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RESEARCH ARTICLE

Multi-phenotyping and genotyping of Spanish groundnuts from diverse crosses to identify sources of fresh seed dormancy and selection of high yielding stable genotypes

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Abstract

Groundnut breeding is focused on developing high-yielding Spanish–type varieties with fresh seed dormancy (to avoid sprouting). Fourteen advanced breeding lines were multi-phenotyped and genotyped for fresh seed dormancy under different germination tests. Further, the genotypes were evaluated for their performance and adaptability using GGE biplots. Thus, widely adapted genotypes were PBS 11077 and PBS 15014 for pod yield per plant (PYLP); PBS 14064 for sound mature kernels (SMKs); PBS 16023 for hundred pod weight (HPW); and PBS 11077 for hundred kernel weight (HKW). PBS 14064 and PBS 15056 (for PYLP), PBS 15056 and PBS 15022 (for SMKs), PBS 16022, PBS 16044 and PBS 14060 (for HPW) and PBS 14064, PBS 14060 and PBS 14068 (for HKW) were appropriate for a specific environment. So, the fresh dormant genotypes PBS 11077, PBS 16023, PBS 14064 and PBS 15014 performed well across all test locations and were designated as ideal in terms of fresh seed dormancy, yield, stability, and emerged as the top fresh dormant genotypes.

Keywords: Groundnut, dormancy, stable, yield, GGE biplots.

Introduction

Groundnut, [*Arachis hypogaea* L. (2n = 4x = 40, AABB)] is a legume crop of the pea family, Fabaceae, comprising important edible oil used as both seed and feed. Groundnut is a significant oilseed crop in India and can be grown in three seasons: *kharif*, pre-*rabi*, *rabi,* or summer across the country (Ali et al. 2022). Spanish (subsp. *fastigiata* var. *vulgaris*) groundnuts are most preferred owing to their short life cycle, but they lack fresh seed dormancy (Nautiyal et al. 2001). However, in India, groundnut is mainly cultivated as a *kharif* crop under rainfed conditions with an average yield of 1635 kg/ha. So, almost 85 percent of the groundnut area remains rainfed, with approximately 80 percent falling under dryland with no irrigation facilities. *In-situ* germination caused by erratic rains during crop maturity may lead to 20-50% reduction in the yield of Spanish types (Kumar et al. 2019). The yield losses due to viviparous germination can be avoidable if we have varieties possessing a high intensity of dormancy (>90%) for a short period (2-3 weeks). So, to develop high-yielding Spanish bunch cultivars with *2-3 weeks* of fresh seed dormancy is an important objective for plant breeders. Breeders frequently sort and select genotypes of specific phenotypic expression under mega environment tests using yield and its components. The environmental conditions such as humidity, soil texture and fertility, precipitation, and temperature may all play a role in the yield fluctuation and variable phenotypic expressions (Oladosu et al. 2016). The performance of genotypes varies with different environmental conditions. This interaction between genotype and environment (GEI) which is responsible for yield instability or variation

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in phenotypic expression, has been reported in several crops (de Vita et al. 2010; Ajay et al. 2019). So, a prerequisite for newly generated fresh dormant advance lines is to undertake a multi-environment trial to determine the superior and stable groundnut genotypes. So, to get a better understanding of genotypic stability patterns, multivariate methods or biplots is an effective tool (Myint et al. 2019). GGE biplots-based multi-environment trail (MET), has been successfully executed for identifying phenotypically stable and superior cultivars across several environments (Oladosu et al. 2017; Ajay et al. 2019; Kumar et al. 2019; Lal et al. 2021; Gangadhara et al. 2023). As a consequence, the current study aims to identify superior fresh dormant genotypes with high and stable yield performance over a wide range of environments**.**

Materials and methods

The experiment involving fourteen advanced breeding lines along with four released check varieties *viz*., Girnar 3, TAG 24, Dh 86 and TG 37A was conducted at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat, India in a medium black calcareous soil (Supplementary Table S1). The experiment was arranged in a randomized complete block design (RCBD) with three replications. Each accession was planted in a single row of 3 m in length, with a spacing of 60 cm between rows × 10 cm between plants.

Evaluation of Spanish bunch advanced breeding lines (ABLs) for fresh seed dormancy

The genotypes were evaluated for fresh seed dormancy for four seasons *viz., kharif* 2019, *kharif* 2020, *rabi* 2020 and *rabi* 2021 by testing them under i) laboratory conditions, ii) field testing, iii) *in situ*-germination test, and iv) GMFSD panel screening. For laboraratory, screening standard SOP for germination test was followed as proposed by Janila et al. (2018). For field tests, seeds from freshly harvested pods were treated with carbendazim (3 g/kg of seed) and sown in a randomized complete block design with three replications. The data on the number of seeds germinated were recorded at weekly interval for up to 21 days to calculate the intensity of dormancy (IOD) as described by Gangadhara et al. 2023. For the *in-situ* germination test, 10 to 15 plants were left standing in the field for more than 3 weeks after they attained maturity in each replication. After three weeks, plants were uprooted and the presence/absence of *in-situ* germination was recorded for test genotypes. For both field and *in-situ* tests, moisture was maintained in the soil at field capacity throughout the experiment. For molecular validation, the fresh dormant ABLs were genotyped on a validation panel comprising a marker GMFSD-1, an allele-specific marker for fresh seed dormancy, as described by Kumar et al. (2019).

Evaluation of fresh dormant ABLs for yield and its components

The same set of fourteen Spanish advanced breeding lines were evaluated for yield and its component traits (direct and positively contributing traits with yield) such as sound mature kernels (SMKs) in%, hundred pod weight (HPW) and hundred kernel weight (HKW) in grams for five seasons namely, *kharif* 2019, *rabi* 2019, *kharif* 2020, *rabi*-summer 2020 and *rabi*-summer 2021. Standard agricultural practices and plant protection measures were adopted for healthy crop production. The data were recorded from five randomly selected plants of each genotype under each replication.

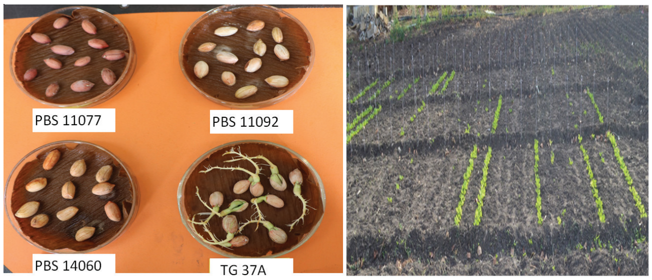
Statistical analysis

The traits were subjected to analysis of variance (ANOVA) using DSAASTAT software. The multivariate stability of genotypes was estimated over seasons graphically using GGE biplot in the R package GGEBiplotGUI (Bernal and Villardon 2016). Further AMMI stability value (ASV) was calculated, as suggested by Purchase (1997) with the agricolae package (de Mendiburu 2017) of R (R core team 2022).

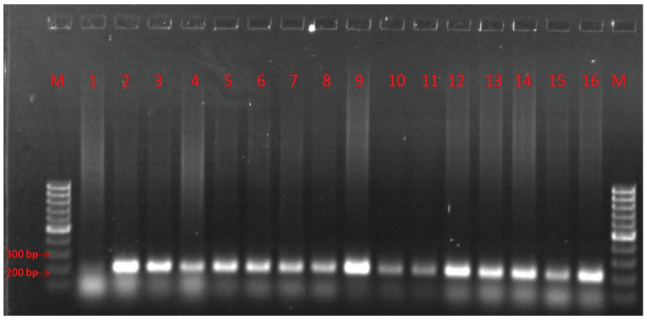
Results and discussion

Evaluation of Spanish bunch ABLs for fresh seed dormancy

The combined analysis of variance (ANOVA) showed that mean squares from genotype and G×E interactions were significant indicating significant variation among the genotypes under study, and also genotypes respond differently from season to season (Supplementary Table S2). Mean values for IOD at 21 days after sowing as calculated from SOP of germination test (pooled over four seasons) are presented in Supplementary Table S3 and season-wise performance of genotypes under different screening methodologies is presented in Supplementary Table S4. As per SOP for germination test (Janila et al. 2018; Fig. 1a), genotypes PBS 16023, PBS 15014, PBS 14064, and PBS 11077 were identified with 100% intensity of dormancy at 21 DAS and were stable across environments as explained by GGE biplots (Gangadhara et al. 2023). The graph generated for IOD at 21 days based on a) multi-environment evaluation (which-won-where pattern), b) Genotype evaluation (mean *vs* stability), and c) GGE biplot genotypes ranking pattern for genotype comparison with ideal genotype under four seasons as described by Gangadhara et al. (2023). Further, other ABLs namely, PBS 11092 (95.4%), PBS 14060 (96.7%), PBS 14064 (99.2%), PBS 14068 (97.3%), PBS 15022 (98.8%), PBS 15027 (95%), PBS 15028 (99.1%), PBS 16022 (95.8%), and PBS 16044 (94.6%) were identified with grand mean of more than 90% fresh seed dormancy at 21 DAS from four seasons *viz*., *kharif* 2019, *kharif* 2020, *rabi* -summer 2020 and *rabi*-summer 2021 (Gangadhara et al. 2023). Under germination test in field in *rabi*-summer 2021



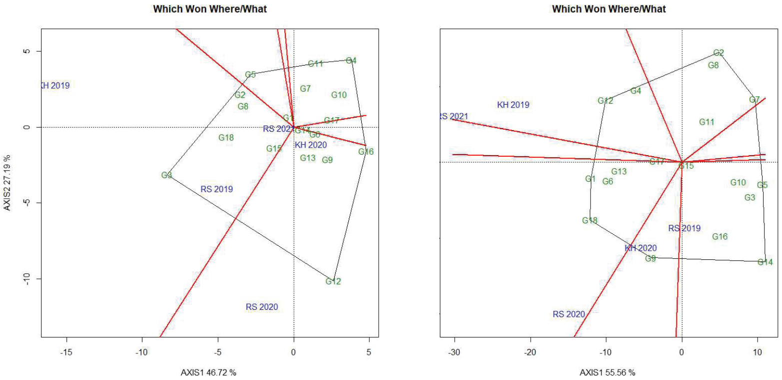
(a) (b)



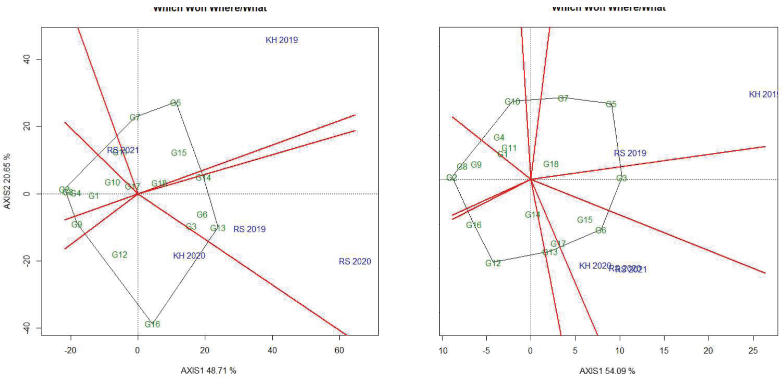
(c)

Fig. 1. (a) Germination test in petriplate; (b) *in-situ* germination test of freshly harvested kernels in the field and (c) Fresh seed dormant ABLs validated on a validation panel comprising a marker GMFSD-1, an allele-specific marker for fresh seed dormancy (Kumar et al. 2019).

and *kharif*-2021, PBS 16023 recorded 100% IOD, while all other ABLs except PBS 11092 showed > 90% dormancy intensity at 21 DAS (Fig. 1b; Supplementary Table S4). Further *in-situ* test showed germination in PBS 14060, PBS 15027, PBS 15028, PBS 16022 and PBS 16033 in *kharif*-2021, while PBS 15022, PBS 15056 and PBS 16022 from summer-2021, when rogued out at 21 days of attaining maturity, whilst other ABLs had no any *in-situ* germination observed. From the cumulative observation, three genotypes, namely, PBS 14064, PBS 15014 and PBS 16023 were identified to have constantly more than 90 percent dormancy in each individual screening test. Whilst**,** ABLs *viz.,* PBS 11077, PBS 15022, PBS 15028, PBS 15056 and PBS 16044 constantly had more than 85 percent dormancy in each screening test. The remaining ABLs showed good percentage of dormancy compared to standard non-dormant checks *namely*, Dh 86, TG 37A and TAG 24 (Supplementary Table S4). Further, these ABLs phenotyped for germination percentage were also genotyped with allele-specific marker GMFSD1 (Kumar et al. 2019) to validate the dormancy. The marker showed clear polymorphism between dormant (> 80% IOD, 21 DAS) and non-dormant parents (< 10% IOD, 21DAS) and co-segregated with the dormant phenotype equivalent or more than 80 percent intensity of dormancy calculated as



Pattern A Pattern B



Pattern C Pattern D

Fig. 2. The "Which-Won-Where" GGE biplot for groundnut genotypes evaluated for PYPL (Pattern A), SMKs (Pattern B), HPW (Pattern C) and HKW (Pattern D) in five environments during *kharif* 2019, *kharif* 2022, *rabi/summer* 2019, *rabi-summer* 2020, and *rabi-summer* 2021

per SOP of germination test at 21 days after sowing (Fig. 1c).

Yield evaluation of fresh dormant spanish bunch advanced breeding lines (ABLs)

The combined analysis of variance (ANOVA) given in Supplimentary Table S5 showed that mean squares from genotype and environment obtained for pod yield per plant and other studied component traits were significant, indicating significant variation among genotypes under study, offering great scope for improvement of traits through breeding line selection (Ajay et al. 2020; Kamdar et al. 2020; Lal et al. 2019; Singh et al. 2015). GEI were significant for pod yield, hundred pod weight, and kernel weight (Supplementary Table S5), suggesting that genotypes respond differently from season to season, which is in agreement with the results of earlier studies (Akbar et al. 2017; Rani et al. 2023). Mean values for pod yield and its component traits (pooled over five years) are presented in Table S3. Pod yield per plant ranged from 11.2 g for PBS 11077 to 5.1 g in PBS 16044, with 6.8, 7.0, 7.1 and 8.7 g, respectively in high-yielding checks *viz*., Dh 86, TAG 24, Girnar 3 and TG 37A respectively with a mean value of 7.34 g. Other superior genotypes identified for higher pod yield compared to superior checks were PBS 15056 (9.0 g) and PBS 15014 (8.3 g). The presence of GEI resulted in differential yield performance among the genotypes across five testing environments. The HPW ranged from 81 (PBS 16023) to 56 g (Girnar 3) with mean value of 69.55 g. Hundred kernel weight ranged from 37.4 (PBS 14064) to 26.5 g (Girnar 3) with the mean value of 31.85 g. Further, the percentage of sound mature kernels was in range of 61 (TG 37A), to 49 (PBS 14068 and PBS 15014). As breeding was performed to select high-yielding fresh dormant Spanish ABLs, there was a wide difference between the two extreme genotypes. So, advanced breeding lines PBS 11077 showed higher pod yield and PBS 15014 had more pod yield and higher SMKs compared to check (TAG 24) on average over five years. Two breeding lines, PBS 11077 (high average pod yield) and PBS 15056 (moderate pod yield), and the check variety TG 37A, were found to be the stable genotypes. Further, changes in genotype ranking were observed between seasons for PYLP, HPW, HKW, SP, and SMK that indicate the presence of crossover interactions which in turn indicate the presence of genotype-environment interactions for these traits. Further, no recognizable pattern of GE was observed between environments [*kharif* (KH) and *rabi*-summer (RS)] and each environment has to be considered as one mega-environment with unpredictable GE (Yan and Tinker 2006). A genotype that is stable to yield in a diversified environment is highly accepted by any researchers in a breeding program to reduce the danger of yield loss owing to adverse climatic conditions (Oladosu et al. 2017). In such a situation, when genotype performance is inconsistent in a diverse environment, the selection of genotype is difficult, so to select stable high-yielding genotypes, stability models such as AMMI and GGE biplots are being adopted extensively (Ajay et al. 2019; 2020).

Ranking of genotypes for pod yield by simultaneous consideration of mean performance and stability index

Based on mean pod yield over seasons, PBS 11077 was most desirable, followed by PBS 15056, TG 37A, PBS 15014 and PBS 16022, whereas PBS 16044 was most undesirable (Table 1). Since yield is polygenically controlled and highly influenced by the environment superiority of genotypes based on yield alone may not be effective (Kamdar et al. 2020). Along with high yield, an acceptable level of stability is one important criterion to be considered in any breeding program. The lower the average stability index (ASV), the more stable the genotype. Based on ASV, PBS 16023 was highly stable, followed by PBS 15027 and PBS 16022. Moreover, the most stable genotypes do not always have the best yield performance so, the simultaneous selection index (SSI) was computed by adding the ranks of stability parameter and average yield. The low value of this parameter shows desirable genotypes with high mean pod yield and stability (Farshadfar et al. 2011). The SSI score for each genotype is presented in Table 1. So, PBS 16022 (8) was most desirable, followed by PBS 16023 (11.5), PBS 15014 (14), PBS 16033 (14), PBS 14064 (14), and PBS 11077 (16).

Table 1. Simultaneous selection indices for yield and stability for 18 genotypes of groundnut

Code	Genotypes	SP	SSI	rSP	rY	Means
G1	Dh 86	0.172	17	4	13	6.87
G2	Girnar 3	0.459	26	17	9	7.13
G3	PBS 11077	0.399	16	15	1	11.27
G4	PBS 11092	0.531	34	18	16	6.27
G5	PBS 14060	0.362	20	13	7	7.67
G6	PBS 14064	0.194	14	6	8	7.53
G7	PBS 14068	0.371	24.5	14	10.5	7.13
G8	PBS 15014	0.249	14	10	4	8.40
G9	PBS 15022	0.259	25	11	14	6.60
G10	PBS 15027	0.072	20	2	18	5.53
G11	PBS 15028	0.199	24	7	17	5.87
G12	PBS 15056	0.622	21	19	2	8.93
G13	PBS 16022	0.150	8	3	5	7.93
G14	PBS 16023	0.036	11.5	1	10.5	7.13
G15	PBS 16033	0.212	14	8	6	7.73
G16	PBS 16044	0.417	35	16	19	5.13
G17	TAG 24	0.243	21	9	12	7.00
G18	TG 37 A	0.336	15	12	3	8.80

SP= stability parameter values, SSI = Simultaneous selection index for yield and stability, rSP = Ranks of the stability parameter, and rY = Ranks of the mean yield of genotypes, means-the mean yield of the genotypes

Biplot pattern for elucidation of multivariate analysis

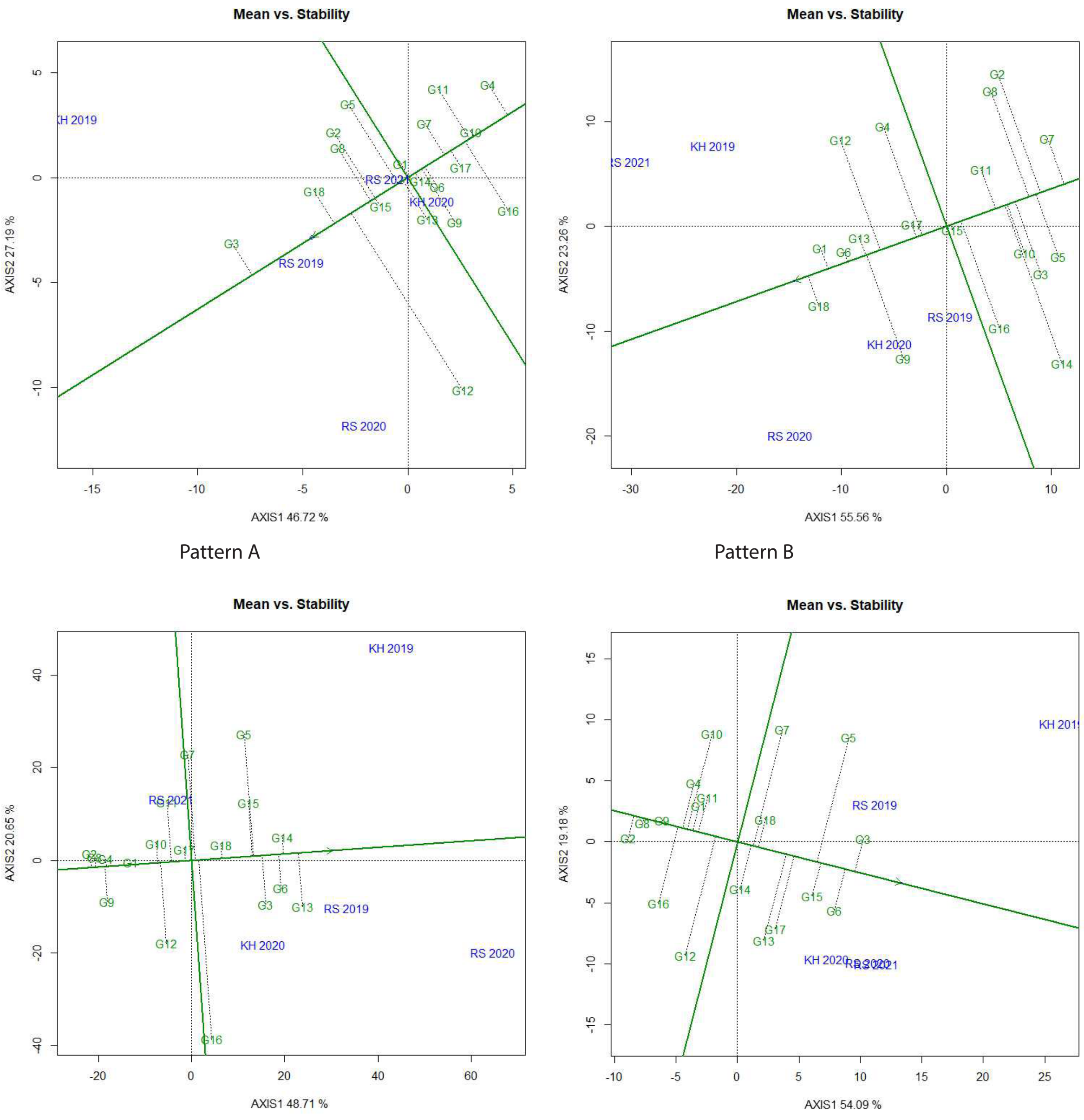
The presence of substantial interaction between genotype and environment necessitates researchers to perform stability analysis of genotypes using GGE biplot analysis (Oladosu et al. 2017). The main effect of genotype (G) plus G×E interactions is the principal source of variation in assessing genotypes under multi-environment trials (MET) (Yan et al. 2000). Three major components can be elucidated using the biplot such as (a) 'which-won-where' pattern or MET, is an effective approach to visualize the pattern of GEI based on the correlation between G and E; (b) stability *vs* mean performance over the environment for genotype evaluation; and (c) ranking of genotypes. The greater PC1 value indicates greater yielding ability whereas the lower PC2 value signifies stability. The cumulative variance of the first principal component (PC1) and the second interaction principal component (PC2) respectively clarified 46.72 and 27.19% of the total GEI for pod yield, 55.56 and 23.26% for SMKs, 48.71 and 20.65% for HPW and 54.09 and 19.18% for HKW. Suppose the first two PCs explain more than 60% of the variability in the data, and the combined effect accounts for more than 10% of the total variability. In that case, the biplot adequately approximates the variability in GEI data (Lal et al. 2019).

Which-won-where

In the which-won-where pattern of GGE biplot, the captivating genotype is always positioned at the vertex of the polygon where both sides of the polygon meet that vertical stripe, generating a borderline of that segment. Fig. 2 illustrates the polygon view of GGE biplot pattern for pod yield per plant (pattern A), sound mature kernels (pattern B), hundred pod weight (pattern C), and hundred seed weight (pattern D). The G+G×E variation was recorded as 73.91, 78.82, 69.36, and 73.27% for PYLP, SMKs, HPW and HKW. GGE biplot was divided into 6, 8, 7, and 9 sections for PYLP, SMKs, HPW, and HKW, respectively. Environmental indicators were positioned into 2, 3, 4, and 2 segments or sections of biplot for PYLP, SMKs, HPW, and HKW, respectively with different genotype winning in each segment confirming the presence of distinct interactions between genotype and environment for all traits evaluated. For pod yield, the hexagon had five genotypes *viz.*, PBS 11092, PBS 14060, PBS 11077, PBS 15056 and PBS 16044 at the vertices of which PBS 11077 was a winner in the first mega-environment (RS 2019, KH 2019, and RS 2021) and PBS 15056 and PBS 16044 in second mega-environment (KH 2020 and RS 2020). However, genotypes PBS 11092 and PBS 14060 did not accommodate in any of the test environments, indicating that they are low yielders in at least one of the test environments. Genotype PBS 15056 in KH 2019 and RS 2021, genotype TG 37A in RS 2020 and, genotype PBS 15022 in KH 2020 and RS 2019 was highly stable with high-sound mature kernels. For hundred pod weight genotypes PBS 16022 in RS 2019 and RS 2020, whereas PBS 16044 in KH 2020 and PBS 14060 in third mega environment KH 2019 was found as a highly stable and best-performing line. For HPW, environments RS 2019 and RS 2020 with PBS 16022 as the winning genotype, PBS 16044 as the winning genotype in the second mega environment KH 2020 and PBS 14060 as superior in the third mega environment KH 2019 was recorded. For HKW, the polygon view identified two mega environments, with PBS 14064 identified as superior in first and PBS 14060 and PBS 14068 as winning genotypes in the second mega environment. Our study's findings agree with the report stated by Oladosu et al. 2017 who considered ten environments. Such differential ranking of genotypes across different environments suggests the possible existence of crossover GEI, which conforms with previous works (Junjittakarn et al. 2016).

GGE biplot pattern of mean vs. stability analysis and ideal genotype assessment

The GGE biplot ranks the genotypes based on their mean performance and stability across environments. In graphical GGE biplot analysis, the ideal genotype should have a high IPCA1 score and an IPCA2 score close to zero (more stable) (Yan and Tinker 2006). The arrow sign on the AEC abscissa line directed the ranking of genotypes in increasing order with a greater value of traits evaluated. The mean *vs* Stability pattern of GGE biplot for pod yield (pattern A), SMK (pattern B), HPW (pattern C) and HKW (pattern D) is presented in Fig. 3. Genotypes PBS 11077 and TG 37A had the highest mean pod yield and genotype PBS 11092 had low yield in the test environments. Genotypes PBS 16023, PBS 16033, PBS 14064, and Dh 86 were highly stable and PBS 15056 was the least stable for yield among environments tested but had low pod yield compared to PBS 11077 and TG 37A. Genotypes PBS 11077 and TG 37A were high-yielders and were fairly stable across the environments tested. The GGE biplot of genotype-focused scaling for SMKs depicted genotypes TG 37A, Dh86, and PBS 14064 had the highest SMKs and genotype PBS 14068 had the least. Genotype PBS 16033, PBS 14064 and TAG 24 were highly stable owing to their closeness to AEC abscissa and PBS 16023, which was away from AEC abscissa, is highly unstable. Among the genotypes tested for SMK, Dh 86, and PBS 14064 recorded high SMK and were also showed stable performance. PBS 16022 and Girnar 3 had high and low HPW, respectively. While PBS 16044 and Dh 86 were, respectively, very unstable and highly stable genotypes. Among the genotypes tested PBS 16023 had high HPW and was stable over environments tested. Genotypes PBS 11077, PBS 14064 and PBS 16033 had high HKW and Girnar 3 the least, PBS 15014 and PBS 15022 were highly stable and PBS 15056 was highly unstable. Genotype PBS 11077 had high HKW and was fairly stable across environments tested. Similar trends with respect to mean



Pattern A

Pattern B

Pattern C

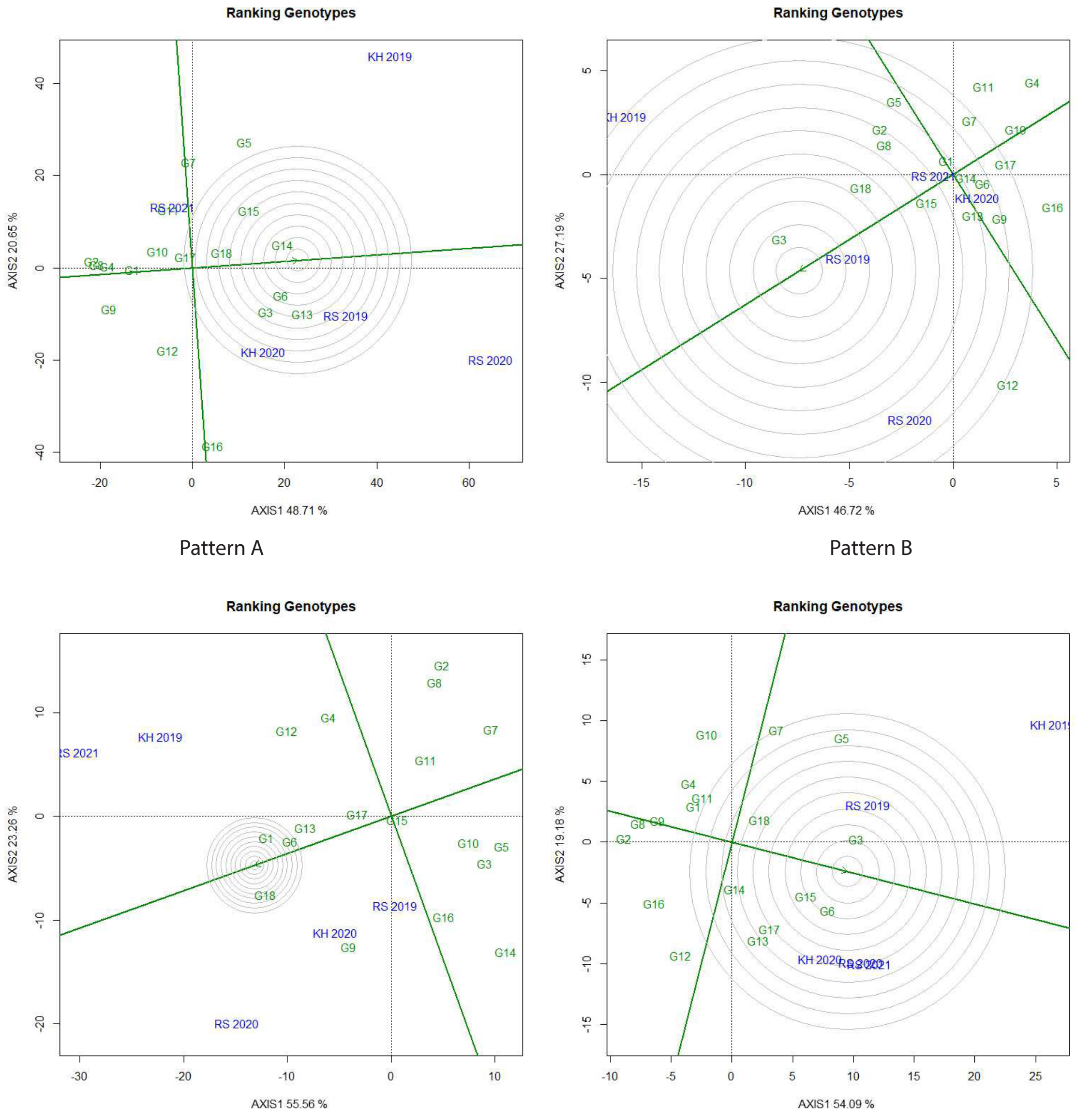
Pattern D

Fig. 3. The mean *vs.* stability pattern of GGE biplot illustrating the interaction effect of 18 genotypes under five seasons for PYPL (Pattern A), SMKs (Pattern B), HPW (Pattern C) and HKW (Pattern D). The biplots were created based on Centering = 0, singular value partitioning (SVP) = 1, and scaling = 0

vs stability analysis have been observed earlier (Oladosu et al. 2017; Hashim et al. 2021; Sabri et al. 2020).

Best and ideal genotype assessment

We can detect an ideal genotype in contrast to other genotypes evaluated through the genotype ranking biplot. Genotype ranking relative to ideal genotype for PYPL (Pattern A), SMK (Pattern B), HPW (Pattern C) and HKW (Pattern D) is presented in Fig. 4. An ideal genotype should have both high mean performance and high stability across environments. Also, genotypes located closer to the 'ideal genotype' are more desirable than others. The genotypes PBS 11077, Dh86, PBS 16023, and PBS 11077 were closer to ideal genotypes for PYPL, SMKs, HPW and HKW respectively. Plant breeders used data from yield performance evaluations based on mean and stability to choose genotypes best suited to a specific environment within a multi-environment, while genotypes close to the ideal genotype were also more promising or appropriate. So, the genotype ranking based on ideal genotype for PYPL was PBS 11077>TG 37 A>Girnar 3>PBS 15014>PBS 14060>PBS 16033>Dh 86. Oladosu et al. (2017) also found similar findings across environments as evidence of our



Pattern A

Pattern B

Pattern C

Pattern D

Fig. 4. The GGE biplot genotypes ranking pattern for genotype comparison with ideal genotype showing G + G × E interaction effect of 18 genotypes under five seasons for PYPL (Pattern A), SMKs (Pattern B), HPW (Pattern C) and HKW (Pattern D).The biplots were created based on Centering = 0, SVP = 2, and scaling = 0. The ideal genotype is signified by a circle within innermost concentric circles on average environment coordinate (AEC) abscissa which passed through biplot origin

result. Based on multi-seasons trial genotypes PBS 11077 and PBS15014 for PYLP, PBS14064 for SMKs, PBS 16023 for HPW and PBS11077for HKW were identified on well suited to a range of environments. The basic criteria for the second category are genotypes with specific adaptation but high performance.

Supplementary material

Supplementary Tables S1 to S5 are presented at www.isgpb.org

Author's contribution

Conceptualization of research (KR, SKB); Designing of the experiments (KR, SKB); Contribution of experimental materials (KR, GK); Execution of field/lab experiments and data collection (KR, GK, ABC, PK); Analysis of data and interpretation (ABC, KR, SS, GK), preparation of the manuscript (KR, PK, SS, NK).

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Supplementary Table S1. **Pedigree information for the developed advanced breeding lines (ABLs)**

ABLs	Pedigree
PBS 11077	TAG 24 X MH 2
PBS 11092	TAG 24 X MH 2
PBS 14060	Kadiri-3 x GG-2
PBS 14064	Girnar-1 x PBS 11003
PBS 14068	GG-2 mutant
PBS 15014	GG 2 x NRCG 1339
PBS 15022	(ICGV 86031 x TAG 24) x ICGS 76
PBS 15027	(ICGV 86031 x TAG 24) x CSMG 84-1
PBS 15028	(ICGV 86031 x TAG 24) x CSMG 84-1
PBS 15056	TAG 24 x ICGV 86031
PBS 16022	GG 2 x PBS 190
PBS 16023	GG 2 x PBS 190
PBS 16033	TAG 24 x M 13
PBS 16044	TAG 24 x ICGS 11

Supplementary Table S2. **Pooled analysis of variance for germination percentage at weekly intervals averaged over four seasons** *viz*.**,** *Kharif* **2019,** *Kharif* **2020,** *Summer* **2020,** *Summer* **2021**

Source of Variation	DF	7 DAS		14 DAS		21 DAS	
		MSS	% ss	MSS	% ss	MSS	% ss
Rep	1	206.05	0.18	44.28	0.03	131.05	0.09
Environment (E)	3	160.71**	0.43	263.66*	0.60	158.81	0.32
Genotype (G)	16	5915.88**	83.65	7191.71**	88.00	7787.69**	82.72
E*G	48	274.56**	11.65	204.41**	7.50	373.09**	11.89
Residual	67	69.21	4.10	75.28	3.86	112.10	4.99
Total	135	838.21		968.58		1115.78	
CV		9.57		10.22		13.02	

*Significance at P< 0.05 level, **Significance at P< 0.01 level

Supplementary Table S3. **The average performance of genotypes in terms of Pod yield/plant, Hundred pod weight (HPW), Hundred kernel weight (HKW), Sound mature kernels (SMKs) and IOD (21 DAS)**

Genotypes	IOD 21 DAS	Pod	Hundred pod weight (HPW) (gm)	Hundred kernel weight (HKW) (gm)	Sound mature kernels (SMKs) (%)
Dh 86	11.5	6.8	62	29.9	60
Girnar 3	91	7.1	56	26.5	50
PBS 11077	100	11.2	78	36.7	51
PBS 11092	95.4	6.2	63	29.6	56
PBS 14060	96.7	7.5	75	35.8	50
PBS 14064	99.2	7.5	79	37.4	59
PBS 14068	97.3	7.1	71	32.8	49
PBS 15014	100	8.3	60	27.1	49
PBS 15022	98.8	6.5	56	27.9	56
PBS 15027	95	5.4	62	29.5	52
PBS 15028	99.1	5.8	70	29.9	52
PBS 15056	80.0	9.0	72	30.8	56
PBS 16022	95.8	7.9	78	33.6	57
PBS 16023	100	7.0	81	32.4	51
PBS 16033	85.8	7.9	73	35.9	54
PBS 16044	94.6	5.1	69	29.7	54
TAG 24	37.3	7.0	73	34.9	55
TG 37A	3.1	8.7	74	32.9	61

Supplementary Table S4. Intensity of dormancy (IOD) in advanced breeding lines 21 days after sowing

Genotypes	*Kharif*-2019	Summer-2020	*Kharif*-2020	Summer-2021			*Kharif*-2021		
	Laboratory test			Laboratory test	Field test	*in-situ* test*	Laboratory test	Field test	*in-situ* test*
Dh 86	0	12.5	33.35	0	12	Present	10	18	Present
Girnar 3	100	100	100	97	99	Absent	93	95	Absent
PBS 11077	100	100	100	100	100	Absent	87	91	Absent
PBS 11092	100	95	86.7	100	90	Absent	80	100	Absent
PBS 14060	100	100	86.65	100	100	Absent	80	88	Present
PBS 14064	100	100	100	100	99	Absent	100	100	Absent
PBS 14068	100	92.5	93.35	100	100	Absent	78	90	Absent
PBS 15014	100	100	100	100	100	Absent	97	98	Absent
PBS 15022	100	95	100	100	92	Present	85	91	Absent
PBS 15027	100	90	90	100	96	Absent	82	90	Present
PBS 15028	96.5	97.5	100	100	100	Absent	87	92	Present
PBS 15056	90.2	60	93.35	50	100	Present	99	96	Absent
PBS 16022	90	60	93.35	100	100	Present	83	87	Present
PBS 16023	100	100	100	100	100	Absent	98	100	Absent
PBS 16033	83.35	70	100	100	97	Absent	82	94	Present
PBS 16044	96.65	100	93.35	95	100	Absent	88	90	Absent
TAG 24	37.3	55	67	45	75	Present	36	78	Present

Supplementary Table S5. Pooled analysis of variance for genotype (G), environment (E) and GxE interaction on pod yield, SMK (%), HPW and HKW and their pooled heritability estimates

Sources of variation	df	MSS			
		PLYP	HPW	HKW	SMKs
Environment (E)	4	698.5**	5413.6**	1649.5**	3215.2**
Rep (ENV)	10	10.64	362.18	17.44	1.045**
Genotype (G)	17	29.32**	909.7**	163.9**	219.3**
GxE	72	18.39**	414.4**	46.39**	81.46
Residual	180	8.9	199.8	21.6	77.85
Vg		0.72	33.0	7.83	9.19
V_{GxE}		3.13	71.54	8.25	1.203
Vp		1.95	60.65	10.9	14.62
h^2 (%)		37.2	54.44	71.7	62.8

**, impliesP ≤ 0.01; PYLP = pod yield (g/plant), HPW= hundred pod weight, HKW= hundred kernel weight, SMK= sound mature kernels