Insights into genetic variability parameters and character associationamong agro-morphological and biochemical traits in little millet (*Panicumsumatrense* Roth. Ex. Roem and Schultz)

ABSTRACT

A set of 64 little millet genotypes was evaluated for their genetic variability parameters, principal components, and their contribution to total variance using seven agro-morphological and four biochemical traits in alpha lattice design with two replications. The mean performance revealed the presence of substantial variability for the characters studied. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimated ranged from 18.28% to 43.75% and 10.06% to 42.75%, respectively. Even though PCV was found to be significantly greater than GCV for the number of tillers, a slightly higher PCV over GCV was observed for all the other traits, suggesting a limited environmental influence for the majority of the traits. High heritability was observed for all agro-morphological and biochemical traits (84.00-94.00%), except for the number of tillers (42.00%), which exhibited moderate heritability. Genetic advance as a percentage of mean (GAM) was high for most of the traits, viz., days to 50% flowering, plant height, panicle length, single plant yield, test weight, grain protein, iron, zinc, and calcium contents. suggesting the predominance of additive gene action and the greater possibility of genetic improvement through simple phenotypic selection. Majority of the contribution towards the total divergence by days to 50% flowering, days to maturity, plant height, number of tillers, panicle length, single plant yield, and grain calcium content coupled with significant and positive correlations of majority of grain yield components with grain yield suggestedthat these traits are the key drivers of variability that could be exploited through a little millet improvement program.

Keywords:*little millet, genetic variability, grain yield, biochemical traits, principal components, character association*

1. INTRODUCTION

The cultivation of millets is gaining prominence during the International Year of Millets due to efforts on the promotion of their cultivation, climate-resilient nature, and awareness of their health benefits. Moreover, in the current scenario of climate change, these millets can also fit in as a contingent crop due to the limited availability of water and drought situations. Hence, the demand for millets will increase in the coming years, and there is an immense need to increase the production of millets. This could be achieved by increasing the area of cultivation under millets and by increasing the productivity of millets through the development of high-yielding cultivars. Small millets are grown under diverse environmental conditions, and efforts to improve through recombination breeding over the years have been limited due to the difficulty of hybridization due to the small size of the spikelet. Emasculation and crossing techniques for small millets have been reported, and improvements have been made in recent years (reviewed by Nagaraja [1]), Hence, there is an immense need for the identification of genetically diverse and desirable parents for use in recombination breeding programs.

Little millet (*Panicumsumatrense* Roth. Ex. Roem and Schultz) is an indigenous crop to India that is predominantly cultivated in the eastern parts of our country. It is widely grown in the states of Madhya Pradesh, Chhattisgarh, Tamil Nadu, Karnataka, Odisha, Andhra Pradesh, Jharkhand, and Bihar, forming an integral part of tribal agriculture. The crop is highly tolerant to moisture stress and drought, and to some extent to water logging, which offer ample scope for its adoption in diverse situations [2]. The grains are rich in dietary fiber, antioxidants, phytochemicals, and polyphenols, which exhibit positive impacts on human health [3].

Germplasm accessions are important resources for any crop improvement program since they harbor valuable genes or alleles for important target traits. A systematic evaluation of germplasm accessions or breeding lines for grain yield and biochemical traits is an essential step in any crop breeding program, which helps in the selection of suitable donors for further use in the recombination breeding program. Even though a good number of germplasms is conserved in the Genebanks at All India Coordinated Small Millets Improvement Project (AICSMIP), Bengaluru, and International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, very few studies have been reported on the evaluation of agro-morphological traits [4, 5, 6] and grain nutritional traits [7, 8, 9].

Characterization of little millet genotypes using agro-morphological and biochemical traits will help in the selection of desirable parents for hybridization for recombination, culminating in the development of high-yielding nutrition-rich cultivars. Hence, this study was executed with the objectives of assessing the genetic variability parameters to determine the true potential of genotypes and understanding the number and nature of principle components and their contribution to total variance to decide on effective selection criteria.

2. MATERIALS AND METHODS

The plant material for this study comprised 64 little millet genotypes, which included 49germplasm accessions and 15released varieties (K-1, Paiyur-1, Paiyur-2, TNAU-63, Co-2, Co-3, Co-4, ATL-1, CG-Kutki-01, CG-Kutki-02, CG-Kutki -03, JK-8, CLMV-1, BL-6 and DHLM-36-3). When a more number of genotypes are used for evaluation, the replication size increases and soil heterogeneity poses a problem. Hence, to control the experimental error, alpha lattice design is used, which is considered as more powerful in controlling experimental error than randomized complete blocks design.The above mentioned genotypes were grown in the research farm at the ICAR - Indian Institute of Millets Research, Hyderabad, Telangana, India, during rabi 2022-23 in Alpha-Lattice design with eight blocks of eight genotypes per block in two replications. A healthy crop was raised by following the recommended agronomic practices and plant protection measures. The observations were recorded on five randomly chosen plants for seven yield-related characters, viz., plant height, number of tillers per plant, panicle length, test weight, and single plant yield from both replications, except for days to 50% flowering and days to maturity, which were recorded on a plot basis. Biochemical analysis (grain protein and minerals) was performed using the dehulled grains of all 64 little millet genotypes. Grain protein content was determined using the standard Macro Kjeldahl method [10] while grain iron, zinc, and calcium contents were determined by the standard method of microwave digestion and atomic absorption spectrometry [11].

The analysis of variance for the Alpha-Lattice Design was worked out as suggested by Patterson and Williams [12]. In this design, the sum of squares due to blocks will be bifurcated into sum of squares due to replications and sum of squares between blocks within replications. The statistical procedure as suggested by Patterson and Williams (1976) was followed as given below:

$$y_{ijk} = \mu + t_i + r_j + b_{jk} + e_{ijk}$$

where y_{ijk} denotes the value of observed trait for the i^{-th} treatment received in the k^{-th} block within j^{-th} replicate (superblock), t_i is the fixed effect of the i^{-th} treatment (i = 1,2,…..t); r_j is the effect of the j^{-th} replicate (superblock) (j = 1,2,…,r); b_{jk} is the effect of the k^{-th} incomplete block within the j^{-th} replicate (k = 1,2,…s) and e_{ijk} is an experimental error associated with the observation of the i^{-th} treatment in the k^{-th} incomplete block within the j^{-th} complete replicate.The variances at the genotypic and phenotypic levels and genetic advance (GA) were calculated according to Burton [13] and Johnson et al. [14], respectively. Phenotypic and genotypic coefficients of variation were analyzed according to Falconer [15]. Heritability in the broad sense for grain yield and its attributing traits as well as biochemical traits was worked out as suggested by Hanson et al. [16]. A principal component analysis (PCA) was performed on agro-morphological and biochemical traits to identify the variables contributing the most to the total variance.The analysis of agro-morphological and biochemical data for the analysis of variance through alpha lattice design was performed using the R package Agricolae [17] while estimation of genetic variability parameters and correlation coefficient analysis were performed by the package Variability [18]. Principal component analysis was performed using the R package FactoMineR [19], whereas the Factoextra [20] package was used for the visualization of the data.

3.RESULTS AND DISCUSSION

3.1 Mean Performance

About 64 little millet genotypes, including germplasm accessions and released varieties, were evaluated for seven agro-morphological and four biochemical characters. The analysis of variance revealed significant differences between the genotypes for all the agro-morphological and biochemical traits studied (Table 1). The mean performance of the little millet genotypes revealed the presence of wide variation for all the seven agro-morphological and four biochemical traits. Early flowering and early maturity were observed in JK-8 (51.50 days) and IC048304237 (82.00 days), respectively, whereas late flowering and late maturity were recorded in IPMR-1042 (77.00 days) and IPMR-1036 (113.50 days), respectively. The tallest genotype was IPMR-897 (159.95 cm), whereas the shortest genotype was IPMR-718 (49.30 cm). The genotype IMPR-767 (16.30) had more tillers, while the genotype GPMR-252 (7.00) had a lesser number of tillers. The longest panicle was observed in IPMR-712 (61.90 cm), while the shortest panicle was found in CG-KUTKI-03 (9.40 cm). Lower test weight was noticed in the genotypes IPMR-825, IPMR-1040, IPMR-97, and IC0483193 (1.55 g) while higher test weight was observed in IC0483133 and IPMR-807 (3.65 g). With respect to single plant yield, the genotypes IPMR-449 and IC0483042 (3.05 g) recorded the lowest, while the genotype IPMR-855 (18.55 g) recorded the highest. With respect to grain yield and its contributing traits, the wide variation observed in this study was also reported in other studies [21, 6].

High grain protein, iron, zinc, and calcium contents were observed in IC048330 (18.35%), IPMR-718 (39.20 ppm), IC0483302 (40.20 ppm), and IPMR-983 (206.80 ppm), respectively, while low grain protein, iron, zinc, and calcium contents were observed in IPMR-1035 and IPMR-1040 (7.00%), IPMR-1035 (16.05 ppm), IPMR-891 (18.50 ppm), and IPMR-825 (90.90 ppm), respectively. With respect to the micro-nutrients, the concentration of grain zinc (18.50 ppm to 40.20 ppm) was greater than that of iron (16.50 ppm to 39.20 ppm). Similarly, the calcium content (90.90 ppm to 206.80 ppm) in the grain was higher than the zinc (18.50 ppm to 40.20 ppm) and iron (16.50 ppm to 39.20 ppm) contents. Wide variation was also observed for the micro-nutrients and the concentration of grain zinc was greater than that of iron, which is in concurrence with the results reported by Kundgol et al. [22]. Similarly, the calcium content in the grain was higher than the zinc and iron contents, and these observations are similar with those reported earlier [7, 23, 24]. Based on the mean performance of genotypes for agro-morphological characters, the promising donor genotypes for early flowering (JK-8), early maturity (IC0483042), tall plant type (IPMR-897), more number of tillers (IMPR-767), long panicle (IPMR-712), more test weight (IC0483133 and IPMR-807), and high single plant yield (IPMR-855) were identified. Promising donor genotypes for nutritional characters such as high protein (IC0483302) and zinc (IC0483302) contents, iron (IPMR-718), and calcium contents (IPMR-983) were also identified. These genotypes exhibit significant potential for further breeding efforts.

3.2Genetic Variability

The estimates of PCV ranged from 18.28% (zinc content) to 43.75% (single plant yield), while those of GCV ranged from 10.06% (days to maturity) to 42.75% (single plant yield). Among the characters studied, high PCV and GCV were exhibited by the majority of the traits except days to 50% flowering, days to maturity, number of tillers, grain zinc, and calcium contents, highlighting the presence of substantial variability for these traits. In this study, PCV was substantially greater than GCV for the number of tillers, indicating a strong environmental influence, while it was slightly greater than GCV for the remaining yield characters and all four biochemical characters, highlighting a limited influence of environment in the expression of these characters. Similar observations were reported earlier for grain yield and its components in little millet [25, 26, 27]. Substantially greater PCV than GCV for the number of tillers, highlighted a strong influence of environment in its expression. However, PCV slightly greater than GCV for the remaining yield-related characters and all four biochemical characters, highlighted a limited influence of environment in their expression. Similar to this study, PCV was reported to be greater than GCV for grain yield and its component traits in earlier studies also [28, 25, 26]. The genetic variability parameters for agro-morphological and biochemical traits are given in Table 2.

High heritability was observed for all the agro-morphological and biochemical traits in the present investigation, except for the number of tillers, which recorded a moderate heritability. This observation revealed the predominance of genetic variation with a limited influence of environment in all the characters except the number of tillers, which will aid in the effective selection of genotypes for all the traits except the number of tillers. These results are in agreement with earlier reports in little millet by Selvi et al., [28] for 1000-grain weight, Jyothsna et al., [29] for days to 50% flowering and grain yield, and Matere et al., [30] for number of tillers, panicle weight, seed yield, and iron content. High heritability for grain yield and its component traits was also reported earlier [26, 4, 31]. High estimates of GAM were exhibited by days to 50% flowering, plant height, panicle length, single plant yield, test weight, and grain protein, iron, zinc, and calcium contents. Similar to the high estimates of GAM in this study, some of the recent reports also revealed high estimates of GAM for grain yield and its component characters [26, 30, 31], and iron content [30]. High heritability coupled with high GAM was exhibited by all the characters studied except days to maturity and number of tillers, which suggested the involvement of additive gene action in the inheritance of grain yield and the majority of its component characters. Therefore, the genetic improvement of grain yield and its component characters could be accomplished by employing a simple phenotypic selection.

3.3Principal Components

Principal component analysis (PCA) is performed to reduce the dimensionality of the dataset while retaining most of the variance. The analysis revealed 11 principal components (PCs), of which, the first three principal components explained 76.02% of the total variance. In a similar study in little millet involving grain yield and nutritional traits, Patel et al., [32] reported that the first two principal components accounted for 92.14% of the total variation. However, in another study involving grain yield and its component traits, Gopikrishnan et al., [33] reported that the first three principal components contributed about 69.10% of cumulative variance.

Eigenvalues are the coefficients of the eigenvectors and they reflect the importance of directional data. Eigenvalue associated with each PCs indicates the amount of variation in the data set it explains.Eigenvalues, proportion of variance, and cumulative proportion of variance in different principal components are presented in Table 3. PC1 was positively associated with variables such as days to 50% flowering (0.3580), days to maturity (0.3688), plant height (0.3181), panicle length (0.1860), and single plant yield (0.3338), indicating their strong influence in PC1, while negatively associated with number of tillers (-0.1916), test weight (-0.2355), protein (-0.3730), Fe (-0.3189), and Zn contents (-0.3534). PC 4 was positively associated with panicle length (0.7069), plant height (0.0873), test weight (0.0783), and single plant yield (0.0621) and negatively associated with days to 50% flowering (0.2035), days to maturity (-0.1549), number of tillers (0.2242), protein content (0.0889), iron content (0.0057), zinc content (0.1556), and calcium content (0.5787). Other principal components show varying degrees of association with different variables, suggesting diverse underlying relationships. The positive association of PC1 with days to 50% flowering, days to maturity, plant height, panicle length, and single plant yield, indicated that it might be allied with growth-related factors, as genotypes with positive scores appear to have growth-promoting traits. Also, PC 4, to some extent contribute to the growth-related factors due to their positive scores for panicle length, plant height, test weight, and single plant yield. Interestingly, PC1 to PC11 follow a similar pattern of decreasing proportions of variance and eigenvalues, indicating that they capture a progressively smaller amount of variance compared to the earlier principal components.

The PCA is graphically depicted as a bi-plot that combines both the scores (data points projected PCs) and loadings (contribution of each variable to the PCs) into a single plot, which reveals inter-unit distances and clustering of units along variances and correlations of variables.The bi-plot analysis (Figure 1) categorized the genotypes into groups over four quadrants based on seven agro-morphological and four biochemical traits. All the 64 little millet genotypes were dispersed across the four quadrants, highlighting the presence of substantial genetic variability. A similar pattern of dispersion of little millet millets genotypes was reported recently [32] while evaluation for grain yield and biochemical traits. The genotypes grouped in the bottom right quadrant were found to be promising for grain yield ant its component traits whereas those grouped in the bottom left quadrant were found to be promising for the nutritional traits, except the calcium content. Also, the genotypes in the bottom left quadrant were found to be promising for grain yield component traits viz., number of tillers and test weight. The bi-plot further revealed that the genotypes IPMR 712, IPMR 807, and IPMR 980 were the most divergent among the 64 genotypes, which can serve as potential parents in the little millet breeding programs due to their differences in agro-morphological and biochemical traits from other genotypes. The genotype IPMR 1037 was promising for plant height, CG-Kutki-03 was promising for test weight, GPMR 252 was promising for single plant yield, IC0483133 was promising for protein content, ATL-1 was promising for iron content, IC0483040 was promising for zinc content, and GPMR 960 was promising for calcium content. Hence, the deployment of the diverse genotypes and the promising donors for important yield and nutritional traits in the crossing program will help in the generation of segregating material with wider variability helping the crop breeder to select desirable genotypes for further advancement towards the development of high-yielding nutritional-rich little millet cultivars.

3.4Character Association

The appropriate knowledge of inter-relationships between grain yield components can help the plant breeders in deciding the selection criteria for achieving the genetic improvement in grain yield. In addition, understanding of the inter-relationships between biochemical characters can help in focusing the selection for the improvement of nutritional trait(s). The genotypic and phenotypic correlation coefficients for grain yield and its components as well as biochemical traits are given in Table 4. The characters such as days to maturity (r_p = 0.761**, r_g = 0.844**) followed by days to 50% flowering (r_p = 0.687**, r_g = 0.766**), plant height (r_p = 0.587**, r_g = 0.621**) and panicle length (r_p = 0.469**, r_g = 0.508**) recorded a significant and positive correlation with single plant yield at both phenotypic and genotypic levels and calcium content (r_p = 0.226**) at phenotypic level, indicating that these characters play an important role in selection for the improvement of grain yield. On the contrary, protein content (r_p = -0.748**, r_g = -0.831**), zinc content (r_p = -0.704**, r_g = -0.773**), iron content (r_p = -0.429*, r_g = -0.471**) and test weight (r_p = -0.547**, r_g = -0.596**) exhibited a significant negative correlation with single plant yield at phenotypic and genotypic level and number of tillers (r_g = 0.508*) at genotypic level. With respect to biochemical traits, protein content exhibited a significant positive correlation with zinc content (r_p = 0.854**, r_g = 0.897**) and iron content (rp = 0.760**, rg = 0.784**) at phenotypic and genotypic levels. A significant positive association of iron content was observed with zinc content (r_p = 0.733**, r_g = 0.761**) whereas a significant negative association was noticed with calcium content (r_p = -0.567**, r_g = -0.618**), both at phenotypic and genotypic levels. Similar results for phenotypic and genotypic correlations with grain yield were reported by Ashok et al. [34] for days to 50% flowering and days to maturity and Gopikrishnan et al. [33] for days to 50% flowering, plant height, number of productive tillers and panicle length in little millet.

In the present study, the genotypic correlation coefficients were relatively higher than phenotypic correlation coefficients for all the agro-morphological and biochemical traits, which indicated the presence of strong inherent association among them and a very limited role of environment in their phenotypic expression. Grain yield displayed a significant and positive correlation with the traits such as days to maturity followed by days to 50% flowering, plant height and panicle length at the phenotypic and genotypic levels. Conversely, a significant negative association between grain yield and the traits such as protein content, zinc content, iron content and test weight in the present study revealed that the grain yield improvement could be achieved through the selection of effective target traits such as plant height and panicle length, since these characters exhibited significant positive correlations with single plant yield. However, simultaneous improvement of grain yield and grain nutritional characters may not be possible due to the presence of negative correlation between them. In line with this study, a significant and positive correlation of the traits such as days to 50% flowering, days to maturity, plant height, number of productive tillers and panicle length with grain yield were reported earlier in this crop [35, 36].

4. CONCLUSION

The study revealed the presence of significant variability and a substantial genetic influence on traits such as plant height, panicle length, test weight, single plant yield, protein content, and Fe content. In addition, high heritability combined with high genetic advance as per cent of mean was exhibited by plant height, panicle length, test weight, single plant yield, Fe content, Zn content, and Ca content, indicating the predominance of additive gene action with minimal impact of environmental factors. Therefore, prioritizing the selection of these traits in breeding materials has the potential to result in genetic improvements. Principal component analysis revealed that key growth-related characters such as days to 50% flowering, days to maturity, plant height, number of tillers, panicle length, and single plant yield are the key drivers of variability, which can be exploited in the genetic improvement of little millet. Since majority of the yield components also exhibited significant and positive correlations with grain yield, giving priority for these traits in selection process will help in the genetic improvement of little millet. However, negative correlations of biochemical traits with grain yield will hinder the simultaneous improvement of grain yield and nutritional quality.

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Table 1 Analysis of variance of agro-morphological and biochemical traits for the little millet genotypes

Source of Variation	**df**	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Number of tillers**	**Panicle length**	**Single plant yield**	**Test weight**	**Protein content**	**Iron content**	**Zinc content**	**Calcium content**
Replication	1	1.12	13.78	1.73	4.88	4.13	0.20	0.03	0.37	39.71*	22.86*	47.78
Genotype	63	113.36**	206.08**	1409**	7.65**	124.18**	30.08**	0.51**	13.65**	54.30**	50.29**	1272**
Block	14	9.76	18.69	48.50	4.15	3.73	0.87	0.04	1.10	3.67	2.09	39.27
Error	49	11.86	12.45	59.76	2.73	6.40	0.78	0.04	0.68	3.54	2.60	52.24

df - degrees of freedom * Significant at $P < 0.05$, ** Significant at $P < 0.001$.

Table 2 Genetic variability parameters for agro-morphological and biochemical traits in little millet genotypes

Traits	PCV (%)	GCV (%)	Heritability %	G A	G A M
Days to 50% flowering	24.04	11.21	84.00	13.66	21.21
Days to maturity	21.31	10.06	87.00	18.88	19.37
Plant height	24.04	23.08	92.00	51.42	45.66
Number of tillers	21.31	13.97	42.00	2.04	18.87
Panicle length	27.82	26.55	91.00	15.12	52.19
Test weight	21.89	20.28	85.00	0.92	38.72
Single plant yield	43.75	42.75	94.00	7.67	85.43
Protein content	23.69	22.37	89.00	4.93	43.53
Iron content	21.78	20.39	87.00	9.71	39.33
Zinc content	18.28	17.40	90.00	9.58	34.12
Calcium content	19.58	18.83	92.00	49.00	37.32

PCV – phenotypic coefficient of variation, GCV – genotypic coefficient of variation, GA – genetic advance, GAM – genetic advance as percentage of mean.

Table 3 Eigenvalues, proportion and cumulative proportion of variances explained in different principal components in little millet

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Days to 50% flowering	0.3580	-0.1853	0.1511	-0.2035	0.1248	0.0734	-0.4134	0.3854	-0.0053	0.1313	0.6446
Days to maturity	0.3688	-0.2046	0.0393	-0.1549	0.0690	0.1606	-0.3603	0.2794	-0.0882	-0.0645	-0.7391
Plant height	0.3181	-0.1915	0.1246	0.0873	0.1449	-0.8550	-0.0694	-0.2702	0.0756	0.0268	-0.0519
Number of tillers	-0.1916	-0.1749	-0.7674	0.2242	0.3338	-0.1760	-0.0424	0.3298	-0.1583	0.1241	0.0113
Panicle length	0.1860	-0.4272	0.2046	0.7069	-0.2482	0.1147	0.2999	0.2646	0.0228	-0.0709	0.0329
Test weight	-0.2355	-0.1730	0.4034	0.0783	0.8301	0.1756	0.1331	-0.0728	0.0152	0.0236	-0.0453
Single plant yield	0.3338	-0.2814	-0.2685	0.0621	0.0225	0.3693	-0.0315	-0.6362	-0.0413	0.4328	0.0415
Protein content	-0.3730	-0.0556	0.1471	0.0889	-0.1647	-0.0716	-0.2582	0.1392	0.5151	0.6493	-0.1521
Iron content	-0.3189	-0.4510	-0.1133	0.0057	-0.0859	0.0730	-0.4204	-0.2563	0.3246	-0.5607	0.0846
Zinc content	-0.3534	-0.0956	0.2442	0.1556	-0.1775	-0.0832	-0.3676	-0.1222	-0.7575	0.1405	0.0070
Calcium content	0.1751	0.5909	-0.0208	0.5787	0.1734	0.0952	-0.4532	-0.1077	0.1203	-0.1181	0.0145
PV (%)	55.96	11.02	9.04	7.60	5.76	3.50	2.94	1.67	1.09	0.75	0.32
CPV (%)	55.96	66.98	76.02	83.98	89.74	93.24	96.18	97.85	98.94	99.68	100.00

PV – proportion of variance, CPV – cumulative proportion of variance

Table 4. Correlation coefficients for agro-morphological and biochemical traits amonglittle millet genotypes

		Days to 50% flowering	Days to maturity	Plant height	Number of tillers	Panicle length	Test weight	Protein content	Iron content	Zinc content	Calcium content	Single plant yield
Days to 50% flowering	**P**	1.000	0.945**	0.684**	-0.397**	0.343**	-0.375**	-0.716**	-0.540**	-0.677**	0.205*	0.687**
	G	1.000	0.961**	0.769**	-0.650**	0.406**	-0.441**	-0.833**	-0.648**	-0.772**	0.182	0.766**
Days to maturity	**P**		1.000	0.671**	-0.350**	0.384**	-0.427**	-0.772**	-0.544**	-0.723**	0.223**	0.761**
	G		1.000	0.755**	-0.565**	0.448**	-0.502**	-0.870**	-0.626**	-0.799**	0.240	0.844**
Plant height	**P**			1.000	-0.260**	0.434**	-0.235**	-0.651**	-0.517**	-0.582**	0.238**	0.587**
	G			1.000	-0.483**	0.492**	-0.257*	-0.708**	-0.568**	-0.637**	0.259**	0.621**
Number of tillers	**P**				1.000	-0.167	0.963	0.281**	-0.429**	0.217*	-0.135	-0.124
	G				1.000	-0.249*	0.107	0.437**	0.674**	0.347**	-0.247*	-0.249*
Panicle length	**P**					1.000	-0.105	-0.303**	-0.180*	-0.212*	0.172	0.469**
	G					1.000	-0.121	-0.319*	-0.186	-0.247*	0.182	0.508**
Test weight	**P**						1.000	0.522 **	0.448 **	0.525 **	-0.475**	-0.547**
	G						1.000	0.610**	0.508 **	0.592 **	-0.523**	-0.596**
Protein content	**P**							1.000	0.760**	0.854**	-0.355**	-0.748**
	G							1.000	0.784**	0.897**	-0.416**	-0.831**
Iron content	**P**								1.000	0.733**	-0.567**	-0.429**
	G								1.000	0.761**	-0.618**	-0.471**
Zinc content	**P**									1.000	-0.327**	-0.704**
	G									1.000	-0.383**	-0.773**
Calcium content	**P**										1.000	0.226*
	G										1.000	0.220
Single plant yield	**P**											1.000
	G											1.000

* Significant at 5% level of probability ** Significant at 1% level of probability

P – Phenotypic G – Genotypic.

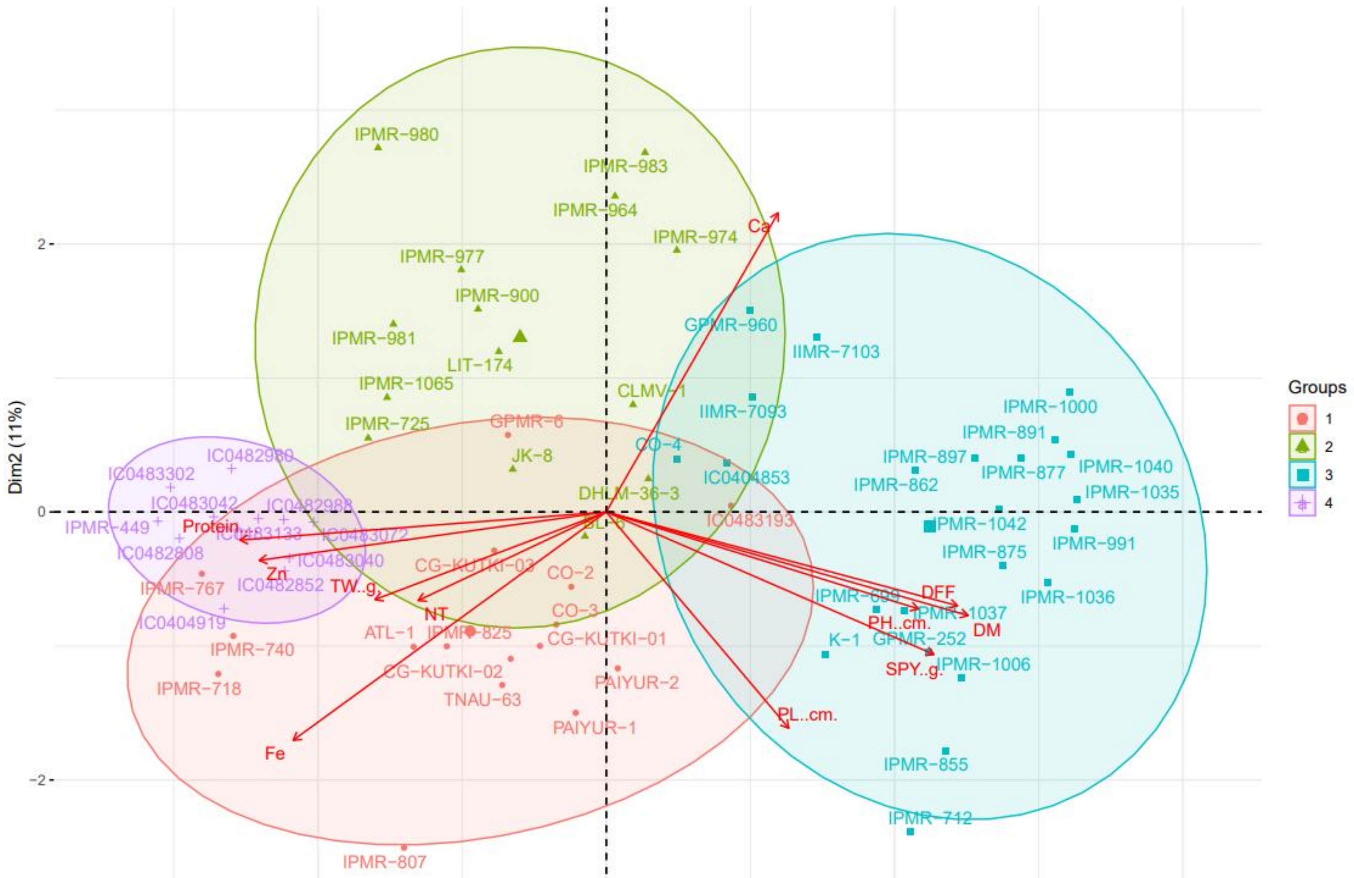

Fig. 1 Bi-Plot representing the similarity or differences between the genotypes

DFF - days to 50% flowering; DM – days to maturity; PH – plant height; NT – number of tillers; PL – panicle length; TW – test weight; SPY – single plant yield; Protein – protein content; Fe – iron content; Zn – zinc content; Ca – calcium content