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STUDIES ON GENETIC DIVERSITY AND ASSOCIATION OF QUANTITATIVE TRAITS IN RECOMBINANT INBRED LINES (RILS) OF FINGER MILLET (*ELEUSINE CORACANA* L. GAERTN.)

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ABSTRACT

Finger millet (*Eleusine coracana* L. Gaertn.) is a nutrient-rich and climate-resilient crop with wide adaptability. The present study was conducted during *Kharif* 2024 at ARS, Hagari, Ballari, to assess genetic diversity and trait associations among 267 F_6 RILs along with three checks. Mahalanobis D^2 statistics grouped the genotypes into nine distinct clusters, indicating substantial genetic divergence within the population. The highest intra-cluster distance was recorded for Cluster I, reflecting greater heterogeneity among its genotypes, while the maximum inter-cluster divergence observed between clusters I and VIII suggested their suitability as potential parents for hybridization. Cluster mean analysis revealed that clusters VI, III and II exhibited superior performance for grain yield and its component traits, whereas Cluster I was ideal for earliness. Thousand seed weight, number of fingers per ear head and finger length contributed most to the overall genetic divergence, emphasizing their importance in genotypic differentiation. Phenotypic correlation analysis among nine quantitative traits revealed that grain yield per plant showed significant positive associations with thousand seed weight, days to 50 per cent flowering and days to maturity, indicating that bolder seeds and extended crop duration contribute positively to yield improvement in finger millet. In contrast, number of leaves per plant, finger length and number of productive tillers per plant exhibited significant negative correlations with grain yield, suggesting that excessive vegetative growth and higher tillering may reduce reproductive efficiency and grain production. Days to 50 per cent flowering was strongly and positively correlated with days to maturity, plant height and thousand seed weight, reflecting coordinated developmental progression and enhanced biomass accumulation in late-maturing genotypes. Plant height showed a significant negative correlation with number of productive tillers per plant, indicating a resource allocation trade-off between vertical growth and tiller production. The observed genetic diversity and significant trait associations among the RILs provide valuable scope for effective selection in finger millet improvement programmes.

***Key words*: Genetic diversity, Correlation, Clusters and RILs**

Introduction

Millets represent a vital group of crops recognized for their wide adaptability to varied ecological conditions, strong tolerance to biotic and abiotic stresses and low input needs. Among them, finger millet (*Eleusine coracana* L. Gaertn.) occupies a significant position as a staple food crop, providing sustenance to millions of resource limited populations inhabiting arid and semi-arid regions across Africa and Asia. From a cytogenetic standpoint, it is an allotetraploid species (2n=4x=36) possessing an AABB genome structure and it predominantly reproduces through self-pollination, with natural cross-pollination occurring at less than one per cent (Barbeau and Hilu, 1993).

The crop is believed to have originated from its wild progenitor, *Eleusine coracana* subsp. *africana*, which belongs to the subfamily *Chloridoideae* of the family *Poaceae*. The centre of origin is localized in the highlands of Ethiopia and Uganda in East Africa, from where the species was introduced into the Indian subcontinent around 2000 BC. Since then, it has become an essential component of traditional agricultural systems and local diets (Kulkarni, 1980).

At the global level, finger millet ranks third among the cultivated millets in area and production, next to pearl millet (*Pennisetum glaucum*) and foxtail millet (*Setaria italica*). It is extensively cultivated under semi-arid tropical and subtropical conditions (Reddy *et al.*, 2009). Nutritionally, it is considered superior to most cereals, containing 5-8 per cent protein, 65-75 per cent carbohydrates and 15-20 per cent dietary fibre, with an average energy value of 336 Kcal per 100 g. The grain is particularly enriched with minerals such as calcium (264-365 mg/100 g), iron (3.60-7.31 mg/100 g) and potassium (294-1160 mg/100 g), far exceeding the levels found in other millets and cereals (Chetan and Malleshi, 2007; Shashi *et al.*, 2007). Additionally, it exhibits low concentrations of anti-nutritional factors like tannins (0.30 mg/100 g) and phytates (0.34 mg/100 g), which enhances its bioavailability of nutrients (Devi *et al.*, 2010).

Finger millet cultivation is widespread across the dry and semi-arid tracts of Africa and Asia, notably in countries such as India, Nepal, Sri Lanka, Madagascar, Malaysia, Uganda and Japan. Among these, India stands as the foremost producer in Asia, with an estimated cultivation area of 1.162 million hectares, producing 1.692 million tonnes and achieving an average productivity of 1456 kg per hectare. Within the country, the principal finger millet growing states include Karnataka, Tamil Nadu, Maharashtra, Uttarakhand, Odisha, Jharkhand and Andhra Pradesh. Karnataka contributes the largest share to national production, covering about 8.73 lakh hectares, yielding nearly 12.34 lakh tonnes, with an average productivity of 1414 kg per hectare (Anon., 2024).

The existence of genetic variability and a clear understanding of genetic relationships among genotypes are essential prerequisites for the success of any crop improvement programme, including that of finger millet. Precise knowledge of the magnitude and pattern of genetic diversity enables breeders to identify and select genetically distinct parents for developing superior hybrids. Greater emphasis should be placed on the traits that contribute most significantly to overall genetic divergence while determining suitable clusters for selection and identifying promising parental lines for hybridization (Jagadev *et al.*, 1991).

Correlation studies play a crucial role in the selection of superior genotypes by revealing the degree and direction of association among yield and its component traits. Such relationships help plant breeders to identify characters that are closely associated with yield and other economically important traits, thereby improving the efficiency of selection. The observed correlations among traits may arise due to pleiotropic gene action, genetic linkage, or physiological and developmental relationships between characters, and they represent the net effect of several segregating genes.

In some cases, genes may simultaneously influence two traits in the same direction, resulting in positive correlations, while in other cases, improvement in one trait may be associated with a reduction in another, leading to negative correlations. Therefore, understanding the interrelationship among yield and its component traits is essential for assembling an optimal combination of desirable characters in a single genotype. Correlation analysis, based on estimates of variances and co variances, provides valuable information on these mutual relationships and helps in identifying effective selection criteria for genetic improvement of yield.

The present investigation was conducted to assess genetic diversity and trait associations among recombinant inbred lines (RILs) of finger millet. The study aimed to understand the extent of variability and the interrelationship among yield and its component traits to facilitate the identification of agronomically superior lines. The results provide valuable insights into the genetic divergence within the population and support effective selection of stable and high-performing genotypes.

Materials and methods

The experiment was conducted at the Agricultural Research Station, Hagari, Ballari, Karnataka during *Kharif* season of 2024. The material for the present study consisted of 267 recombinant inbred lines (RILs) in the F_6 generation derived from the cross PR 202 × GPU 48, along with three check varieties, namely PR 202, GPU 48 and HR 13. For the purpose of evaluation, a total of 270 genotypes were utilized, which included 267 RILs and three checks.

The experiment was laid out in an augmented block design (Federer, 1956) to effectively address the objectives outlined in the present investigation. The experimental layout consisted of 14 compact blocks, each accommodating 22 entries comprising 19 RILs and three checks. The RILs were unreplicated, while the three checks were repeated in each block. Each entry was sown in a single row of 3 m length with a spacing of 45

Table 1: Clustering pattern of F_6 recombinant inbred lines (RILs) of finger millet.

Clusters number	Number of RILs	Name of the RILs
I	16	HR 13, HR 3814-1, HR 3830, HR 3834, HR 4061, HR 3853, HR 3859, HR 3889, HR 3899, HR 3907, HR 3908, HR 3960, HR 3984, HR 4034, HR 4049, HR 4060
II	27	GPU 48, HR 3857, HR 3865, HR 3874, HR 3880, HR 3883, HR 3905, HR 3906, HR 3909, HR 3917, HR 3925, HR 3930, HR 3934, HR 3958, HR 3961, HR 3976, HR 3977, HR 3993-1, HR 4001, HR 4002, HR 4005, HR 4006-1, HR 4006-2, HR 4007, HR 3810, HR 4029, HR 4050
III	35	PR 202, HR 3827, HR 3854, HR 3878, HR 3882, HR 3812, HR 3892, HR 3894, HR 3895, HR 3897, HR 3911, HR 3913, HR 3915, HR 3924, HR 3926, HR 3927, HR 3932, HR 3813, HR 3940, HR 3953, HR 3954, HR 3956, HR 3979, HR 3995, HR 4003, HR 4009, HR 4013, HR 4014, HR 4023, HR 4028, HR 4030, HR 4036, HR 4039, HR 4042, HR 4047-2
IV	45	HR 3805-1, HR 3815-2, HR 3824, HR 3825, HR 3826, HR 3828, HR 3829, HR 3831, HR 3844, HR 3852, HR 3864, HR 3866, HR 3867, HR 3868, HR 3873, HR 3876, HR 3886-2, HR 4062, HR 3901, HR 3912, HR 3914, HR 3923, HR 3941, HR 3949, HR 3955, HR 3966, HR 3970, HR 3973, HR 3974, HR 3978, HR 3980, HR 3996, HR 4000, HR 4010, HR 4015, HR 4022, HR 4026, HR 4033, HR 4038, HR 4040, HR 4041, HR 4046, HR 4054, HR 4055, HR 4057
V	41	HR 3805-2, HR 3806, HR 3807, HR 3809, HR 3815-1, HR 3816, HR 3818, HR 3819, HR 3820, HR 3821, HR 3823, HR 3833, HR 3835, HR 3839, HR 3840, HR 3841, HR 3845, HR 3811, HR 3851, HR 3855, HR 3858, HR 3860, HR 3861, HR 3863, HR 3871, HR 3872, HR 3877, HR 3881, HR 3884, HR 3885, HR 3886-1, HR 3887HR 3890, HR 3893, HR 3900, HR 3916, HR 3935, HR 3982, HR 3998, HR 4004, HR 4008
VI	29	HR 3808, HR 3870, HR 3891, HR 3898, HR 3904, HR 3931, HR 4063, HR 3946, HR 3959, HR 3964, HR 3967, HR 3975, HR 3983, HR 3999, HR 4016, HR 4017, HR 4018, HR 4020, HR 4021, HR 4025, HR 4035, HR 4037, HR 4044, HR 4045, HR 4048-1, HR 4048-2, HR 4052, HR 4053, HR 4059
VII	21	HR 3814-2, HR 3817, HR 3822, HR 3832, HR 3836, HR 3837, HR 3838, HR 3842, HR 3843, HR 3846, HR 3847 HR 3848, HR 3879, HR 3888, HR 3936, HR 3950, HR 3993-2, HR 4019, HR 4043, HR 4051, HR 4058
VIII	27	HR 3849, HR 3850, HR 3869, HR 3896, HR 3902, HR 3903, HR 3920, HR 3921, HR 3922, HR 3937, HR 3944, HR 3945, HR 3947, HR 3948, HR 3963, HR 3969, HR 3972, HR 3985, HR 3986, HR 3987, HR 3988, HR 3991, HR 3994, HR 4012, HR 4024, HR 4047-1, HR 4056
IX	29	HR 3862, HR 3875, HR 3910, HR 3918, HR 3919, HR 3928, HR 3929, HR 3933, HR 3938, HR 3939, HR 3942, HR 3943, HR 3951, HR 3952, HR 3957, HR 3962, HR 3965, HR 3968, HR 3971, HR 4064, HR 3981, HR 3989, HR 3990, HR 3992, HR 3997, HR 4011, HR 4027, HR 4031, HR 4032

cm between rows and ten days after sowing, seedlings were thinned by maintaining 10 cm between plants within a row.

Fertilizers were applied at the recommended dose of 40:20:20 N, P_2O_5, K_2O kg per acre and all other cultural practices were carried out at regular intervals as per the recommended package of practices to ensure the successful growth of a healthy crop. Data were recorded on five randomly selected plants from each genotype, including both RILs and check varieties. Observations were taken for key agronomic traits such as days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, number of productive tillers per plant, finger length, number of fingers per ear head, 1000 seed weight and grain yield per plant. Each trait was measured at the appropriate growth stage using standard procedures to ensure consistency and accuracy across all entries.

The genetic diversity among recombinant inbred lines (RILs) of finger millet was estimated using Mahalanobis D^2 statistics as proposed by Mahalanobis (1936). The analysis was performed using R Studio (ver. 2025.05.1+513) software developed by Posit PBC. The pairwise D^2 values obtained were utilized for clustering the genotypes following the hierarchical method suggested by Sokal and Sneath (1963).

All the [n(n-1)/2] D^2 values were subjected to hierarchical clustering to classify the genotypes into different groups based on genetic similarity. The intra-cluster and inter-cluster distances were calculated as per the methods outlined by Singh and Chaudhary (1977). These distances helped in assessing the degree of genetic divergence within and between clusters, respectively.

The contribution of individual traits towards total genetic divergence was estimated to determine the relative importance of each character in differentiating the genotypes. The percentage contribution of each trait was calculated following the procedure suggested by Singh and Chaudhary (1977). Traits showing higher contributions were considered more important in distinguishing the genotypes and were prioritized for use in breeding and selection programmes.

Correlation studies were undertaken to assess the degree and direction of linear association between dependent and independent variables. The correlation coefficient varies from -1, representing a perfect negative relationship, to +1, indicating a perfect positive relationship. In the present investigation, correlation coefficients among different pairs of characters were computed following the statistical procedure outlined by Panse and Sukhatme (1964). The significance of the estimated correlation coefficients was tested at (n-2) degrees of freedom using the '*t*' test, with reference to Fisher and Yates tables at 0.05 and 0.01 probability levels.

Results and Dscussion

Genetic divergence determined by inherent genetic factors, forms the basis of heritable variation within a species and is essential for understanding adaptation, population differentiation and trait evolution. Estimating genetic divergence helps in grouping genotypes and identifying those with unique or desirable traits. The magnitude of variability within a population indicates its evolutionary potential and adaptability, guiding effective germplasm utilization for diversity, conservation and crop improvement studies.

Data on nine yield and its related traits from 267 recombinant inbred lines (RILs) and three checks of finger millet were analysed using Mahalanobis D^2 statistics and clustering was performed following the hierarchical method proposed by Sokal and Sneath (1963). The analysis revealed considerable variation among the genotypes, indicating the presence of a wide range of genetic diversity within the population.

A total of 270 genotypes (comprising 267 RILs and 3 checks) were classified into nine distinct clusters based on genetic divergence, as presented in Table 1 and Fig. 1. Cluster IV was the largest, comprising 45 genotypes, followed by clusters V and III with 41 and 35 genotypes, respectively. The higher number of genotypes in these clusters suggests a relatively narrow genetic base, indicating similarity in their trait composition. Clusters VI and IX, each containing 29 genotypes, along with clusters II and VIII with 27 genotypes each, represented moderately large groups reflecting considerable genetic variation. Cluster I (16 genotypes) and cluster VII (21 genotypes) showed a moderate degree of diversity. The absence of monogenotypic clusters signifies that all genotypes exhibited notable genetic divergence, with none being distinct enough to form a separate cluster.

Genetic divergence among the nine clusters of finger millet RILs was assessed using Mahalanobis D^2 statistics, where diagonal values denote intra-cluster distances and off-diagonal values represent inter-cluster distances. The

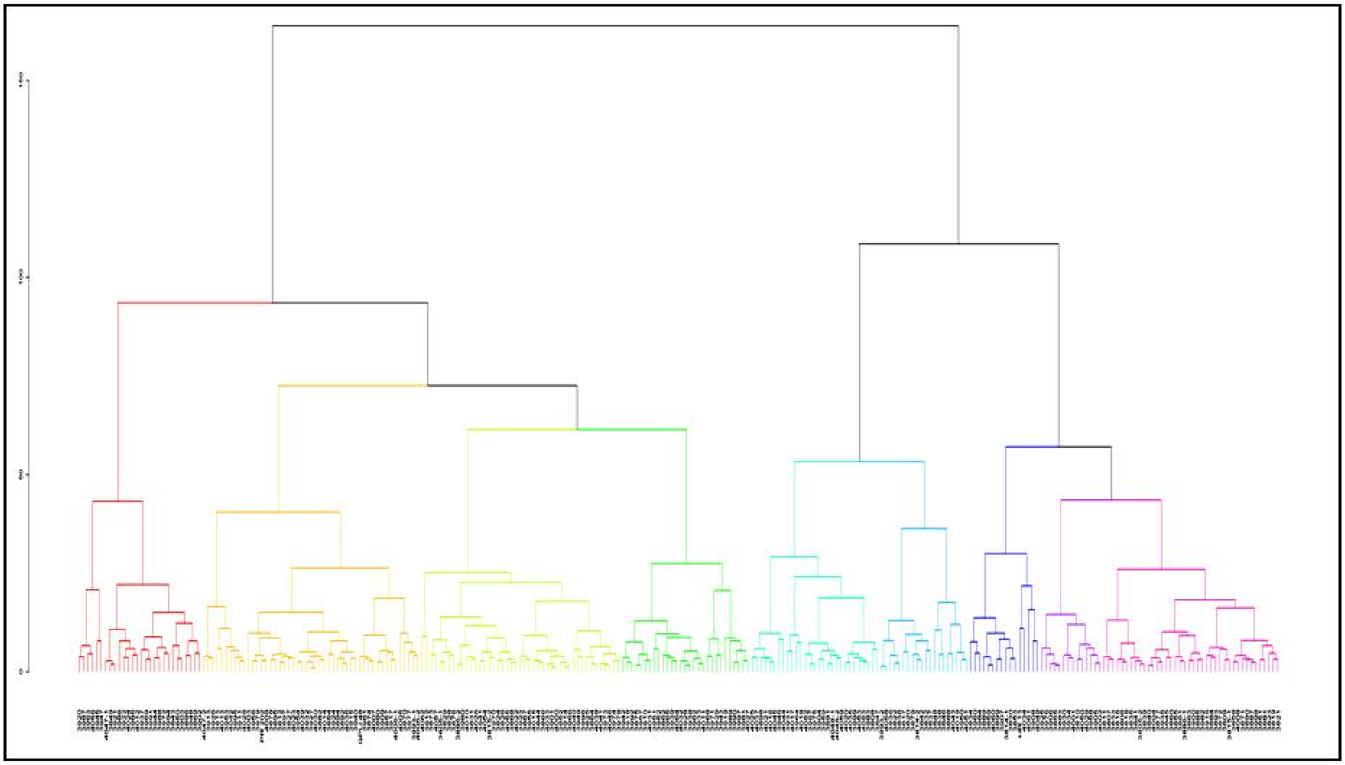

Fig. 1: Heirarchial cluster dendrogram of F_6 RILs of finger millet.

Table 2: Average intra (diagonal) and inter cluster distances for yield and yield contributing traits in F_6 RILs of finger millet.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**4.03**	2.39	3.27	2.58	1.86	4.59	3.84	5.27	3.71
II		**2.83**	1.27	2.09	1.78	2.89	3.04	3.65	2.56
III			**2.77**	1.83	2.23	2.88	3.28	2.98	1.65
IV				**2.77**	1.31	3.71	3.02	3.32	1.34
V					**2.63**	3.34	2.32	3.53	2.33
VI						**3.70**	2.16	2.45	3.68
VII							**3.55**	2.62	3.42
VIII								**3.91**	2.70
IX									**3.23**

computed intra and inter-cluster distance values are summarized in Table 2.

The intra-cluster distances among the nine clusters ranged from 2.63 to 4.03, indicating variable genetic diversity within clusters. Cluster I exhibited the highest intra-cluster distance (4.03), reflecting greater heterogeneity among its genotypes, followed by clusters VIII (3.91), VI (3.70) and VII (3.55), which also showed moderate diversity. In contrast, clusters V (2.63), III and IV (2.77) and II (2.83) recorded lower intra-cluster distances, suggesting close genetic similarity among their constituent genotypes.

The inter-cluster distances varied from 1.27 to 5.27, denoting considerable genetic divergence among clusters. The maximum divergence was observed between clusters I and VIII (5.27), followed by I and VI (4.59) and I and VII (3.84), indicating these combinations as potential parents for hybridization to exploit heterosis. Conversely, the minimum inter-cluster distance was found between clusters II and III (1.27), followed by IV and V (1.31) and IV and IX (1.34), suggesting close genetic relationships and limited variability between these clusters.

Cluster mean analysis revealed wide variability among the nine clusters of recombinant inbred lines (RILs) of finger millet, reflecting substantial genetic divergence across all studied traits presented in Table 3. For days to 50 per cent flowering, mean values ranged from 59.49 days (Cluster I) to 71.48 days (Cluster VIII), while for days to maturity, values varied from 92.13 days (Cluster I) to 104.10 days (Cluster VI), indicating the presence of both early and late maturing genotypes. Cluster I, characterized by early flowering and early maturity, represents a valuable source for developing short duration cultivars capable of escaping pink stem borer infestation. Plant height ranged from 89.96 cm (Cluster I) to 120.40 cm (Cluster IX), suggesting that Cluster IX and VIII possessed tall and vigorous genotypes, whereas Cluster I harboured compact plant types desirable for lodging resistance. Number of leaves per plant showed moderate variation (10.50-11.55), with Cluster VIII exhibiting the highest leaf count and Cluster I the lowest, indicating differential vegetative growth potential among clusters.

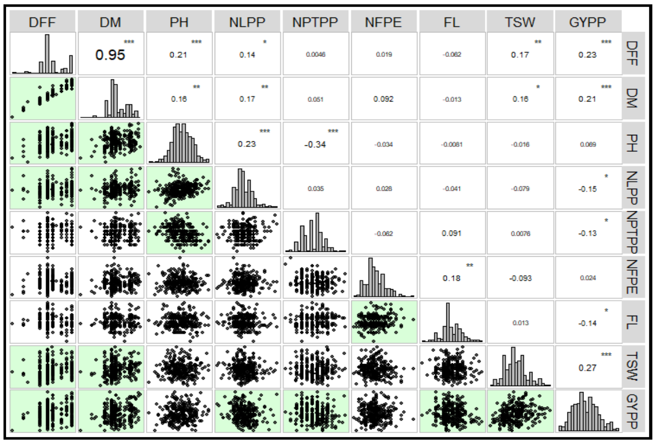

Fig. 2: Diagrammatic representation of phenotypic correlation of quantitative traits in finger millet.

Yield and its related traits also displayed marked variation across clusters. Productive tillers per plant ranged from 4.05 (Cluster VIII) to 5.02 (Cluster VII), identifying Cluster VII and I as ideal for improving tiller productivity. Finger length varied from 6.52 cm (Cluster VI) to 7.00 cm (Cluster IV), while the number of fingers per ear head ranged from 7.30 (Cluster VIII) to 7.74 (Cluster VI), highlighting Clusters IV and VI for superior ear head traits. Thousand seed weight spanned from 2.58 g (Cluster IV) to 2.97 g (Clusters II and VI), indicating that these clusters harbour bold seeded genotypes preferred for seed vigour and yield stability. Grain yield per plant showed the widest range, from 20.46 g (Cluster V) to 31.45 g (Cluster VI), demonstrating the existence of high-yielding RILs in Clusters VI, III and II. Overall, clusters VI, III and II emerged as promising sources for yield enhancement, while Cluster I serves as a valuable pool for early maturity and stress-escape traits. The observed cluster differentiation confirms the presence of considerable genetic diversity, offering scope for selecting contrasting parents in hybridization to develop high-yielding and disease-resistant cultivars of finger millet.

The per cent contribution of nine traits to genetic divergence (Table 4) revealed that thousand seed weight (13.11%), number of fingers per ear head (12.21%), finger length (11.64%) and plant height (11.13%) were the major contributors, indicating their key role in differentiating genotypes. Moderate contributions were recorded for days to 50 per cent flowering (11.05%),

Table 3: Cluster mean values for yield and yield contributing traits in F_6 RILs of finger millet.

Cluster	DFF	DM	PH	NLPP	NPTPP	FL	NFPE	TSW	GYPP
I	59.49	92.13	89.96	10.50	4.82	6.75	7.48	2.59	21.39
II	62.76	95.06	101.31	10.94	4.50	6.79	7.50	2.97	29.77
III	63.15	95.63	112.48	10.98	4.27	6.79	7.58	2.86	30.09
IV	62.31	94.78	110.38	11.19	4.40	7.00	7.68	2.58	20.85
V	63.20	96.15	101.08	11.06	4.74	6.80	7.42	2.74	20.46
VI	71.31	104.10	104.79	10.86	4.65	6.52	7.74	2.97	31.45
VII	70.14	103.14	100.67	11.49	5.02	6.84	7.35	2.81	21.59
VIII	71.48	103.41	120.35	11.55	4.05	6.75	7.30	2.94	24.66
IX	63.17	95.59	120.40	11.36	4.15	6.69	7.49	2.62	23.12

DFF = Days to 50 per cent flowering; **NLPP** = Number of leaves per plant; **NFPE** = Number of fingers per ear head;
DM = Days to maturity; **NPTPP** = Number of productive tillers per plant; **TSW** = Thousand seed weight (g);
PH = Plant height (cm); **FL** = Finger length (cm); **GYPP** = Grain yield per plant (g)

days to maturity (10.94%), number of leaves per plant (10.45%) and grain yield per plant (10.32%), while the lowest was from number of productive tillers per plant (9.15%). The narrow range of contribution values (9.15-13.11%) suggests that genetic divergence was governed by the collective influence of multiple traits rather than a single dominant factor, indicating a balanced and multidimensional pattern of variability among the recombinant inbred lines (Sankara *et al.*, 1998).

Karl Pearson mathematically formalized the correlation concept in 1895 by introducing the Pearson correlation coefficient (r), which continues to be the most widely applied measure for quantifying linear relationships between two variables. Correlation analysis serves as a vital tool in breeding programs, enabling indirect selection strategies, multi-trait enhancement and optimal resource utilization. In finger millet improvement, knowledge of trait associations allows breeders to simultaneously improve multiple characteristics, especially grain yield and quality, the primary objectives of finger millet breeding programs.

Phenotypic correlation analysis was performed among nine quantitative traits to identify direct trait associations and formulate efficient selection strategies for characters strongly correlated with yield performance (Table 5). Thousand seed weight (0.2678) exhibited the highest significant positive correlation with grain yield per plant, suggesting that genotypes with bolder seeds achieve superior productivity. This was followed by days to fifty per cent flowering (0.2291) and days to maturity (0.2121), indicating that extended growth duration facilitates prolonged photosynthetic activity and enhanced dry matter accumulation, thereby improving yield potential. These results are in accordance with the findings of Anuradha *et al.*, (2013), Patil *et al.*, (2013), Brunda *et al.*, (2015), Ezeaku *et al.*, (2015), Jyothsna *et al.*, (2016), Manoj Kumar *et al.*, (2015) and Chavan *et al.*, (2020).

Conversely, number of leaves per plant (-0.1477) showed a significant negative association with grain yield per plant, implying that excessive vegetative growth may redirect photosynthates from reproductive organs to foliage, ultimately reducing grain production. Similarly, finger length (-0.1404) and number of productive tillers per plant (-0.1308) demonstrated negative correlations with yield. The negative relationship with tiller number suggests intra-plant competition, wherein excessive tillering produces numerous but inadequately filled fingers. This finding emphasizes that achieving an optimal tiller number, rather than maximizing tiller production, is critical for yield enhancement in finger millet. These results are consistent with the findings of Manyasa *et al.*, (2016) and Madhavilatha *et al.*, (2021).

Days to 50 per cent flowering exhibited a highly significant positive correlation with days to maturity (0.9538), followed by plant height (0.2091), thousand seed weight (0.1716), and number of leaves per plant (0.1396). These associations indicate that late-flowering genotypes undergo extended vegetative growth, enabling greater stem elongation and biomass accumulation, though breeders must consider lodging risks in taller types. The positive relationship with seed weight reflects prolonged grain-filling duration, facilitating enhanced photosynthate

Table 4: Per cent contribution of nine characters towards genetic divergence in F_6 RILs of finger millet.

Traits	Per cent contribution
Days to 50 per cent flowering	11.05
Days to maturity	10.94
Plant height (cm)	11.13
Number of leaves per plant	10.45
No. of productive tillers per plant	9.15
Finger length (cm)	11.64
Number of fingers per ear head	12.21
Thousand seed weight (g)	13.11
Grain yield per plant (g)	10.32

Table 5: Phenotypic correlation coefficient between yield and its attributing traits in finger millet.

	DFF	DM	PH	NLPP	NPTPP	NFPE	FL	TSW	GYPP
DFF	1	0.9538**	0.2091**	0.1396*	0.0046	0.0188	-0.0621	0.1716**	0.2291**
DM		1	0.1619**	0.1654**	0.0509	0.0922	-0.0133	0.1557*	0.2121**
PH			1	0.2329**	-0.3410**	-0.0337	-0.0081	-0.0160	0.0690
NLPP				1	0.0346	0.0282	-0.0406	-0.0788	-0.1477*
NPTPP					1	-0.0618	0.0907	0.0076	-0.1308*
NFPE						1	0.1795**	-0.0932	0.0244
FL							1	0.0128	-0.1404*
TSW								1	0.2678**
GYPP									1

Note: *Significance at 5 %; ** Significance at 1 % ; **DFF** = Days to 50 per cent flowering; **NLPP** = Number of leaves per plant; **NFPE** = Number of fingers per ear head; **DM** = Days to maturity; **NPTPP** = Number of productive tillers per plant; **TSW** = Thousand seed weight (g); **PH** = Plant height (cm); **FL** = Finger length (cm); **GYPP** = Grain yield per plant (g)

accumulation in developing seeds. Similarly, late-flowering genotypes produce more foliage, potentially increasing photosynthetic capacity. However, balanced selection for optimal leaf number remains crucial to maximize efficiency without excessive resource competition that could compromise grain yield. Comparable results were documented by Chavan *et al.*, (2020).

Days to maturity demonstrated a highly significant positive correlation with days to 50 per cent flowering (0.9538), confirming the strong developmental linkage between these growth phases. Additional positive associations were observed with number of leaves per plant (0.1654), plant height (0.1619), and thousand seed weight (0.1557). Plant height demonstrated significant positive correlations with number of leaves per plant (0.2329), days to fifty per cent flowering (0.2091), and days to maturity (0.1619), revealing that taller genotypes produce more foliage and exhibit extended growth duration. Conversely, the significant negative correlation between plant height and number of productive tillers per plant (-0.3410) indicates a critical resource allocation trade-off between vertical growth and lateral branching. This inverse relationship suggests that taller plants prioritize upward development over tiller production, reflecting a compensatory developmental mechanism where resources are differentially partitioned between stem elongation and tillering capacity. These results are in line with previous findings reported by Mahanthesha *et al.*, (2018).

Number of leaves per plant exhibited significant positive correlations with plant height (0.2329), days to maturity (0.1654), and days to 50 per cent flowering (0.1396), while number of productive tillers per plant showed a significant negative correlation with plant height (-0.3410). Number of fingers per ear head and finger length demonstrated a significant positive correlation (0.1795), indicating that genotypes with more fingers tend to produce longer fingers as well. This association reflects coordinated inflorescence development, where increased panicle branching occurs alongside extended finger growth. This relationship is breeding-favourable, as concurrent enhancement of both traits expands the grain-bearing surface area, potentially improving yield capacity when adequate grain filling across all fingers is ensured. Similar observations were recorded by Chavan *et al.*, (2020). Thousand seed weight showed significant positive correlations with days to fifty per cent flowering (0.1716) and days to maturity (0.1557), confirming that extended crop duration promotes the development of bolder seeds through prolonged grain-filling periods that allow greater photosynthate accumulation in developing grains.

The phenotypic correlation analysis revealed that thousand seed weight, days to fifty per cent flowering, and days to maturity were positively correlated with grain yield, while excessive vegetative traits showed negative associations. The strong correlation between flowering time and maturity indicates coordinated developmental phases. Critical trade-offs were identified between plant height and tillering capacity and between vegetative growth and reproductive success. These findings emphasize that optimal rather than maximum expression of vegetative traits is essential for yield improvement. Selection strategies should prioritize balanced plant architecture, moderate growth duration and enhanced seed weight to achieve superior grain yield in finger millet.

Conclusion

The study revealed considerable genetic variability among 267 RILs and three checks of finger millet, which were grouped into nine distinct clusters using Mahalanobis D^2 statistics. The wide distribution of genotypes across clusters indicated substantial genetic divergence and a broad genetic base. High inter-cluster distances, particularly between clusters I and VIII, suggest their suitability as potential parents for hybridization to exploit maximum heterosis. Cluster mean analysis identified clusters VI, III and II as promising for yield related traits, while clusters I and IV were superior for early maturity and panicle attributes. Traits such as thousand seed weight, number of fingers per ear head and finger length contributed most to total genetic divergence, underscoring their importance in selection. Phenotypic correlation analysis revealed that thousand seed weight, days to 50 per cent flowering and days to maturity were positively associated with grain yield in finger millet. Strong interrelationships among flowering, maturity and plant height indicated coordinated growth and development, while negative associations of excessive vegetative traits with yield emphasized the importance of balanced plant architecture. Hence, selection for optimal growth duration, moderate tillering and higher seed weight would be effective for yield improvement.

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