55	70.97	90.60	90.14	85.32
7	Number of Male flowers per panicle	60.34	63.03	91.70	85.41	80.12
8	Number of fruits per panicle (Marble Stage)	56.10	61.67	82.80	7.31	70.14
9	Number of fruits at panicle (Harvest)	37.93	47.92	62.70	0.70	61.85
10	Fruit Retention (%)	58.09	71.35	66.30	18.78	97.44
11	Fruit weight	53.35	58.19	84.00	12.37	77.00
12	Stomatal Density (stomata/mm ²)	30.99	34.50	80.70	93.62	57.33
13	Phenol Content (mg/g)	13.18	17.46	57.00	86.21	20.51
14	Fresh Bark wood weight/Dry bark wood weight	22.56	23.77	90.10	2.60	44.12
15	Fresh bark weight/fresh wood weight	54.55	57.05	91.40	1.27	55.00
16	Fruit yield per tree	26.72	28.45	88.20	0.35	51.68

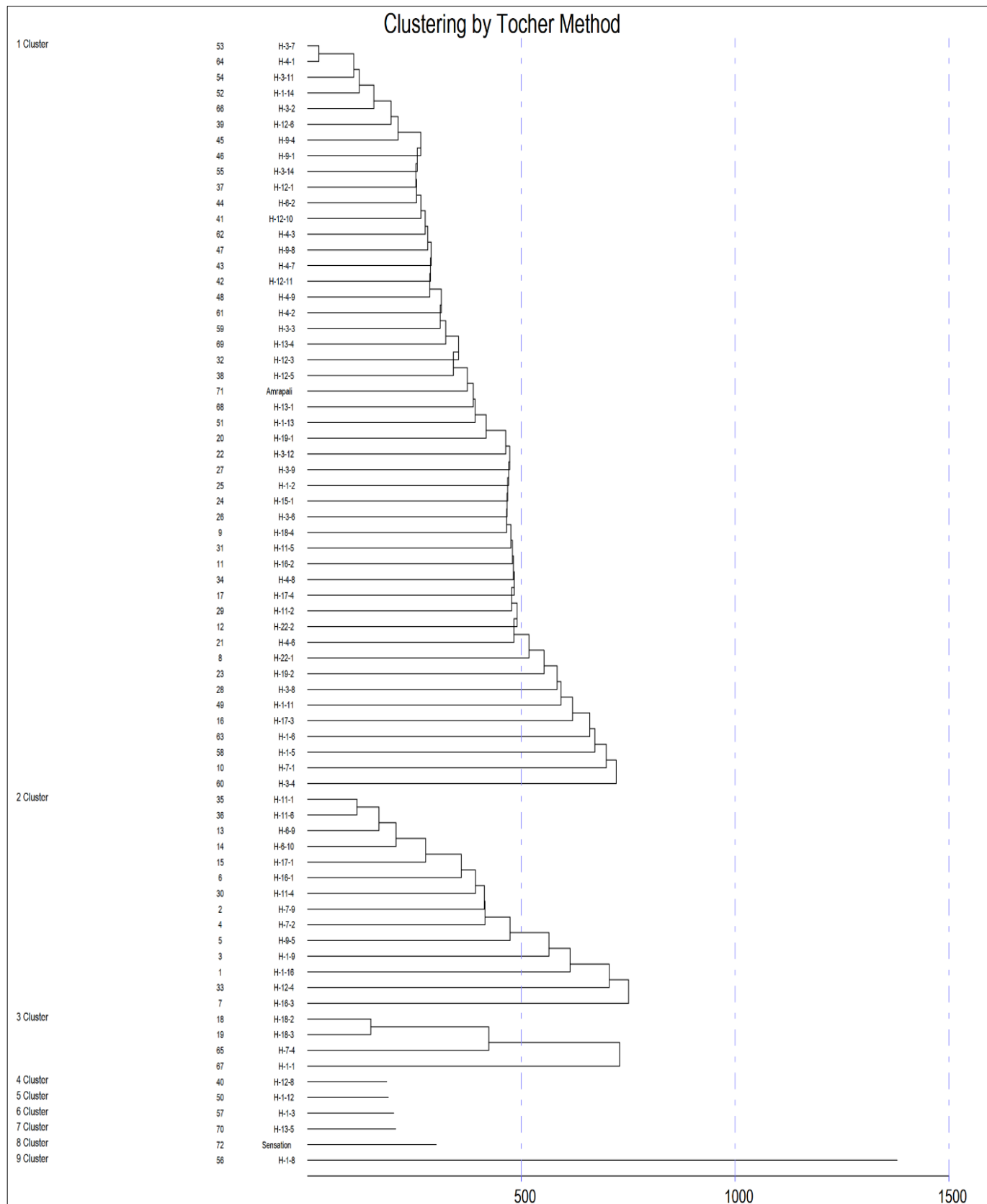


Fig 1: Dendrogram representing distance among 72 mango hybrids and parents

Table 4: Cluster Groups among 72 mango hybrids and parents using Mahalanobis D² analysis

Cluster Group	Number of Genotypes	List of Genotypes
1 Cluster	48	h-3-7, h-4-1, H-3-11, H-1-14, h-3-2, H-12-6, H-9-4, H-9-1, H-3-14, H-12-1, h-6-2, H-12-10, h-4-3, H-9-8, H-4-7, H-12-11, H-4-9, h-4-2, h-3-3, H-13-4, H-12-3, H-12-5, Amrapali, H-13-1, H-1-13, H-19-1, H-3-12, H-3-9, h-1-2, H-15-1, h-3-6, H-18-4, H-11-5, H-16-2, H-4-8, H-17-4, H-11-2, H-22-2, h-4-6, H-22-1, H-19-2, H-3-8, H-1-11, H-17-3, h-1-6, h-1-5, h-7-1 & h-3-4
2 Cluster	14	H-11-1, H-11-6, H-6-9, H-6-10, H-17-1, H-16-1, H-11-4, H-7-9, h-7-2, H-9-5, H-1-9, H-1-16, H-12-4 & H-16-3
3 Cluster	4	H-18-2, H-18-3, H-7-4 & H-1-1
4 Cluster	1	H-12-8
5 Cluster	1	H-1-12
6 Cluster	1	H-1-3
7 Cluster	1	H-13-5
8 Cluster	1	Sensation
9 Cluster	1	H-1-8

Table 5: Per cent contribution of various growth and yield traits in mango hybrids and parents

Sl. No.	Source	Contribution (%)	Times ranked 1st
1	Plant height (m)	1.20	31
2	Tree Girth (cm)	7.79	202
3	Total number of panicles	6.49	168
4	Inflorescence length (cm)	2.00	52
5	Inflorescence Width (cm)	0.43	11
6	Number of Hermaphrodite flowers per panicle	13.58	352
7	Number of Male flowers per panicle	6.85	178
8	Number of fruits per panicle (Marble Stage)	11.45	297
9	Number of fruits at panicle (Harvest)	4.54	118
10	Fruit Retention (%)	7.50	194
11	Fruit weight	0.63	16
12	Stomatal Density (stomata/mm ²)	2.54	66
13	Phenol Content (mg/g)	2.39	62
14	Fresh Bark wood weight/Dry bark wood weight	12.54	325
15	Fresh bark weight/fresh wood weight	4.85	126
16	Fruit yield per tree	15.22	395
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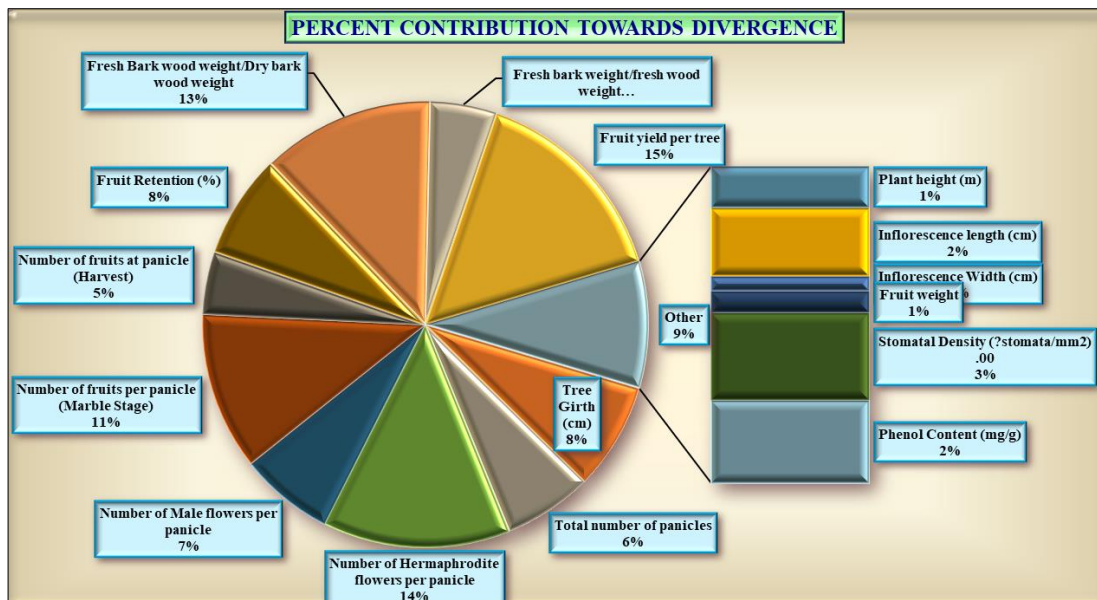


Fig 2: Diagrammatic representation of percent contribution by various traits in mango hybrids and parents

Table 6: Cluster distances among various clusters in mango

Cluster Distances									
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	498.91	952.74	1034.36	777.65	853.9	787.36	802.39	1137.87	2957.82
Cluster 2		579.9	1589.91	1475.34	1776.95	1911.35	1872.26	2189.76	4182.05
Cluster 3			723.06	1546.2	1302.18	1604.86	1358.51	1890.57	2866.95
Cluster 4				0.00	1252.50	688.71	764.55	985.35	2525.95
Cluster 5					0.00	453.57	531.40	879.67	1772.66
Cluster 6						0.00	205.97	300.81	1740.34
Cluster 7							0.00	521.84	1526.44
Cluster 8								0.00	1379.31
Cluster 9									0.00

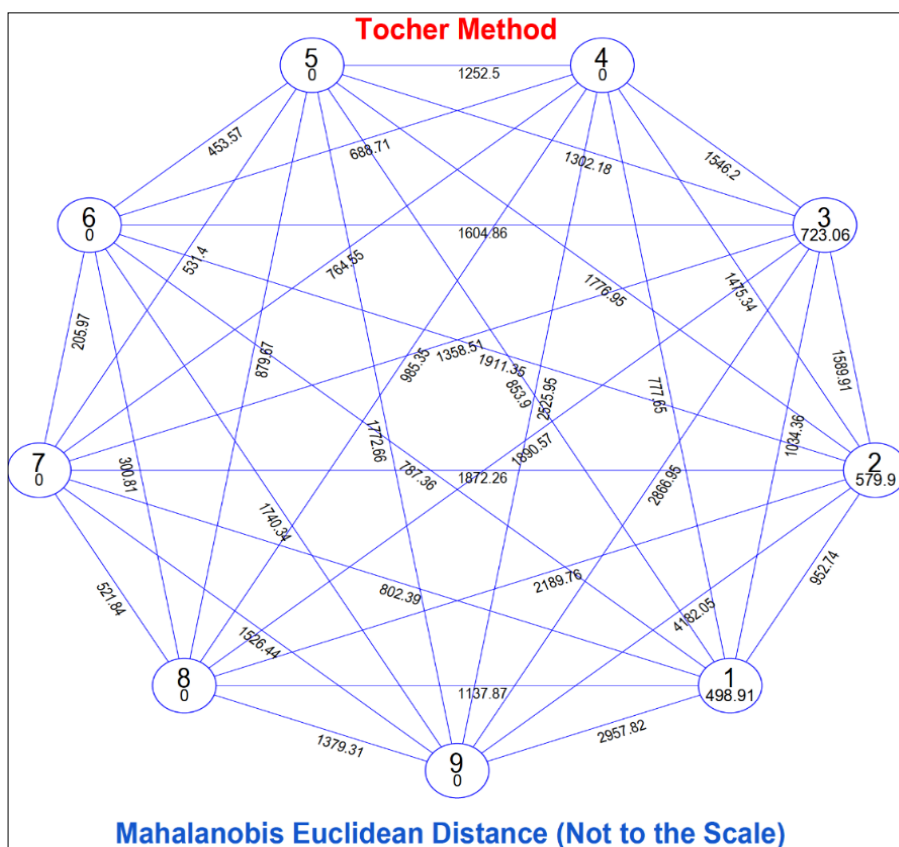


Fig 3: Diagrammatic representation of cluster distances among various clusters in mango

Table 7: Cluster means for various traits in 72 mango hybrids and parents

	TH	TG	TNP	IL	IW	NHF	NMFPT	NFFPT	NFP	FR	FW	SD	PC	FBWW/DBWW	FBW/FWW	FYPT
Cluster 1	6.79	71.29	132.86	25.23	19.71	99.37	432.93	6.8	1.07	16.86	170.76	623.62	5.76	0.99	0.65	12.28
Cluster 2	4.61	39.87	74.36	23.52	19.27	111.63	370.82	4.59	1.37	35.03	144.55	696.17	6.86	2.09	0.71	9.39
Cluster 3	7.03	82.79	124.37	26.81	23.13	298.04	782.67	10.06	1.51	17.36	192.79	590.7	6.09	0.84	0.59	9.63
Cluster 4	6.33	76.66	227.5	27.25	17.75	97.37	949.4	6.15	1.5	23.07	230	627.37	5.11	0.83	0.98	22.61
Cluster 5	7.16	85.73	195.5	24.75	20.75	48.6	226.45	17.5	0.95	5.42	131.62	588.95	5.61	0.67	0.95	12.4
Cluster 6	8.88	116.22	271.5	24.25	18.25	48.25	255.6	11.5	0.8	6.51	189.62	607.85	3.63	0.85	0.69	20.78
Cluster 7	10.11	121.38	198	27.5	22	59.98	332	12.95	1.6	12.58	280.85	447.45	4	0.7	0.61	22.45
Cluster 8	9.04	121.22	252.5	25.5	21.75	90.92	171.9	10.45	1.1	10.57	99.58	1125	4.18	0.7	0.69	30
Cluster 9	7.84	99.46	283.5	27.75	19.25	254.18	356.72	24.65	2	8.21	175.51	581.7	5.06	0.92	0.72	42.96

Table 8: Correlation coefficient among various yield and yield related traits in mango hybrids and parents

Correlation matrix																
	TH	TG	TNP	IL	IW	NHF	NMFPT	NFFPT	NFP	FR	FW	SD	PC	FBWW/DBWW	FBW/FWW	FYPT
TH	1.0000	0.805**	0.489**	0.290**	-0.0946	-0.0884	0.0658	0.329**	-0.0376	-0.209*	0.1292	-0.183*	-0.589**	-0.621**	-0.0791	0.379**
TG		1.0000	0.683**	0.357**	-0.0378	0.1006	0.190*	0.492**	0.0732	-0.361**	0.277**	-0.269**	-0.735**	-0.672**	-0.0372	0.474**
TNP			1.0000	0.397**	0.0236	0.0835	0.146*	0.476**	0.169*	-0.303**	0.208*	-0.178*	-0.538**	-0.489**	-0.0284	0.602**
IL				1.0000	0.591**	0.196*	0.252**	0.169*	0.160*	-0.0608	0.258**	-0.0900	-0.156*	-0.185*	0.0728	0.343**
IW					1.0000	0.262**	0.151*	0.0437	-0.0353	-0.169*	0.158*	0.0132	0.250**	0.0892	0.0478	0.1215
NHF						1.0000	0.524**	0.218*	0.281**	-0.0732	0.317**	-0.0847	0.0404	0.0711	0.0434	0.0179
NMFPT							1.0000	0.0366	0.260**	-0.0188	0.417**	-0.0164	-0.0304	-0.0471	0.0896	-0.0414
NFFPT								1.0000	0.250**	-0.534**	0.144*	-0.156*	-0.396**	-0.311**	0.0874	0.427**
NFP									1.0000	0.455**	0.0254	-0.0317	-0.0055	0.0161	-0.0860	0.173*
FR										1.0000	-0.195*	0.1060	0.285**	0.292**	-0.1211	-0.176*
FW											1.0000	-0.370**	-0.170*	-0.211*	-0.0767	0.1057
SD												1.0000	0.263**	0.410**	0.0658	0.0208
PC													1.0000	0.544**	-0.0748	-0.394**
FBWW/DBWW														1.0000	0.155*	-0.312**
FBW/FWW															1.0000	-0.0872
FYPT																1.0000

Table 9: Path coefficient analysis among fruit yield and yield related traits in mango hybrids and parents

Path matrix of fruit yield per tree																
	TH	TG	TNP	IL	IW	NHF	NMFPT	NFFPT	NFP	FR	FW	SD	PC	FBWW/DBWW	FBW/FWW	FYPT
TH	0.0504	0.0406	0.0246	0.0146	-0.0048	-0.0045	0.0033	0.0166	-0.0019	-0.0105	0.0065	-0.0092	-0.0296	-0.0313	-0.0040	0.379**
TG	0.0002	0.0003	0.0002	0.0001	0.0000	0.0000	0.0001	0.0002	0.0000	-0.0001	0.0001	-0.0001	-0.0002	-0.0002	0.0000	0.474**
TNP	0.2121	0.2958	0.4334	0.1722	0.0102	0.0362	0.0631	0.2061	0.0732	-0.1314	0.0902	-0.0770	-0.2333	-0.2118	-0.0123	0.602**
IL	0.0149	0.0183	0.0204	0.0513	0.0303	0.0100	0.0129	0.0087	0.0082	-0.0031	0.0132	-0.0046	-0.0080	-0.0095	0.0037	0.343**
IW	-0.0149	-0.0060	0.0037	0.0932	0.1578	0.0413	0.0239	0.0069	-0.0056	-0.0267	0.0249	0.0021	0.0395	0.0141	0.0075	0.1215
NHF	0.0014	-0.0016	-0.0013	-0.0031	-0.0041	-0.0156	-0.0082	-0.0034	-0.0044	0.0011	-0.0049	0.0013	-0.0006	-0.0011	-0.0007	0.0179
NMFPT	-0.0120	-0.0348	-0.0267	-0.0461	-0.0277	-0.0960	-0.1830	-0.0067	-0.0475	0.0034	-0.0764	0.0030	0.0056	0.0086	-0.0164	-0.0414
NFFPT	0.0713	0.1066	0.1030	0.0366	0.0095	0.0472	0.0079	0.2166	0.0541	-0.1157	0.0312	-0.0338	-0.0858	-0.0673	0.0189	0.427**
NFP	-0.0014	0.0027	0.0063	0.0060	-0.0013	0.0105	0.0097	0.0093	0.0373	0.0170	0.0009	-0.0012	-0.0002	0.0006	-0.0032	0.173*
FR	-0.0261	-0.0450	-0.0378	-0.0076	-0.0211	-0.0091	-0.0023	-0.0667	0.0568	0.1248	-0.0244	0.0132	0.0355	0.0364	-0.0151	-0.176*
FW	0.0112	0.0239	0.0180	0.0224	0.0136	0.0274	0.0361	0.0125	0.0022	-0.0169	0.0865	-0.0320	-0.0147	-0.0182	-0.0066	0.1057
SD	-0.0393	-0.0578	-0.0381	-0.0193	0.0028	-0.0182	-0.0035	-0.0335	-0.0068	0.0228	-0.0793	0.2146	0.0564	0.0881	0.0141	0.0208
PC	0.0883	0.1103	0.0808	0.0234	-0.0376	-0.0061	0.0046	0.0595	0.0008	-0.0427	0.0255	-0.0395	-0.1501	-0.0816	0.0112	-0.394**
FBWW/DBWW	0.0164	0.0178	0.0129	0.0049	-0.0024	-0.0019	0.0012	0.0082	-0.0004	-0.0077	0.0056	-0.0108	-0.0144	-0.0264	-0.0041	-0.312**
FBW/FWW	0.0064	0.0030	0.0023	-0.0058	-0.0038	-0.0035	-0.0072	-0.0070	0.0069	0.0097	0.0062	-0.0053	0.0060	-0.0125	-0.0803	-0.0872
FYPT	0.379**	0.474**	0.602**	0.343**	0.1215	0.0179	-0.0414	0.427**	0.173*	-0.176*	0.1057	0.0208	-0.394**	-0.312**	-0.0872	1.0000

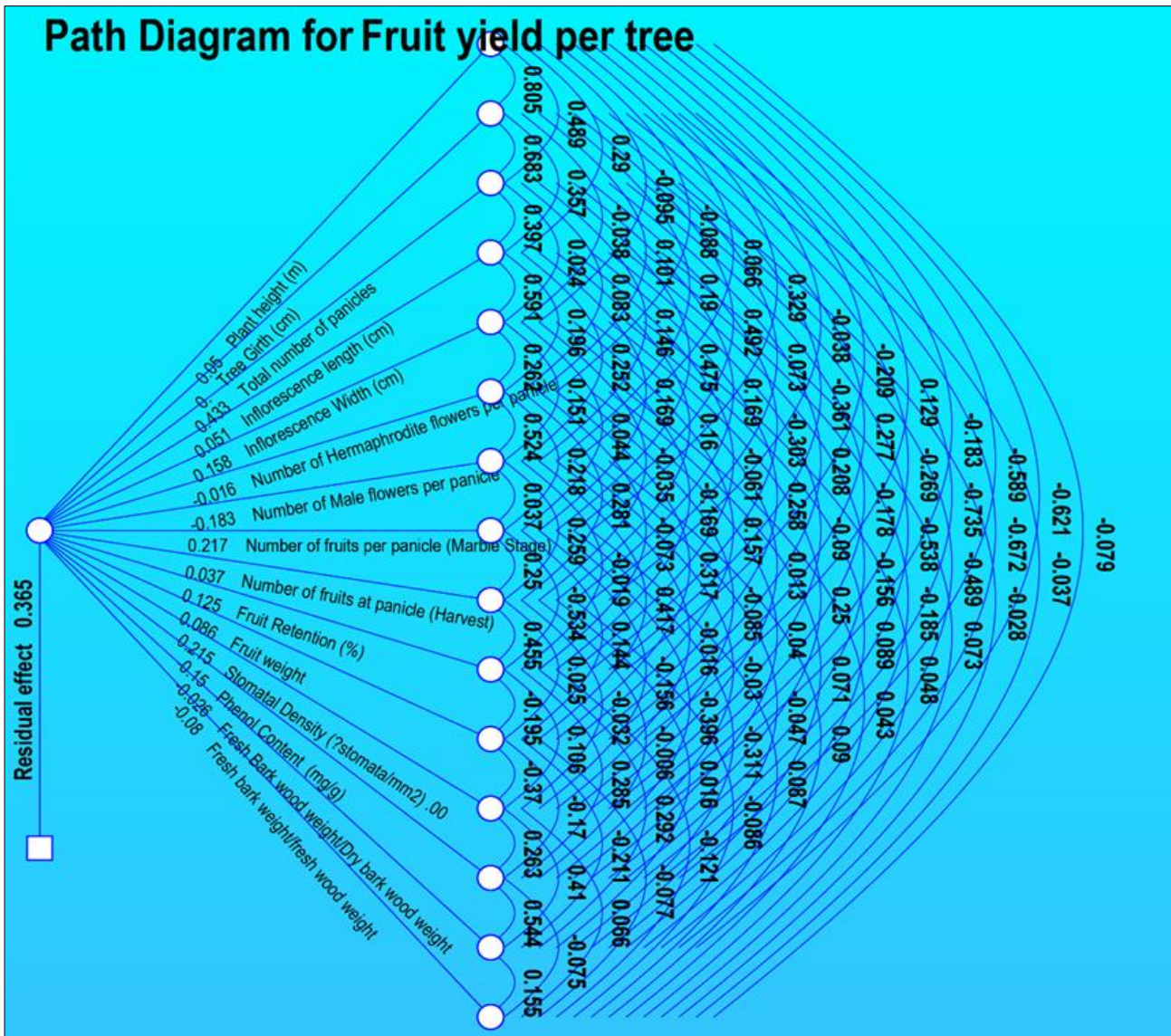


Fig 4: Path diagram representing direct and indirect effects on fruit yield per tree in mango hybrids and parents

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