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RESEARCH ARTICLE

Assessment of extra early field pea (*Pisum sativum* L.) genotypes performance using GGE biplot

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Abstract

Extra earliness in terms of flowering and maturity coupled with higher grain yield is an ultimate strategy for field pea promotion in short-season environments and to escape prevailing terminal stresses. Therefore, the development of stable, extra early and high-yielding genotypes has been the focus of the field pea breeding program. The study aimed to understand the role of genotype, environment, and their interaction in the performance of extra-early genotypes. The integration of GGE biplot analysis and multiple comparison tests detected that a higher proportion of variation in studied traits was due to genotypes as an interactive factor followed by genotype x environment interaction, justifying the requisite of multi-environment testing. The present study effectively recognized "Mega environment" for environment-specific breeding. The GGE biplot identified genotypes namely IPFD 18-14 and IPFD 18-20 as 'ideal' genotypes for earliness and grain yield, respectively, and these genotypes could be exploited in the future breeding programme for developing extra early and high-yielding field pea varieties.

Keywords: Earliness, Grain yield, G x E interaction, GGE biplot.

Introduction

Field pea or dry pea (*Pisum sativum* L.) is regarded as one of the nutritionally rich cool season legume crop with high yield potential thus holds immense promise for alleviating protein malnutrition to the resource poor society (Pandey et al. 2021). It is being cultivated worldwide in over 8.14 mha area with a production of about 16.20 mt, catering the need of consumer as food, feed and fodder. The global productivity of dry pea is near to 2.0 tonnes per hectare whereas the productivity of this crop in India is very low and fluctuates between 800–1000 kg/ha owing to countless ubiquitous biotic and abiotic stresses (FAOSTAT 2019), of which powdery mildew, rust and high temperature are the major concerns (Lamichaney et al. 2021; Parihar et al. 2022). The given stresses cause noteworthy damage to crop if occurred at flowering or terminal stage (Sudheesh et al. 2015). It has been observed that farmers' are also seeking suitable genotypes for late planting and rice fallow conditions wherein the crop is exposed to different terminal stresses causing considerable yield losses.

Earliness is an imperative trait that allows a genotype to escape or avoid terminal stresses, thus sustains the productivity (Jeuffroy et al. 2010). Since, crop phenology i.e. flowering, podding and maturity plays instrumental role in adjustment of crop cultivars into diverse environments (Berger et al. 2006), earliness is desirable in field pea for its adaptation to short season environments and to escape terminal heat, drought and diseases which are the most serious constraints to field pea productivity in the semi-arid tropics. In addition, earliness also helps in realization of maximize yield per unit time and per unit area in different cropping system (Dixit et al. 2014). Therefore, the present attempt has been made to identify extra early and high yielding genotypes to promote this crop in untapped areas like rice fallows, tal areas, where it is not being taken due to non-availability of extra early cultivars and use of long duration cultivars leads to exposure of crop to

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high temperature, drought and disease incidence. Also, availability of extra early cultivars will facilitate late planting in these areas and timely harvesting giving enough time for preparation and sowing of next crop particularly during spring/summer.

In any breeding programme it is very important to evaluate the effect of environment and genotype and their interactions on genotypic performance for targeted trait(s) (Parihar et al. 2017a). While approximating performance of genotypes for any trait, it is indispensable to minimize environmental variation to ease out genetic effect. The environmental variables to a large extent affect response to selection due to genotype by environment interaction (GEI) effects (Tolessa et al. 2013). Therefore, the precise understanding of the GEI serves as a decisive apparatus, particularly to made any recommendation regarding release of varieties for particular condition (Yan 2011). To define GEI, breeders perform multi-environmental trials in order to identify the most superior genotype for wide or specific cultivated areas (Tolessa et al. 2013). The quantitative traits are highly influenced by GEI and cannot be interpreted as based on G and E means alone (Tan et al. 2012). During recent past, various approaches have been used in pea to determine the influence of G and GE interaction on phenotypic performance of seed yield and other agronomically important traits (Bocianowski et al. 2019). Of them, GGE biplot technique, which graphically illustrates both G and GEI components, has become popular among the researchers for better explanation of G and GEI effects on targeted traits in various crops (Parihar et al. 2017b; Singh et al. 2020, Reddy et al. 2022). Since, both components are indispensable sources of variations that play instrumental role towards cultivar evaluation and need to be considered simultaneously for appropriate genotype and environment evaluation. Therefore, an attempt has been made to ascertain the influence of GEI on earliness and grain yield using a panel of extra early field pea genotypes. These genotypes were tested across the environments to identify stable and superior genotypes that could be used as varieties or suitable donors to breed short duration varieties for wider adaptation.

Materials and methods

Preliminary work

On the basis of previous characterization carried out in a set of 400 field pea genotypes, few early type genotypes were identified to be used as donor in hybridization programme. Crosses were synthesized between early type genotypes i.e., Arkel, VRP 6, AGETA 6, DDR 30, DDR 23 and VRP 22 in winter season of 2011-12 for developing extra early genotypes. The subsequent generations were advanced following pedigree method in succeeding winter season during 2012-13 to 2016-17. Finally, 44 extra early field pea genotypes were developed and were further evaluated during winter season of 2017-18 and 2018-19.

Planting materials, experimental site, design and observation recorded

During 2017-18, a panel of 50 genotypes comprised of 44 extra early genotypes and six released varieties viz., Arkel, VRP 6, AGETA 6, DDR 30, DDR 23 and VRP 22 was timely planted (E1) as per recommended package of practices in randomized complete block design (RCBD) with three replications. The same panel was further evaluated in 2018-19 through staggered planting at three different dates viz., normal planting (04/11/2018; E2), late planting (29/12/2018; E3) and extreme late planting (12/01/2019; E4). The experiment was executed at main farm of ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh, India. The experimental location is situated in semi-arid northern plains with a latitude of 26.28° North, a longitude of 80.21° East and an elevation of 152.4 meters above mean sea level. The genotypes were seeded with hands in one row of 4.0 m length, spaced 60 x 10 cm between plant and rows, in RCBD with three replications in all the environments. The experiment was properly managed to avoid unwanted stresses and recommended package of practices were adopted to raise a healthy crop. The days to flowering (DF), days to maturity (DM) and grain yield/plant (g) (GY) were recorded according to the descriptor list of genus Pisum L. (Pavelková et al. 1986).

Data analysis

The analysis of variance (ANOVA) was performed via SAS GLM Procedure (SAS 9.4). The GGE biplot analysis was done using 'R' software (R development core Team 2012) following a model of Yan (2002).

Results and discussion

Earliness is a very important trait that allows a crop to escape different stresses occurring during the sensitive reproductive phase (Jeuffroy et al. 2010). If field pea is to be introduced in rice fallows and similar new niches, earliness is the most important trait to be considered, since sowing at rice fallows is usually done late and use of early maturing genotype will allow the crop to escape terminal stress and also facilitates timely harvesting for growing of next crop. Thus, to identify high-yielding and stable extra early genotypes in order to increase the production and promote field pea in new niches where it is not being taken due to availability of long duration varieties which exposes the terminal stages to various biotic and abiotic stresses.

A panel of 50 field pea genotypes was evaluated in four environments normal sowing (2017-18, E1; 2018-19, E2), late sowing (2018-19, E3) and extremely late sowing (2018-19, E4). Consequently, field pea crop was exposed to different thermal regimes during various growth stages in winter

Table 1. Details of different temperature regimes during different growth stages in different environments

Environment	Cropping season (°C)		During flowering (°C)		During maturity (°C)	
	Minimim	Maximum	Minimim	Maximum	Minimim	Maximum
E1(Timely planting, 2017-18)	11.2	24.1	9.4	20.4	11.62	25.94
E2(Timely planting, 2018-19)	10.11	26.12	7.68	24.08	11.02	25.45
E3 (Late planting, 2018-19)	11.49	26.94	10.60	24.70	17.00	34.93
E4 (Extreme late planting, 2018-19)	12.60	28.03	13.25	28.15	21.27	37.48

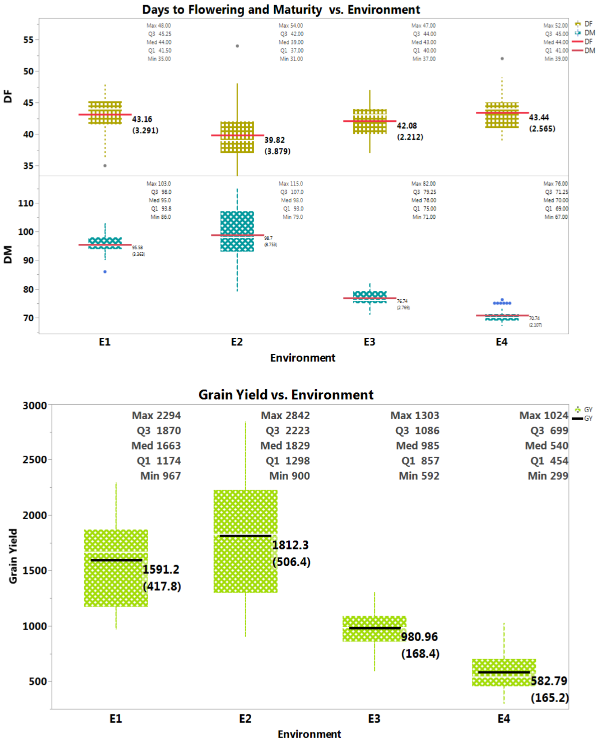

Fig. 1. Box plot illustration of DF, DM and GY of 50 field pea genotypes in four environments. The box represents the area from the first quartile to the third quartile. A white horizontal line goes through the box at the median and the black horizontal line indicates mean along with SD. The whiskers (vertical line) go from each quartile to the minimum or maximum. Dots indicate outliers in the box

season 2017-18 and 2018-19 (Table 1). The level of exposure of field pea crop to different temperature regimes during different growth stages strongly supported different dates of planting as individual environments. The analysis of variance (Table 2) revealed that the effect of genotype and environment were significant for all characters. The tested genotypes exhibited variable response for days to flowering (DF), days to maturity (DM) and grain yield (GY) in each tested environments. The mean performance of the tested field pea genotypes for maturity and grain yield in grain in Table 3. Genotype IPFD 18-14 took the least number of days for flowering (35.75 days) and maturity (76.50 days). In case of grain yield, the best performing genotype was IPFD 18-20 (1733 kg/ha) followed by IPFD 18-24 (1723 kg/ha) (Fig. 1). Based on mean per se performance the best performing genotype in term of early maturity was IPFD 18-14 (10) with <77 days and for grain yield IPFD 18-20 with >1.7t/ha productivity.

In case of DF, the partitioning of TSS revealed that 56.75% of the total variation is explained by the differences between genotype means which is indicated by the red-coloured area in the mosaic plot. The green-coloured area in the mosaic plot represents the variation due to genotype by environment effects (43.25% of the total variation). In addition, mosaic plot also represented the contribution of G and GEI effects in individual principal component by red and green colour portion in columns of individual PCs, respectively. The first two principal components used here to construct the GGE biplot jointly account for 83.44 % of the TSS, 99.37% of the sum of squares due to genotype (SSG), and 62.53% of the sum of squares due to genotype by environment (SSGE). In case of DM, 44.21% and 55.79% of the total variation is accounted by the differences between genotype means and genotype-by environment, respectively. In addition, initial two PCs collectively described 93.61% of the TSS, 96.40% of

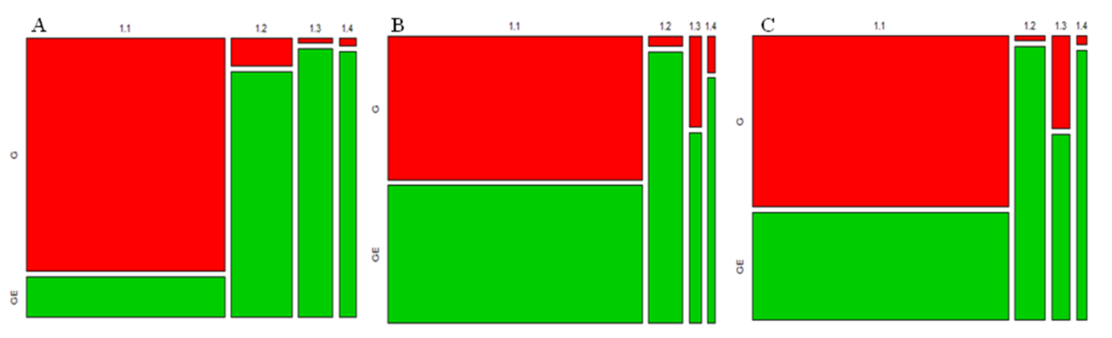

Fig. 2. Mosaic plot visualizing the two- way partitioning of the total sums of squares into genotype (G) and genotype-by-environment (GE) components along each principal components axis for individual traits DF (A), DM (B) and GY(C)

Table 2. Analysis of variance for 50 extra early genotypes of field pea

Source of variation	df	Days to flowering	Days to maturity	Grain yield
Environments	3	135.26**	9507.12**	15832938.74**
Genotypes	49	21.20**	44.23**	254009.20**
Error	147	5.38	18.60	77546.17
Total	199			

**, * Significant at the 0.01 and 0.05%, respectively.

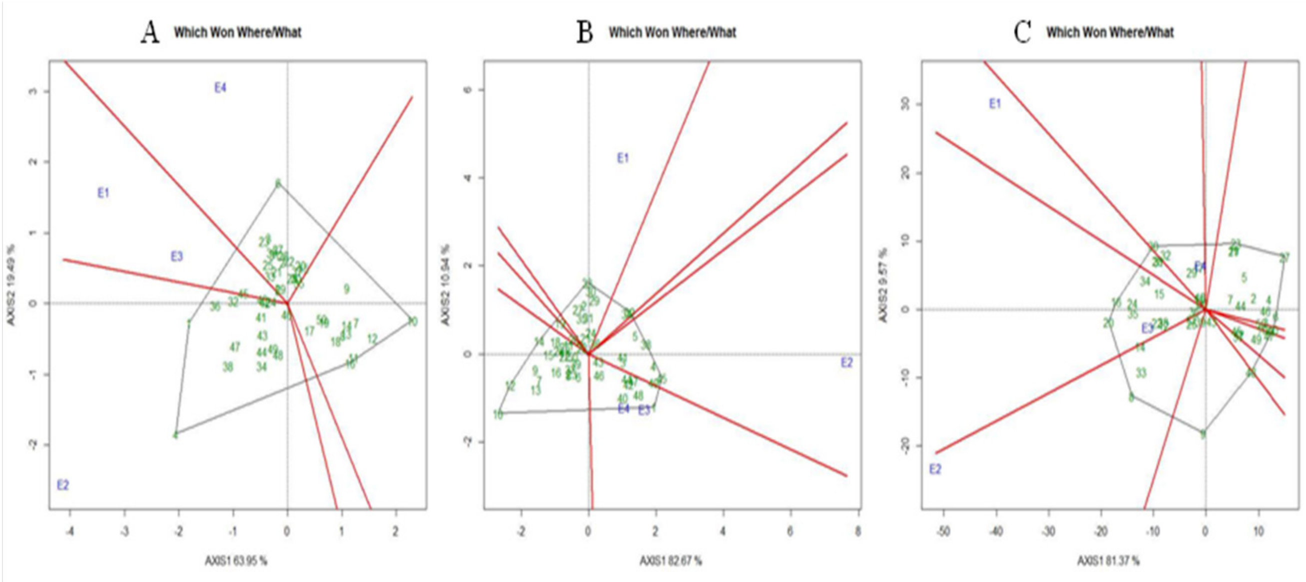

Fig. 3. The 'which-won-where' view of the GGE biplot of field pea genotypes in diverse environments. (A) Days to flowering (B) Days to maturity and (C) Grain yield. No transformation of data (transform = 0); and data were centred by means of the environments (centring = 2). The biplot was based on 'symmetric scaling', i.e. genotype and environment focused singular-value partitioning, and therefore it is most appropriate for displaying the relationship between both genotypes and environments. Numbers correspond to genotypes is listed in Supplementary Table S1.

the SSG, and 91.40 % of the SSGE. Similarly, in case of GY the G and GEI effects accounted for 52.20% and 47.80 % of the total variation, respectively. Also, first two PCs were responsible for 90.95% of the TSS, 96.08% of the SSG, and 85.34% of the SSGE (Fig. 2). The source of variation demonstrated that largest variation in all the studied traits was accounted due to genotypic effect followed by GE interaction effects. The presence of GEI demonstrated a significant difference in genotypic performance for targeted traits across the environments. Likewise, extra early genotypes of field pea demonstrated variable response over the environments for examined traits also validating GE influence. These finding confirmed the presence of cross over interaction (COI) across the environments, thus implying importance of multi-environment testing. The GEI affecting the ranking of genotypes across the environments which reflected GE interaction is crossover type and this has been reported for grain yield and other agronomic traits in field pea (Tolessa et al. 2013; Bocianowski et al. 2019). Presence of COI is non-additive and non -separable in nature suggesting for breeding of specific adaptation (Yan and Hunt 2002; Rakshit et al. 2012). The genotypic responses for different traits speckled in different environments may be due to variation in the genetic architecture of genotypes or environments or other factors (Bocianowski et al. 2019; Rich and Watt 2013).

The "which-won-where" biplot was used to identify genotypes for a specific environment (Fig. 3). The contribution of PC1 and PC2 witnessed the complex interaction between genotypes and environments for all traits. The perpendicular lines were drawn from the origin of the biplot to each side of the polygon separating the biplot into several sectors with winning genotype. Those genotypes which registered lowest and highest value for DF, DM and GY were at different vertices of the polygon (convex hull) and contributed maximum to the interactions whereas the genotypes located nearer to the origin was less responsive than the farthest genotypes placed in the vertex. The equality lines partitioned the graph into three sectors for DF and DM and in four sectors for GY. These sectors could be entitled as "Mega Environment" affirming environmental variability and existence of COI. The environments which develop small angles among each other are indicative

Table 3. Mean performances of tested field pea genotypes for earliness and grain yield

S.N.	Genotypes	Days to flowering					Days to maturity					Grain yield(kg/ha)			
		E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E4	mean
1	ARKEL	48	48	47	45	47.00	92	114	80	75	90.25	1656	1892	888	1365
2	DDR- 23	43	39	44	46	43.00	100	98	73	70	85.25	1268	1333	693	1012
3	VRP- 22	42	40	46	49	44.25	94	108	77	67	86.50	1096	1250	413	907
4	AGETA- 6	46	54	44	42	46.50	96	114	77	75	90.50	1134	1167	714	964
5	DDR- 30	42	41	43	46	43.00	98	110	77	70	88.75	1447	1292	511	1057
6	VRP -6	44	38	42	52	44.00	94	96	76	76	85.50	1011	1125	620	935
7	IPFD- 18 -11	**36**	37	38	44	38.75	90	89	71	69	79.75	1426	1538	714	1166
8	IPFD- 18 -12	37	38	39	43	39.25	92	95	74	70	82.75	1780	2825	474	1572
9	IPFD- 18 -13	38	36	39	45	39.50	92	87	74	69	80.50	1048	2242	522	1244
10	IPFD- 18 -14	**35**	31	37	40	35.75	86	79	72	69	76.50	1027	1333	860	1052
11	IPFD- 18 -15	38	37	38	40	38.25	95	95	73	69	83.00	1751	1867	309	1167
12	IPFD- 18 -16	38	34	39	39	37.50	90	81	74	69	78.50	1862	2267	458	1413
13	IPFD- 18 -17	40	36	39	40	38.75	90	87	75	69	80.25	1707	1975	299	1248
14	IPFD- 18 -18	39	36	40	41	39.00	96	87	75	70	82.00	1868	2625	1024	1668
15	IPFD- 18 -19	44	37	41	44	41.50	95	89	77	70	82.75	1981	2217	855	1564
16	IPFD- 18 -20	39	37	38	39	38.25	93	91	79	68	82.75	2294	2658	708	1733
17	IPFD- 18 -21	42	38	43	40	40.75	95	93	76	70	83.50	1802	1700	738	1372
18	IPFD- 18 -22	39	37	42	40	39.50	96	91	75	70	83.00	1684	1842	641	1269
19	IPFD- 18 -23	39	39	39	44	40.25	98	92	74	70	83.50	1670	1300	416	1093
20	IPFD- 18 -24	44	37	42	44	41.75	95	92	74	71	83.00	2274	2842	696	1723
21	IPFD- 18 -25	44	40	42	46	43.00	97	98	76	70	85.25	1643	1292	533	1142
22	IPFD- 18 -26	44	38	43	45	42.50	95	93	76	71	83.75	1954	2400	423	1366
23	IPFD- 18 -27	47	39	43	46	43.75	93	95	76	71	83.75	1680	1292	492	1070
24	IPFD- 18 -28	44	41	43	44	43.00	98	99	77	70	86.00	2211	2533	481	1551
25	IPFD- 18 -29	47	39	43	44	43.25	96	93	77	70	84.00	1647	2000	510	1287
26	IPFD- 18 -30	45	38	43	45	42.75	97	95	76	71	84.75	1678	1833	422	1206
27	IPFD- 18 -31	46	38	43	45	43.00	100	96	75	70	85.25	1187	900	894	917
28	IPFD- 18 -32	44	39	40	45	42.00	95	98	75	68	84.00	2160	2150	822	1537
29	IPFD- 18 -33	44	41	39	46	42.50	101	100	75	69	86.25	1878	1825	566	1311
30	IPFD- 18 -34	43	38	43	44	42.00	102	99	75	69	86.25	2274	2150	743	1521
31	IPFD- 18 -35	47	38	43	44	43.00	100	98	78	70	86.50	2161	2117	696	1511
32	IPFD- 18 -36	47	44	43	45	44.75	101	108	77	71	89.25	2160	2017	549	1438
33	IPFD- 18 -37	47	39	43	43	43.00	103	98	75	69	86.25	1820	2650	461	1527
34	IPFD- 18 -38	45	44	40	41	42.50	100	108	75	70	88.25	2189	2267	539	1575
35	IPFD- 18 -39	45	37	42	42	41.50	99	97	75	70	85.25	2156	2517	440	1573
36	IPFD- 18 -40	47	46	44	46	45.75	97	100	77	71	86.25	1687	1892	428	1295
37	IPFD -18 -41	45	37	42	43	41.75	93	95	76	69	83.25	1259	1633	418	975
38	IPFD- 18 -42	47	46	43	41	44.25	98	112	80	70	90.00	1845	2242	630	1502
39	IPFD- 18 -43	47	38	44	44	43.25	95	95	80	70	85.00	1578	1892	561	1278
40	IPFD- 18 -44	44	42	43	45	43.50	92	107	77	75	87.75	985	1242	611	898
41	IPFD- 18 -45	45	42	43	43	43.25	97	106	80	73	89.00	1011	1250	470	887
42	IPFD- 18 -46	43	42	44	45	43.50	95	107	82	75	89.75	1244	1583	478	1029
43	IPFD- 18 -47	43	43	44	43	43.25	96	100	82	70	87.00	1479	1800	677	1245
44	IPFD- 18 -48	45	43	42	41	42.75	95	107	80	75	89.25	1356	1467	540	1051
45	IPFD- 18 -49	47	43	42	45	44.25	96	115	82	75	92.00	1278	1567	424	1057
46	IPFD- 18 -50	44	39	44	41	42.00	95	100	82	72	87.25	1090	1250	820	1008
47	IPFD- 18 -51	44	46	44	44	44.50	94	109	80	72	88.75	1011	1275	415	879
48	IPFD- 18 -52	42	42	44	41	42.25	93	110	82	72	89.25	967	1575	498	991
49	IPFD- 18 -53	43	42	44	41	42.50	94	114	80	72	90.00	1063	1428	637	998
50	IPFD- 18 -54	40	37	44	41	40.50	95	95	76	71	84.25	1125	1292	410	946
	Mean	43.16	39.82	42.08	43.44	42.13	95.58	98.70	76.74	70.74	85.44	1591.24	1812.31	582.79	1241.83

Table 4. Top 10 genotypes for earliness and grain yield based on mean and stability

S. no.	Character	Best performing genotypes
1	Days to flowering (<40 days)	IPFD18 -14, IPFD 18-16, IPFD 18-20, IPFD 18-15, IPFD 18-17, IPFD 18-11, IPFD 18-18, IPFD 18-12, IPFD 18-22, IPFD 18-13
2	Days to maturity (<83 days)	IPFD 18-14, IPFD 18-16, IPFD 18-11, IPFD 18-17, IPFD 18-13, IPFD 18-18, IPFD 18-20, IPFD 18-12, IPFD 18-19, IPFD 18-15
4	Grain yield (>1.5 t/ha)	IPFD 18-20, IPFD 18-24, IPFD 18-18, IPFD 18-38, IPFD 18-39, IPFD 18-12, IPFD 18-19, IPFD 18-28, IPFD 18-32, IPFD 18-37

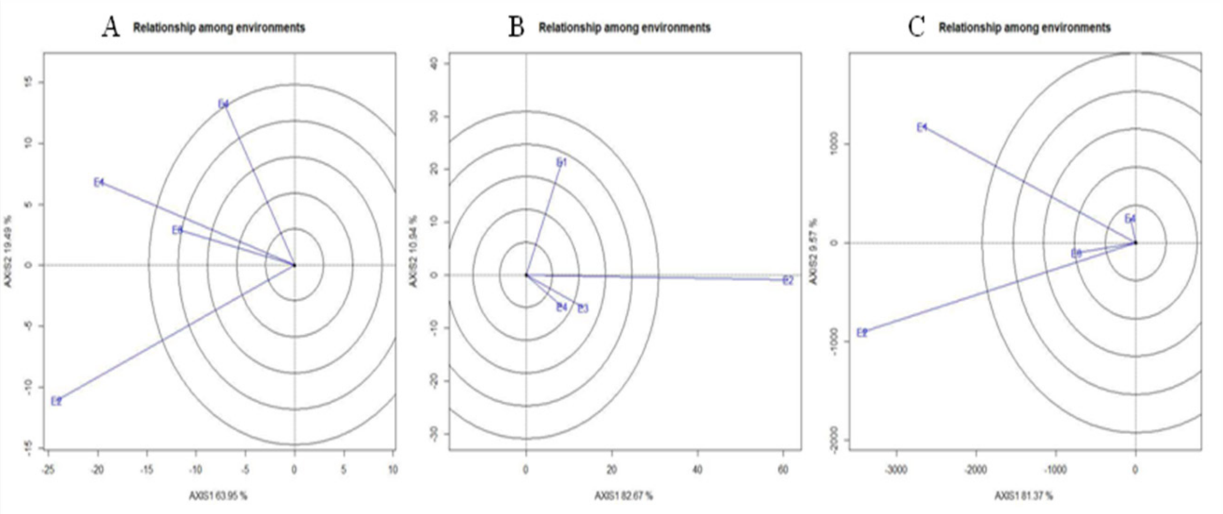

Fig. 4. Relationship among the test environments based on the GGE biplot analysis of 50 field pea genotypes across diverse environments for three traits, (A) days to flowering, (B) days to maturity and (C) grain yield. No transformation of data (transform = 0); and data were centred by means of the environments (centring = 2). The biplot was based on 'column metric preserving', i.e. environment-focused singular-value partitioning, and thus it is most suitable for representing the relationship among environments. Numbers correspond to genotypes is listed in Supplementary Table S1

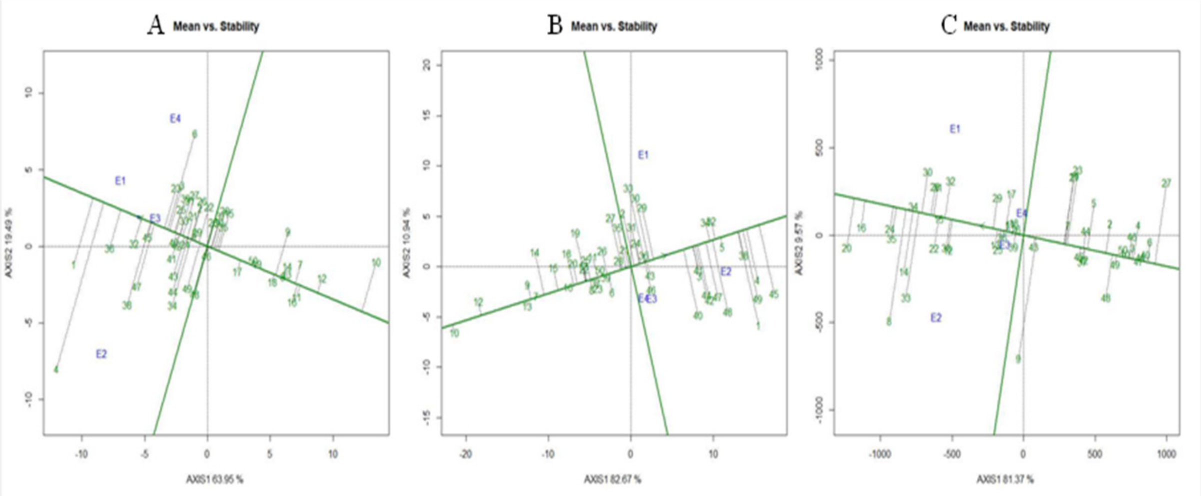

Fig. 5. Mean vs. Stability view of the GGE biplot of field pea genotypes in diverse environments for three traits, (A) Days to flowering (B) Days to maturity and (C) Grain yield. There was no transformation of data (transform = 0), and data were centered by means of the environments (centring = 2). The biplot was based on "row metric preserving." i.e. genotype focused singular value partitioning, and thus it is best suitable for displaying the association between genotypes. Numbers correspond to genotypes is listed in Supplementary Table S1

of positive association. For instance, in DF environments E1 and E3 had an acute angle and are considered to be positively associated, while, obtuse angle between E2 and E4 represents negative association. Likewise, for DM, E2, E3 and E4 had acute angle with each other while E1 had acute angle with E2 but had obtuse angle with E3 and E4. In GY, all the environments had different magnitude of positive relationship among each other (Fig. 4). The high GEI effects on traits of interest across the test locations warranted the use of the GGE biplot to explain the G and GEI effects from multi-environmental trials (Yan et al. 2015; Luoet al. 2015a). In addition, earlier reports acknowledged the significance of cross over interaction in breeding programme and strongly recommended the implication of breeding strategies for specific adaptation (Rakshit et al. 2012; Ullah et al. 2012, Krishnamurthy et al. 2017). Therefore, field pea breeders are hereby advised to plant the best genotypes of particular location in the most desirable environments to exploit positive GEI effects. In the present investigation, GGE biplot methodology successfully illustrated mega environment using "which-won-where" view. The prime intention of mega-environment (ME) identification was to comprehend the intricate genotype x environment interaction pattern within ME for exploiting specific adaptation as well as increase of selection responses (Yan et al. 2011). In present attempt the GGE biplot evaluation for DF, DM and GY revealed that the used environments to test field pea performance can be divided into three and four mega-environments, respectively. In particular mega-environment genotypic performance remains consistent or similar across the years (Yan and Rajcan 2002; Yan and Tinker 2006). Thus, breeding efforts in environment specific manner holds great significance for improving the precision in breeding programme. The positive and negative association among the environments suggested the existence of non cross over and cross over interaction (COI) with consistent and inconsistent genotypic response in these environments, respectively. Thus one of the environments from non-cross over interaction could be dropped in future testing program to reduce cost of testing and to improve efficiency with minimum test environments. In the same data set both cross over and non-cross over interaction is corroborated with the previous reports of existence of twin interactions in multi-environment testing (Yihunie and Gesesse 2018; Tolessa et al. 2013; Rakshit et al. 2012).

The "mean versus stability" view of the biplot demonstrated that IPFD 18-14 (10) genotype was earliest in terms of both flowering and maturity and IPFD 18-24 (20) was the highest yielding. The most stable genotypes are those that records highest negative projection on AEC i.e. close to 0 (Yan and Rajcan 2002). Accordingly, for DF and DM, IPFD 18-16 (12) and IPFD 18-14 (10), respectively, were the most ideal genotypes having short projection from AEC abscissa. Genotypes located closer to the ideal genotype are more desirable than others. Therefore, genotypes IPFD 18-15 (11) for DF and IPFD 18-17 (13), IPFD 18-13 for DM were considered as desirable genotypes. In case of GY, genotype IPFD 18-20 (16) was the most ideal genotype and IPFD 18-24 (20), IPFD 18-28 (24) and IPFD 18-39 (35) were considered as most desirable (Fig. 5). These ideal and desirable genotypes identified in the present study would be valuable genetic resources for comprehensive breeding programme of field pea for developing high yielding varieties with earliness. These strategies have been successfully deployed for identifying stable and good performing genotypes in different crops for different traits (Girgel and Cokkizgin 2019; Tolessa et al. 2013; Tekalign et al. 2017). The best performing 10 genotypes for earliness and grain yield is presented in Table 4. Genotypes IPFD 18-14, IPFD 18-16, IPFD 18-11 etc showed earliness but was not a high yielding genotype. While, genotypes IPFD 18-51, IPFD 18-52, IPFD 18-53 showed late maturity (>87 days) but had low yield (<1 t/ha). However, genotypes, IPFD 18-20, IPFD 18-12, IPFD 18-18, IPFD 18-19 were early (< 83 days) and high yielding (> 1.5 t/ha) (Table 3; Supplementary Table 1), therefore these are the ideal genotypes that could be considered for cultivation in the area where short crop window is available.]

Author's Contribution

Conceptualize and wrote the draft of manuscript (AKP, AL); Supervised and edited manuscript (GPD); Statistical analysis (DS); Execution of field experiment and data recording (AKP, AKS); All authors read and approved the final manuscript.

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