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Assessment of genetic diversity for yield and quality traits of rice landraces of Telengana by multivariate analyses

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Abstract

The present investigation on 'Assessment of genetic diversity for yield and quality traits of rice landraces of Telengana by multivariate analyses', was conducted during the *kharif-2021*, which characterize 23 rice landraces with 21 yield and quality traits. All the genotypes were significantly different for every trait. The genetic variability studies emulated, high PCV and GCV was absorbed for the traits followed, number of fertile spikelets per panicle, elongation ratio, kernel length breadth ratio, protein content, water uptake ratio, harvest index, number of effective tillers per plant, alkali spread value, biological yield and grain yield per plant. High heritability coupled with high genetic advance was observed on the following characters *viz.*, harvest index, grain breadth, alkali spread value, protein content, number of fertile spikelets per panicle, grain yield per plant, grain length, biological yield, plant height, kernel length breadth ratio, amylose content and thousand grain weight. It explains that there is scope of improvement through selection in these characters. Principal Component Analysis revealed usage of Akshaya ponni, Nagara, Halla batta, Gadakadhiya Mahi, Aashudhee, Ghalima and Kukuda Munde would be rewarding in crop improvement for good yield, likewise, Bhairojlu, Daddigha, Gadakadhiya Mahi, Kaala Jeera, Krishtampeta gold and Kumar Gorla would be rewarding in improvement of quality traits.

Keywords: PCV, GCV, Heritability, selection and principal component analysis

Introduction

For around half of the world population, rice is considered to be primary source on energy intake. Over a hundred of nations farm rice on around 158 million hectares, which yielding 470 million tons of white rice per year (Ricepedia, IRRI, Bollinedi *et al.*, 2020) ^[4]. Rice landraces have been farmed and nourished since the dawn of civilization, and they play a critical role in livelihood and food security. Rice landraces have a wide range of agromorphological characteristics, and some of them show promise in terms of yield. Some rice landraces provide surprising health benefits such as protection against several chronic diseases such as cardiovascular disease, type-2 diabetes, obesity, cancer and have the potential to heal certain disorders like haemorrhage, diarrhoea, fertility, fever and many more (Okarter and Liu 2010, Sanghamitra *et al.*, 2017, Hedge *et al.*, 2013, Pokhrel *et al.*, 2020) ^[14]. Due to the increasing awareness of health benefits in rice landraces, there is a rising need for the rice variety with good cooking and nutritive qualities (Asghar *et al.*, 2012) ^[2]. There always been a need for increase in the food production to curtail the hunger of raising human population. Though the rice landraces have a low yielding potential, they are believed to have more local adaptability and better-quality traits (Tiwari *et al.*, 2018) ^[21]. In order to use landraces in breeding efforts, the comprehend genetic variability of the genotypes has to be studied. The estimation of genetic variability is the fundamental principle in the crop improvement program (Madhubabu *et al.*, 2020) ^[11]. The genetic parameters like coefficient of variance, heritability and genetic advance are the excellent tools for effective selection in breeding program (Behera *et al.*, 2018, Gyawali *et al.*, 2018) ^[3, 9]. Principal component analysis is a statistical technique for selecting superior lines in a diverse population. It is used for transforming a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components without losing important information of

original data (Nachimuthu *et al.*, 2014, Pachauri *et al.*, 2017) [12, 15]. The results will then be used as selection criteria for improvement of grain yield in rice land races and to assist the future breeding programs for yield improvement and to identify the elite genotypes for yield and quality parameters.

Materials and Methods

The present investigation on ‘Assessment of genetic diversity for yield and quality traits of rice landraces of Telengana by multivariate analyses’, was conducted during the *kharif*-2021 at Bagusala farm, Centurion University of Technology and Management, Paralakhemundi, Odisha. In terms of topography and fertility, the experimental area was rather uniform. Coordination is the location. 84.139883°E, 18.806853°N. The experimental material consists of 23 germplasm lines of rice genotypes obtained from Seed Farms from Telangana. These lines were laid out in a randomized block design and planted in the spacing 20 X 20 cm with three replications. The recommended package of practices was followed to raise a normal crop, including irrigation with alternate wetting and drying and necessary plant protection measures. Fertilizers were applied to the main field at the rate of 150:50:50 NPK kg/ha at different crop stages including transplanting, early tillering and booting stage.

Data recordings

The rice landraces were examined based on the 21 quantitative and quality traits. The data was collected on 1) days to 50 % flowering, 2) days to maturity, 3) number of tillers per plant, 4) number of effective tillers per plant, 5) plant height, 6) panicle length, 7) number of fertile spikelets per panicle, 8) spikelet fertility, 9) panicle density, 10) thousand grain weight, 11) biological yield, 12) harvest index, 13) grain yield per plant, 14) grain length, 15) grain breadth, 16) kernel length breadth ratio, 17) elongation ratio, 18) water uptake ratio, 19) alkali spread value, 20) amylose content and 21) protein content. In these traits, protein content was estimated with Lowry’s method, rest of traits

were measured or recorded as per the guidelines of DUS (Distinctiveness, Uniformity and Stability) from Directorate of Rice Research. These data on 21 traits were recorded from 5 randomly selected representative plants in all the genotypes, except for the trait days to 50 % flowering and days to maturity, where observation was made on plot-by-plot basis.

Data analysis

The data from the 21 quantitative and quality traits were analyzed in ‘RStudio (4.1.2)’ using various packages. ANOVA, Genetic parameters (Phenotypic and Genotypic Coefficient of variance, Heritability, Genetic Advance per Mean), Correlation and Path Coefficient Analysis were done using the ‘Variability’ package and the Multivariate Analysis *i.e.*, Principal Component Analysis was performed using ‘Facto Mine R’ and ‘Factoextra’ Packages.

Result and Discussion

Estimation of Genetic Parameters

The analysis of variance revealed the presence of significant differences among all the genotypes for all the traits observed (Table 1). The genetic variability studies emulated, high PCV and GCV was absorbed for the traits followed, Number of fertile spikelets per panicle, Elongation ratio, Kernel length breadth ratio, Protein content, Water uptake ratio, Harvest index, Number of effective tillers per plant, Alkali spread value, Biological yield and Grain yield per plant (Table 2). In this finding, PCV was higher than GCV for all the characters, which explains there was the influence of environmental factors. The estimates of ECV explains the same. Some characters were less affected by environment, such as thousand grain weight, days to maturity, amylose content, grain length, days to 50 % flowering, plant height, kernel length breadth ratio, panicle length, spikelet fertility, grain breadth, number of fertile spikelets per panicle, biological yield and panicle density. While, harvest index, water uptake ratio, grain yield per plant, alkali spread value, number of effective tillers per plant and elongation ratio have high environmental influence.

Table 1: Analysis of variance (ANOVA) for 21 traits\

S. No.	Parameters	Mean Sum of Square		
		Replication (df=2)	Genotypes (df=22)	Error (df=44)
1	Days to 50 % flowering	20.348	59.235**	11.545
2	Days to maturity	28.101	62.332**	12.344
3	Number of tillers per plant	2.6317	13.368**	1.7519
4	Number of effective tillers per plant	1.5924	12.649**	2.4177
5	Plant height	7.35	1595.75**	32.58
6	Panicle length	1.0014	12.5134**	2.0108
7	Number of fertile spikelets per panicle	182.95	2568.55**	131
8	Spikelet fertility	49.418	197.775**	30.221
9	Panicle density	1.3571	1.5315**	0.4907
10	Thousand grain weight	0.008	35.419**	0.144
11	Biological yield	14.42	1771.05**	68.37
12	Harvest index	11.856	208.614**	14.933
13	Grain yield per plant	11.8	319.614**	14.065
14	Grain length	0.00993	2.17841**	0.09269
15	Grain breadth	0.00013	0.85833**	0.05822
16	Kernel length breadth ratio	0.00045	1.26112**	0.0194
17	Elongation ratio	2.2014	4.3885**	1.6199
18	Water uptake ratio	315.1	4402.6**	729.9
19	Alkali spread value	0.1014	7.2042**	0.4651
20	Amylose content	0.006	51.541**	0.581
21	Protein content	0.0132	7.8139**	0.4627

High heritability coupled with high genetic advance was observed on the following characters *viz.*, harvest index, grain breadth, alkali spread value, protein content, number of fertile spikelets per panicle, grain yield per plant, grain length, biological yield, plant height, kernel length breadth ratio, amylose content and thousand grain weight. It explains that there is scope of improvement through selection in these characters.

These genetic parameter study revealed that number of fertile spikelets per panicle, kernel length breadth ratio, biological yield, protein content, harvest index, alkali spread value and grain yield per plant can be improved through selection. Heterosis breeding will be helpful for the improvement of remaining traits such as days to maturity, days to 50 % flowering, panicle length, grain length, spikelet fertility, panicle density, plant height, thousand grain weight and amylose content.

Table 2: GCV, PCV, Heritability and Genetic Advance per Mean for 21 traits

S. No.	TRAITS	PCV	GCV	HB	GAM	CD(5%)
1	Days to 50 % flowering	5.7	4.34	57.93	6.81	5.59
2	Days to maturity	4.3	3.26	57.44	5.08	5.78
3	Number of tillers per plant	20.64	17.13	68.85	29.28	2.18
4	Number of effective tillers per plant	33.24	25.42	58.52	40.06	2.56
5	Plant height	16.77	16.27	94.11	32.51	9.39
6	Panicle length	9.81	7.82	63.52	12.83	2.33
7	Number of fertile spikelets per panicle	23.67	21.97	86.12	42.01	18.83
8	Spikelet fertility	12.93	10.42	64.89	17.28	9.05
9	Panicle density	14.28	9.19	41.42	12.18	1.15
10	Thousand grain weight	17.81	17.7	98.79	36.25	0.63
11	Biological yield	28.24	26.68	89.25	39.92	13.61
12	Harvest index	42.32	38.14	81.22	41.80	6.36
13	Grain length	10.51	9.87	88.23	19.10	0.5
14	Grain breadth	20.14	18.25	82.09	34.05	0.4
15	Kernel length breadth ratio	24.6	24.05	95.52	43.42	0.23
16	Elongation ratio	58.38	35.17	36.29	43.65	2.09
17	Water uptake ratio	31.68	25.07	62.65	40.88	1.12
18	Alkali spread value	47.54	43.27	82.85	41.13	1.25
19	Amylose content	19.75	19.42	96.69	39.34	1.12
20	Protein content	41.49	38.06	84.12	38.90	44.46
21	Grain yield per plant	56.25	52.73	87.87	48.82	6.17

The attributes number of fertile spikelets per panicle, kernel length breadth ratio, biological yield, water uptake ratio, number of effective tillers per plant, protein content, harvest index, alkali spread value, grain yield per plant and elongation ratio all have high GCV and PCV. The findings of this study are consistent with those of previous researchers such as Ranjith *et al.*, 2018 ^[16], Saha *et al.*, 2019 ^[17] and Kujur *et al.*, 2019 ^[10] for the traits number of fertile spikelets per panicle, number of effective tillers per plant, biological yield, harvest index and grain yield per plant. For kernel length breadth ratio, Kujur *et al.*, 2019 ^[10] and Bollinedi *et al.*, 2020 ^[4] finding showed similar result. Thongbam *et al.*, 2012 ^[20], Dhanwani *et al.*, 2013 ^[6], Nirmaladevi *et al.*, 2015 ^[13] showed similar results for alkali spread value and water uptake ratio. But Protein content, and elongation ratio results were contrasting to Thongbam *et al.*, 2012 ^[20] and Bollinedi *et al.*, 2020 ^[4]

In the present study, high heritability coupled with high genetic advance per mean was observed for harvest index, grain breadth, alkali spread value, protein content, number of fertile spikelets per panicle, grain yield per plant, biological yield, plant height, kernel length breadth ratio, amylose content and thousand grain weight. This result was confirmed by findings of Gokulakrishnan *et al.*, 2014 ^[7], Tuhina-Khatun *et al.*, 2015 ^[22], Behera *et al.*, 2018 ^[3], Ranjith *et al.*, 2018 ^[16], Saha *et al.*, 2019 ^[17] and Gupta *et al.*, 2021 ^[8].

Principal Component Analysis

PCA gives a method for reducing a complicated data set to a lower dimension, revealing the often hidden, simplified

structures that lie beneath it. Principle component analysis is useful for collecting measurements for a large number of observed variables and constructing a smaller number of novel variables (called Principal Component) that account for the majority of the variance in the observed variables. The underlying structure of the new dimension can be used envisaged using a logical regression formula with the eigen value and corresponding loading vector of the individuals from the PCA. In this study, PCA was used to analyse 21 yield and quality traits in 23 rice genotypes. The PCs with eigen values >1 and that explained at least 5% of the variation in the data were evaluated in the current investigation, according to the criteria provided by Brejda *et al.* (2000) ^[5]. The PC with the highest eigen values and variables with the highest factor loading were deemed to be the most indicative of system characteristics. Out of 21, seven principal components (PCs) *viz.* PC1 with 5.895(28.07%), PC2 with 3.31(15.76 %), PC3 with 2.66 (12.68 %), PC4 with 2.06 (9.807 %), PC5 with 1.65 (7.84 %), PC6 with 1.31 (6.226 %) and PC7 with 1.16 (5.523%) exhibited more than 1.00 eigen value, and showed about 85.9% cumulative variability (Fig 1) among the traits studied (Table 5). The PC1 component, which accounted for the most variability (28.1%), was mostly positively related to traits like water uptake ratio and kernel length breadth ratio, but negatively related to traits like grain yield per plant, number of tillers per plant, number of effective tillers per plant, grain breadth, biological yield, harvest index, number of fertile spikelets per panicle, panicle length, and plant height. These findings contradicted those of Tuhina-Khatun *et al.*, 2015 ^[22] and Prafull Kumar *et al.*, 2015.

However, in terms of flag leaf length, this conclusion matched that of Allam *et al.*, 2017^[1]. Panicle density and alkali spread value were the most associated features on a positive scale in PC5, whereas protein content, amylose content, days to maturity, kernel length breadth ratio, and panicle length were on a negative scale. Bollinedi *et al.*, 2020^[4] also came to similar conclusions deemed to be the most indicative of system characteristics. Out of 21, seven principal components (PCs) viz PC1 with 5.895(28.07%), PC2 with 3.31(15.76 %), PC3 with 2.66 (12.68 %), PC4 with 2.06 (9.807 %), PC5 with 1.65 (7.84 %), PC6 with 1.31 (6.226 %) and PC7 with 1.16 (5.523%) exhibited more than 1.00 eigen value, and showed about 85.9% cumulative variability (Fig 1) among the traits studied (Table 5). The PC1 component, which accounted for the most variability

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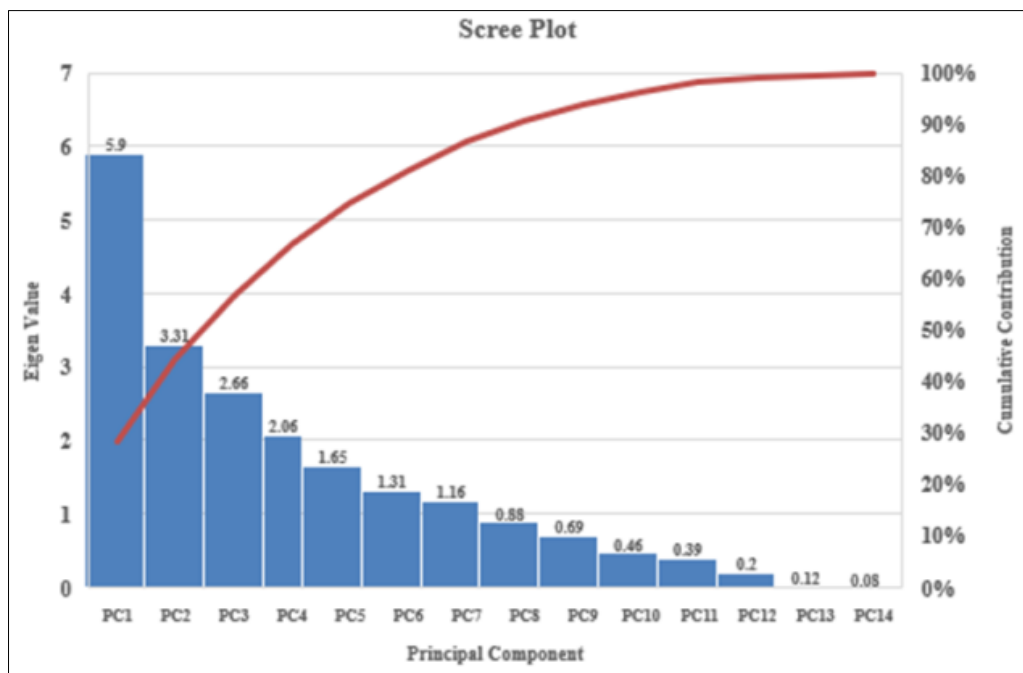


Fig 1: Scree Plot of Variation in Eigen Value Blue bar indicates the Eigen Value; Red line indicates the cumulative contribution to the total variance by each Principal Component

Table 3: Eigen value, Contribution of variance and components of Principal Component

Principal components	Eigenvalues	Contribution	Cumulative Contribution
PC1	5.9	28.07	28.07
PC2	3.31	15.76	43.83
PC3	2.66	12.68	56.51
PC4	2.06	9.807	66.319
PC5	1.65	7.84	74.16
PC6	1.31	6.226	80.385
PC7	1.16	5.523	85.909
PC8	0.88	4.193	90.101
PC9	0.69	3.285	93.386
PC10	0.46	2.172	95.558
PC11	0.39	1.866	97.424
PC12	0.2	0.952	98.376
PC13	0.12	0.575	98.951
PC14	0.08	0.387	99.337
PC15	0.06	0.298	99.635
PC16	0.03	0.142	99.778
PC17	0.02	0.092	99.869
PC18	0.02	0.084	99.953
PC19	0.01	0.03	99.983
PC20	0	0.016	99.999
PC21	0	0.001	100

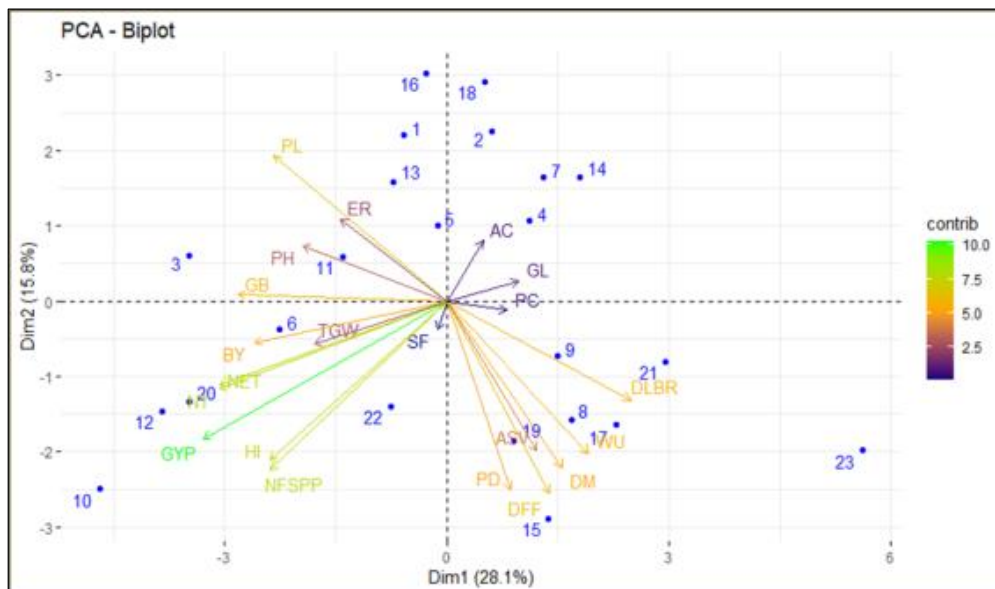
Table 4: PCA scores of rice genotypes

Genotypes	PC1	PC2	PC3	PC4	PC5	PC6	PC7
ThalamGour	0.25	6.43	2.97	0.31	2.07	3.55	0.54
Phodisi	0.27	6.67	0.04	0.53	0.27	5.76	9.53
Halla batta	8.97	0.48	0.15	0.6	0.35	1.47	0.43
Jhadjadhan	0.91	1.5	8.53	2.81	0.52	0.48	1.66
Phuda Malu	0.01	1.33	0.26	18.6	8.29	0.98	1.69
Daddigha	3.77	0.19	0.49	21.56	5.34	8.53	0.26
Kaala Jeera	1.25	3.53	7.55	8.31	1.93	4.24	27.86
Krishtampeta gold	2.08	3.27	1.86	0.71	0.4	27.92	16.31
Dhomdha	1.66	0.7	12.7	2.42	18.48	0.08	1.92
Kukuda Munde	16.25	8.18	0.3	0.03	8.26	0.01	0.19
Mudimuringi	1.45	0.46	0.33	2.26	0.56	0.66	2.95
Nagara	10.91	2.79	4.43	0.1	9.25	0.21	0
Pohaki	0.38	3.3	0.71	0.57	2.21	3.92	1.44
Eesakawada	2.37	3.55	0.59	0.13	0.09	0.37	5.19
Ghalima	1.4	11.04	3.05	1.93	0.53	2.41	0.03
Gadakadhiya Mahi	0.06	12.06	2.08	11.81	3.54	0.29	7.83
Kumar Gorla	3.83	3.55	21.58	2.32	2.74	15.53	1.25
Aashudhee	0.19	11.2	7.99	0.96	2.3	6.53	0.63
Agma Kundha	0.6	4.48	11.65	8.64	0.33	0.45	6.29
Bhairajlu	8.93	2.36	0.22	0.03	0.73	6.83	0
Vedhuru Sanna	6.45	0.84	5.4	4.66	1	0.75	0.11
Tharang	0.42	2.57	2.32	5.44	26.11	4.3	9.55
Akshaya ponni	23.26	5.18	0.46	0.92	0.36	0.39	0

PCA score of each genotype (Table 6) revealed the performance of the genotype in the respective Principal Component. Top performing Genotypes were enlisted in the table 7.

Table 5: Top genotypes from PCA scores

Principal Component	Genotypes
PC1	Akshaya ponni, Kukuda Munde, Nagara, Halla batta
PC2	Gadakadhiya Mahi, Aashudhee, Ghalima, Kukuda Munde
PC3	Kumar Gorla, Dhomdha, Agma Kundha, Jhadjadhan
PC4	Daddigha, Phuda Malu, Gadakadhiya Mahi, Agma Kundha
PC5	Gadakadhiya Mahi, Daddigha, Kukuda Munde, Phuda Malu
PC6	Krishtampeta gold, Kumar Gorla, Daddigha, Bhairajlu
PC7	Kaala Jeera, Krishtampeta gold, Tharang, Phodisi

**Fig 2:** Biplot of PC1 and PC2

The biplot was made for the individuals and variables in PC1 and PC2 (Fig 2), which constitute the total variation of 43.83%. the biplot depicts these PCs mostly dominated by yield traits such as days to 50 % flowering, days to maturity, number of tillers per plant, number of effective tillers per plant, plant height, panicle length, number of fertile

spikelets per panicle, panicle density, biological yield, harvest index and Grain yield per plant. The genotypes responsible for this variation were mainly, Akshaya ponni, Nagara, Halla batta, Gadakadhiya Mahi, Aashudhee, Ghalima and Kukuda Munde.

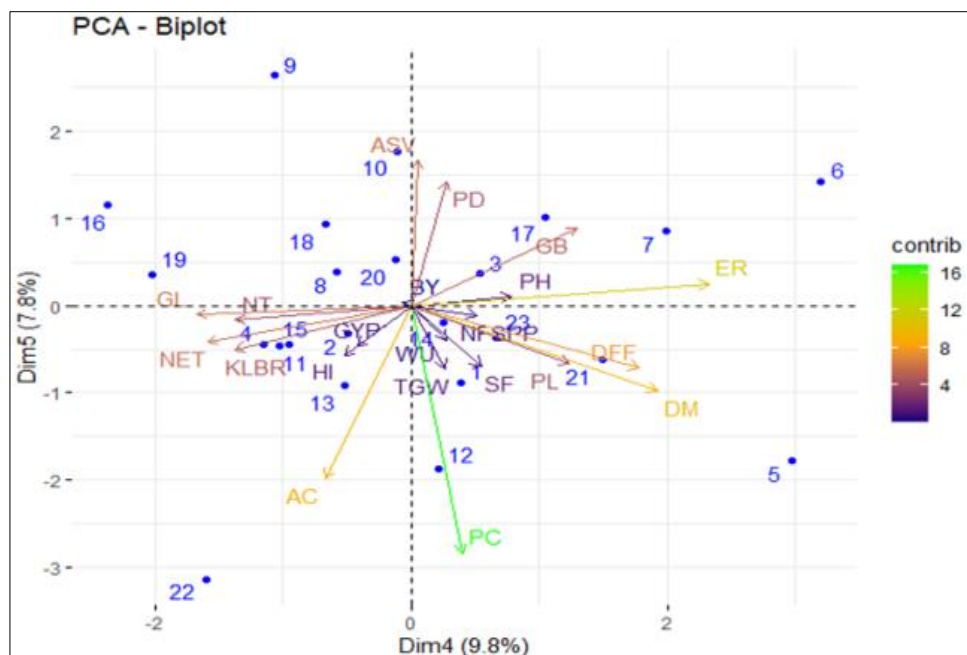


Fig 3: Biplot of PC4 and PC5

Most of the quality traits are dominated more in PC4 and PC5 (Fig 3), together they constitute for 17.64% of variation. The traits which are dominated in these PCs were grain length, grain breadth, kernel length breadth ratio, elongation ratio, water uptake ratio, alkali spread value, amylose content and protein content. The genotypes contributing to these variations were Bhairojlu, Daddigha, Gadakadhiya Mahi, Kaala Jeera, Krishtampeta gold, Kukuda Munde, Kumar Gorla, Phodisi, Phuda Malu and Tharang.

Conclusion

In the present study, explains all the genotypes were significantly different for every trait, in the genetic parameter studies revealed that number of fertile spikelets per panicle, kernel length breadth ratio, biological yield, protein content, harvest index, alkali spread value and grain yield per plant can be improved through selection. Heterosis breeding will be helpful for the improvement of remaining traits such as days to maturity, days to 50 % flowering, panicle length, grain length, spikelet fertility, panicle density, plant height, thousand grain weight and amylose content. Thus, selection based on these traits will be help to improve grain yield per plant. PCA revealed usage of Akshaya ponna, Nagara, Halla Batta, Gadakadhiya Mahi, Aashudhee, Ghalima and Kukuda Munde would be rewarding in crop improvement for good yield, likewise, hairojlu, Daddigha, Gadakadhiya Mahi, Kaala Jeera, Krishtampeta gold and Kumar Gorla would be rewarding in improvement of quality traits.

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