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RESEARCH PAPER

Studies on correlation and genetic divergence in passion fruit (*Passiflora*.spp) genotypes

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Abstract: Passion fruit (*Passiflora* spp.) is a perennial, woody vine recognized for its distinctive flavour, high nutritional composition and economic significance, leading to its widespread cultivation across tropical and subtropical regions. However, in India, commercial production still depends largely on narrow genetic base, with 'Kaveri' being the only released hybrid available for cultivation. Hence, correlation and divergence studies were carried out by involving 50 genotypes and two checks *viz* Kaveri and JJ-51to identify the diversified genotypes and the traits to be considered while developing a variety. The experiment was laid out in augmented design in farmer's field in Ranganathpura village in Shivamogga district, during 2024-25. Fruit yield per vine was significantly and positively correlated with traits *viz.,* fruit dimensions, pulp weight and juice content at genotypic and phenotypic levels. Among the traits studied, fruit weight contributed maximum genetic divergence (27.90%). The genotypes were classified into eight clusters of which cluster II was largest which contains 30 genotypes. The greatest inter-cluster distance (102.00) was observed between cluster VI and cluster VII. The highest intra-cluster distance (57.32) was in the cluster II. Cluster IV,V,VI,VII and VIII exhibited greatest genetic diversity. Thus selecting the genotypes from this cluster would yield a broad range of segregating progeny.

Keywords: Cluster analysis, Correlation, Divergence, Fruit yield, Passion fruit

Introduction

Passion fruit is a underutilized fruit crop belongs to family Passifloraceae which was originated in Brazil. It is a perennial, woody vine cultivated widely in tropical and subtropical regions. In India, passion fruit is gradually gaining importance as farmers opt for exotic fruit crops to enhance diversification and income (De-pari *et al.,* 2002*)*. However, 'Kaveri' continues to be the only released hybrid recommended for commercial cultivation, indicating the narrow genetic base utilized so far. Research on genotype evaluation under different ecological conditions, particularly in Karnataka, is limited (Tripathi, 2018). Since varietal improvement requires cost and time efficient approaches, assessment of existing genetic variability through correlation and divergence studies provides valuable insights in identifying promising genotypes with superior yield and quality traits. To address this gap, the present investigation was carried out in farmer's field with the objective of evaluating genetic divergence and trait associations to aid future breeding strategies in passion fruit.

Material and methods

An investigation was conducted in farmer's field in Ranganathpura village in Shivamogga district, Karnataka, India during the year 2024-25. It is located between 13° 77' N latitude and 75° 61' E longitude with an elevation of 650 m above mean sea level. The experimental site is located in Southern Transition Agro-climatic zone of Karnataka with sandy loam soil and annual rainfall of 886.90 mm. The experiment was laid out in augmented design with two checks and 50 genotypes. Morphological traits of fruit were recorded by taking the mean of 10 fruits. The titratable acidity of different samples was estimated by titrating against 0.1N sodium hydroxide solution. Total sugars present in the samples were estimated by Anthrone reagent method andare expressed in percentage. Presence of amount of ascorbic acid in different genotypes was estimated by 2,6-dichlorophenol indophenol (DCPIP) dye titration method outlined as Ranganna 1986. The free radical scavenging activities of the extracts were determined byusing 2, 2- Diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging method described by Maizura *etal*., 2011. The total phenolic content of all plant extract was determined by using the Folin-ciocalteu reagent as described by Sadasivam and Manikam, 1991.The phenotypic and genotypic correlation co-efficient analysis was done using standard formulae described by Al- Jibouri *et al.,* 1958.

$$r_p(xy) = \frac{Cov_p(xy)}{\sqrt{\sigma^2 p(x).\ \sigma^2 p(y)}}$$

$$r_p(xy) = \frac{Cov_g(xy)}{\sqrt{\sigma^2 g(x).\ \sigma^2 g(y)}}$$

Where,

rp (xy) = Phenotypic correlation coefficient between characters'x'and'y'

rg(xy) = Genotypic correlation coefficient between characters 'x' and 'y'

$Cov_p(xy)$ = Phenotypic covariance of character 'x' and 'y'

$Cov_g(xy)$ = Genotypic covariance of character 'x' and 'y'

$\sigma^2p(x)$ = Phenotypic variance of character 'x'

$\sigma^2p(y)$ = Phenotypic variance of character 'y'

$\sigma^2g(x)$ = Genotypic variance of character 'x'

$\sigma^2g(y)$ = Genotypic variance of character 'y'

The genetic diversity among 50 genotypes and checks was assessed by using D^2 Mahalanobis statistics by Mahalanobis, 1936. The grouping of accessions was done using Tocher's method, as described by Rao, 1952.

Results and discussion

Correlation analysis helps identify relationships among plant traits, where positive associations suggest traits increase or decrease together, often due to shared genetics or pleiotropy, while negative correlations indicate opposing trends. Such insights are vital in plant breeding, guiding trait selection, revealing genetic linkages and supporting the development of improved crop varieties for evolving agricultural needs.

Phenotypic correlation coefficient studies (Table 1) revealed that fruit length (0.79**), fruit width (0.82**), fruit weight (0.98**), fruit volume (-0.91**), pulp weight (0.98**) and juice content (0.78**) had significantly positive association with fruit yield per vine. Fruit yield per vine was non-significant and positively correlated with titratable acidity (0.16), total sugars (0.41), TSS:acid (0.21), sugar:acid (0.18), ascorbic acid (0.05), antioxidant activity (0.09) and total phenols (0.08). Whereas, pericarp thickness (-0.95**), number of seeds per fruit (0.91**) and TSS (-0.26**) had significantly negative correlation with fruit yield per vine. Fruit length and width has significantly negative correlation with pericarp thickness (-0.79** and -0.85**), number of seeds per fruit (-0.77** and -0.87**). Pericarp thickness was significantly and positively associated with number of seeds per fruit (0.98**) and TSS (0.22**).

Genotypic correlation analysis (Table 2) showed that fruit length (0.88), fruit width (0.85**), fruit weight (0.93**), fruit volume (0.98**), pulp weight (0.97**) and juice content (0.78**) exhibited a significant positive association with fruit yield per vine. Yield per vine was also positively correlated, though non-significantly with titratable acidity (0.14), total sugars (0.13), TSS: acid ratio (0.19), sugar: acid ratio (0.15), ascorbic acid (0.02), antioxidant activity (0.06) and total phenols (0.11). In contrast, pericarp thickness (-0.96**), number of seeds per fruit (-0.92**) and TSS (-0.26**) showed a significant negative relationship with fruit yield per vine. Furthermore, fruit length and width exhibited significant negative associations with pericarp thickness (-0.92** and -0.91**) and number of seeds per fruit (-0.92** and -0.94**). Pericarp thickness was, however significantly and positively correlated with number of seeds per fruit (0.98**) and TSS (0.21**).

The strong positive correlation of fruit size parameters, pulp weight, and juice content with yield per vine highlights their role as key determinants of fruit productivity. Conversely, the negative association of pericarp thickness, seed number, and

Table 1. Phenotypic correlation coefficient between yield and quality parameters of Passion fruit genotypes

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
X1	1.00	0.94**	0.81**	0.85**	0.80**	-0.79**	-0.77**	0.68**	-0.20**	0.14	0.06	0.17	0.13	0.44**	0.01	0.01	0.79**
X2		1.00	0.84**	0.84**	0.84**	-0.85**	-0.87**	0.81**	-0.16	0.12	0.04	0.14	0.11	0.30**	0.04	0.04	0.82**
X3			1.00	0.92**	0.95**	-0.96**	-0.94**	0.82**	-0.29**	0.22**	0.19	0.25**	0.23**	0.07	0.08	0.04	0.98**
X4				1.00	0.90**	-0.96**	-0.91**	0.87**	-0.24**	0.21**	0.18	0.25**	0.23**	0.07	0.08	0.04	0.91**
X5					1.00	-0.98**	-0.92**	0.85**	-0.28**	0.20**	0.16	0.24**	0.21**	0.05	0.08	0.02	0.98**
X6						1.00	0.98**	-0.83**	0.22**	-0.11	-0.10*	-0.15	-0.12	-0.04	-0.08	-0.07	-0.95**
X7							1.00	-0.84**	0.15	-0.06	-0.07	-0.10	-0.08	-0.07	-0.07	-0.07	-0.91**
X8								1.00	-0.22**	0.15	0.19	0.18	0.19	0.06	0.06	0.00	0.78**
X9									1.00	-0.58**	-0.04	-0.76**	-0.46**	-0.27**	-0.12	-0.13	-0.26**
X10										1.00	0.16	0.93**	0.84**	0.40**	0.10	0.47**	0.16
X11											1.00	0.17	0.62**	0.04	0.16	0.18	0.41
X12												1.00	0.84**	0.41**	0.15	0.37**	0.21
X13													1.00	0.31**	0.17	0.28**	0.18
X14														1.00	0.09	0.37**	0.05
X15															1.00	-0.01	0.09
X16																1.00	0.08
X17																	1.00

*- Significant at 5% **- Significant at 1 %

X1- Fruit length (cm),X2- Fruit width (cm),X3- Fruit weight (g),X4- Fruit volume (cc),X5- Pulp weight (g), X6- Pericarp thickness (mm), X7- Number of seeds per fruit, X8- Juice content (%), X9- TSS (^{0}B), X10- Titratable acidity (%), X11- Total sugars (%), X12- TSS: Acid, X13- Sugar: Acid, X14- Ascorbic acid (mg/ 100g), X15- Antioxidant activity (%), X16- Total phenols (mg GAE/100 g dry weight), X17- Fruit yield per vine (kg)

Table 2. Genotypic correlation coefficient between yield and quality parameters of Passion fruit genotypes

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17
X1	1.00	0.95**	0.89**	0.88**	0.87**	-0.92**	-0.92**	0.81**	-0.16	0.05	0.09	0.09	0.07	0.20**	0.00	0.10	0.88**
X2		1.00	0.87**	0.85**	0.89**	-0.91**	-0.94**	0.88**	-0.12	0.04	0.08	0.07	0.06	0.13	0.00	0.04	0.85**
X3			1.00	099**	0.98**	-0.94**	-0.91**	0.82**	-0.28**	0.19	0.18	0.22**	0.21**	0.04	0.06	0.07	0.93**
X4				1.00	0.99**	-0.96**	-0.92**	0.83**	-0.28**	0.18	0.17	0.23**	0.22**	0.05	0.07	0.08	0.98**
X5					1.00	-0.95**	-0.93**	0.84**	-0.27**	0.17	0.16	0.22**	0.19	0.03	0.06	0.07	0.97**
X6						1.00	0.98**	-0.82**	0.21**	-0.08	-0.11	-0.13	-0.09	-0.02	-0.06	-0.10	-0.96**
X7							1.00	-0.84**	0.15	-0.03	-0.08	-0.07	-0.05	-0.05	-0.04	-0.11	- 0.92 **
X8								1.00	-0.23**	0.16	0.19	0.18	0.19	0.03	0.04	0.01	0.78**
X9									1.00	-0.57**	-0.05	-0.76**	-0.45**	-0.32**	-0.13	-0.09	-0.26**
X10										1.00	0.19	0.92**	0.83**	0.42**	0.09	0.42**	0.14
X11											1.00	0.20**	0.65**	0.01	0.15	0.16	0.13
X12												1.00	0.83**	0.43**	0.15	0.31**	0.19
X13													1.00	0.34**	0.16	0.24**	0.15
X14														1.00	0.01	0.35**	0.02
X15															1.00	-0.03	0.06
X16																1.00	0.11
X17																	1.00

*- Significant at 5% **- Significant at 1 %

X1- Fruit length (cm), X2- Fruit width (cm), X3- Fruit weight (g), X4- Fruit volume (cc), X5- Pulp weight (g), X6- Pericarp thickness (mm), X7- Number of seeds per fruit, X8- Juice content (%), X9- TSS (^{0}B), X10- Titratable acidity (%), X11- Total sugars (%), X12- TSS: Acid, X13- Sugar: Acid, X14- Ascorbic acid (mg/ 100g), X15- Antioxidant activity (%), X16- Total phenols (mg GAE/100 g dry weight), X17- Fruit yield per vine (kg)

TSS with yield reflects a developmental trade-off, wherein higher allocation towards structural tissues and seeds limits pulp proportion and reduces harvestable yield. Therefore, selecting genotypes with larger fruits, greater pulp recovery and thinner pericarp would be beneficial for enhancing both yield and quality in passion fruit improvement programmes.The non-significant positive associations of yield with biochemical parameters such as titratable acidity, sugars, ascorbic acid, antioxidants and phenols indicate that quality related traits vary independently of yield implying that improvement of fruit quality may be possible without adversely affecting yield potential.The difference between genotypic and phenotypic correlation coefficients was minimal, indicating a strong, inherent association among the traits analyzed. This small gap suggests that environmental factors had limited influence on the expression of these characters, especially for fruit yield per tree, reflecting robust genetic control within the tested material. Similar findings were noted by Usha *et al.* (2018), Ndukwe and Baiyeri *et al.* (2019), Shivakumar *et al.* (2025).

Fruit weight showed the highest contribution to genetic divergence at 27.90%, followed by fruit volume (22.02%), total sugars (14.78%), TSS (4.50%), antioxidant activity (4.00%), ascorbic acid (3.60%), juice content (3.40%), fruit width (2.87%), fruit length (2.52%), pericarp thickness (2.27%), pulp weight (2.19%), sugar: acid ratio (2.00%), number of seeds per fruit (2.00%), titratable acidity (1.90%), TSS: acid ratio (1.50%), total phenols (1.50%), and fruit yield per vine (1.05%). (Fig. 1).This suggests that selection based on fruit weight, volume, and sugar content would be most effective for differentiating genotypes and improving breeding outcomes. The high contribution of these traits implies they are major factors underlying genetic variability among the genotypes, making them key targets in breeding programs aimed at enhancing fruit quality and yield. Less contributing traits, although important for overall characterization, have a smaller role in defining genetic divergence.

The genotypes, including checks were classified into eight distinct clusters as shown in (Fig. 2). Cluster II contained the largest number of genotypes with thirty entries (JJ-11, JJ-12, JJ-13, JJ-15, JJ-17, JJ-2, JJ-20, JJ-21, JJ-22, JJ-23, JJ-26, JJ-27, JJ-28, JJ-29, JJ-3, JJ-31, JJ-32, JJ-34, JJ-36, JJ-37, JJ-39, JJ-41, JJ-43, JJ-

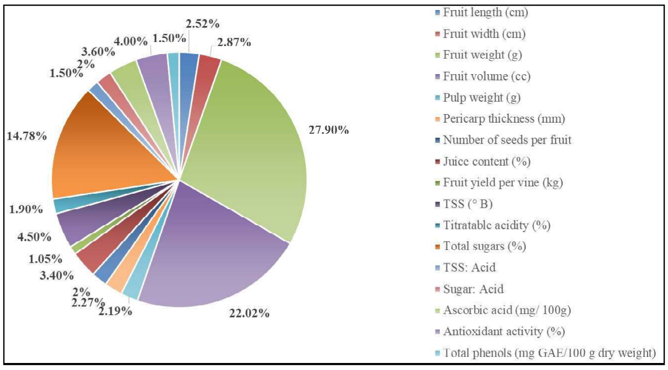

Fig. 1. Pie chart showing contribution of different characters towards total genetic divergence in Passion fruit genotypes

Table 3. Average intra and inter cluster distance (D^2) for yield and quality parameters formed by Passion fruit genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	52.57	59.83	68.06	78.75	79.41	80.59	80.59	80.51
Cluster II		57.32	68.95	79.28	80.18	81.34	81.34	81.25
Cluster III			27.36	87.57	88.55	89.62	89.62	89.58
Cluster IV				0.00	98.31	100.09	100.09	99.91
Cluster V					0.00	100.86	100.88	100.87
Cluster VI						0.00	102.00	101.91
Cluster VII							0.00	101.92
Cluster VIII								0.00

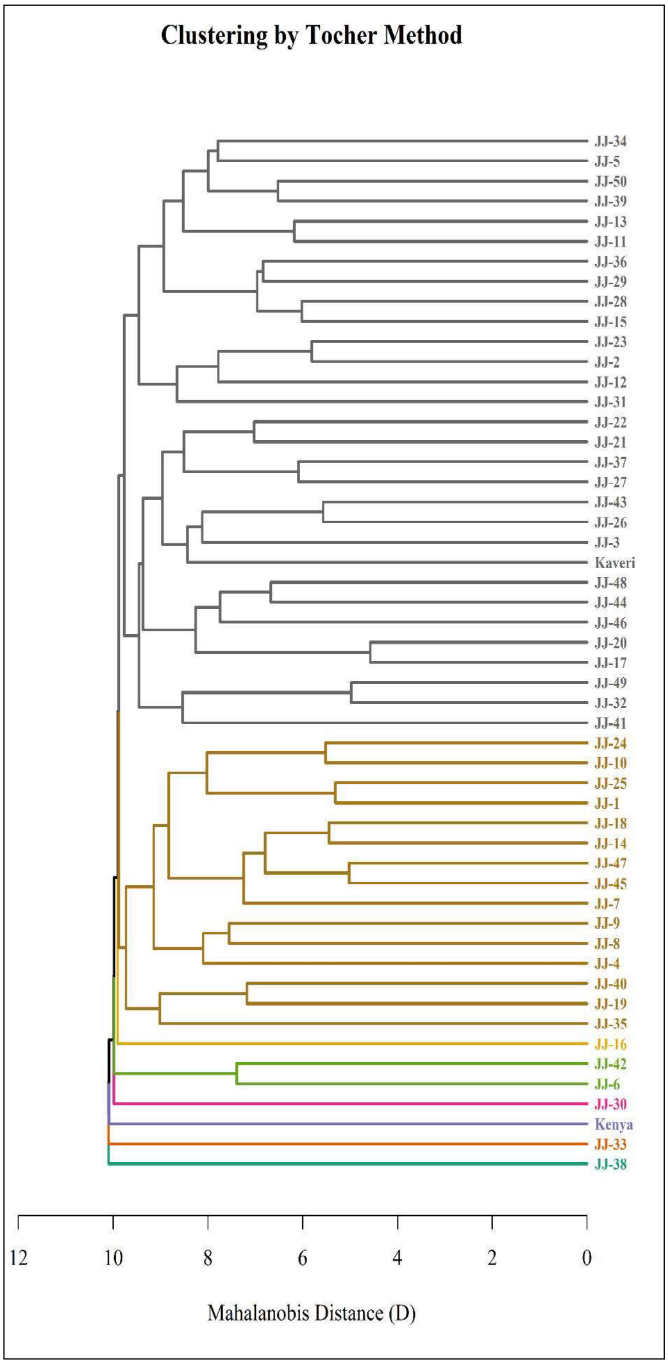

Fig 2. Dendrogram showing the genetic diversity among different genotypes of Passion fruit

44, JJ-46, JJ-48, JJ-49, JJ-5, JJ-50, and Kaveri), followed by cluster I with fifteen genotypes (JJ-1, JJ-10, JJ-14, JJ-18, JJ-19, JJ-24, JJ-25, JJ-35, JJ-4, JJ-40, JJ-45, JJ-47, JJ-7, JJ-8, and JJ-9). Cluster III comprised two genotypes (JJ-42 and JJ-6), while clusters IV, V, VI, VII, and VIII each consisted of a single genotype (JJ-16, JJ-30, JJ-33, JJ-38, and JJ-51, respectively).The predominance of genotypes in clusters I and II indicates low intra- cluster divergence and higher degree of similarity among their genotypes, while the occurrence of solitary genotypes in clusters IV, V, VI, VII and VIII reflects wide inter- cluster distances suggesting the unique genetic constitution. Such distinctness may be exploited as potential donors in hybridization to maximize heterosis and genetic gain. Similar findings were recorded by Pooja *et al.* (2018), Guruprasad *et al.* (2021)*,* Viera *et al.* (2022) and Swaroop *et al.* (2023).

The inter-cluster D^2 values varied from 59.83 to 102.00. The greatest inter-cluster distance of 102.00 was observed between cluster VI and cluster VII, followed closely by the distance of 101.92 between cluster VII and cluster VIII. The smallest inter-cluster distance of 59.83 was recorded between cluster I and cluster II.The intra-cluster D^2 values ranged from 0.00 to 57.32. The highest intra-cluster distance was observed in cluster II (57.32) followed by cluster I (52.57) and cluster III (27.36). The minimum intra-cluster distance of 0.00 was recorded in clusters IV, V, VI, VII and VIII (Table 3). This indicates that genotypes in the clusters IV, V, VI, VII and VIII are genetically more divergent from each other. This suggests that crossing genotypes from these clusters would likely result in greater heterosis and wider variation in offspring.

Conclusion

Fruit yield per vine showed significant positive correlations with fruit length, fruit width, fruit weight, fruit volume, pulp weight, and juice content at both genotypic and phenotypic levels. Among the traits analyzed, fruit weight contributed the most to genetic divergence. The genotypes in the clusters IV, V, VI, VII and VIII are more divergent which can be selected for further crop improvement and varietal development.

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