



Research Article

Characterization of little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz) landraces and varieties for genetic diversity and association of traits

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Abstract

Little millet is one of the least explored small millets and has several nutritional benefits with features of climate resilience. In this study, seventeen little millet landraces and varieties were characterized for eleven quantitative and six qualitative traits. The diversity of the accessions for quantitative traits with major contributors as 1000 seed weight and plant height grouped the genotypes into five clusters. Five genotypes each were grouped under cluster III and cluster V. The maximum inter cluster distance was found between cluster I and cluster II. Subsequently, cluster I had higher desirable mean for plant height, number of basal tillers, panicle length, number of branches per panicle and grain yield per plant while cluster III had early flowering. The qualitative traits viz., grain colour, panicle compactness and pigmentation of leaf sheath were also highly variable in the present material and were grouped into six clusters based on these traits. Hence, these highly variable qualitative traits could be employed as major indicators in the identification of these landraces. In addition, out of the fourteen traits, five traits viz., number of branches per panicle, panicle length, flag leaf length, flag leaf width and number of basal tillers, exhibited significant influence on yield through direct and indirect effects. Thus, these traits could be used as effective selection indicators for improving the yield parameters in little millet.

Keywords: little millet landraces, D² analysis, correlation and path analysis

INTRODUCTION

Little millet (*Panicum sumatrense* Roth. ex. Roem. and Schultz) is one of the underutilized small millets reported to be originated from South East Asia and is currently cultivated largely in India and Nepal. India produces about 0.12 million tonnes per year and serves as the largest producer in the world. It is grown widely in the states of Karnataka, Andhra Pradesh, Tamil Nadu, Orissa, Bihar, Maharashtra and Madhya Pradesh (Meena *et al.*, 2021).

This crop is a highly self - pollinated owing to the presence of cleistogamous flowers and it belongs to the family of *Poaceae*. Little millet is an allotetraploid crop with a chromosome number of $2n = 4x = 36$. Being a quick growing crop, it is the first food to be consumed among the tribal people and is the staple food for millions of people (Selvi *et al.*, 2014). It is comparatively rich in protein, fibre, iron and is free of gluten. Thus, people with

nutrient deficiencies and diabetes would be benefitted by consuming little millet in their dietary bowl (Ambati and Sucharita, 2019). Due to these incredible nutraceutical benefits and the importance given by the Government towards these millets, they are getting popularity in urban regions as well. This crop is also highly drought tolerant and it has been historically serving as a reserve food crop as it can be stored for a long period of time without deterioration (Ganapathy, 2017).

Little millet, an orphan crop, has not yet been utilized by researchers and the variability present in this crop is also not yet well explored. Little millet endows a greater variability in its genus and its landraces are still cultivated as a heritage by Malayali tribes of Kolli hills (Arunachalam *et al.*, 2005). The variability of these landraces is yet to be analysed and this study focuses on analysing the diversity of the novel features in little millet landraces for future breeding programmes. Recent studies on characterization of little millet genotypes by D² analysis grouped them into six clusters and it was observed that yield was the major trait that contributed to genetic divergence (Suryanarayana and Sekhar, 2018a). Successively, in another study by Venkataratnam *et al.* (2019a), the genotypes were grouped into seven clusters with days to 50% flowering as the major contributor towards variability. Thus, analysing and observing the genetic diversity in genotypes provides a base for the scope of selection and improvement in little millet genotypes. This study is thereby conducted with an aim to characterize the little millet landraces for various yield attributing and qualitative traits which could be utilized in future.

MATERIALS AND METHODS

The experiment was conducted with seventeen little millet landraces and varieties collected from different parts of South India (Table 1). They were evaluated at Karunya Institute of Technology and Sciences, situated at about 11° 56' N latitude and 76° 44' E longitude at an altitude of 467 m above MSL. The genotypes were grown in Randomized Block Design with three replications at a spacing of 30 × 10 cm during *Kharif* 2022 and recommended package of practices were adopted. Randomly selected five plants were tagged and observations for eleven quantitative traits *viz.*, number of basal tillers, days to 50% flowering, peduncle length (cm), flag leaf blade length (cm), flag leaf blade width (cm), leaf area index, panicle length (cm), number of branches per panicle, plant height (cm) 1000 seed weight (g) and grain yield per plant as well as six qualitative traits *viz.*, inflorescence shape, panicle compactness, pigmentation at leaf sheath, leaf sheath pubescence, grain shape and grain colour were recorded. The qualitative traits were recorded based on the DUS (Distinctiveness, Uniformity and Stability) descriptors provided by PPV & FRA (Protection of Plant Varieties and Farmers' Rights Authority). The data recorded were subjected to D² analysis developed by Mahalanobis (1936) using hierarchical clustering on principal components method. Correlation among the morphological traits was analysed as per the method suggested by Johnson *et al.* (1955) and path coefficient analysis was estimated as the method suggested by Dewey and Lu (1959). The analyses were computed using the packages 'Biotools', 'Agricolae' and 'Metan' in R software version 4.2.2.

Table 1. List of Genotypes and their place of collection

S.No	Genotype Name	Place of collection
1	ATL 1	Center of Excellence in Millets, Athiyandal
2	Kolundhan samai	Jawadhu hills
3	Chittan samai	Jawadhu hills
4	IR 20 samai	Kolli hills
5	Kottathara samai	Attapadi, Kerala
6	CO 4 (samai)	TNAU, Coimbatore
7	Vellai samai	Jawadhu hills
8	Periya samai	Kolli hills
9	IR 8 Samai	Jawadhu hills
10	Siru samai	Jawadhu hills
11	Kalman samai	Jawadhu hills
12	Kothu samai	Jawadhu hills
13	Paakulam Karunsamai	Attapadi, Kerala
14	Jawadhu local samai	Jawadhu hills
15	Perunkolai samai	Jawadhu hills
16	Kochchamai	Kolli hills
17	Perunsamai	Jawadhu hills

RESULTS AND DISCUSSION

The ANOVA revealed significant differences among the seventeen genotypes for 11 quantitative traits. This indicated the presence of variation among the genotypes for all the characters studied (Table 2). From the D² analysis it could be observed that, the seventeen genotypes were grouped into five clusters. Among the five clusters, five genotypes each were grouped under cluster III and cluster V, respectively. Three genotypes were grouped under cluster I and two each were grouped in cluster II and cluster IV, respectively (Table 3). These genotypes were thus grouped into clusters based on the per cent contribution of the traits and it was observed that the 1000 seed weight followed by plant height were the major contributors for divergence (Table 4). Selvi *et al.* (2015) and Arya *et al.* (2018) also reported 1000 seed weight and plant height as major contributors in D² analysis. Hence, these traits could be exploited in future breeding programmes.

The inter and intra cluster distances assess the diversity among and within the cluster of genotypes (Handl *et al.*, 2005). Among the clusters, high inter cluster distance was observed between cluster I and cluster II. This presented a higher degree of genetic diversity among the genotypes of the cluster I and cluster II. However, the lowest inter cluster distance was observed between cluster II and

cluster III. This exhibited a genetic similarity and closeness prevailing among these clusters (Table 5). The clusters I and II genotypes can be exploited in future hybridization programmes to develop high yielding recombinants. Although the genotypes were distributed in different clusters, there were few variations within the clusters for the traits other than the major contributing traits. Among all the clusters, high intra cluster distance was exhibited by cluster I (Table 5). This portrayed a wider genetic diversity among the genotypes for all the yield attributing traits in cluster I. However, intra cluster distance in cluster IV was low and it comprised of the genotypes IR 20 samai and Perunkolai samai. Thus, these two genotypes were observed to share the genetic similarity for the traits recorded. Similar reports on higher and lower intra cluster distances in little millet was reported by Patel *et al.* (2018).

Regarding the cluster means for all traits, cluster I performed superior with the highest mean for plant height, number of basal tillers, panicle length, number of branches per panicle and grain yield per plant. The cluster III had early flowering genotypes with higher 1000 seed weight (Table 6). On comparison with the landraces, the varieties ATL 1 and CO 4 (samai) recorded higher mean for four major yield attributing traits with higher yield (Table 7). Inclusively, among the landraces, Perunsamai recorded higher mean for single plant yield

Table 2. ANOVA for 11 quantitative traits

S.No	Traits	Mean sum of squares		
		Replication	Genotypes	Error
1	Days to 50% flowering	27.08	563.93**	18.35
2	Number of basal tillers	0.14	65.49**	10.88
3	Flag leaf length	0.85	527.10**	65.24
4	Flag leaf width	0.02	1.21**	0.15
5	Peduncle length	11.75	239.12**	83.67
6	Panicle length	0.07	439.93**	59.61
7	Plant height	43.06	6048.84**	193.20
8	Number of branches per panicle	1.80	34.62**	3.33
9	1000 seed weight	0.00	2.85**	0.03
10	Leaf area index	0.00	0.08**	0.01
11	Grain yield per plant	0.55	244.03**	12.53

** significant at 1% level,

Table 3. Distribution of 17 genotypes among different clusters

Clusters	Number of genotypes	Name of genotypes
I	3	ATL 1, CO 4 (samai), Paakulam Karunsamai
II	2	Kolundhan samai, IR 8 samai,
III	5	Chittan samai, Kottathara samai, Siru samai, Jawadhu local samai, Perunsamai
IV	2	IR 20 samai, Perunkolai samai
V	5	Vellai samai, Periya samai, Kalman samai, Kothu samai, Kochchamai

Table 4. Contribution of quantitative characters towards genetic divergence

Traits	% contribution
1000_seed_weight	42.00
Plant height	14.70
Grain yield per plant	8.90
Leaf area index	7.10
Flag leaf length	6.90
Panicle length	5.40
Number of branches per panicle	5.00
Days to 50% flowering	4.20
Number of basal tillers	2.60
Flag leaf width	2.30
Peduncle length	1.00

Table 5. Average inter and intra cluster D² values among five clusters

	C1	C2	C3	C4	C5
C1	4.86	16.72	9.42	12.34	16.57
C2		1.46	5.90	6.84	10.35
C3			1.09	11.02	11.74
C4				0.54	13.78
C5					3.92

Table 6. Cluster mean values for 11 quantitative traits

Traits	I	II	III	IV	V
Days to 50% flowering	62.67	52.00	51.60	58.67	80.66
Plant height	103.13	83.58	86.73	90.12	99.29
Number of basal tillers	7.74	6.00	7.52	6.00	5.75
Flag leaf length	28.77	18.09	21.97	22.22	21.82
Flag leaf width	1.25	0.77	0.94	1.06	0.99
Leaf area index	0.13	0.09	0.09	0.11	0.16
Peduncle length	14.00	12.73	12.86	14.57	16.34
Panicle length	23.60	19.34	23.02	20.22	22.58
Number of branches per panicle	5.57	3.68	4.98	3.82	4.52
Grain yield per plant	18.06	12.27	15.09	12.31	13.99
1000 seed weight	2.49	2.36	2.76	2.27	2.56

and number of branches per panicle. However, the 1000 seed weight was the highest in Jawadhu local samai. In line with these, Chittan samai was found to have an early flowering while Periya samai had the highest mean for plant height. These genotypes produced higher number of tillers than the rest of the genotypes. Among all the collected landraces, Perunsamai and Chittan samai could be identified as promising genotypes for major yield attributing traits like grain yield per plant, number of branches per panicle, number of basal tillers and days to 50% flowering (Table 7). Therefore, these genotypes could be utilized in the future crop improvement programmes for the development of high yielding varieties (Fig. 1).

Further, the D² analysis was carried out for five qualitative traits for the seventeen genotypes. The qualitative traits among landraces serve as an essential tool in characterization as they exhibit a higher variability for qualitative traits (Dixit and Nizar, 2013). As a result of this from the D² analysis, the genotypes were grouped into six clusters (Table 8). Among all the clusters, cluster I and cluster II included four genotypes each respectively. Followed by this, cluster IV and cluster V had three genotypes each respectively. Two genotypes were included in cluster III and a single genotype was grouped under cluster IV and cluster VI respectively. The traits namely, grain colour, panicle compactness and

Table 7. Mean performance of the genotypes for quantitative traits

Genotypes	DFF	PHT	BT	FLL	FLW	PEL	PL	NBP	1000 SW	GYP
ATL 1	48.00	103.60	8.47	27.38	1.21	11.84	24.61	6.12	2.52	20.43
Kolundhan Samai	52.33	91.95	5.53	18.75	0.83	12.10	18.23	4.12	2.28	11.89
Chittan Samai	49.00	96.45	7.27	21.45	0.93	14.46	22.41	4.82	2.84	15.94
IR 20 Samai	57.67	95.67	5.67	22.79	1.03	14.72	22.98	4.12	2.24	13.09
Kottathara Samai	54.67	73.57	6.60	24.57	1.10	11.49	23.88	4.16	2.76	14.68
CO 4 (Samai)	56.33	98.68	7.13	29.27	1.23	13.67	26.07	5.24	2.62	18.62
Vellai Samai	80.67	96.84	6.17	20.78	1.08	16.37	24.06	5.10	2.72	14.39
Periya samai	83.30	112.06	5.83	21.43	0.88	13.33	21.42	4.62	2.66	13.86
IR 8 Samai	51.67	75.20	6.47	17.42	0.71	13.35	20.45	3.24	2.44	12.64
Siru Samai	51.00	77.47	9.73	20.43	0.83	13.45	20.14	5.20	2.60	13.51
Kalman Samai	85.00	84.16	5.47	22.16	1.07	15.35	28.76	4.09	2.56	14.25
Kothu samai	83.00	99.10	5.53	22.06	0.89	16.40	19.42	4.68	2.20	13.82
Paakulam Karunsamai	83.67	107.10	7.63	29.67	1.30	16.50	20.13	5.35	2.32	15.14
Jawadhu_Local_Samai	51.00	89.42	6.81	20.90	0.91	13.17	24.22	4.52	2.86	15.19
Perunkolai_Samai	59.67	84.57	6.33	21.64	1.09	14.41	17.46	3.52	2.30	11.52
Kochchamai	71.33	104.31	5.73	22.68	1.05	20.23	19.24	4.13	2.68	13.64
Perunsamai	52.33	96.73	7.17	22.51	0.95	11.72	24.43	6.21	2.74	16.14
Max	85.00	112.06	9.73	29.67	1.30	20.23	28.76	6.21	2.86	20.43
Min	48.00	73.57	5.47	17.42	0.71	11.49	17.46	3.24	2.20	11.52
Standard deviation	14.41	11.23	1.16	3.33	0.16	2.23	3.03	0.82	0.22	2.25

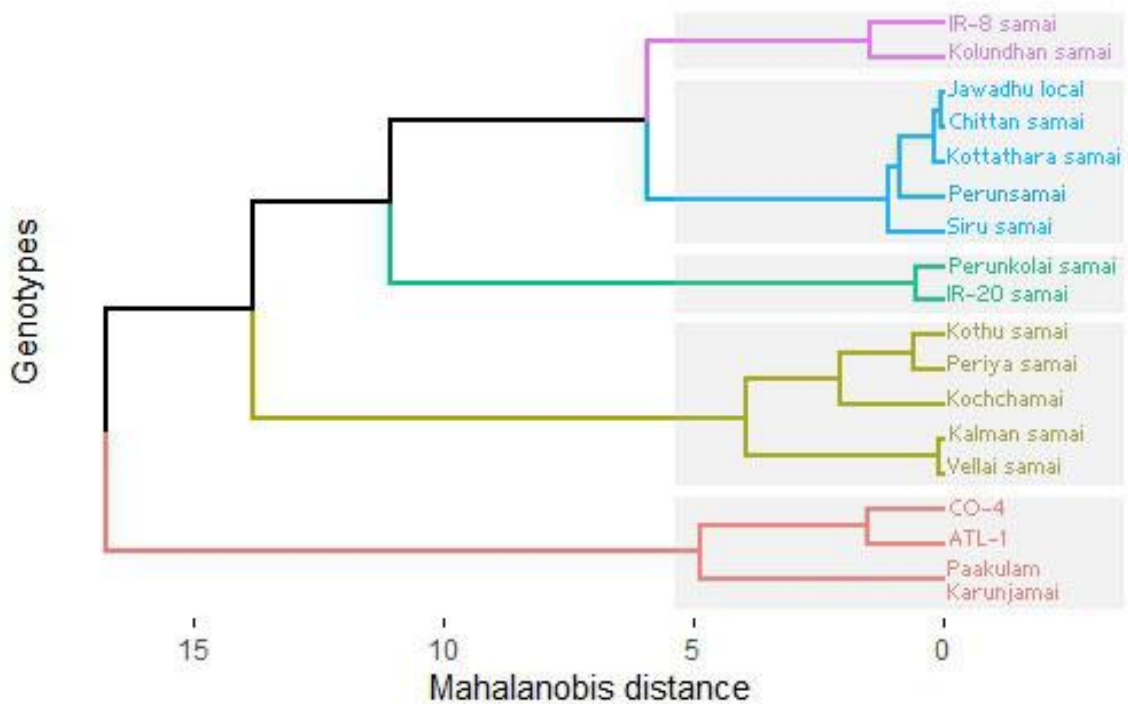


Fig. 1. Dendrogram based on Hierarchical clustering for little millet landraces (Quantitative traits)

Table 8. Distribution of seventeen genotypes among different clusters based on D² analysis with qualitative traits

Clusters	Number of genotypes	Name of genotypes
I	4	ATL-1, C0-4, Kothu samai, Kochchamai
II	4	Kolundhan samai, Chittan samai, Periya samai, Paakulam Karunsamai
III	2	IR 20 samai, Perunkoai samai
IV	3	Kottathara samai, Kalman samai, Perunsamai
V	3	Vellai samai, Siru samai, Jawadhu local samai,
VI	1	IR 8 samai

pigmentation at leaf sheath were the major contributors towards variability. Thus, these traits were the major influencing factors in the clustering of the genotypes into six clusters (Table 12). These qualitative traits could further be evaluated in other trials and could be used as morphological markers for the identification of true to type landraces from the hilly regions. Similar results for qualitative analysis and DUS characterization were also reported by (Natesan *et al.*, 2020)

Genotypes with arched inflorescence, compact panicle and round grains were included in the cluster I and cluster III (Table 9). Among these two clusters, cluster III contained genotypes with pigmentation at the leaf sheath while pigmentation was absent in the genotypes grouped under cluster I. However, the cluster V and cluster VI included genotypes with globose inflorescence and elliptical grains. Moreover, the genotypes with oval seeds were separately grouped under cluster II while the genotype with pubescence at leaf sheath was grouped separately under cluster VI (Table 10). Similar variation for Qualitative traits among little millet genotypes was also recorded by Katara *et al.* (2019).

Regarding the inter cluster distances, maximum inter cluster distance was observed between cluster I and cluster VI. Also, high inter cluster distances were observed between cluster VI and every other remaining cluster (Table 11). This indicates that the genotype grouped under cluster VI was significantly diverse from the other genotypes. The inter cluster distance was the lowest between cluster IV and cluster V indicating a genetic similarity among

the genotypes in these clusters for qualitative traits. The highest intra cluster distance was observed in the cluster I. This indicated the presence of a high degree of variability among the genotypes of the cluster I. The intra cluster distance exhibited by cluster VI was zero as it included only a single genotype. Whereas, it was observed that the intra cluster distance was also recorded zero for the cluster III despite comprising two genotypes. This could be as a result of the similar behaviour of the traits that were recorded across the genotypes in the clusters III (Fig. 2). Among all the genotypes, the landrace IR 8 samai grouped under cluster VI was the most distinctive as it was the only genotype with the pubescence presence on its leaf sheath. Similarly, the landraces, IR 20 samai and Perunkolai samai were distinct from the other genotypes as they scored for the absence for pigmentation at the leaf sheath (Table 13). These distinctive traits could be further exploited in the identification of the specific genotypes from different sources (Katara *et al.*, 2019).

Thus, the present study revealed that the landraces collected from the same geographical locations were grouped into different clusters and it is observed that the geographical diversity did not have a significant influence in the genetic diversity of the genotypes. Similar findings for this variation were also reported by Kumar *et al.* (2010) in finger millet. The major variable traits noted among the landraces in the present study were 1000 seed weight plant height, grain colour, panicle compactness and pigmentation at leaf sheath. The diverse genotypes from the clusters I and II namely ATL 1, CO 4 (samai), Paakulam Karunsamai, Kolundhan samai, IR 8 samai

Table 9. Cluster mean values for six qualitative traits

Traits	I	II	III	IV	V	VI
Inflorescence shape	3.00	4.50	3.00	5.67	5.00	5.00
Panicle compactness	3.00	6.00	3.00	5.67	5.67	7.00
Pigmentation at leaf sheath	9.00	9.00	1.00	9.00	9.00	9.00
leaf sheath pubescence	1.00	1.00	1.00	1.00	1.00	9.00
Seed shape	2.00	4.00	2.00	2.00	2.00	2.00
Grain colour	4.00	5.50	3.00	5.33	2.67	3.00

Table 10. Grouping of the genotypes based on DUS descriptors for qualitative traits

Traits	State	Genotypes
Inflorescence shape	Arched	ATL 1, Kolundhan samai, IR 20 samai, CO 4 (samai), Kothu samai, Perunkolai samai, Kochchamai
	Globose- elliptic	Chittan samai, Vellai samai, Periya samai, IR 8 samai, Siru samai, Kalman samai, Paakulam karunsamai, Jawadhu local samai, Perunsamai
	Diffused	Kottathara samai
Panicle compactness	Compact	ATL 1, IR 20 samai, CO 4 (samai), Kothu samai, Perunkolai samai, Kochchamai
	Intermediate	Kottathara samai, Vellai samai, Periya samai, Kalman samai, Paakulam karunsamai, Jawadhu local samai
	Open	Kolundhan samai, Chittan samai, IR 8 samai, Siru samai, Perunsamai
Pigmentation at leaf sheath	Absent	ATL 1, Kolundhan samai, Chittan samai, Kottathara samai, CO 4 (samai), Vellai samai, Periya samai, IR 8 samai, Siru samai, Kalman samai, Kothu samai, Paakulam Karunsamai, Jawadhu local samai, Kochchamai, Perunsamai
	Present	IR 20 samai, Perunkolai samai
Leaf sheath pubescence	Absent	ATL 1, Kolundhan samai, Chittan samai, IR 20 samai, Kottathara samai, CO 4 (samai), Vellai samai, Periya samai, Siru samai, Kalman samai, Kothu samai, Paakulam Karunsamai, Jawadhu local samai, Perunkolai samai, Kochchamai, Perunsamai
	Present	IR 8 samai
Grain shape	Elliptical	ATL 1, IR 20 samai, Kottathara samai, CO 4 (samai), Vellai samai, Siru samai, Kalman samai, Kothu samai, Jawadhu local samai, Perunkolai samai, Kochchamai, Perunsamai
	Oval	Kolundhan samai, Chittan samai, Periya samai, Paakulam Karunsamai
Grain colour	Straw white/cream	
	Golden yellow	Vellai samai, Kochchamai
	Light Brown	ATL 1, IR 20 samai, IR-8 Samai, Siru samai, Jawadhu local samai, Perunkolai samai
	Brown	Kolundhan samai, Chittan samai, Kottathara samai, Periya samai, Kalman samai, Kothu samai
	Grey	CO 4 (samai), Perunsamai
	Dark Grey	Paakulam Karunsamai

Table 11. Average inter and intra cluster D² values among six clusters

	C1	C2	C3	C4	C5	C6
C1	1.63	9.14	4.52	5.08	3.59	21.38
C2		1.478	10.76	12.29	10.42	21.23
C3			0	14.66	8.79	17.36
C4				1.33	1.98	19.08
C5					0.44	13.94
C6						0

Table 12. Contribution of characters towards genetic divergence

Trait	% contribution
Grain colour	31.08
Panicle compactness	20.27
Pigmentation at leaf sheath	20.27
Leaf sheath pubescence	12.16
Inflorescence shape	9.46
Grain shape	6.76

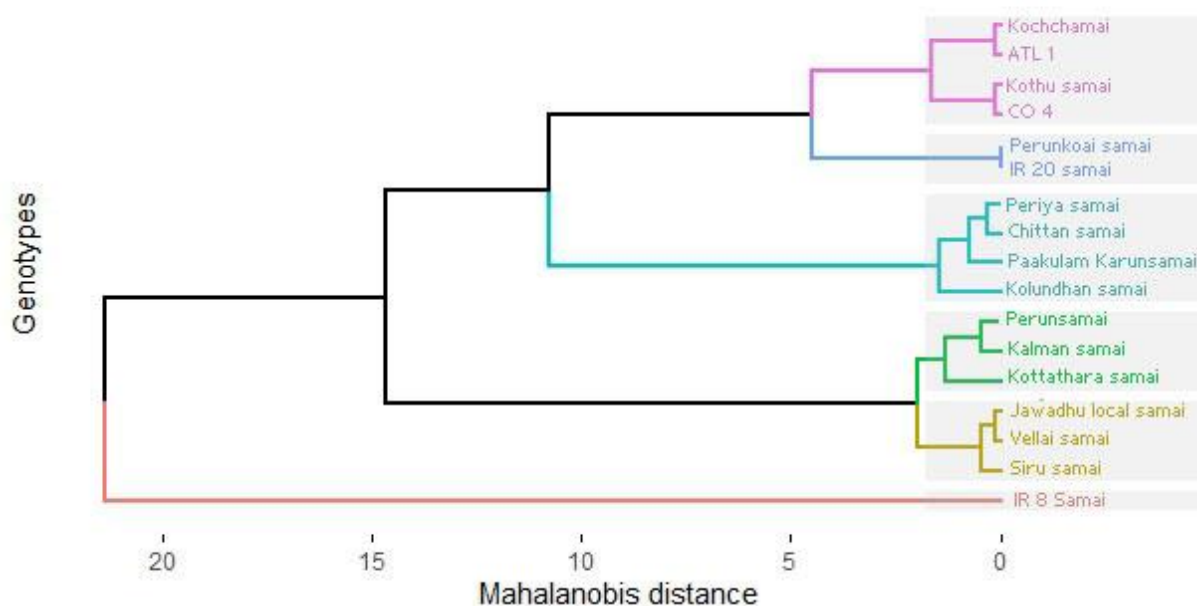


Fig. 2. Dendrogram based on Hierarchical clustering for little millet landraces (Qualitative traits)

Table 13. Recorded Observations for Qualitative Traits

Genotypes	IS	PC	PLS	LSP	GS	GC
ATL 1	3	3	9	1	2	3
Kolundhan samai	3	7	9	1	4	5
Chittan samai	5	7	9	1	4	5
IR 20 samai	3	3	1	1	2	3
Kottathara samai	7	5	9	1	2	5
CO 4 (samai)	3	3	9	1	2	6
Vellai samai	5	5	9	1	2	2
Periya samai	5	5	9	1	4	5
IR 8 Samai	5	7	9	9	2	3
Siru samai	5	7	9	1	2	3
Kalman samai	5	5	9	1	2	5
Kothu samai	3	3	9	1	2	5
Paakulam Karunsamai	5	5	9	1	4	7
Jawadhu local samai	5	5	9	1	2	3
Perunkolai samai	3	3	1	1	2	3
Kochchamai	3	3	9	1	2	2
Perunsamai	5	7	9	1	2	6

PLS: Pigmentation at leaf sheath, IS: Inflorescence shape, PC: Panicle compactness, PLS: Pigmentation at leaf sheath, LSP: Leaf sheath pubescence, GS: Grain shape, GC: Grain colour.

could be utilized as parents in hybridization programmes of little millet (Fig. 3 and 4). The correlation and path analysis for various traits could help us in improving the process of selection and hybridization among the little millet genotypes. The correlation of the traits revealed

significant positive association of number of branches per panicle, panicle length, flag leaf length, flag leaf width and number of basal tillers with grain yield per plant (Table 14). This suggests that these traits could be used as major selection indices for improving the yield

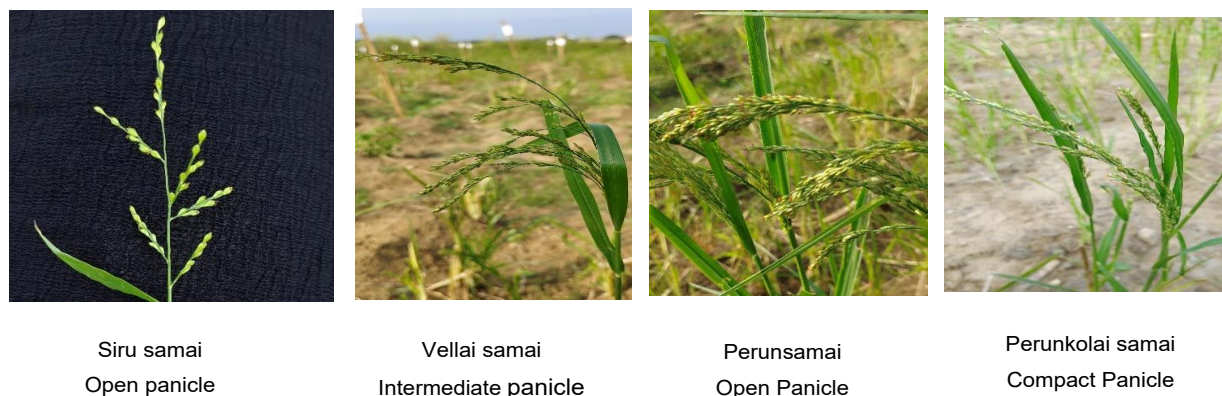


Fig. 3. Panicle compactness of the desirable little millet landraces



Fig. 4. Grain colour variations in the little millet landraces

parameters in little millet. Similar observations for this relationship were also reported by Selvi *et al.* (2014) and Anuradha *et al.* (2017). Among the correlated traits, significant inter correlations were observed between flag leaf length, number of basal tillers and plant height with number of branches per panicle. Significant positive correlation was also observed between flag leaf length and flag leaf width indicating that selection of these inter correlated traits would also have positive influence in the grain yield per plant. Similar results for these observations were also reported by Gopikrishnan *et al.* (2021).

The path analysis exhibited the highest positive direct contribution of plant height, number of basal tillers, flag leaf length, panicle length, and number of branches per panicle towards grain yield per plant. (Table 15). In addition, other traits were also observed to influence the yield parameters indirectly. Flag leaf length had strong association with grain yield per plant *via* plant height and number of branches per panicle and moderately through panicle length. The high indirect effect of number

of branches per panicle on yield was observed through number of basal tillers, panicle length and days to 50% flowering while moderate effect was observed through plant height and flag leaf length. The indirect effect of panicle length was observed as high through number of branches per panicle and low by flag leaf length (Nirmalakumari *et al.*, 2010).

Similarly, the influence of number of basal tillers was observed high through number of branches per panicle and negligible through days to 50% flowering. Flag leaf width had high positive indirect effect on grain yield per plant through plant height, number branches per panicle and flag leaf length and had a moderate effect through panicle length. The direct and indirect association of these traits were also reported by Venkataratnam *et al.* (2019b) and Suryanarayana and Sekhar (2018b). Thus, the traits, number of branches per panicle, flag leaf length, panicle length, number of basal tiller and flag leaf width were observed to have a major influence on grain yield per plant through direct and

Table 14. Correlation of morphological traits to Grain yield per plant

	DFF	PHT	BT	FLL	FLW	PEL	PL	NBP	1000 SW	GYP
DFF	1.00									
PHT	0.43	1.00								
BT	-0.46	-0.13	1.00							
FLL	0.13	0.44	0.31	1.00						
FLW	0.24	0.36	0.14	0.89**	1.00					
PEL	0.63**	0.36	-0.33	0.06	0.21	1.00				
PL	0.01	-0.04	0.05	0.32	0.34	-0.24	1.00			
NBP	-0.06	0.48*	0.59*	0.54*	0.38	-0.20	0.35	1.00		
1000 SW	-0.22	-0.05	0.26	-0.03	-0.02	-0.14	0.49*	0.28	1.00	
GYP	-0.22	0.37	0.48*	0.69**	0.54*	-0.25	0.61**	0.76**	0.39	1.00

Table 15. Path analysis of morphological traits to Grain yield per plant

	DFF	PHT	BT	FLL	FLW	PEL	PL	NBP	1000 SW	GYP
DFF	-0.38	0.39	-0.32	0.09	-0.03	-0.09	-0.03	0.17	-0.03	-0.22
PH	-0.16	0.89	-0.11	0.22	-0.05	-0.05	-0.03	-0.32	-0.01	0.37
BT	0.18	-0.14	0.69	0.15	-0.02	0.06	0.06	-0.48	0.01	0.48*
FLL	-0.08	0.44	0.23	0.44	-0.12	-0.01	0.26	-0.41	-0.02	0.69**
FLW	-0.08	0.34	0.10	0.43	-0.12	-0.03	0.26	-0.32	-0.01	0.54*
PEL	-0.24	0.35	-0.31	0.04	-0.03	-0.13	-0.17	0.22	-0.02	-0.25
PL	0.01	-0.04	0.06	0.16	-0.04	0.03	0.73	-0.31	0.04	0.61**
NBP	-0.48	0.29	0.46	0.25	-0.19	-0.21	0.31	0.32	0.02	0.76**
1000 SW	0.15	-0.13	0.11	-0.10	0.02	0.03	0.36	-0.20	0.07	0.39

DFF: Days to 50% flowering, PH: Plant height (cm), BT: Number of basal tillers, FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), PEL: Peduncle length (cm), PL: Panicle length (cm), NBP: Number of branches per panicle, 1000 SW: 1000 seed weight (g), LAI: Leaf area index, GYP: Grain yield per plant (g), PLS: Pigmentation at leaf sheath, IS: Inflorescence shape, PC: Panicle compactness, PLS: Pigmentation at leaf sheath, LSP: Leaf sheath pubescence, GS: Grain shape, GC: Grain colour.

indirect parameters. Hence, these traits can be used as major selection indices for improvement of yield in little millet breeding programmes.

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