



Research Article

Assessment of Genetic Parameters, Agro-Morphologic Stability and Clustering Pattern of Promising Candidate Basmati Rice (*Oryza sativa* L.) Lines

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Abstract | In the present study, genetic parameters, agro-morphologic stability and clustering pattern of twenty promising elite basmati rice (*Oryza sativa* L.) lines including three checks were investigated in advance generation. Triplicated randomized complete block design (RCBD) was used during three consecutive years from 2016 to 2018 and the data were subjected to combined ANOVA, correlation, principal component, GGE biplots in order to demonstrate the stability and performance of these advance Basmati lines. A highly significant and exploitable level of genetic variability was found existed among tested inbred lines. Higher broad sense heritability (%) was observed among tested genotypes which specifies higher proportion of phenotypic variation attributed by genetic values. Correlation matrix portrayed significantly positive relationship of grain yield with maturity days; significantly positive relationship of plant height with days to maturity and highly negative with panicle length and thousand grains weight. Dendrograms divided the genotypes into six distinct Clusters. Based on GGE biplots, PK10324-1-1 followed by PK9444-8-1-2 and PK10029-13-2-1 were identified to be most superior and potential candidate Basmati lines with better yield and stability across three years (growing seasons). Whereas, Super Basmati (check), PK 10436-2-1-1, PK10437-14-2-1 exhibited lowest yield stability across test environments. Test-environment analysis indicated that genotypes PK10324-1-1 and PK9444-8-1-2 were best suited for 2017 season, genotypes PK10967-30-1, Chenab Basmati and PK 10355-13-2-1 were best suited for 2018, genotypes PK9966-10-1 and PK 10434-6-2-1 were best suited for 2016 season, whereas genotype PK10029-13-2-1 performed equally well in 2017 and 2018. Principal Component Analysis (PCA) also displayed stability in performance relative to all studied traits in all the advance Basmati lines. Convincingly, the higher yielding and more stable among the studied advance Basmati lines can be utilized as new candidate Basmati lines as compared to existing Basmati varieties used as checks.

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Keywords | Rice (*Oryza sativa* L.), Agro-morphological traits, Yield stability, Clustering, principal component analyses (PCA), Correlation, GGE analysis



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Introduction

Rice (*Oryza sativa* L.) is energy source for about half of the world's population and ranks second amongst the cereal grain crop (Manjappa and Hittalmani, 2014). Agriculture is the major segment of the economy of Pakistan which contributes principally in the livelihood of majority of the population (>65-70%) in the country. After wheat, rice crop holds an important place in food crops in the agriculture economy. It contributes 3.5 percent of value added in agriculture and 0.7 percent in Gross Domestic Production (GDP) (PES, 2020-21).

Rice production in Pakistan can be sub-divided into three categories including basmati (aromatic), fine (non-aromatic) and coarse types. During previous year 2020-21, rice crop was cultivated on an area of 3.335 million hectares, reflecting a drastic increase of 9.9% as compared to last year's cultivated area *i.e.* 3.034 million hectares and the year 2020-21 exhibited a record production growth of 13.6% to 8.419 million tons as compared to previous year's production of 7.414 million tons. The increase in production was basically due to high yielding varieties, rising per unit prices as well as increased demands for the country's rice in international markets (Agri. statistics of Pak., 2020-21).

Basmati belongs to a special group of rice which is worldly renowned for its specific smell of aroma and taste, long and slender grains which elongates after cooking. Scientific findings of previous few decades have proved that traditional basmati quality is ecologically specific for its unique Basmati characteristics which can only be attained when the basmati cultivars are grown in the traditional basmati area locally named as 'kallar tract' located in Punjab province of Pakistan along with specific areas of India (Akhter and Haider, 2020). Histochemical analyses have emphasized the major aroma compound *2-acetyl-1-pyrroline* (2AP) is primary compound present in mature rice grain of basmati rice varieties responsible for its specific Basmati aroma (Setyaningsih *et al.*, 2019).

Development of high yielding and early maturing varieties are common objective of breeding owe to feed the burgeoning population and continuously reducing cultivated land. Crop breeding is a basic tool which facilitates crop improvement and principally depends upon range and level of genetic diversity available in

the gene-pool. Traits of interest may be governing by single or multiple genes that are responsible for qualitative and quantitative inheritance in rice crop. The knowledge and behavior of these responsible genes is vital for adopting appropriate procedure after hybridization for genes introgression and fixation in following generations (Mishu *et al.*, 2016).

The phenomenon of transmission of characters from parents to offspring is usually measured in terms of heritability and genetic advance (GA) *viz.* a measure of genetic gain under selection, which expresses the direct relationship between heritability and response to selection (Shukla *et al.*, 2004). Heritability and genetic advance are two important selection parameters, which play important role in predicting genes behavior in next generations and helpful in predicting the gene fixation under selection than heritability estimates alone (Lingaiah, 2015; Sharma *et al.*, 2020; Siger *et al.*, 2018). Therefore, this investigation was made with an objective to identify the elite Basmati rice genotypes for yield parameters.

These fixed genes sometime behave different under various environment and creates phenotypic differences. These differences are the outcome of genes interaction with environment and demand to adopt strategy to minimize the environmental influence on plant genes (Hub, 2011). For this purpose, we split the total variation into different components, and separate genetic variation from other environmental variation and find out environmental responsive and non-responsive genotypes.

The genotypic coefficient of variation (GCV) estimates the heritable variability, whereas phenotypic coefficient of variance (PCV) measures the influence of environment on the genotype. High value of the PCV and low value of the GCV for a character indicates high influence of environment in its expression (Bagudam *et al.*, 2018). This method would facilitate in selection of stable genotypes who perform better in all environments along with region specific genotypes (Boukar *et al.*, 2019; Yaqoob *et al.*, 2012; Bagati *et al.*, 2016).

Rice yield is a complex trait, polygenic in inheritance, associated with diverse yield contributive traits, more prone to environmental fluctuations. Development of high yielding genotypes require a comprehensive information of genetic variation of yield associating

characters (Würschum *et al.*, 2018). Several scientists has reported the genes that contribute to plant growth and development that are components of directly and indirectly for rice yield improvement (Lipi, *et al.*, 2021; Mallimar *et al.*, 2015). Therefore, it is necessary to have a good knowledge of these characters that have vital association with yield as a result, they can be used to direct selection criteria or indices to enhance performances of varieties in a new plant population (Bagati *et al.*, 2016).

Considering the above points, the aim of this study is to evaluate twenty elite and promising Basmati rice genotypes to select those that have better and stable yield attributes over checks for incorporation into breeding programme and to use them directly as potential candidate lines for future varieties.

Materials and Methods

The present study was carried out at the research area of Rice Research Institute, Kala Shah Kaku (RRI, KSK) for three successive seasons 2016, 2017 and 2018. The experimental material consisted of twenty rice genotypes (commercial and promising rice lines) including three check varieties (Super Basmati, Basmati 515 and PK1121 aromatic) tested in Randomized Complete Block Design (RCBD) with three replications. Genotypes were grown in 5 meters apart maintaining 20 cm×20 cm plant spacing of individual genotype and all the recommended cultural practices was applied. Observations on ten quantitative parameters *i.e.* plant height (PH), days to maturity (DM), number of tillers per plant (NTP), number of panicles (NP), number of grains per panicle (NGP), panicle length (PL), thousand grain weight (TGW), grain yield (GY), husk percentage (HP), milling recovery percentage (RP) were noted from ten consecutive plants from each replication and then averaged. The data recorded for these characters were subjected to combined Analysis of Variance to test the significance for each character (Steel and Torrie, 1980). PCV and GCV were calculated by the formula given by Burton (1952), heritability by Burton and De Vane (1953) and genetic advance *i.e.* the expected genetic gain was calculated by using the procedure given by Johnson *et al.* (1955) in order to estimate the genetic variation. Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance (Singh and Ceccarelli, 1996). The heritability gives information on the transmission of traits from

parents to offspring hence, aiding in selection given as:

$$H^2 = \delta^2g / \delta^2p$$

Where;

H^2 : Broad sense heritability; δ^2g : Genotypic variance; δ^2p : Phenotypic variance.

Expected genetic advance (GA) under selection was computed according to the formula given by Johnson *et al.* (1955) expressed as:

$$GA = (\delta^2g / \delta p) \times K$$

Where;

δ^2g : Genotypic variance; δp : Phenotypic standard deviation of the original population; K: Selection differential with level of selection intensity at 5%.

Descriptive statistics, violin frequency distribution graphs and PCA was carried out using SPSS ver. 26. PCA Biplots shows the relationship between the traits depending on the angle between the vector for respective trait. Lesser the angle between the vectors of two traits, higher the degree of association; and *vice versa*. The lines near the vector of a traits represents more value of that trait. Length of the vector portrays the variation explained by that trait or variable out of total variation present in the population. Clustering was done using Mega ver. X software whereas GGE biplot analysis was conducted using R software ver. 4.0.3.

Results and Discussion

Combined analysis of variance and genetic variability

It was performed to find out significance of genetic variability among studied traits for genotypes and years of study. Highly significant ($p < 0.01$) and exploitable level of genetic variability existed among tested genotypes for majority of the traits along with acceptable co-efficient of variation (%) (Table 1). Only two traits, husk (%) and RP (%), showed non-significant levels of genetic variability among tested twenty (20) genotypes. Whereas, non-significant and unexploitable levels of genetic variability existed among blocks. Previously, significant genetic variability among advanced rice genotypes has been reported for PH, DM, NTP, NP, NGP, PL, TGW and GY (Yaqoob *et al.*, 2012; Anis *et al.*, 2016), whereas non-significant

Table 1: Combined Analysis of Variance results of elite Basmati rice lines for studied traits.

	PH	DM	NTP	NP	NGP	PL	TGW	GY	HP	RP
RSS	1.67	26.12	63.35	58.05	396.07	11.72	2.32	0.01	0.02	8.45
GSS	254.39**	64.59**	24.39**	9666.79**	2199.30**	37.64**	13.32**	1.33**	3.63 ^{NS}	6.13 ^{NS}
E	6.53	2.45	4.49	28.47	6.07	4.03	2.47	0.02	1.48	4.40
CV %	2.13	1.45	11.32	1.46	2.57	7.83	7.47	2.88	9.97	3.63
R ²	0.951	0.932	0.776	0.994	0.995	0.828	0.733	0.975	0.170	0.301
F	35.421	24.664	6.258	307.388	332.920	8.735	4.959	70.269	0.370	0.780
Pr > F	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	0.991	0.724
GEN	39.147	26.138	5.431	339.530	361.092	9.348	5.382	77.657	0.409	0.717
	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	0.980	0.779
Year	0.024	10.660	14.108	2.039	65.286	2.911	0.936	0.076	0.005	1.378
	0.976	< 0.0001	< 0.0001	0.144	< 0.0001	0.067	0.401	0.927	0.995	0.265

NS: non-significant; ****:** highly significant at $\alpha = 0.01$; *****: significant at $\alpha = 0.05$; **RSS:** Replication sum of squares; **GSS:** Genotypic sum of squares; **E:** Error; **CV%:** Coefficient of variance (Percentage); **R-squared:** Coefficient of determination; **F:** F-tabulated value; **Pr>F:** Probability of significance of results ($\alpha = 0.05$); **GEN:** Part of variations due to genotypes; **Year:** Part of variations due to years; **PH:** Plant height; **DM:** Days to maturity; **NTP:** Number of tillers per plant; **NP:** Number of panicles per plant; **NGP:** Number of grains per panicle; **PL:** Panicle length; **TGW:** Thousand grain weight; **GY:** Grain yield; **HP:** Husk percentage; **RP:** Milling recovery percentage.

variability for HP and RP (Kumar *et al.*, 2019), which support the consistency and accuracy of our experimental conditions and research data. Coefficient of variation (CV%) showed percentage of total variations present in the genotypes for the traits. All the traits showed less than 10% CV except NTP (11.32%). Low CV percentages might be due to the reason that the genotypes were uniform and homogenous for all the studied traits (Table 1). R-squared (R²) is the coefficient of determination that shows the proportion of the variability in the studied genotypes for the considered traits being explained by the explanatory variables. The results (Table 1) have depicted that almost all the traits explained more than 90 percent of the total variability in case of PH, DM, NP, NGP and GY. All the other traits also explained more than 70% of the total variation except HP and RP which showed 0.170 and 0.301 (R-squared values) as given in Table 1. Results of combined ANOVA further elucidated the proportion of total variations explained by genotypes and years of studies. Highly significant ($p < 0.001$) results were observed for all the studied traits among genotypes, except HP and RP. Likewise, highly significant ($p < 0.001$) results were detected in all the three years for DM, NTP and NGP which shows inconsistent behavior of genotypes for these traits studied in all the three years (2016, 2017 and 2018). However, all the other traits displayed consistent behavior in all the three years of study as represented by non-significant ($p > 0.05$) results for years portraying the stability of genotypes for these phenotypes (Table 1).

Figures 1 (a – j) show violin plots depicting frequency distribution of all the genotypes / promising lines for studied traits during 2016, 2017 and 2018 represented with different colors in each plot. The plot areas show the similarity in performance of genotypes during all the consecutive three years showing the stability for traits and consistency of phenotypes in every year except in case of NTP and RP suggesting that these traits were highly influenced by environmental factors such as weather, rainfall and temperature dissimilarities in studied years.

Genetic parameters of traits for elite Basmati lines studied for three years

Genetic parameters indicated wide range of genetic variation among tested genotypes for studied traits. Higher phenotypic variance and co-efficient of variation values were observed for all traits as compared to genotypic variance and co-efficient of variation values (Table 2), which indicated influence of environmental factors on expression of these traits. The higher genotypic and phenotypic co-efficient of variation values (28% - 55%) were observed for NGP and TGW which indicate wider variability spectrum for these traits and potential for early generation trait selection through phenotypic selection. Moderate genotypic and phenotypic coefficient of variation values (13% - 18%) were recorded for NTP, NP and PL, indicating these traits were under influence of environmental factors and moderate genetic variation existed for further improvement. Whereas, PH, DM, GY, HP and RP had lower genotypic and phenotypic

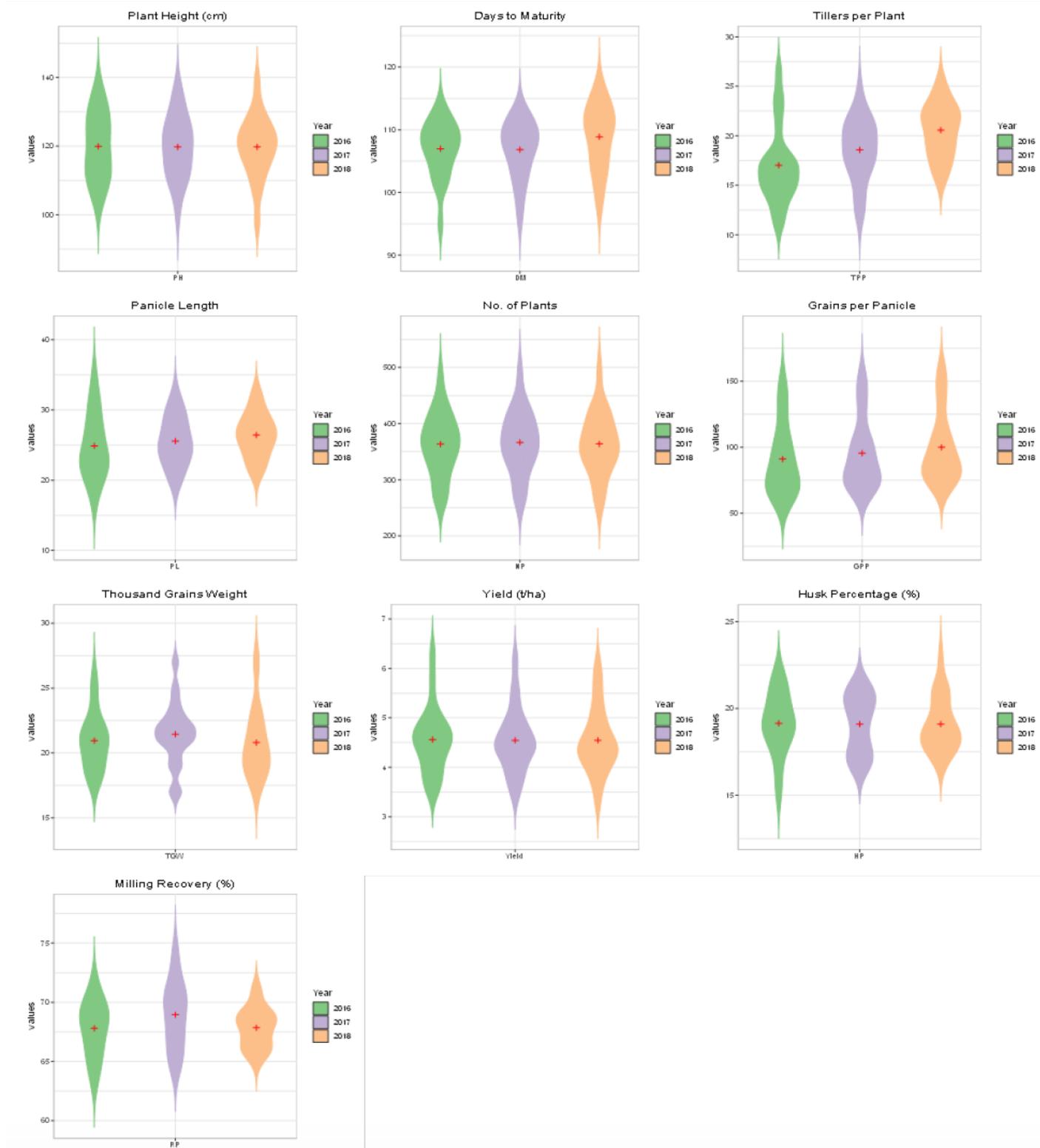


Figure 1 (a – j): Violin plots depicting frequency distribution of all the genotypes / promising lines for studied traits during three years 2016, 2017 and 2018 represented with different colors in each plot.

co-efficient of variation values (1% - 8%), suggesting that these traits were greatly under environment influence and narrow genetic variation for further improvement. These results are in accordance with those reported by (Anyaocha *et al.*, 2018).

Higher broad sense heritability (%) was observed for

the traits which showed higher proportion of variation is due to genetic values and it ranged from 59% (TGW) to 99% (NP and NGP) (Table 2). Whereas, HP and RP showed lower heritability. Higher heritability coupled with high genetic advance indicate prevalence of additive gene action inheritance, lesser environmental influence on performance of traits and

amenable of simple phenotypic selection (Sumanth *et al.*, 2017). High heritability and genetic advance estimates were observed for NP, NGP and PH. Whereas, all other traits showed good heritability along with lower to moderated genetic advance estimates, indicating that these traits were under control of additive and non-additive gene actions and were also influenced by the environment. In recent years, similar results have been reported in other studies (Karim *et al.*, 2016; Sumanth *et al.*, 2017; Iqbal, 2018; Saha *et al.*, 2019).

Table 2: Genetic parameters.

Traits	GM	σ^2_g	σ^2_p	CVg	CVp	H ²	GA
PH	119.95	82.62	89.15	7.58	7.87	92.68	15.36
DM	107.58	20.71	23.16	4.23	4.47	89.42	7.55
NTP	18.73	6.63	11.12	13.75	17.81	59.63	3.49
NP	364.50	3212.77	3241.24	15.55	15.62	99.12	99.04
NGP	95.67	731.08	737.15	28.26	28.38	99.18	47.26
PL	25.63	11.20	15.23	13.06	15.23	73.54	5.04
TGW	4.55	3.62	6.09	41.77	54.19	59.42	2.57
GY	21.07	0.44	0.46	3.14	3.21	95.62	1.13
HP	19.12	0.72	2.20	4.43	7.75	32.63	0.85
RP	68.20	0.58	4.98	1.11	3.27	11.59	0.45

GM: Grand mean; **σ^2_g :** Genotypic variance; **σ^2_p :** Phenotypic variance; **CVg:** Genotypic coefficient of variation; **CVp:** Phenotypic coefficient of variation; **H²:** Broad sense heritability (%); **GA:** Genetic advance; **PH:** Plant height; **DM:** Days to maturity; **NTP:** Number of tillers per plant; **NP:** Number of panicles per plant; **NGP:** Number of grains per panicle; **PL:** Panicle length; **TGW:** Thousand grain weight; **GY:** Grain yield; **HP:** Husk percentage; **RP:** Milling recovery percentage.

Mean performance for yield and related traits

Mean performance of studied traits differs significantly, except for HP and RP which showed non-significant differences among tested genotypes (Supplementary Table 1). Maximum PH was observed in PK10029-13-2-1 (136 cm) and minimum in Kissan Basmati (101 cm). Basmati 515 and PK10437-14-2-1 were matured in 113 days, whereas Kissan Basmati taken only 96 days for maturity. Since, short stature and early maturity are desirable characters for earliness (Yuan, 2017; Dreccer *et al.*, 2019), Kissan basmati had both of these, thus good candidate line for replacing the current commercial rice cultivars. For NTP, maximum was observed in PK9966-10-1 (25) and minimum in PK10437-14-2-1 (13). Likewise, PK9966-10-1 had highest (490) and PK10437-14-2-1 had lowest (260) NP area due to difference in their tillering ability. For NGP, Chenab and Punjab

Basmati had highest 154 and 148 grains, respectively, whereas PK 10436-2-1-1 had lowest grains (66). Maximum PL was observed in Punjab Basmati (32.40 cm) and minimum in PK10967-30-1 (19.05 cm). Regarding TGW, PK 1121 aromatic had maximum weight (24.67 g) and Basmati 515 had minimum weight (18.67 g). Finally, PK10324-1-1 yielded maximum GY production (6.18 t/ha) with average performance of all studied traits, whereas PKBB15-116 yielded minimum GY production (3.44 t/ha) due to lower TGW potential. All tested genotypes showed low husk proportion ($\leq 20\%$) and very good RP ($\geq 65\%$) (S1).

Overall, four genotypes PK10324-1-1, PK9444-8-1-2, PK10029-13-2-1 and Chenab Basmati yielded ≥ 5.0 t/ha GY production. Among these, PK10324-1-1, PK9444-8-1-2 and PK10029-13-2-1 are good candidates for transplanted rice because all these developed optimum NTP and NP (Tian *et al.*, 2017). Chenab Basmati showed average PH, taken moderate DM, developed lower NTP and NP, produced highest NGP along with long panicles and very good yielding potential thus ideal candidate for direct seeded rice (Jain *et al.*, 2018). Other genotypes are also good, either for GY potential or for individual traits thus can be utilized for improvement of rice plant (Figure 2).

Correlation and coefficients of determination analyses

Figure 3 (a, b) show the results of correlations and coefficient of determination analyses among traits depicting the trends of associations among traits including PH, DM, NTP, PL, NP, NGP, TGW, yield, HP and RP of all the studied promising genotypes of rice in average for three consecutive years 2016, 2017 and 2018. Correlation matrix (Supplementary Table 2) among traits portrayed highly significant and strong ($p \leq 0.0001$) positive relationship of PH with DM ($r^2 = 0.535$) and highly significant ($p \leq 0.05$) negative with PL and TGW emphasizing that PH portrayed negative effects on PL ($r^2 = -0.319$) and TGW ($r^2 = -0.337$) in studied Basmati genotypes whereas positive effects on DM (S2). Longer plants were late to mature as compared to short stature plants directing the breeders to select the plants with short stature with the intent of reducing growth duration in rice. Similarly, DM described negative association ($p \leq 0.01$) with yield ($r^2 = -0.333$). NGP are highly ($p \leq 0.0001$) and positively associated with PL ($r^2 = 0.772$). NP were highly ($p \leq 0.05$) negatively associated with TGW ($r^2 = -0.318$) representing the opposite

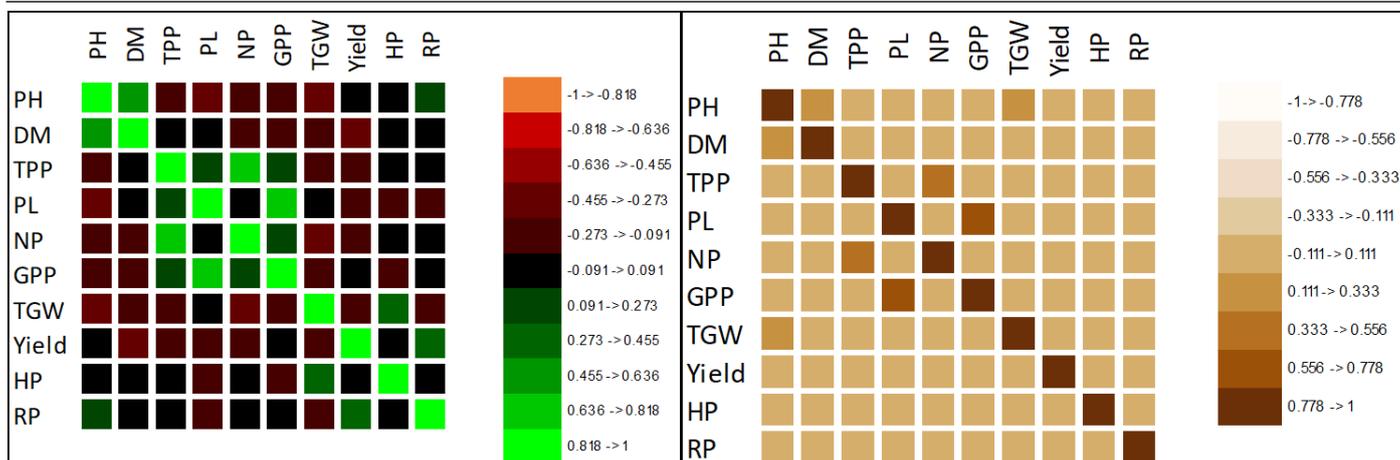


Figure 3 (a, b): Diagrams are showing correlations and coefficients of determinations matrix within studied agronomic and physiological yield related traits. Level of significance was adjusted at 5%.

PH: Plant height; **DM:** Days to maturity; **NTP:** Number of tillers per plant; **NP:** Number of panicles per plant; **NGP:** Number of grains per panicle; **PL:** Panicle length; **TGW:** Thousand grain weight; **GY:** Grain yield; **HP:** Husk percentage; **RP:** Milling recovery percentage.

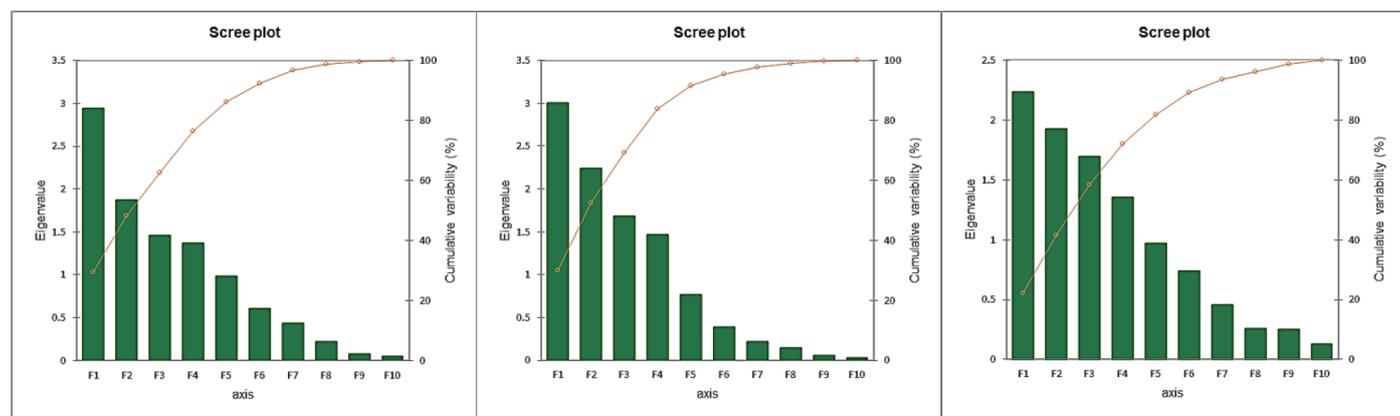


Figure 4: Eigenvalues of all components in PCA for all the three years (left to right) indicating the proportions of total variance attributed to studied ten traits in target genotypes.

Eigenvalues (Figure 4) indicated the percentage of total variance attributed to studied ten traits in target genotypes. Cumulative variability percentages depicted the addition of variance percentage attributed to components or factors. PCAs showed that more than 80% of the total variation due to studied traits in genotypes, is represented by first four components in all the three years, as depicted by Figure. Biplots in Figures 5 (a – i) depict the performance of genotypes / pure lines during three years of studies and data collected for agronomic traits for all the genotypes during three years 2016 – 2018. In year 2016, Kissan Basmati, followed by Chenab Basmati, Punjab Basmati, PK10324 and PK9444 were highest yielder (Figure 5a and b) considering first three factors. PK10324 and PK9444 respectively were the yielder while considering all the first four factors representing 76.39% of the total variations explained by given variables under study. Likewise, during 2017, PK10324, PK9444 and Kissan Basmati were the highest yielder (Figure 5d – f) and during 2018, PK10029, PK9444, PK10324

followed by PK9966 and PK10683 were amongst the highest yielder pertaining to the first four factors which explain 83.91% and 72.05% of the total variation present in the experimental material during 2017 and 2018 respectively (Figure 5a – i).

Figure 6 shows dendrogram or clustering of genotypes / promising lines studied in three consecutive years from 2016 to 2018 for ten morphological traits related to yield. Dendrogram divided the genotypes into six distinct Cluster as portrayed in Figure 6 a and b. In total of studied lines, eleven lines were contained by first Cluster C1 containing PK9444-8-1-2, PK10029-13-2-1, PK10324-1-1, PK10967-30-1, RRI-3, PKPB-8, Kissan Basmati, PK 1121 Aromatic, PK10436-2-1-1, PK10683-12-1, PK10355-13-2-1; Cluster 2 (C2) containing only one lines i.e. PK9966-10-1, Cluster 3 (C3) contained four genotypes i.e. PKBB15-116, PK8892, Super Basmati and Basmati 515; and forth Cluster (C4) and fifth Cluster (C5) contained one genotypes i.e. Punjab Basmati and

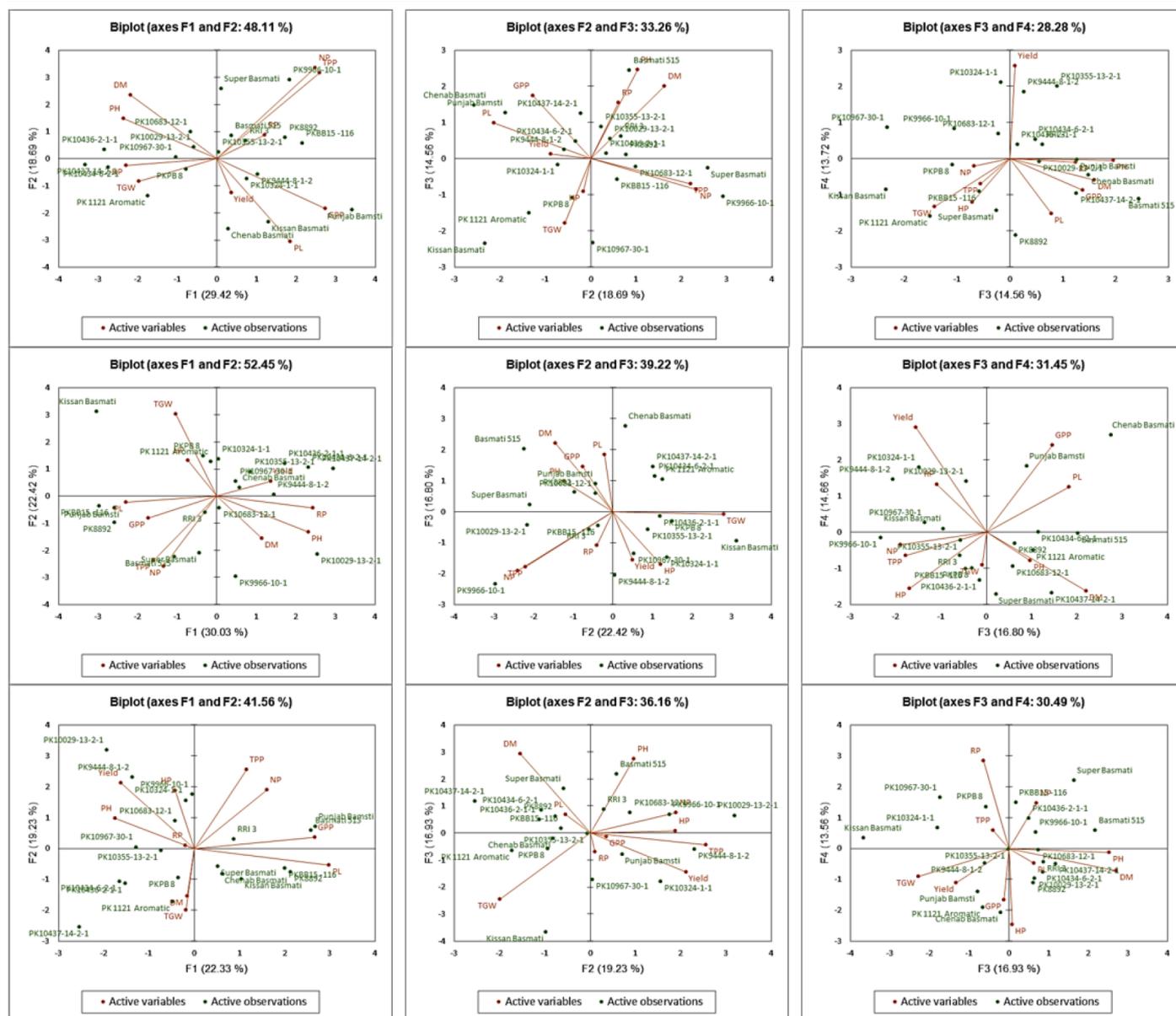


Figure 5 (a – i): Results of principal component analyses (PCA) of ten morphological and yield components in the studied promising rice lines. PH: Plant height; DM: Days to maturity; NTP: Number of tillers per plant; NP: Number of panicles per plant; NGP: Number of grains per panicle; PL: Panicle length; TGW: Thousand grain weight; GY: Grain yield; HP: Husk percentage; RP: Milling recovery percentage.

Table 3: Phenotypic characteristics of promising Basmati rice lines / genotypes in each Cluster.

Class	PH	DM	NTP	PL	NP	NGP	TGW	HP	RP	GY
1	119	106	18	25	358	85	22	19	68	5
2	116	109	25	21	490	80	19	19	69	5
3	121	109	21	28	420	114	20	19	68	4
4	108	104	21	32	360	148	20	18	67	5
5	118	110	14	30	280	154	20	19	68	5
6	130	112	14	22	270	70	22	19	69	4

PH: Plant height; DM: Days to maturity; NTP: Number of tillers per plant; PL: Panicle length; NP: Number of panicles per plant; NGP: Number of grains per panicle; TGW: Thousand grain weight; HP: Husk percentage; RP: Milling recovery percentage; GY: Grain yield.

Chenab Basmati respectively whereas sixth Cluster (C6) consisted of two genotypes *i.e.* PK10437-14-2-1 and PK10434-6-2-1, as depicted in Figure 6a and b. Phenotypic characters of each Cluster are given in Table 3.

Genotype-by-environment interaction analysis

To select superior and stable genotypes with better yield across different environments, biplot analysis was executed on three consecutive years data (as different environments) in 20 studied genotypes. Biplot analysis revealed important information about three important aspects including mega-environment analysis, genotype evaluation and test-environment evaluation. Overall, biplot analysis demonstrated that 99.36% of the total variation across different environ

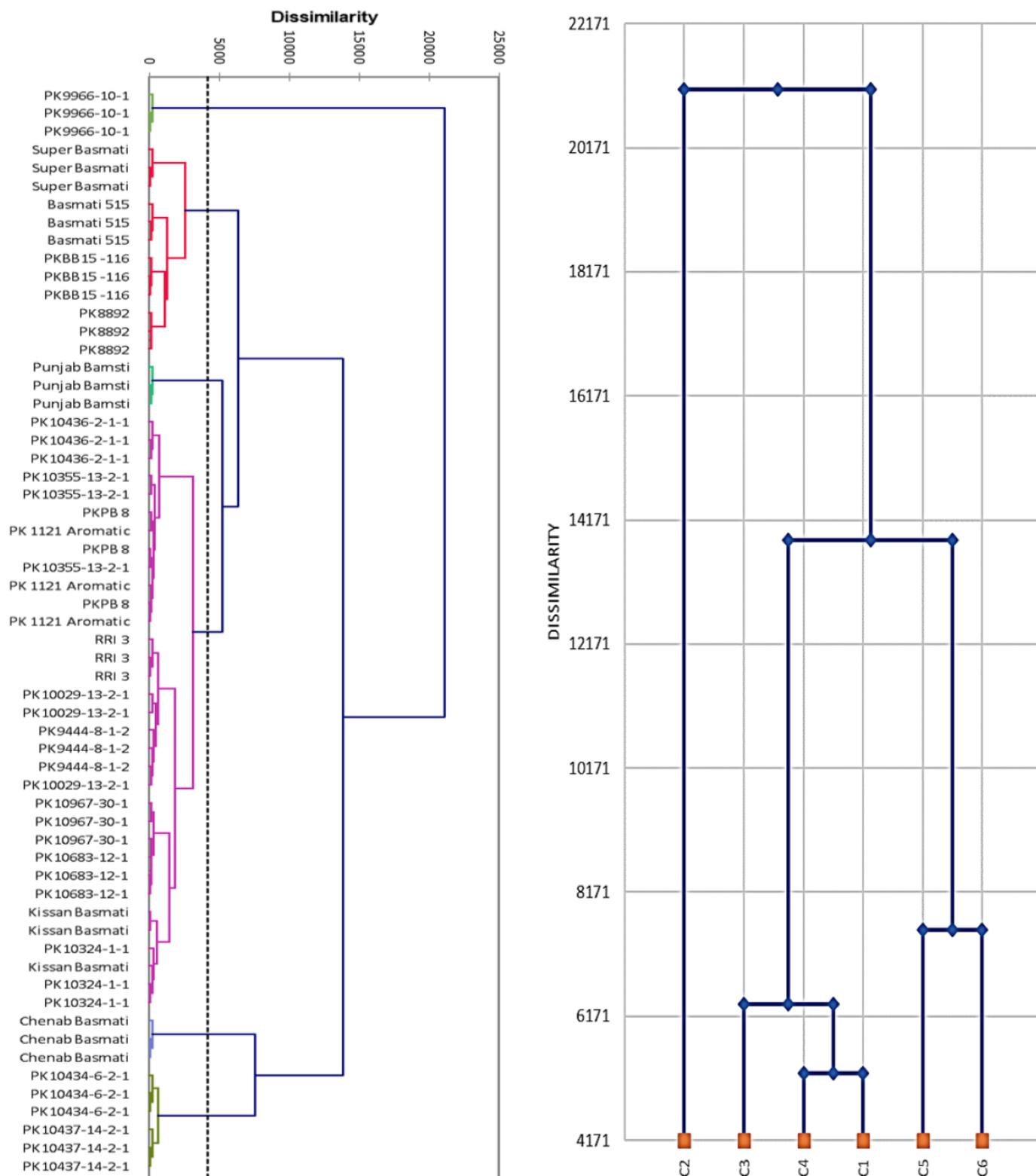


Figure 6: dendrogram or Clustering of genotypes / promising lines studied in three consecutive years from 2016 to 2018 for ten morphological traits related to yield.

ments was explained by two major principal components (PC1 96.2%, PC2 3.16%).

Mega-environment analysis (which-won-where/what) highlighted that all test environments (2016, 2017 and 2018) fell into a single sector and at least eight genotypes (G4, G1, G3, G11, G19, G2, G5,

G20) grouped into this sector (Figure 7A). These results indicate that these eight genotypes had highest yield ($G4 > G1 > G3 > G11 > G19 > G2 > G5 > G20$) in all test environments. Mean performance and stability analysis across test environments (Figure 7B) revealed that among all genotypes, G15 was most stable but had below average yield performance.

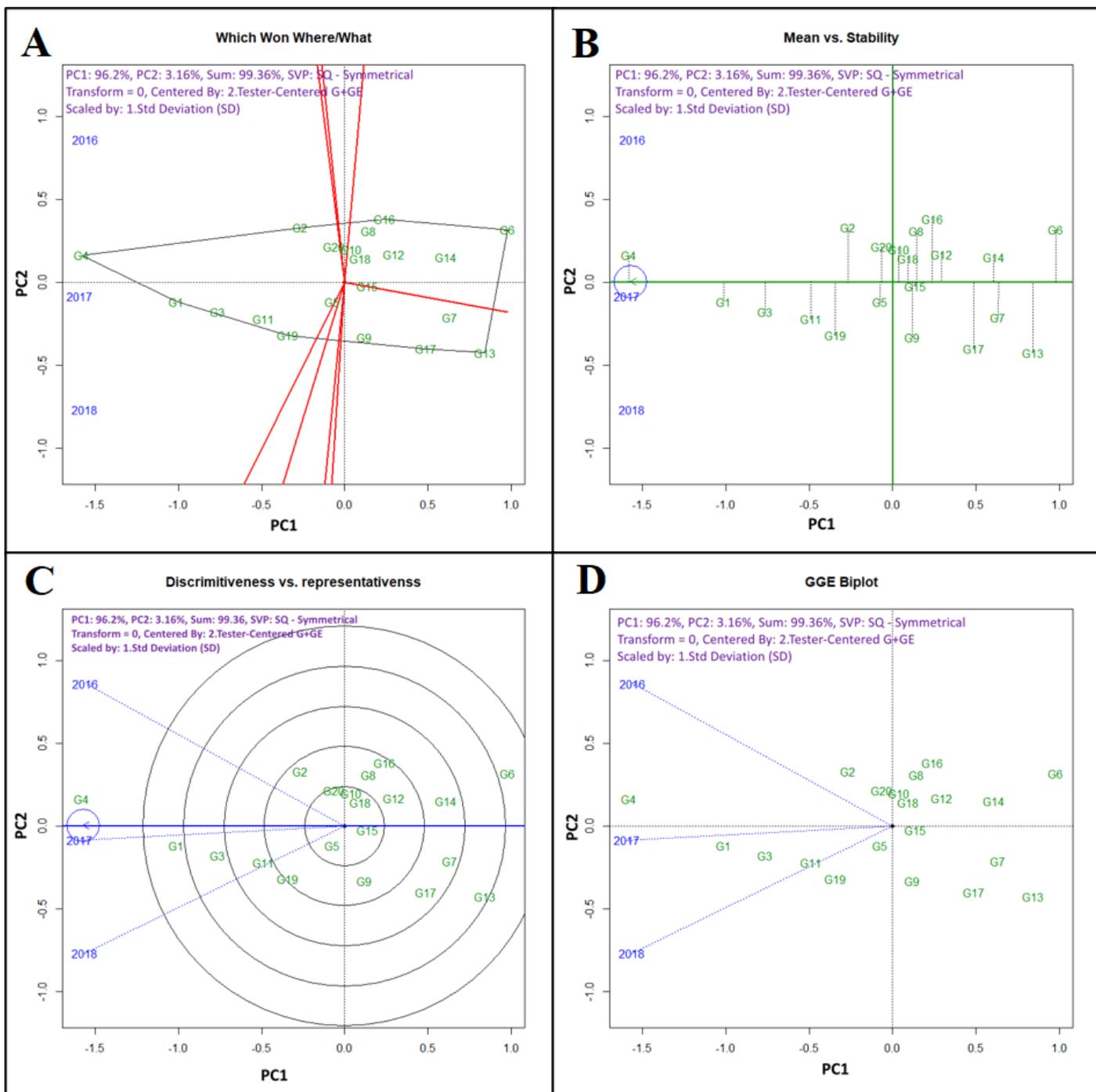


Figure 7: (A) Mega-environment (which-won-were/what) analysis (B) mean performance and stability of genotypes (C) test-environment (discrimitiveness and representativenss) and (D) cumulative biplot analysis views based on GY data of investigated genotypes.

Similarly, G5 > G1 > G4 showed more stability in their respective order along with better yield performance. Whereas, among all studied genotypes, G13, G16 and G17 exhibited lowest yield stability across test environments. Test-environment analysis (discrimitiveness vs representativenss) indicated that genotypes G4 and G1 were best suited for 2017 environment, genotypes G5, G11 and G19 were best suited for 2018 environment, genotypes G2 and G20 were best suited for 2016 environment, whereas genotype G3 performed equally well in 2017 and 2018 en-

vironments (Figure 7C). Collectively, based on GGE biplot analysis results, G4 > G1 > G3 were identified to be most superior genotypes with better yield and stability across multiple environments (Figure 7D).

PK9444-8-1-2 (G1), PK9966-10-1 (G2), PK10029-13-2-1 (G3), PK10324-1-1 (G4), PK10967-30-1 (G5), PKBB15 -116 (G6), PK8892 (G7), RRI-3 (G8), PKPB-8 (G9), Punjab Basmati (G10), Chenab Basmati (G11), Kissan Basmati (G12), Super Bas-

mati (G13), Basmati 515 (G14), PK1121 Aromatic (G15), PK 10436-2-1-1 (G16), PK10437-14-2-1 (G17), PK 10683-12-1 (G18), PK 10355-13-2-1 (G19) and PK 10434-6-2-1 (G20).

Conclusions and Recommendations

Higher yield along with stability in performance over years are the straightforward criteria for developing new cultivars in crop breeding. The attained results revealed presence of exploitable genetic variability among tested twenty (20) elite Basmati genotypes for majority of the traits along with acceptable co-efficient of variation (%) except for HP and RP. Likewise, violin plot areas also showed observable stability in performance of genotypes in terms of studied traits during all the consecutive three years (2016 – 2018) with the exception of two traits *i.e.* NTP and RP. Higher phenotypic variance and co-efficient of variation values were observed for all traits as compared to genotypic variance and co-efficient of variation values which indicated multigenic traits with high influence of environmental factors on expression of these traits. Higher broad sense heritability (%) was also observed which showed higher proportion of total variability is owing to genetic values. Correlation matrix portrayed significantly positive relationship of GY with DM indicating late maturing genotypes were high yielding; significantly positive relationship of PH with DM and highly negative with PL and TGW emphasized longer plants are late to mature as compared to short stature plants. It accentuates the selection of plants with shorter stature with the intent of reducing growth duration in rice. Furthermore, a short duration variety is better than a long duration variety, even with same yield returns. A variety with shorter growth duration would require less water, would be less exposed to hazards such as insects, pests, droughts and floods and more the interval of fellow land available for other crop plantings.

NGP are highly and positively associated with PL, whereas, NP are highly negatively associated with TGW. Such associations represented the opposite relations between two traits and showed that number of grains reduces with increased selection of heavier grains. Dendrograms divided the genotypes into six distinct Cluster with significantly distinct agronomic and morphologic traits depicting significant existence of exploitable variations present. Collectively, based on GGE biplot analysis results, PK10324-1-1

> PK9444-8-1-2 > PK10029-13-2-1 were identified to be most superior genotypes with better yield and stability across three years. PCA results also showed stability in performance relative to all studied traits in all the advance Basmati lines revealing that these lines can be used as direct and indirect material as new Basmati lines and as a parental material to evolve new higher yielding superior quality Basmati lines respectively.

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Novelty Statement

The newly evolved advance Basmati rice lines displaying higher stability in performance and yield tested over three consecutive years in comparison with existing check varieties *i.e.* Super Basmati, Basmati 515 and PK1121 aromatic being cultivated on more than 50% of rice growing area, may be used as novel candidate Basmati lines and may be subjected to national trials to be approved for general cultivation.

Authors contribution

MA, ZH, SSA, TL, RARK, AR, TB, M Ijaz, MAR, M Iqbal and MR acknowledge equal participation in conducting the experiments, outcome of research & development of advance Basmati inbred lines. ZH, QR, AR and TB contributed in writing the manuscript, ZH and RARK conducted the analyses. ZH, SSA and QR analyzed the results. MAR conducted the quality analyses of genotypes, MA and MR improved the final draft of the manuscript.

Supplementary Material

There is supplementary material associated with this article. Access the material online at: <https://dx.doi.org/10.17582/journal.sja/2022/38.....>

Conflict of interest

The authors have declared no conflict of interest.

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