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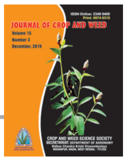

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GGE Biplot analysis for appraisal of basmati rice (*Oryza sativa* L.) genotypes under transplanted and direct seeded condition

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ABSTRACT

The present investigation was planned to identify the stable and adaptable Basmati rice genotypes by using GGE biplot method. Thirty-six genotypes were tested in Randomized Block Design at two locations (Kaul and Uchani) for two growing seasons' viz., kharif 2016 and 2017.The pooled analysis of variance indicated that genotypes, environments and genotype x environment interaction differed significantly for the studied parameters. Based on the GGE biplot analysis, Pusa Sugandh 5 (G31), HKR - 11-509 (G6), PAU 6295-2 (G25),SJR-70-3-2(G33) and Pusa Sugandh 3 (G30) were identified as stable genotypes for number of tillers per plant, biological yield per plant and grain yield per plant across the environments. Pusa 1734-8-3-85 (G21) and CSR-30 (G2), SJR-70-3-2 (G33) and HKR 98-476 (G14), Pusa 1734-8-3-85 (G21) and UPR-386-9-1-1 (G36) under direct seeded condition and Pusa Basmati 1121 (G27) and HKR 11-447 (G13), HKR 06-434 (G9) and HKR -11-509 (G6), Pusa Sugandh 5 (G31) and Pusa Basmati 1 (G26) for transplanted condition showed specific adaptation for number of tillers per plant, biological yield plant and grain yield per plant, respectively.

Keywords: Basmati, environment,G x E interaction, GGE, rice.

Rice is the staple food for more than 50% of the global population and more than 90% of the total rice is produced and consumed in Asian countries (Chauhan *et al.,* 2017). To fulfill the food demands of burgeoning population, the world rice production is needed to increase by 50% from 2010 to 2030 (Avnery *et al.,* 2013). At present more than 70% of the total rice of the globe is produced on irrigated lands (Chakraborty *et al.*, 2017). In South Asian countries, rice is mainly cultivated by transplanting of about one month old seedlings in puddled soil which require a huge amount of water during the growing season and labor for transplanting (Pal *et al.,* 2018). The conventional method of rice cultivation possesses the serious problem of water and labor scarcity in many parts of the world and impacted the rice production (Jabran *et al.,* 2017). Alternative method of rice cultivation like alternate wetting and drying (Lampayan *et al.,* 2015), aerobic or dry direct-seeded rice (Bhushan *et al.*, 2007) which requires less water than conventionally transplanted methods are under investigation. Farmers are adopting direct seeded Rice (DSR) method of rice growing as an alternative in many conventional transplanted (TPR) areas (Sun *et al.,* 2015).

DSR requires less water and laborers in comparison to TPR however, the water stress during the growing season negatively affect the yield, its component, physical and cooking quality of grains (Gunaratne *et al.,* 2011). Number of studies have been planned to measure the yield and quality differences between TPR and DSR. Some studies showed that yield under DSR equals or exceeded the TPR yield however some studies were found against these reports (Xu *et al.,* 2019). To what extent, the DSR practices influence the performance of different genotypes for yield and component traits in comparison to TPR is still under investigation. The response of crops to different environmental conditions depends on the genotype and growth stages. Significant amount of variability among the rice genotypes have been reported in response to varying environmental conditions (Yamakawa *et al.,* 2007).Till now, no specifically adapted genotypes have been developed for DSR and already released varieties for TPR do not perform well under DSR. These variable responses of genotypes over the multi-environments are the main challenges for plant scientists. Significant G × E interaction is the main reason for the variable response of genotypes. Genotype and environment interaction analysis is an important prerequisite to select the stable and specifically adapted genotypes to different environments (Yan, 2011). The potential gene expression of quantitative traits is often affected by growing environments, resulting in poor genetic gain from artificial selection (Horn *et al.*, 2018). A large number of studies have been conducted to identify the stable and adaptable rice genotypes for different ecologies (Tariku, 2017; Katsura *et al.*, 2016). By keeping the above facts in mind, the present investigation was designed to assess the stability and adaptability of thirty-six Basmati rice genotypes under direct seeded and transplanted method ofrice cultivation.

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MATERIALS AND METHODS

The experiment was conducted under two different cultivation methods namely TPR and DSR at two locations, Rice research station, Kaul (Kaithal) and Regional Research Station, Uchani (Karnal) which falls under sub-tropical region of North India during *kharif* 2016 and *kharif* 2017. Thirty-six basmati rice genotypes were planted in randomized block design (RBD) in three replications (Table 1). Plot size consisted of 5 rows of 1m length. In DSR cultivation method, overnight pre-germinated seeds were dibbled at 15 x 20 cm^2 spacing. Irrigation was applied at an interval of 6-7 days when hair cracks developed on the surface. In conventional TPR method, 27 days old 2-3 seedlings per hill spaced at 15 × 20 cm^2 were transplanted. The inorganic fertilization @ N (90 kg ha^{-1}), P (30 kg ha^{-1}) and K (30 kg ha^{-1}) was used. Irrigation was applied at 3 days interval up to 90-100 DAT in TPR. Seed rate under both TPR and DSR was 20 kg ha^{-1}. Description of environment was given in Table 2.

Statistical analysis

The data analysis for number of tillers per plant, biological yield per plant (g) and grain yield per plant (g) was done by using GGE biplot methodology. This methodology emphasizes the two source of variation, genotype (G) and genotype environment (GE) to be considered simultaneously for genotype and environment evaluation (Yan, 2001). GGE biplots were used to identify (i) the mega-environment using which-won-where pattern, to recommend the genotypes for specific mega-environments (ii) the stable genotypes that can be recommended across the environments (iii) the target environments for different genotypes under study.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

A broad range of variation in the mean performance of genotypes across the locations under DSR and TPR were observed for the studied traits (Table 3). The variability for number of tillers per plant ranged from 6.48-14.15 and 10.33-17.10 with mean value 10.54 and 14.01; for biological yield per plant from 28.62-48.76 and 37.62-54.50 with mean 38.50 and 43.70; for grain yield per plant from 7.87-15.72 and 12.37-18.21 with mean 12.09 and 15.65 under DSR and TPR, respectively.Under DSR, highest value for grain yield and number of tillers per plant were observed for genotypes Pusa 1734-8-3-8, CSR-30 and Pusa 1656-10-705.While under TPR, Pusa Sugandh 5, Pusa Basmati 1 and 6 had maximum value for grain yield per plant and Pusa Basmati 1121 Pusa Sugandh 5 and HKR 11-447 for number of tillers per plant. Similarly, SJR-70-3-2, HKR 98-476 and Pusa 1734-8-3-85 under DSR while, HKR 06-434, HKR -11-509 and Taraori Basmati under TPR had maximum value for biological yield per plant. The results of the pooled ANOVA for number of tillers per plant and biological yield per plant were indicated in Table 4. The results suggested that all sources of variation *viz.,*environments, genotypes and genotype × environment (GE) interaction differed significantly at 5% probability level. The G × E interaction further partitioned in interaction principal components (IPC) and first two IPCs contributed 91.6% and 90.7% of the total variation for number of tillers per plant, biological yield per plant and grain yeild per plant respectively. Mostafavi *et al.* (2011), Tariku (2017) and Zewdu *et al.* (2020) evaluated the rice genotypes under multi-environmental conditions and selected the genotypes generally and specifically adapted to different environments.

Polygon view

The polygon view of the biplot represents the desirable genotype(s) in each environment or groups of environments (Yan and Hunt, 2002). The polygon is formed by connecting the vector length of the vertex genotypes from the origin of biplot in such a way that the remaining genotypes come inside the polygon. The vertex genotypes viz., G14 (HKR 98-476), G21 (Pusa 1734-8-3-85), G27 (Pusa Basmati 1121), G8 (HKR 08-417), G4 (Haryana Basmati 1) and G3 (CSR TPB-1)for number of tillers per plant (Fig. 1), G9 (HKR 06-434), G33 (SJR-70-3-2), G14 (HKR 98-476), G2 (CSR-30), G3 (CSR TPB-1) and G35 (Taraori Basmati) for biological yield per plant (Fig. 4) and G31 (Pusa Sugandh 5), G21 (Pusa 1734-8-3-85), G2 (CSR-30), G17 (PAU-6297-1), G3 (CSR TPB-1) and G4 (Haryana Basmati 1) for grain yield per plant (Fig. 7) have the longest vector length which decides the response of genotypes to different environments.Therefore, the vertex genotypes are the highly responsive genotypes compared to others. Comparison can be made with the vertex genotypes in adjacent sectors of the polygon. For example, genotype G21 (Pusa 1734-8-3-85) and G27 (Pusa Basmati 1121) indicated that G21 (Pusa 1734-8-3-85) had maximum number of tiller per plantin E1, E2, E3 and E4 environments because genotype G21 (Pusa 1734-8-3-85) located in one sector with these environments. The genotype G27 (Pusa Basmati 1121) is better in E5, E6, E7 and E8 environments. G9 (HKR 06-434) had maximum biological yield per plant under E5, E6, E7 and E8 environment whereas G14 (HKR 98-476) had highest biological yield under E1, E2, E3 and E4 environment. Similarly, genotype G31 (Pusa Sugandh 5) had highest grain yield per plant in E5, E6, E7 and E8 environments while G21 (Pusa 1734-8-3-85) performed better in E1, E2, E3 and E4 environment. The rays fractionate the biplot into sectors, and eight environments fall into anyone of these sectors. The vertex genotypes of each sector are best forthe evaluated traits for the environments that come under that particular sector. The genotype G21 (Pusa 1734-8-3-85) followed by G2 (CSR-30) had the maximum number of tillers per plant in E1, E2, E3 and E4

Table 1 : List of genotypes used in the study

Code	Genotypes	Code	Genotypes	Code	Genotypes
G1	Basmati 370	G13	HKR 11-447	G25	PAU 6295-2
G2	CSR-30	G14	HKR 98-476	G26	Pusa Basmati 1
G3	CSR TPB-1	G15	HUBR-16	G27	Pusa Basmati 1121
G4	Haryana Basmati 1	G16	Improved Pusa Basmati 1	G28	Pusa Basmati 1509
G5	Haryana Mahak 1	G17	PAU-6297-1	G29	Pusa Sugandh 2
G6	HKR -11-509	G18	Pusa 1475-03-42-45-119-1	G30	Pusa Sugandh 3
G7	HKR 03-408	G19	Pusa 1637-2-8-20-5	G31	Pusa Sugandh 5
G8	HKR 08-417	G20	Pusa 1656-10-705	G32	Pusa Basmati 6
G9	HKR 06-434	G21	Pusa 1734-8-3-85	G33	SJR-70-3-2
G10	HKR 06-443	G22	Pusa 1826-12-27-1-4	G34	Super Basmati
G11	HKR 06-487	G23	Pusa 1884-3-9-175	G35	Taraori Basmati
G12	HKR 08-425	G24	Pusa 1884-9-12-14	G36	UPR-386-9-1-1

Table 2: Description of different Basmati rice cultivation methods

Cultivation method	Season	Location	Code
Direct Seeded Rice	*Kharif* 2016	Kaul	E1
Direct Seeded Rice	*Kharif* 2017	Kaul	E2
Direct Seeded Rice	*Kharif* 2016	Uchani	E3
Direct Seeded Rice	*Kharif* 2017	Uchani	E4
Transplanted Rice	*Kharif* 2016	Kaul	E5
Transplanted Rice	*Kharif* 2017	Kaul	E6
Transplanted Rice	*Kharif* 2016	Uchani	E7
Transplanted Rice	*Kharif* 2017	Uchani	E8

environments while G27 (Pusa Basmati 1121) followed by G13 (HKR 11-447) had highest tillers per plant in E5, E6, E7 and E8 (Fig. 1). The other vertex genotypes, G14 (HKR 98-476), G4 (Haryana Basmati 1), G3 (CSR TPB-1) and G8 (HKR 08-417) were poorest in all environments because there is no environment in their sectors. G9 (HKR 06-434) followed by G6 (HKR -11-509) produced maximum biological yield under E5, E6, E7 and E8 while G14 (HKR 98-476) followed by G33 (SJR-70-3-2) and G21 (Pusa 1734-8-3-85) had maximum biological yield under environments E1, E2, E3 and E4 (Fig. 4). In the same way, G31 (Pusa Sugandh 5) followed by G26 (Pusa Basmati 1) and G30 (Pusa Sugandh 3) had highest grain yield under E5, E6, E7 and E8 whereas G21 (Pusa 1734-8-3-85), G25 (PAU 6295-2) and G36 (UPR-386-9-1-1) gave maximum grain yield under E1, E2, E3 and E4 (Fig. 7). Check cultivar Sahbhagi Dhan was found suitable for *Rabi* season and Tulasi for *Kharif* season (Balakrishnan *et al.,* 2016). Similarly, Tariku (2017) identify genotype NERICA-13as the winner genotype for Woreta and Pawe location while genotype FOFIFA-4129 as good yielder for Metema location.

Environmental view

The angle among the vectors of the different environments defines the association among them (Yan, 2002). On the basis of angles between the environmental vectors, the eight environments were categorized into two classes. Class 1 have E1, E2, E3, E4 and class 2 have E5, E6, E7 and E8 environments for number of tillers (Fig. 2), biological yield per plant (Fig. 5) and grain yield per plant (Fig. 8). The small angle among the four environments of each class indicated positive correlation between them for all the studied traits. These environments provide similar information about the genotypes. Whereas the large angle between the environments of class 1 and class 2 shows the poor association between them. Another major fact from the environmental view of the biplot is the length of the environment vectors which depicts the discriminating ability and representativeness. An ideal environment is denoted by a small circle. An ideal test environment is one having most extended vector among the environments and placed on AEC abscissa (Yan and Kang, 2003). Environment E2 and E8 were the most discriminating indicating that these environments are suitable for the selection of specially adapted genotypes for number of tillers per plant (Fig. 2) biological yield per plant (Fig. 5) and grain yield per plant (Fig. 8). The line passing through the origin of biplot and the mean environment is AEC. The angle between the AEC axis and the vector of an environment indicates the representativeness of the environment. In present study none of the environment is most representative for either

Table 3 : Mean performance of 36 Basmati rice genotypes under DSR and TPR over the locations and years for number of tillers, biological yield and grain yield per plant

Genotypes	Number of tillers per plant		Biological yield per plant		Grain yield per plant	
	DSR	TPR	DSR	TPR	DSR	TPR
Basmati 370	8.43	12.08	35.37	46.50	9.95	13.55
CSR-30	13.13	14.02	41.90	40.25	14.62	15.05
CSR TPB-1	6.48	10.33	28.62	37.62	7.87	12.37
Haryana Basmati 1	6.57	12.53	32.17	42.85	8.16	15.17
Haryana Mahek 1	11.31	12.36	42.84	45.68	12.94	13.85
HKR -11-509	11.58	14.08	41.05	48.30	13.05	16.63
HKR 03-408	7.43	12.18	31.55	44.55	9.21	13.39
HKR 06-417	7.16	13.13	31.00	39.30	8.65	14.50
HKR 06-434	11.46	15.04	46.19	54.50	12.95	17.28
HKR 06-443	8.41	13.00	36.43	43.17	10.06	14.50
HKR 06-487	10.26	13.31	34.70	39.49	12.29	14.48
HKR 08-425	12.67	14.46	40.85	45.54	13.93	17.10
HKR 11-447	10.96	16.16	42.97	45.29	12.52	17.10
HKR 98-476	12.08	12.68	48.06	44.50	13.81	14.07
HUBR-16	8.33	14.44	31.86	40.32	9.80	16.08
Improved Pusa Basmati 1	10.78	15.51	37.63	45.15	12.21	16.92
PAU-6297-1	11.71	12.54	44.85	42.05	13.40	13.56
Pusa 1475-03-42-45-119-1	9.08	11.81	35.95	41.75	11.08	14.40
Pusa 1637-2-8-20-5	12.38	14.44	40.49	40.88	13.90	17.04
Pusa 1656-10-705	12.85	15.35	41.17	41.04	14.24	17.10
Pusa 1734-8-3-85	14.15	15.38	46.76	45.37	15.72	17.12
Pusa 1826-12-271-4	11.38	13.90	42.01	42.97	12.96	15.35
Pusa 1884-3-9-175	9.70	15.03	35.79	46.24	10.91	16.80
Pusa 1884-9-12-14	7.15	11.43	31.52	40.45	8.80	12.93
Pusa 6295-2	12.52	15.68	41.75	45.88	14.05	16.25
Pusa Basmati 1	12.46	15.28	37.98	43.00	13.95	17.83
Pusa Basmati 1121	10.40	17.10	36.08	46.30	11.87	17.00
Pusa Basmati 1509	12.60	15.18	38.91	40.26	14.00	16.79
Pusa Sugandh 2	10.25	14.02	36.70	40.93	11.67	15.50
Pusa Sugandh 3	11.44	15.26	37.56	43.57	13.16	17.35
Pusa Sugandh 5	12.53	16.31	40.74	45.68	13.98	18.21
Pusa Basmati 6	11.41	15.97	39.40	46.17	12.83	17.40
SJR-70-3-2	11.28	15.52	48.76	46.53	12.98	17.06
Super Basmati	8.72	12.14	32.68	43.50	10.28	14.31
Taraori Basmati	8.13	12.43	32.15	47.13	9.49	13.65
UPR-386-9-1-1	12.41	14.49	41.55	40.44	13.95	15.54
Range	6.48-14.15	10.33-17.10	28.62-48.76	37.62-54.50	7.87-15.72	12.37-18.21
Overall mean	10.54	14.01	38.50	43.70	12.09	15.65

Table 4 : Analysis of variance of 36 rice genotypes and 8 environments for number of tillers per plant and biological yield per plant

Source	df	Number of tillers plant^{-1}	Biological yield plant^{-1}	Grain yield plant^{-1}
Environment (E)	7	124.60**	287.85**	130.68**
Genotype (G)	35	22.76**	103.57**	22.00**
G x E	245	1.12**	8.96**	1.11**
PC 1	41	20.08**	39.81**	4.64**
PC 2	39	4.00**	4.59**	0.96**
Pooled error	560	0.73	1.29	0.48

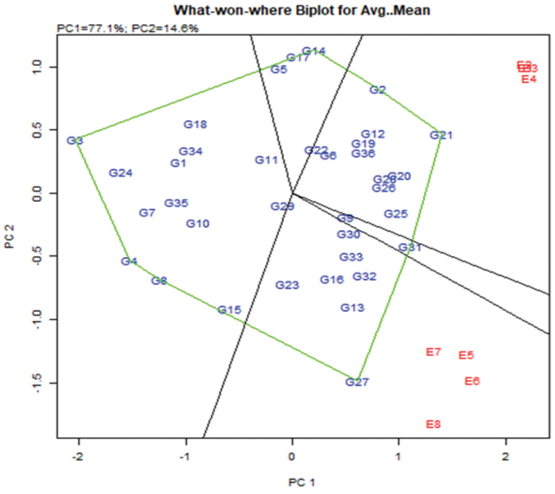

Fig. 1 : Polygon view for number of tillers plant^{-1}

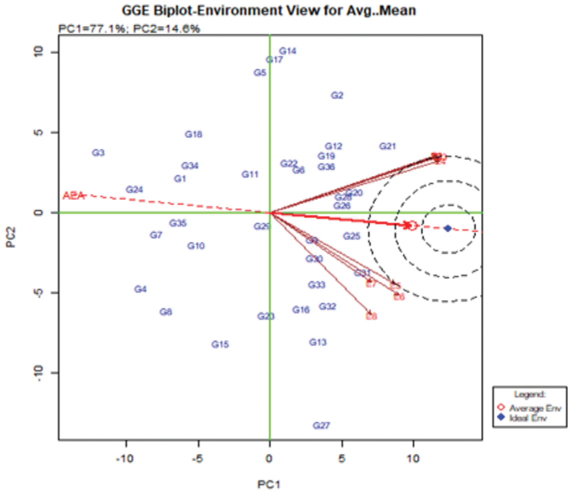

Fig. 2 : Environmental view for number of tillers plant^{-1}

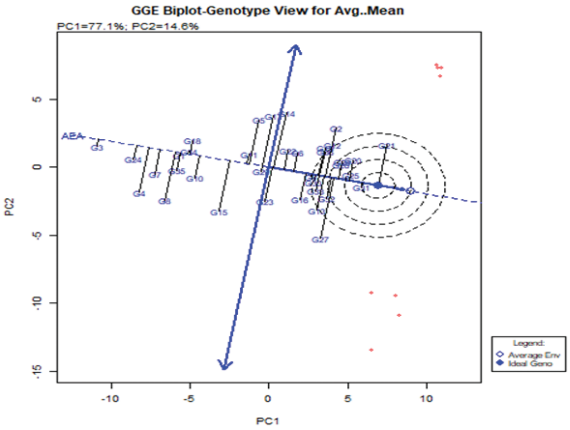

Fig. 3 : Genotypic view for number of tillers plant^{-1}

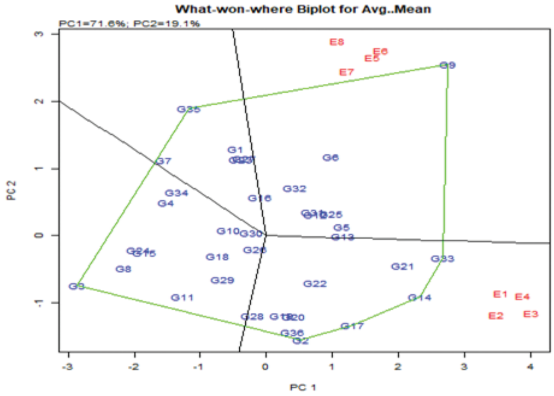

Fig. 4: Polygon view for biological yield plant^{-1}

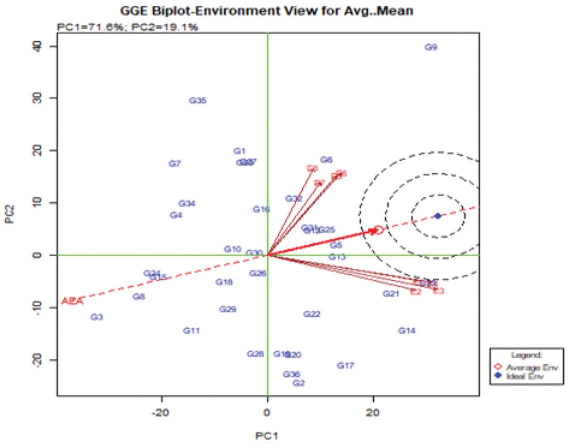

Fig. 5 : Environmental view for biological yield plant^{-1}

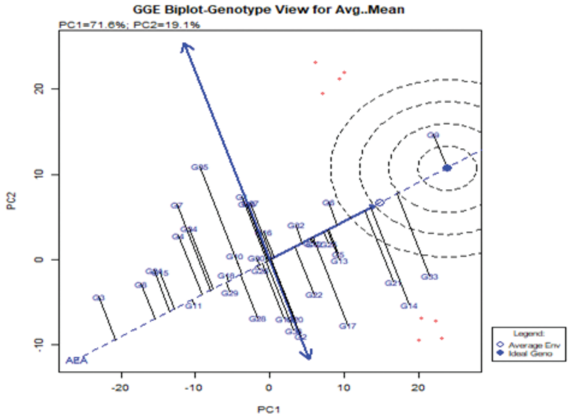

Fig. 6 : Genotypic view for biological yield plant^{-1}

of the trait.The most representative and discriminating environment is good for the identification of generally adapted genotypes. Ram *et al.* (2020) observed late sown irrigated condition as the most desirable environment for the selection of generally adapted genotypes of wheat. Kesh *et al.* (2021) found chemical free cultivation production environment as most representative while direct seeded rice and system of rice intensification as most discriminating.

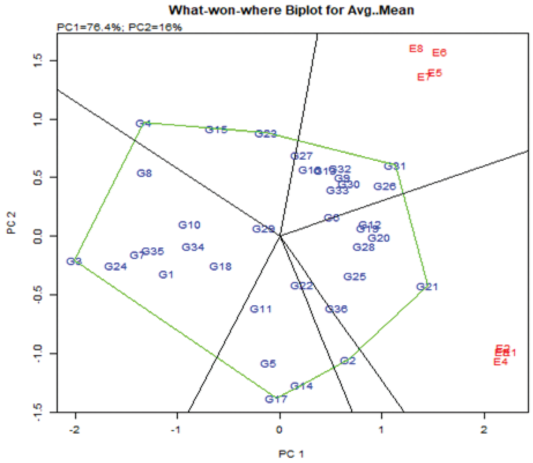

Fig. 7 : Polygon view for grain yield plant^{-1}

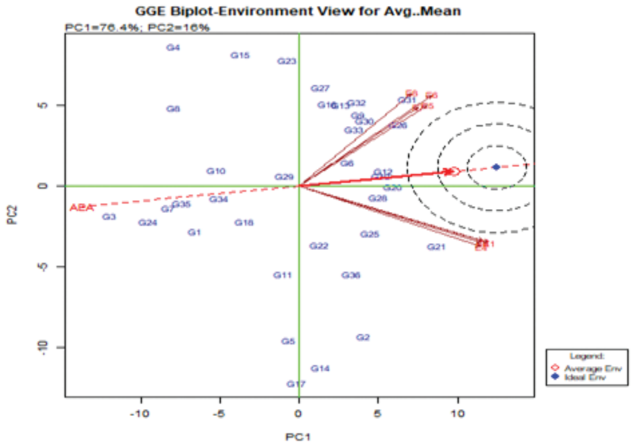

Fig. 8 : Environmental view for grain yield plant^{-1}

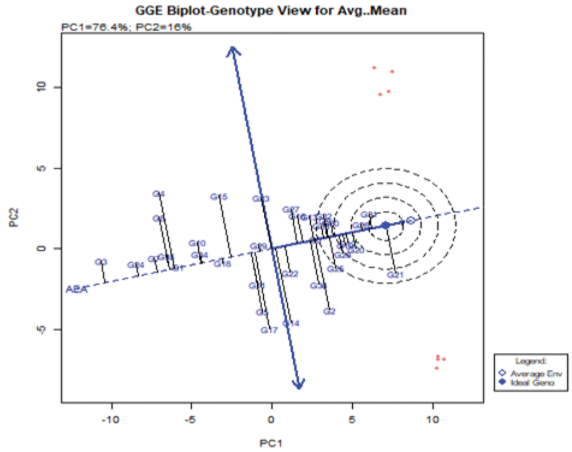

Fig. 9: Genotypic view for grain yield plant^{-1}

Genotype view

Fig. 3 and 6 shows the ranking and distance of the thirty-sixgenotypes by taking the reference of the ideal genotype identified by the average environmental coordinate (AEC). An ideal genotype is the one having large IPCA1 value. i.e., high mean with small IPCA2 value, i.e., more stability (Yan, *et al*., 2000). The filled bluecirclein Fig. 3 and 6denoted the place of ideal genotype. In real situation, the ideal genotype might not exist;but could be taken as a reference for genotypic evaluation (Anothai *et al*., 2009). G31 (Pusa Sugandh 5) for number of tillers per plant (Fig. 3), G6 (HKR -11-509) for biological yield per plant (Fig. 6) and G31 (Pusa Sugandh 5) for grain yield per plant (Fig. 9) were found as most stable genotypes due to their presence nearby the blue circle. The other stable genotypes were G25 (PAU 6295-2), G26 (Pusa Basmati 1), G33 (SJR-70-3-2) and G30 (Pusa Sugandh 3) for number of tillers per plant (Fig. 3);G31 (Pusa Sugandh 5), G25 (PAU 6295-2), G32 (Pusa Basmati 6) and G16 (Improved Pusa Basmati 1) for biological yield per plant (Fig. 6) and G26 (Pusa Basmati 1), G30 (Pusa Sugandh 3), G33 (SJR-70-3-2) and G12 (HKR 08-425) for grain yield per plant (Fig. 9). Improved Pusa Basmati 1 and HUBR-16 were found as stable genotypes for plant height having general adaptation across the environments (Kesh *et al.,* 2018). On the basis of GGEbiplot, Hidassie and NERICA-4 were identified as the most stable and high yielder genotypes (Zewdu *et al.,* 2020). Okra genotypes VRO-112, Kashi Kranti, VRO-110 and VRO-6 were found most desirable genotypes for fruit yield under alkaline environment (Sanwal *et al.,* 2021).

The presence of GEI complicates the selection of desirable genotypes under multi-environmental trials.Both mean yield and stability should be considered simultaneously for making the effective selection of genotypes and to reduce the effect GEI. Based on results it could be concluded that GGE biplot is an efficient technique to identify the high yielding, stable and adaptable genotypes. Genotypes G31 (Pusa Sugandh 5), G6 (HKR -11-509), G25 (PAU 6295-2), G33 (SJR-70-3-2) and G30 (Pusa Sugandh 3) were identified as stable genotypes for all the studied parameters across the environments. G21, G2; G33 (SJR-70-3-2), G14 (HKR 98-476); and G21 (Pusa 1734-8-3-85), G36 (UPR-386-9-1-1) showed specific adaptation to DSR condition while G27 (Pusa Basmati 1121), G13 (HKR 11-447); G9 (HKR 06-434), G6 (HKR -11-509) and G31 (Pusa Sugandh 5), G26 (Pusa Basmati 1) under TPR condition for number of tillers per plant, biological yield per plant and grain yield per plant, respectively.

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