



GGE biplot analysis of finger millet (*Eleusine coracana*) genotypes under diverse agro-climatic conditions of Uttarakhand

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Received: 23 January 2023; Accepted: 8 June 2023

ABSTRACT

Finger millet [*Eleusine coracana* (L.) Gaertn.] is mostly cultivated in the arid and semi-arid regions of India. In this study, 11 finger millet genotypes were evaluated for six traits in a randomized complete block design with three replications at Ranichauri (E1), Dehradun (E2) and Pantnagar (E3) of Uttarakhand during *kharif* 2018 and 2019. The analysis of variance revealed significant variation among genotypes due to genotypes (G), environments (E) and G×E interaction (GEI) effects. The environment contributed for 37.3%, 38.6%, 58.2%, 65.5%, 21.0% and 76.9% of the total variation for days to 50% flowering, plant height, number of tillers, number of heads, number of fingers and grain yield, respectively. Grain yield exhibited a crossover-type GEI effect with a high environmental and GEI variance proportion. The mean grain yield over the locations was ranged from 16.9 (E1) to 38.8 q/ha (E3), whereas the genotypic mean was stretched from 22.7 (PF5) to 34.3 q/ha (PF8). The GGE biplot graphical analysis identified three mega environments, and the best genotypes were PF5, PF6 and PF2 in E1; PF8 in E2; PF10 and PF11 in E3. Based on a hypothetical ideal genotype, PF8 was identified as the best genotype owing to the high mean grain yield and stability over the locations. The ranking of genotypes based on ideal genotype would be as follows: PF8>PF10>PF3>PF7>PF2>PF1>PF11>PF4>PF9>PF6>PF5. The location Dehradun had high discriminating ability and representativeness and considered as the best environment for selecting high-yielding and stable genotypes among the locations.

Keywords: Finger millet, Genotype-by-environment interaction, GGE biplot, Stability, Representativeness

Finger millet [*Eleusine coracana* (L.) Gaertn.] is native to Ethiopian highlands and was introduced into India more than 3000 years ago (Hilu *et al.* 1979). The crop is mostly cultivated under traditional tribal farming system at semi-arid and arid regions in India and East Africa for a long time where other crops fail to produce grain. The grains are rich source of mineral and nutrients (Chandra *et al.* 2016). Finger millet is also known as poor man's crop and used as important staple food after rice, wheat, sorghum and pearl millet (Sharma *et al.* 2022a). Grains are used as food for human consumption and fodder as feed for maintaining livestock populations (Reddy *et al.* 2021, Sharma *et al.* 2022b). Finger millet grows over 9.22 million hectares

(Mha) of land globally and its production registers 11.63 million tonnes (MT) while in India it covers an area of 1.19 Mha and produces 2.0 MT of grains.

Finger millet is a climate-resilient crop yet the physiological production of grain among genotypes are always affected by environment (E), and genotype-by-environment interaction (GEI) effect (Ghaffari *et al.* 2021, Yan and Kang 2003). Suitable genotypes are selected based on their stability and high yielding ability after robust testing across the different environmental conditions over the years (Chand *et al.* 2021) to access the G × E interaction effect among different genotypes of finger millet for general and specific adaptations (Aarthi *et al.* 2020).

Several numerical and graphical stability approaches have been used to analyze the effect of G × E interactions and identify superior genotypes for high yield and stability across diverse environmental conditions. The GGE biplot analysis is a practical graphical approach that provides graphical images of each trait from multi-environment trial (MET) and are considered to be more informative for extracting valuable overview of complex original data (Yan 2015). In this study, finger millet genotypes were evaluated

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at three locations for the identification of–(i) best genotype (high yielding) in each environment, (ii) stable genotype over the locations, (iii) most suitable environment for a genotype, and for (iv) determination of the discriminating ability and representativeness of environments for genotypic evaluation, and (v) ranking of genotypes based on average yield and stability.

MATERIALS AND METHODS

The present study was carried out at Ranichauri (E₁, 30°18'N; 78°24'E; 2200 m amsl); Dehradun (E₂, 30°15'N; 78°10'E; 640 m amsl) and Pantnagar (E₃, 29°02'N; 79°30'E, 243.84 m amsl). Genetic material comprised a set of 11 finger millet genotypes belonging to early, medium, and late maturity groups and were accessed from different centers (Table 1). Soil type, average annual rainfall and temperature at Ranichauri (silty clay soil, 1200–1400 mm, 3–28°C), Dehradun (alluvial, 2000 mm, 5.2–36°C) and Pantnagar (silty loam, 600 mm, 6–37°C) also varied considerably. Seeds were sown on first week of July 2018 and 2019 and experiments were laid out in randomized complete block design (RCBD) with three replications in each site. Plot size was maintained 3.0 × 1.5 m² at each location with five rows. One outer border row on each side of plot was not considered for recording data. Recommended cultural practices were employed during crop season for better plant stand and growth. Data were collected on six characters that included grain yield (GY; q/ha), days to 50% flowering (DTF; days), plant height (PH; cm), number of productive tillers (NPT), number of fingers (NF) per head and number of heads (NH). Field data on PH, NPT and NF were recorded from 10 randomly selected plants, while NH, DTF, and

GY were measured based on each plot. By combining the two year data, GY stability and suitability of the test environment was examined by using combined analysis of variance using PBSTAT-PPB 1.2 software (Suwarno *et al.* 2015), GGE biplot analysis using PB Tools (PBTools, 2014) and PBSTAT-GE software (Suwarno *et al.* 2015). Singular value partitioning (SVP) and symmetric scaling were employed for the study of which-won-where pattern.

RESULTS AND DISCUSSION

Analysis of variance and mean performance: The combined analysis of variance revealed significant differences (P<0.01) among genotypes, environments and GEI effect for all the traits in both the seasons (Table 2). The relative contributions of each source of the total variation (G+E+GE) are depicted in Table 2. However, it showed considerable differences in the magnitude of their relative proportion of variance over total variability among traits. Among the studied traits, environment played most significant role for GY (76.9%), NH (65.5%) and NT (58.2%) in determining phenotypic variation and performance of genotypes. The large GE effect with low G effect were observed for NF (50.6%, 28.4%), PH (34.4%, 27.0%), NH (21.2%, 13.3%) and GY (19.2%, 3.9%), respectively whereas large G effect with low GE effect were recorded for DTF (54.5%, 8.2%) and NT (22.8%, 19.0%), respectively (Table 2). The environment effect was almost similar in 2018 and 2019 for all the traits. In combined analysis, the genotypes accounted for 54.5%, 27.0%, 22.8%, 13.3%, 28.4% and 3.9% of the total variation for DTF, PH, NT, NH, NF and GY, respectively. Likewise, the environment contributed for 37.3%, 38.6%, 58.2%, 65.5%, 21.0% and 76.9% of the total variation for DTF, PH, NT, NH, NF and GY, respectively. Similarly, the contribution of GE was 8.2, 34.4, 19.0, 21.2, 50.6 and 19.2 for DTF, PH, NT, NH, NF and GY, respectively. For grain yield, environment effect accounted for 79.4% of the total variation in 2018 and 75.4% in 2019. Likewise, the proportions of variation explained by GE were 18.5% and 19.2% in 2018 and 2019, respectively.

The high proportion of GEI variance assigned the probable evidence of cross-over type interaction as it shows the high magnitude of GEI effect; however, least proportion GEI variance possibly produces a testimony for non-cross over type interaction. The result of ANOVA highlighted that the proportion of variation due to genotypic variance was higher than the environment and G×E variance for DTF. This suggested that DTF exhibited the non-crossover type of interaction where genotypic differences constituted the major part of variability. However, the proportion of G×E variance was higher over genotypic and environmental variance for NF and showed cross-over type of interaction.

For GY, the proportion of environmental variance was higher than the genotypic and G×E variance (Table 2). It was, therefore, apparent that the environment that varied widely with change in growing site at different locations exerted a significant influence on grain production among finger millet genotypes and showed crossover type of

Table 1 Detailed information on genotypes, maturity groups, testing locations, and their codes used in the study

Genotype	Code	Accessed from	Maturity *	Location
PF1	G1	PCPGR, Pantnagar	Medium	Ranichauri (E1)
PF2 (check)	G2	VPKAS, Almora	Early	Dehradun (E2)
PF3	G3	ICRISAT, India	Late	Pantnagar (E3)
PF4 (check)	G4	ICRISAT, India	Medium	
PF5	G5	ICRISAT, India	Extra Early	
PF6	G6	ICRISAT, India	Medium	
PF7	G7	PCPGR, Pantnagar	Early	
PF8	G8	GBPUA&T, Pantnagar	Late	
PF9 (check)	G9	Local collection, Pithoragarh	Late	
PF10	G10	PCPGR, Pantnagar	Late	
PF11	G11	ICRISAT, India	Late	

*Early, 52–65 days; Medium, 66–80 days; Late, 81 days onwards (number of days required for flowering under Pantnagar environment).

Table 2 The combined analysis of variance (ANOVA) and total variation (G+E+GE) is explained by genotype (G), environment (E), and genotype-by-environment interaction (GEI) for different traits across 2018 and 2019

Trait	Parameter	Source of variation		
		G	E	GEI
DTF 2018	MS	1365.5**	5845.6**	120.9**
	Proportion of G/E/GE (%)	51.8	35.7	12.5
DTF 2019	MS	2465.5**	7015.6**	160.8**
	Proportion of G/E/GE (%)	54.3	38.8	6.9
DTF combined	MS	1956.5**	6683.5**	147.5**
	Proportion of G/E/GE (%)	54.5	37.3	8.2
PH 2018	MS	852.1**	6598.5**	531.6**
	Proportion of G/E/GE (%)	28.8	36.7	34.5
PH 2019	MS	1051.6**	7215.5**	635.2**
	Proportion of G/E/GE (%)	26.3	39.2	34.5
PH combined	MS	972.9**	6968.3**	620.0**
	Proportion of G/E/GE (%)	27.0	38.6	34.4
NT 2018	MS	2.6**	42.8**	0.8**
	Proportion of G/E/GE (%)	21.9	57.9	20.2
NT 2019	MS	6.2**	60.5**	2.8**
	Proportion of G/E/GE (%)	22.3	59.4	18.3
NT combined	MS	4.0**	50.5**	1.6**
	Proportion of G/E/GE (%)	22.8	58.2	19.0
NH 2018	MS	0.6**	34.8**	0.8**
	Proportion of G/E/GE (%)	13.5	63.2	23.3
NH 2019	MS	2.5**	48.4**	2.5**
	Proportion of G/E/GE (%)	12.4	67.2	20.4
NH combined	MS	1.7**	40.6**	1.3**
	Proportion of G/E/GE (%)	13.3	65.5	21.2
NF 2018	MS	8.2**	38.5**	8.7**
	Proportion of G/E/GE (%)	28.7	21.5	49.8
NF 2019	MS	15.4**	49.5**	14.2**
	Proportion of G/E/GE (%)	28.8	20.6	50.6
NF combined	MS	12.0**	44.4**	10.7**
	Proportion of G/E/GE (%)	28.4	21.0	50.6
GY 2018	MS	89.5**	10121.6**	245.8**
	Proportion of G/E/GE (%)	2.1	79.4	18.5
GY 2019	MS	125.9**	11450.8**	302.7**
	Proportion of G/E/GE (%)	5.4	75.4	19.2
GY combined	MS	114.4**	11210.7**	278.9**
	Proportion of G/E/GE (%)	3.9	76.9	19.2

**P<0.01; DTF, Days to 50% flowering; PH, Plant height; NT, Number of productive tillers; NH, Number of heads; NF, Number of fingers and; GY, Grain yield.

interaction (Fig 1A). Bandyopadhyay (2001) also studied the impact of temperature and rainfall on grain production in finger millet at high altitude and suggested that the competence to grain yield largely depends on the physiogenotypic response of the plant. In this study, for grain yield, PF10 performed excellently in E3 but not in E1 and E2. However, PF5 had a high grain yield in E1 and E2

but not in E3 (Fig 1A). It showed that variability in GY production had a greater reliance on overall temperature effect and rainfall distribution to the respective location at the growing site during the entire cropping season of the plant. Based on Euclidean distance for GY, all three locations were constellated into different groups and, likely, genotypes could be grouped into five clusters (Fig 1B). The

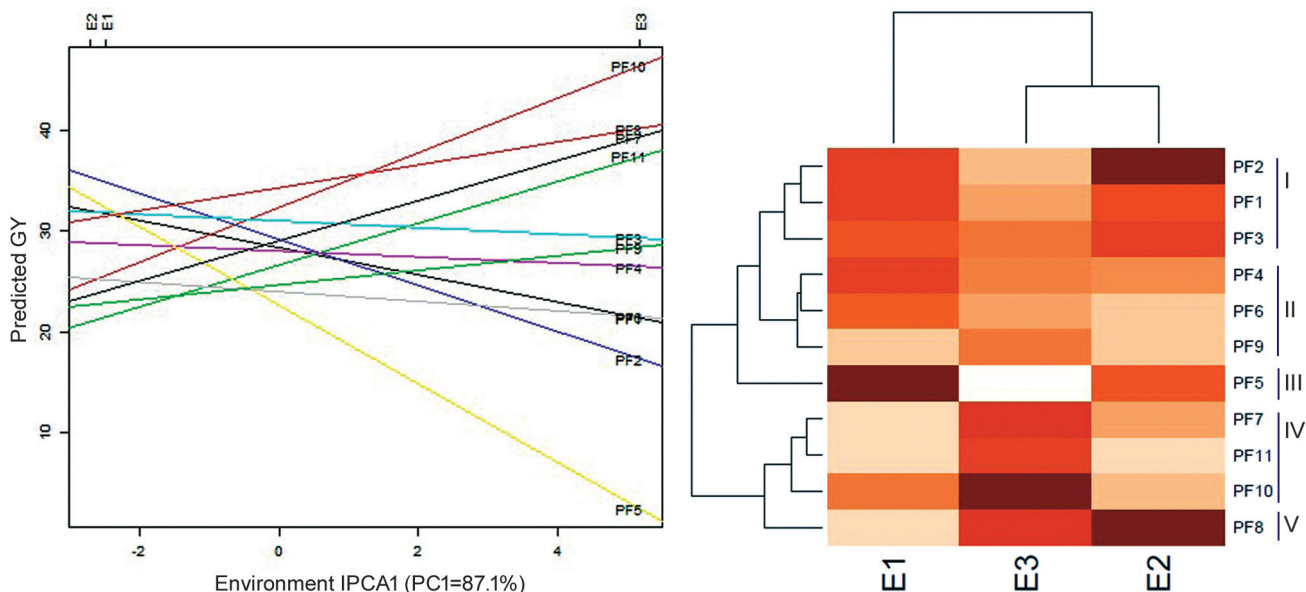


Fig 1 An adaptation map (A) and heat map (B) of 11 genotypes for grain yield over the three environmental conditions.

constellation of genotypes showed that PF2 (early), PF1 (early), PF3 (late) were closer to each other and grouped in cluster I, while PF4 (medium), PF6 (medium), PF9 (late) in cluster II; PF7 (early), PF10 (late), PF11 (late) in cluster IV. Clusters III and V were represented by one genotype for PF5 (early) and PF8 (late), respectively. A higher proportion of GEI reduces the association between a genotypic and phenotypic value of a trait and offers a challenge to plant breeders to select the best genotype for wider adaptability, stability, and high yield (Ghaffari *et al.* 2021). Therefore, it has been suggested to divide diverse environments into small environmental groups, each having more homogeneity to develop genotypes for specific environmental conditions (Yan and Tinker 2006).

The mean DTF value was ranged from 68.3 (E2) to 96.5 days (E1), NT from 1.6 (E1) to 4.1 (E2), NH from 1.6 (E1) to 3.7 (E2), and GY from 16.9 (E1) to 38.8 q/ha in E3 (Table 3). For genotypic mean, the combined value of DTF was ranged from 59.0 (PF5) to 106.3 days (PF9), NT from 1.7 (PF9) to 4.0 (PF5), NH from 1.7 (PF9) to 3.3 (PF4), and GY from 22.7 (PF5) to 34.3 q/ha (PF8). The mean GY order of the environments was as follows: $E1 < E2 < E3$. The mean genotypic GY among the genotypes was as follows: $PF8 > PF10 > PF3 > PF2 > PF7 > PF1 > PF4 > PF11 > PF9 > PF6 > PF5$.

Which-won-where and mega environment identification: The GGE biplot helps to identify mega-environments constructing polygon structure by joining outermost genotypes from the biplot origin. Therefore, all other genotypes come inside the periphery of the polygon. In a polygon, the genotype located on the vertex performed best in environments that fall within a particular sector (Yan and Tinker 2006). In our finding, three mega environments were identified, and vertex genotypes were PF5, PF2, PF8, PF10, PF11 and PF6 (Supplementary Fig 1). Each location was grouped into different mega-environments due to

their different soil types, rainfall, temperature patterns and geographical locations. The first mega environment (ME1) contained only one location (E1: Ranichauri) with high-yielding genotypes (PF5, PF6 and PF2). The second mega environment (ME2) consisted of one location (E2: Dehradun) with PF8, whereas the third mega environment (ME3) also possessed a single environment (E3: Pantnagar) with two high-yielding genotypes, PF10 and PF11. The “which-won-where” pattern of the GGE biplot showed that each mega-environment had different high yielding genotypes and showed cross-over type GEI. Furthermore, superior genotypes located at the vertex of the polygon of each mega-environment show high adaptability and would be rewarding to cultivate them at a specific location.

Mean yield performance and stability of genotypes: Mean yield performance and stability of genotypes must be evaluated across the locations over the years before their identification and release into a particular environment (Yan and Tinker 2006). The average-environment coordination (AEC) abscissa line represented a single arrow line and indicated a high average grain yield across the environment. The AEC ordinate, represented by a straight line that passed through the biplot origin and is perpendicular to AEC abscissa, highlighted the extent of variability (high variability represents poor stability) in either direction (Fig 2). Furthermore, AEC ordinate divides finger millet genotypes into two major groups with higher mean grain yield (right side) and lower mean grain yield (left side) than the overall mean. For instance, PF8 had the highest grain yield, followed by PF10, PF3, PF7 and PF2 (above than mean grain yield). In contrast, PF5 showed minimum grain yield followed by PF6, PF9, PF4 and PF11 (below mean grain yield). The dotted lines connected each genotype to AEC abscissa, and their length show each genotype’s stability. Higher the length of the lines, the less is stability of genotypes and vice-versa. Therefore, PF5, PF10, PF2

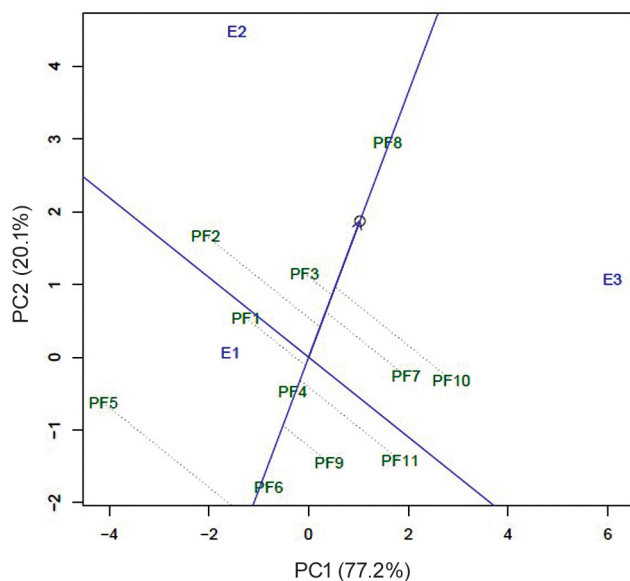


Fig 2 GGE biplot showing “mean vs. stability” of 11 finger millet genotypes across three locations for grain yield.

and PF11 were highly unstable, whereas PF8, PF4 and PF6 were highly stable across the locations. Among the stable genotypes, PF8 was high yielding across the locations (high general adaptation), whereas PF10 was least stable but high yielding which suggested that it might adapt to a particular location.

Identification of ideal genotypes: The ranking GGE biplot can be used to compare genotypes with an ideal genotype. An ideal genotype would have high grain yield and stability across the environments (Yan and Tinker 2006). Therefore, the best genotype would be the one that has the closest distance from the ideal genotype (represented by concentric circles), and the genotype located at the farthest distance would be most undesirable. Genotype PF8 was located closest to the ideal genotype and identified as the best genotype (Supplementary Fig 2). The ranking of genotypes based on ideal genotype under this study would be as follows: PF8 > PF10 > PF3 > PF7 > PF2 > PF1 > PF11 > PF4 > PF9 > PF6 > PF5.

Identification of ideal environments: The concentric rings (centrifugal) on the biplot show the length of environment vectors that represent the standard deviation within the respective environment. The increase in vector length represents more discriminating ability of the environment (Yan and Tinker 2006). In this study, environments E2 and E3 had more discriminating ability (Supplementary Fig 3). The AEA line passes through the average (denoted by a small circle at the end of the arrow) and the biplot origin. The angle between the environmental vector and AEA represents the magnitude of representativeness of the test environment. A smaller angle denotes more representativeness of the test environment and vice-versa. Thus, E2 was more representative than E3 and E1. Test environments having high discriminating and representativeness are best for selecting genotypes that have general adaptation (Yan and Kang 2003). However, a test

Table 3 Year-wise and combined trait means of genotypes and environments over two years of testing in three locations

Genotype/location	Days to 50% flowering			Number of tillers			Number of heads			Number of fingers			Grain yield (q/ha)			
	2018	2019	Combined	2018	2019	Combined	2018	2019	Combined	2018	2019	Combined	2018	2019	Combined	
Genotype^a																
PF1	52.8	91.8	72.3	2.1	3.3	2.7	1.9	2.7	2.3	5.8	6.8	6.3	25.6	31.0	28.3	
PF2	59.5	78.5	69.0	1.9	2.7	2.3	1.8	2.3	2.3	4.1	5.3	4.7	23.5	34.7	29.1	
PF3	84.5	88.9	86.7	2.1	2.5	2.3	1.9	2.7	2.3	5.9	8.1	7.0	25.6	36.4	31.0	
PF4	65.2	88.8	77.0	2.9	3.7	3.3	3.1	3.5	3.3	4.8	5.8	5.3	25.2	30.8	28.0	
PF5	55.8	62.2	59.0	3.5	4.5	4.0	2.1	2.7	2.4	7.9	8.7	8.3	18.1	27.3	22.7	
PF6	74.2	87.2	80.7	1.8	2.2	2.0	1.9	2.7	2.3	6.5	7.5	7.0	26.1	21.9	24.0	
PF7	65.1	74.3	69.7	1.7	2.3	2.0	1.8	2.8	2.3	6.6	8.0	7.3	25.8	32.2	29.0	
PF8	89.5	117.9	103.7	2.6	3.4	3.0	2.5	3.5	3.0	6.2	7.2	6.7	31.2	37.4	34.3	
PF9	96.5	116.1	106.3	1.5	1.9	1.7	1.2	2.2	1.7	6.5	7.5	7.0	26.7	22.7	24.7	
PF10	79.5	93.9	86.7	2.9	3.1	3.0	1.9	3.1	2.5	7.9	8.9	8.4	29.1	34.3	31.7	
PF11	88.4	96.2	92.3	2.5	2.9	2.7	2.1	3.3	2.7	5.9	7.3	6.6	24.6	28.8	26.7	
Location^b																
Ranichauri (E1)	65.1	71.5	68.3	0.8	2.4	1.6	1.2	1.5	1.4	3.4	4.2	3.8	16.1	17.7	16.9	
Dehradun (E2)	75.8	87.4	81.6	3.5	4.7	4.1	3.4	4	3.7	6.1	6.7	6.4	35.6	41.8	38.7	
Pantnagar (E3)	87.5	105.5	96.5	1.5	2.9	2.2	1.7	2.7	2.2	7.5	8.7	8.1	35.9	41.7	38.8	

^aGenotype means are based on 3 location data over the two years; ^blocation means are based on 11 genotypic data over the two years.

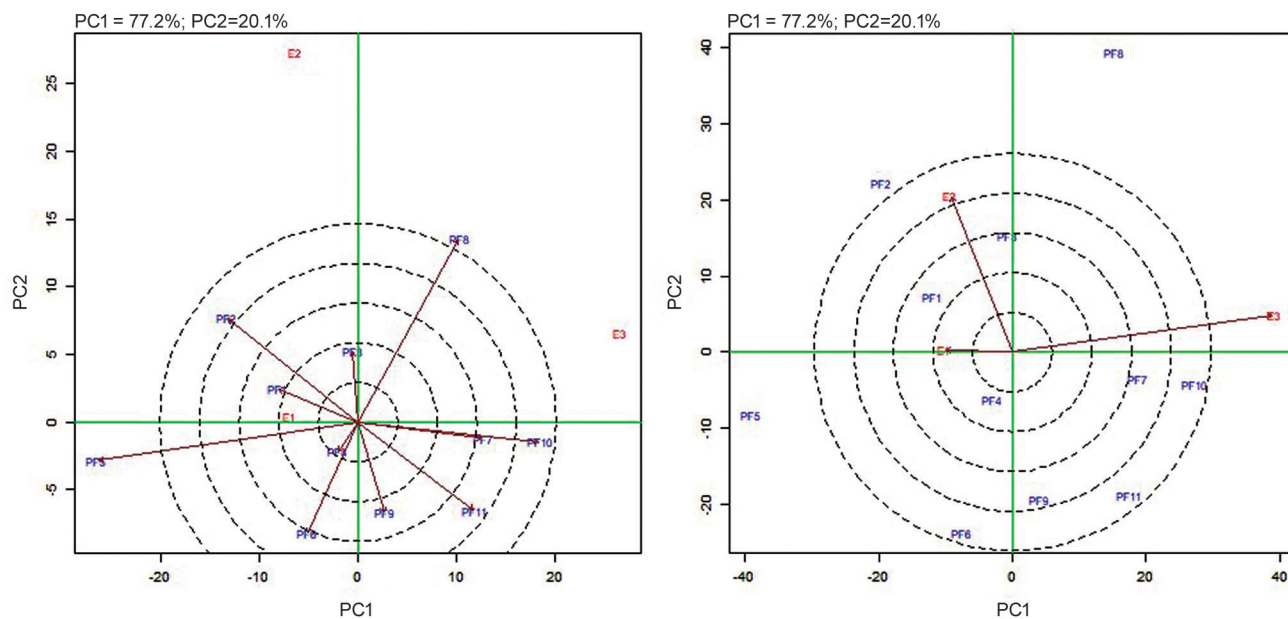


Fig 3 Relationship among genotypes (A) and environments (B) for grain yield.

environment with the high discriminating ability and low representativeness are good for selecting specific genotypes for specific environments. Thus, E2 had high discriminating ability and representativeness than E3 and E1. Therefore, E2 followed by E3 would be ideal environments for selecting widely adapted genotypes across the location.

Relationship among genotypes and environments: The distance between genotypes denotes the Euclidean distance between them and measures the genetic dissimilarity. The angle between genotypes also represents the relationship between them. Therefore, genotypes PF8 and PF5 were very dissimilar, whereas PF7 and PF10 were very close to each other (Fig 3A). The dissimilarity between genotypes might arise due to differences in mean GY and their interaction with climatic conditions. Genotypes near the biplot origin are considered average genotypes, and their contribution is zero to G and GEI (Yan and Tinker 2006). The more vector length represents more genotypic distance from biplot origin and contributes more to G, GEI, or both. Thus, genotypes PF8 and PF5 had the most extended vector amongst all and were considered as best and poorest genotypes, respectively. An acute ($<90^\circ$) angle between PF3 and PF8 signifies that they respond similarly in all environments. However, an obtuse ($>90^\circ$) angle between PF8 and PF5 responded inversely in different climatic conditions, i.e. one genotype performed well in one location but not in other and vice-versa. As relationships between environments are concerned, the angle between environment vectors plays a vital role in determining their association with each other. The acute and obtuse angles between environments show the positive and negative correlation, respectively. However, the right angle (90°) between them displays no correlation. In our finding, environments E1 and E2 had a positive correlation, whereas E3 had a significant negative correlation with E1 and no correlation with E2 (Fig 3B).

However, climatic conditions and geographical locations of E2 and E3 are more similar than E1. The dendrogram represented in the heat map also highlighted their closeness with each other.

In conclusion, grain yield is always affected by genotype, environment and GEI effect. The MET data would help to identify genotypes with general and specific adaptations. The yield advantage of late-maturing genotypes seemed to be associated with the better physio-genetic response of finger millet genotypes over three locations. Genotype PF8 was considered an ideal genotype as it had a high mean grain yield and stability among the other genotypes over the locations. However, it would be desirable to include more testing locations across the Uttarakhand state for two or more years to identify climate-specific or widely adapted genotypes.

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