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Multi-environment evaluation of Spanish bunch groundnut genotypes for fresh seed dormancy

Narendra Kumar*, B. C. Ajay, M. C. Dagla[1], A. L. Rathnakumar, T. Radhakrishnan, C. Lal[2], M. Y. Samdur[3], R. K. Mathur[4] and P. Manivel[5]

ICAR-Directorate of Groundnut Research, Ivnagar Road, P. B. No. 5, Junagadh 362 001, Gujarat; [1]ICAR-Indian Institute of Maize Research, PAU Campus, Ludhiana 141 004; [2]ICAR-Indian Institute of Wheat & Barley Research P.B. No. 158, Karnal 132 001; [3]Centre on Rabi Sorghum (ICAR-Indian Institute of Millets Research) Solapur 413 006, Maharashtra; [4]ICAR-Indian Institute of Oil Palm Research, Pedavegi 534 450; [5]ICAR- Directorate of Medicinal and Aromatic Plants Research, Anand 387 310

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Abstract

The present study was carried out to evaluate eight promising Spanish bunch groundnut genotypes during four consecutive years (2014, 2015, 2016, 2017) to study genotype × environmental interactions and to identify stable sources of fresh seed dormancy in Spanish background in groundnut. Pooled analysis of variance revealed highly significant differences among the genotypes and genotype × environmental interactions for fresh seed dormancy at weekly intervals indicating that differential behavior of genotypes for fresh seed dormancy over the environmental conditions. Based on the results of intensity and duration of dormancy and germination stability index, identified four stable advanced breeding lines *viz*., PBS 12192, PBS 12187, PBS 12191 and PBS 12190 having high fresh seed dormancy of three week and two stable advanced breeding lines *viz*., PBS 12189 and PBS 12171 having high fresh seed dormancy of two week. Therefore, these genotypes can be used as novel genetic stock of fresh seed dormancy in Spanish bunch and they can be integrated into breeding programs to develop high yielding Spanish bunch cultivars with 2-3 weeks of fresh seed dormancy to avoid yield losses due to *in-situ* germination at the time of crop maturity.

Key words: Groundnut, Spanish bunch, fresh seed dormancy, stability, germination stability index

Introduction

Groundnut (*Arachis hypogaea* L.) is an important self-pollinated oilseed crop cultivated in about 4.87 million ha area with the production and productivity of 7.22 million tons and 1543 kg/ha, respectively in triennial average during 2014-15 to 2016-17 (Anonymous, 2017). Among the total cultivated area in India, about 7.5lakh ha area under post-rainy season (*rabi*-summer) which is predominated by Spanish bunch cultivars due to their early maturity and easy harvesting but Sub-species *fastigiata*, Spanish (subsp. *fastigiata* var. *vulgaris*) and Valencia (subsp. *fastigiata* var. *fastigiata*) habit types normally does not have seed dormancy. Lack of seed dormancy in the Spanish bunch varieties have a major problem resulting in 10-20% loss in pod yield due to *in-situ* germination resulting from unpredictable rainfall at harvest and delayed harvesting (Khalfaoui 1991; Nautiyal et al. 2001). To avoid yield losses and poor seed quality due to unexpected rainfall at harvest and delayed harvesting at least 2-3 weeks of fresh seed dormancy would be required in Spanish bunch groundnut cultivars grown in rainy and post rainy seasons. Considerable year-to-year variations observed in fresh seed dormancy due to genotypic difference and occurrence of genotype by environment interaction is most common resulting from the differential expression of genotypes over the environments and it may complicate the selection process of a genotype for a target trait. Therefore, multi-environment trials (METs) are widely used by plant breeders to evaluate the relative performance of genotypes over the environments. Additive Main Effects and Multiplicative Interaction (AMMI) analysis is one of the most popular parametric of multivariate methods to predict adaptation and stability of cultivars

*Corresponding author's e-mail: narendrapb09@gmail.com
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(Gauch 1992). AMMI analysis is a combination of ordinary ANOVA to analyze the main effects (additive part) of the genotypes and the environment together with principal components analysis of the genotype by environment interaction (Zobel et al. 1988; Gauch 1988). GGE biplot analysis was recently developed method to use some of the functions of previous methods jointly. Yan et al. (2000) put the G and GE together and referred as GGE and following the proposal of (Gabriel 1971), biplot technique was used to display the GGE of a multi-environment trials data which jointly referred to as a GGE biplot (Yan 2001). GGE biplot analysis is a data visualization tool, which graphically displays a GE interaction in a two way table. It is very effective tool for mega environment analysis (which-won-where pattern), in which specific genotypes can be recommended to specific mega environments (Yan and Tinker 2006), genotype evaluation (the mean performance vs. stability) and environmental evaluation (power to discriminate among genotypes in target environments). The GGE biplot technique has been successfully utilized in groundnut by many workers (Kasno and Trustinah 2015; Dolinassou et al. 2016; Kebede and Getahun 2017; Ajay et al. 2017; Lal et al. 2019) to identify stable performing genotypes to specific environment and across environments. Therefore, present investigation was undertaken to understand genotype-environment interactions (GEI) of fresh seed dormancy and to assess performance of genotypes over the environments through AMMI and GGE biplot to identify most stable groundnut genotypes with 2-3 weeks of fresh seed dormancy in Spanish bunch background.

Materials and methods

Plant materials and growing conditions

The experimental material comprised of six Spanish bunch advanced breeding lines (PBS 12171, PBS 12187, PBS 12189, PBS 12190, PBS 12191 and PBS 12192) and two high yielding popular Spanish bunch varieties *viz*., TG 37A and Dh 86. These genotypes were harvested at maturity as indicated by blackening of inner parenchyma of the pod (Miller and Burns 1971). To study fresh seed dormancy, a sample of mature pods were randomly selected and shelled immediately after harvesting of summer groundnut and precaution was taken to prevent any damage of the testa, cotyledons and embryo while removing seeds from pods. Before sowing, seeds were treated with carbendazim (3g kg^{-1} of seed) fungicides to protect from soil-borne diseases. A total of eight genotypes were evaluated during 2014 to 2017 (June-July) at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat, India (Lat. 21°31' N, Long. 70°36' E) in medium black calcareous soil. The data of maximum and minimum temperature (^{0}C), relative humidity (%) and solar radiation (W/m^2) for each environment is illustrated in Fig. 1. The experiment was laid out in a randomized complete block design with three replications. Each replication consisted of 20 freshly harvested seeds sown at 2 to 3cm deep for each genotype. The seeds of each genotype were sown at 45 cm spacing between rows and 10 cm between plants. The soil moisture was maintained at field capacity during the growth period up to 35 days after sowing (DAS). The mean pod moisture content was 38.5% at harvest and remaining pods were stored at 7.6% moisture content. The observations were recorded on number of seeds germinated at weekly interval until the end of experiment.

Fresh seed dormancy is characterized by its duration and intensity as per method suggested by Kumar et al. (1991). Duration of fresh seed dormancy was measured by days taken to attain 50 per cent germination by a genotype and intensity of fresh seed dormancy was measured as percentage of non-germinated seed at seven days after sowing. Degree of dormancy was classified using 1-8 scale according to the scale devised by Landfort et al. (1965) where scale 1 = 0-10%, 2 = 11-20, 3 = 21-40, 4 = 41-60, 5 = 61-70, 6 = 71-80, 7 = 81-99 and 8 = 100% non-germinated seeds. The percentage of germinated seeds for an entry at a given date was calculated by the following formula:

Germination (%) = Number of germinated seeds * 100/
Total number of sown seeds

Statistical analysis

Pooled analysis of variance was performed using the statistical package DSAASTAT (Onofri 2007). GGE biplot analysis was used to demonstrate the G and GE effects using principal components (PC) scores from singular value decomposition (SVD). GGE biplot with average-environment coordination (AEC) and polygon view was drawn to describe the stable performance of genotypes within a specific environment and over environment. GGE-biplot analysis was performed in R (R core team 2015). AMMI analysis, the data of germination percentage was subjected to combined analysis of variance and AMMI analysis which is a combination of analysis of

variance and multiplication effect analysis. Analysis of variance was used to partition variance into three components: genotype deviation from grand mean, environment deviations from grand mean, and GE deviation from grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA). R package was used to perform this analysis (R core team 2015). The AMMI stability value (ASV) as described by Purchase (2000) was calculated as follows:

$$ASV = \sqrt{\left[\left(\frac{IPCA1\ sum\ of\ square}{IPCA2\ sum\ of\ square}\right) IPCA1\ score\right]^2 + (IPCA2\ score)^2}$$

where, SSIPCA1/SSIPCA2 is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV scores indicate a more stable genotype across environments.

Germination Stability Index (GSI) was used to identify stable genotypes for fresh seed dormancy. Stability alone can't be the sole criteria for genotypic selection because most stable genotypes should be best performer also. Yield Stability Index (YSI) which takes into consideration both yield and stability was used by Farshadfar et al. (2011) to select stable and high yielding genotypes. This measure was used in the present study to select stable genotypes with fresh seed dormancy and index is denoted as Germination Stability Index (GSI). GSI were calculated by the following formulas:

GSI = RASV + RG

where RASV is the rank of ASV (AMMI stability value) and RG is the rank of mean germination across environments. GSI incorporate both fresh seed dormancy and stability in a single criterion. Low value of this parameter shows desirable genotypes with high fresh seed dormancy (*i.e.*, low germination per cent) and stability.

Results and discussion

Pooled analysis of variance for germination percentage at different weekly intervals

Pooled analysis of variance for germination per cent at weekly intervals revealed highly significant genotypic differences and genotype × year interaction for fresh seed dormancy at different weekly intervals (Table 1). It indicated differential behavior of genotypes under different environments. It might be due to environmental factors also played very important role in inducing dormancy. Large sum of square for genotype showed that there was sufficient genetic variability among all the genotypes for germination per cent at different weekly intervals over the years. The higher genotypic variation relative to environmental counterpart is also consistent with the high autogamous nature of groundnut (Nath and Alam 2002). Significant genotype × year interaction (GEI) effects indicated that germination percent was influenced by year-to-year variation which could be attributed to environmental factors like temperature, relative humidity and solar radiation during the experiment period (Fig. 1). Significant effects of genotype and GEI was found in this study are in agreement with other authors reported by Kumar et al. (2017); Kumar et al. (2018a); Kumar et al. (2018b). Germination is also quantitative trait like yield which is controlled by several genes, groundnut yield is influenced by varied environmental factors like soil type, moisture, sowing time (Mekontchou et al. 2006; Khan et al. 2009).

AMMI analysis of variance for of eight genotypes

Table 1. Analysis of variance for germination percentage at weekly intervals averaged over four year from 2014-17

Sources of variation	DF	7 DAS	14 DAS	21 DAS	28 DAS	35 DAS
Year	3	524.6	221.6	624.5	950.6	2264.1
Rep(Year)	8	58.6	84.1	116.3	158.5	193.0
Genotype	7	5682.7**	14309.2**	13487.5**	8660.6**	7407.8**
Genotype × Year	21	210.2**	206.9**	179.5**	582.8**	633.7**
Residual	56	44.9	52.4	76.0	143.6	154.2
Total	95	513.2	1145.1	1107.8	895.0	864.6

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

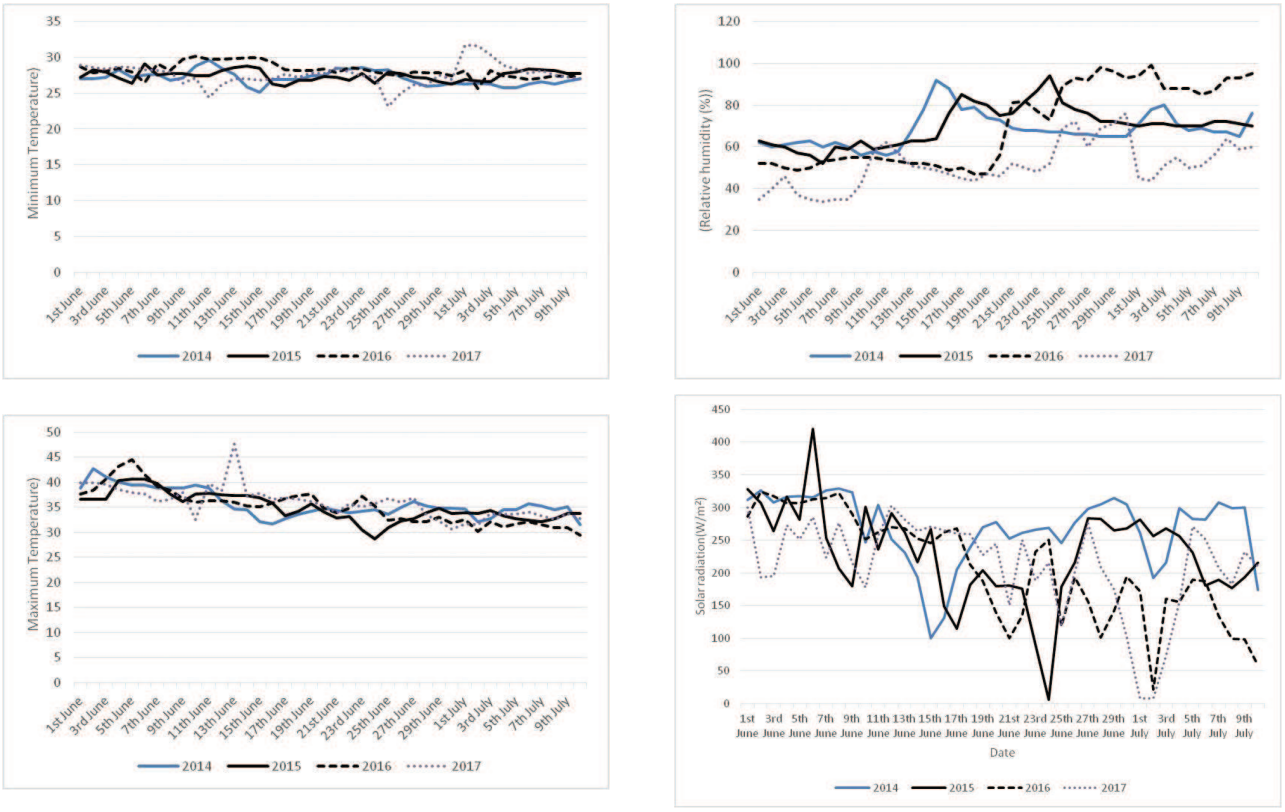

Fig. 1. Maximum and minimum temperature, relative humidity and solar radiation during the experiment period 2014-2017

for fresh seed dormancy (FSD) at 21DAS revealed that highly significant ($P \leq 0.01$) variation among the genotypes, genotype and GE interaction and IPCA1 and significant ($P \leq 0.03$) variation among the environments (Table 2). It indicated that all the genotypes had different FSD at 21DAS across the test environments due to variations in environmental factors like temperature, relative humidity and solar radiation during the experiment period (Fig. 1). Significant GEI for dormancy was also reported by Kumar et al. (2017); Kumar et al. (2018a) and Kumar et al. (2018b). The AMMI analysis of variance showed that 89.7% of the total sum of squares was attributable to the genotypes (G), 1.8% to the environments (E) and 3.6% to GEI effects (Table 2). A large proportion of genotype indicated that the genotypes were more

Table 2. AMMI† analysis of variance of fresh seed dormancy at 21DAS for eight groundnut genotypes grown over four year from 2014-17

Sources of variation	DF	Sum of squares	Mean square	F value	P>F	Percentage of GEI ss
Environment (E)	3	1876.00	625.30	5.39	0.03*	1.8
Rep(E)	8	929.00	116.10	1.53	0.17	0.9
Genotype (G)	7	94363	13480.5	177.22	2.2e-16***	89.7
G×E interaction	21	3774.00	179.40	2.36	0.006**	3.6
IPCA1	9	2813.02	312.56	4.11	0.004***	2.7
IPCA2	7	842.28	120.33	1.58	0.16	0.8
IPCA3	5	119.18	23.84	0.31	0.90	0.1
Residuals	56	4260.00	76.10			

†Abbreviations: AMMI = additive main effects and multiplicative interaction; GEI = genotype × environment interaction; IPCA = interaction principal component analysis axis; significance codes: *** = 0.001, '**' = 0.01, '*' = 0.05

diverse with differences among the means. The small proportion of environment indicated that the variations among the environmental means were not very much high. However, magnitude of GEI was very much smaller than that for the genotype SS, it indicating that the differences in the response of the genotypes across environments were not much large and the variation was mostly due to genotypic differences among the genotypes. The partitioning of GE interaction for germination percent at 21DAS, which was mainly explained by the first principal component axis (IPCA1) with 74.5% (2.7) of GEI sum of squares (3.6). The second and third interaction principal component axis (IPCA 2, IPCA 3) was non-significant and accounted for 22.3% (0.8) and 3.2% (0.1), respectively of GEI sum of squares. They jointly accounted for 25.5% of GEI sum of squares (Table 2).

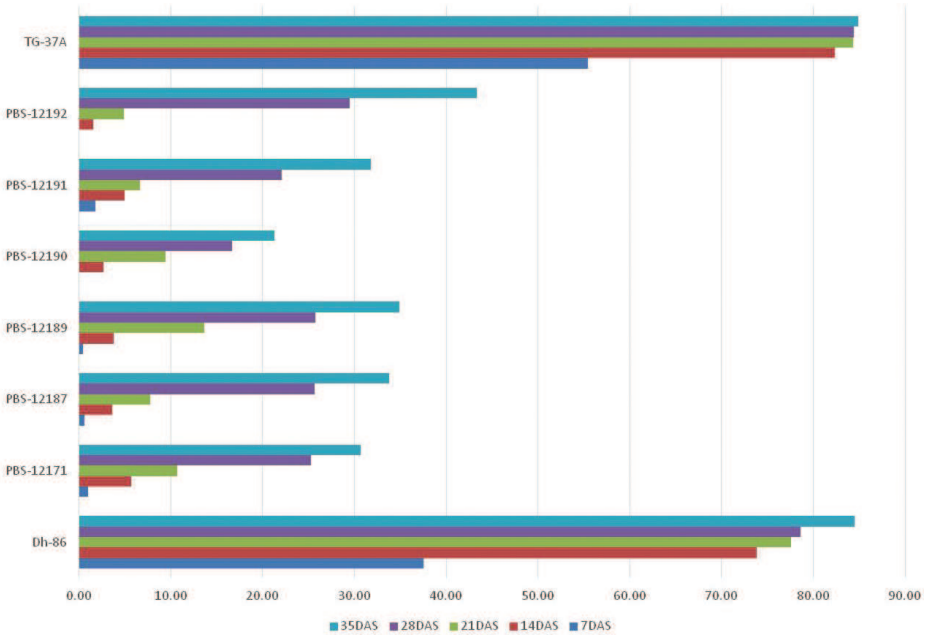

Fig. 2. Stacked bar representing average germination percentage of groundnut genotypes during 2014-2017

Intensity, degree and duration of fresh seed dormancy

Intensity of dormancy is defined as the percentage of seeds that not germinated even seven days after the harvest (Kumar et al. 1991). From practical point of view, high intensity (>90%) along with 2-3week duration is very important rather than at seven days after harvest (Kumar et al. 2017). Average intensity ranged from 45% to 100% at 7 DAS during 2014 to 2017. The results showed that four advanced breeding lines *viz*., PBS 12187, PBS 12189, PBS 12190 and PBS 12192 had an average H"100% intensity of fresh seed dormancy followed by two advanced breeding lines PBS 12171 and PBS 12191 with 99% and 98 %, respectively intensity of fresh seed dormancy while two high yielding varieties *viz*., TG 37A and Dh 86 had only 45% and 63%, respectively intensity of fresh seed dormancy at seven days during 2014-2017 (Table 3, Fig. 2). This large variation in intensity of dormancy could be due to genotypic differences among the genotypes and environmental factors which affects dormancy by their effect

Table 3. Average intensity and degree of fresh seed dormancy across the year from 2014-2017

Genotype	Intensity of dormancy (%)				Average	Degree of dormancy			
	2014	2015	2016	2017		2014	2015	2016	2017
Dh 86	58	80	38	74	63	4	6	3	6
PBS 12171	100	98	98	100	99	8	7	7	8
PBS 12187	98	100	100	100	100	7	8	8	8
PBS 12189	100	100	98	100	100	8	8	7	8
PBS 12190	100	100	100	100	100	8	8	8	8
PBS 12191	100	98	95	100	98	8	7	7	8
PBS 12192	100	100	100	100	100	8	8	8	8
TG 37A	56	51	18	53	45	4	4	2	4

on mother plant and seeds during storage. These findings are in agreement with the results of several researchers published earlier (Kumar et al. 1991; Faye et al. 2009; Naganagoudar et al. 2015; Kumar et al. 2017; Kumar et al. 2018a); Kumar et al. 2018b).

Degree of fresh seed dormancy of genotypes was recorded on 1 to 8 scales of Landfort et al. (1965), wherein scale "1" indicates least dormant and scale "8" indicates most dormant genotype. In the present study degree of dormancy scale ranged from 4 to 8 during 2014-2017 except 2 to 8 scale in the year 2016. It was observed that four advanced breeding lines *viz*., PBS 12187, PBS 12189, PBS 12190 and PBS 12192 had an average score ≈8 while two advanced breeding lines *viz*., PBS 12171 and PBS 12191 had an average score 7.5 across the year at 7DAS. Therefore, based on intensity and degree of dormancy following advanced breeding lines *viz*., PBS 12187, PBS 12189, PBS 12190, PBS 12192, PBS 12171 and PBS 12191 were identified as source of high intensity and degree of fresh seed dormancy in Spanish bunch background at 7 DAS (Table 3). Li and Foley (1997) reported that degree of dormancy is influenced by genetic and environmental factors during the development of seed. Nautiyal et al. (2001) also reported large variation of seed dormancy in Spanish type genotypes. Gaikwad and Bharud (2016) also observed that sufficient genetic variation for fresh seed dormancy at different weekly intervals over the years.

Genotypes having 2-3 weeks of fresh seed dormancy will be more useful especially for those areas where unpredictable rainfall occurs at the time of crop maturity. Prolonged seed dormancy of > 3 weeks is also undesirable in India as the crop is also cultivated under *rabi*/post-rainy season. The duration of dormancy is mainly governed by the intensity of dormancy and environmental factors. Faye et al. (2009) also reported that intensity and duration of dormancy are correlated each other. Genotypes having high intensity of dormancy (>90%) at ideal environmental conditions would be more desirable rather than having low intensity with long duration of dormancy. Based on the results of intensity and duration of fresh seed dormancy, five advanced breeding lines *viz*., PBS 12192, PBS 12191, PBS 12187, PBS 12190 and PBS 12171 having high fresh seed dormancy (≥90%) of three week and one advanced breeding line, PBS 12189 with high fresh seed dormancy (96%) of two week had been identified. These all the advanced breeding lines had almost 100% fresh seed dormancy at 7 DAS (Table 4).

The intensity of FSD depends on genetic constitution of genotype and duration of dormancy. Among advanced breeding lines, highest average per cent reduction in intensity of FSD was observed from 21 to 28 DAS (15.5%) followed by 28 to 35 DAS (8.5%), 14 to 21 DAS (4.9%) and 7-14 DAS (3%) while in case of cultivars average per cent reduction was highest from zero to 7 DAS (46.5%) followed by 7 to 14 DAS (28.5%), 14 to 21DAS (4.2%), 28 to 35 DAS (2.6%) and from 21-28 DAS (2.2%). It revealed that all the advanced breeding lines had 2-3 weeks fresh seed dormancy while both the cultivars had lack of fresh seed dormancy (Table 4). Among the advanced breeding lines highest per cent reduction in intensity of FSD from 21 to 28 DAS was observed in PBS 12192 (24.6%) followed by PBS 12187 (17.9%) and PBS 12191 (16.3%) while in case of cultivars highest average per cent reduction was recorded in TG 37 A (55%) followed by Dh 86 (38%) at zero to 7 DAS (Table 4). In India, groundnut is cultivated in rainy, post-rainy and summer season therefore Spanish genotypes which having 2-3 week dormancy would be more desirable and could be used in further multiplication

Table 4. Mean intensity and duration of fresh seed dormancy at weekly interval over the year from 2014-2017

Genotype	Intensity of dormancy (%)					Degree of dormancy			
	7 DAS	14DAS	21DAS	28DAS	35DAS	2014	2015	2016	2017
Dh 86	62	32	26	22	17	7	14	7	14
PBS 12171	99	95	90	76	70	35	35	28	35
PBS 12187	99	96	92	74	66	35	35	35	35
PBS 12189	100	96	86	74	65	35	35	35	28
PBS 12190	100	97	91	83	79	35	35	35	35
PBS 12191	98	96	95	78	68	35	35	35	28
PBS 12192	100	98	95	71	57	35	35	35	28
TG 37A	45	18	16	15	15	7	7	7	7

Table 5. IPCA1 and IPCA2 scores, mean germination percent at 21DAS and various stability parameters in groundnut genotypes during 2014 to 2017

Genotype	ASV	GSI	RASV	RG	Germination (%)	IPCA1	IPCA2
Dh 86	8.18	15	8	7	77.6	-4.48	0.14
PBS 12171	4.91	12	7	5	10.7	2.60	1.24
PBS 12187	1.59	5	2	3	7.8	-0.15	1.56
PBS 12189	2.78	12	6	6	13.7	0.83	-2.33
PBS 12190	2.74	9	5	4	9.4	0.80	-2.32
PBS 12191	2.16	6	4	2	6.7	0.92	1.36
PBS 12192	1.16	2	1	1	4.9	0.61	0.31
TG 37A	2.05	11	3	8	84.2	-1.12	0.02

ASV = AMMI stability value; GSI = Germination stability index; RASV = Rank of AMMI stability value; RG = Rank of mean germination across environments

and breeding programme than genotypes having more than 3 week dormancy. Mathur et al. (2000) also observed that two advanced breeding lines PBS 12115 and PBS 12126 possessed fresh seed dormancy of 21-28 days and 14-21 days respectively. The variability in fresh seed dormancy among Spanish advanced breeding lines in the present study was in agreement with earlier works (Yaw et al. 2008; Rathanakumar et al. 2009; Faye et al. 2009, Faye et al. 2010; Wang et al. 2012; Gaikwad and Bharud 2016).

Relationship and effect of environmental factors on fresh seed dormancy

Though seed dormancy in groundnut is genetically controlled by dominant allele of a single gene (Upadhyaya and Nigam 1999; Yaw et al. 2008) but it also influenced by the several environmental factors like growing season, temperature, relative humidity, solar radiation, rainfall, soil moisture and soil fertility etc. (Patro and Ray 2016). Correlations between fresh seed dormancy and environmental factors (maximum temperature, relative humidity and solar radiation) revealed values of correlation were high but non-significant findings observed between fresh seed dormancy over the years with environmental factors *viz*., maximum temperature, relative humidity, solar radiation except FSD2014 with maximum temperature in 2016 and FSD2016 with maximum temperature in 2017 while FSD2016 and FSD2017 had negative relationship with relative humidity of 2014 and 2016 (Table 6). Interestingly, FSD over the years had negative relationship with relative humidity. It showed that high relative humidity induces the germination in studied genotypes.

Table 6. Correlations between fresh seed dormancy and environmental factors at 21days after sowing

Indices	FSD 2014	FSD 2015	FSD 2016	FSD 2017
Maxitemp2014	0.90	0.97	0.90	0.87
Maxitemp2015	0.94	0.99	0.87	0.91
Maxitemp2016	1.00**	0.98	0.65	1.00
Maxitemp2017	0.64	0.79	1.00**	0.58
RH2014	-0.67	-0.82	-1.00**	-0.62
RH2015	-0.74	-0.87	-0.99	-0.69
RH2016	-0.99	-0.93	-0.50	-1.00**
RH2017	-0.90	-0.79	-0.24	-0.93
SR2014	0.92	0.98	0.88	0.89
SR2015	0.95	0.99	0.84	0.92
SR2016	0.85	0.94	0.94	0.81
SR2017	0.08	0.29	0.82	0.01

*Significant at P<0.05, **Significant at P<0.01 levels. Abbreviations: FSD=fresh seed dormancy; Maxitemp= Maximum temperature; RH=relative humidity (%); SR= solar radiation (W/m^2)

Table 7. Effect of environmental factors on fresh seed dormancy at weekly interval in groundnut

Indices	FSD (%)	Min. mean temp. (^oC)	Max. mean temp. (^oC)	Mean relative humidity (%)	Mean solar radiation (W/m^2)
FSD7DAS	88	28	40	52	296
FSD14DAS	79	28	37	57	260
FSD21DAS	74	28	35	64	209
FSD28DAS	62	27	34	74	207
FSD35DAS	55	27	33	73	197

Abbreviations: FSD=fresh seed dormancy

Temperature and moisture content played very important role in inducing dormancy in groundnut. Mean FSD at 7DAS was 88% at 40°C temperature and 52% relative humidity. It showed high temperature and low relative humidity inducing dormancy in studied genotypes. It might be due to inhibition of physiological processes and accumulation of growth inhibitor substances required for germination. Maximum reduction (15.5%) of FSD was observed from 21 to 28DAS (62%) at 34°C and at 74% high relative humidity (Table 7). It indicated that this temperature and relative humidity regime were most favourable conditions for induction of germination in studied genotypes. Opio and Photchanachai (2016) reported that highest seed dormancy in peanut was shown by seeds exposed to temperature at 40°C. Toh et al. (2008) observed high temperatures induce accumulation of reactive oxygen species (ROS) and abscisic acid (ABA) which play important role in dormancy and germination control in *Arabidopsis* seeds.

GGE biplot analysis

GGE explains two most important sources of variation *i.e.*, genotype main effect (G) and genotype × environment (GE) interaction effect. The GGE analysis was considered satisfactory as the first two principal components (PC1 and PC2) of the GGE explained 99% variation. GGE-biplot is perfectly suited for analysis involving multiple environments which is based on genetic correlation between environment and the which-won-where pattern; evaluation of environment based on discriminating ability and representativeness; and evaluation of genotype based on mean performance and stability across environments. The GGE biplot graphically displays G+GE of the MET data in a way that facilitates visual variety evaluation and mega-environment identification (Yan et al. 2007).

Which-won-where pattern is viewed as a polygon which is helpful to estimate the existence of possible mega-environments (Yan and Rajcan 2002; Yan and Tinker 2006). The lines dividing the biplot into sectors represent a set of hypothetical environments. Polygon is created by joining all the genotypes which were away from biplot origin. A perpendicular line from the origin is drawn beyond the polygon biplots was divided into several sectors. The genotypes at the vertices of each sector were the best performing genotype at environments than other genotypes in same sector. If a genotype at an angular vertex of the polygon falls within one sector with an environment marker (or with several markers), that means that performance of this genotype was the highest in this particular environment. Another important feature of this biplot is that it indicates environmental groupings, which suggests the possible existence of different mega-environments. Fig. 3 presents a polygon view of Spanish bunch groundnut genotypes evaluated for fresh seed dormancy at 21 DAS during 2014 to 2017. The polygon was divided into five sectors and identified two mega environments. First mega-environment consists of year 2015, 2016 and 2017 along with best performing genotypes PBS 12191 (6), PBS 12190 (5), PBS 12189 (4), PBS 12192 (7) and PBS 12187 (3) whereas second mega-environment consists of year 2014 along with best genotype PBS 12171 (2). It indicated that these genotypes performed best in these two mega environment. Cultivars TG 37A and Dh 86 did not accommodate by any of the environment, it indicating that these cultivars did not have fresh seed dormancy across the years (Fig. 3). The GGE biplot

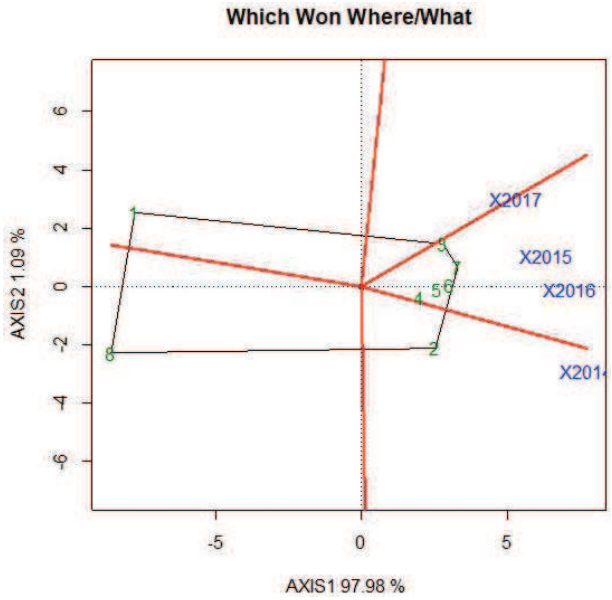

Fig. 3. Polygon views of the GGE-biplot based on symmetrical scaling for the which-won where pattern for groundnut genotypes evaluated for fresh seed dormancy at 21DAS during 2014-2017. (SVP=4, Centring=2, Scaling= 0.), (1=Dh 86, 2 = PBS 12171, 3 = PBS 12187, 4 = PBS 12189, 5 = PBS 12190, 6 = PBS 12191, 7 = PBS 12192, 8 = TG 37A)

ranks genotypes by their mean germination percent and stability over environments (Fig. 4). The axis of average environment coordination (AEC) abscissa is a single arrowed line that passes through the biplot origin with an arrow indicating to the direction of the

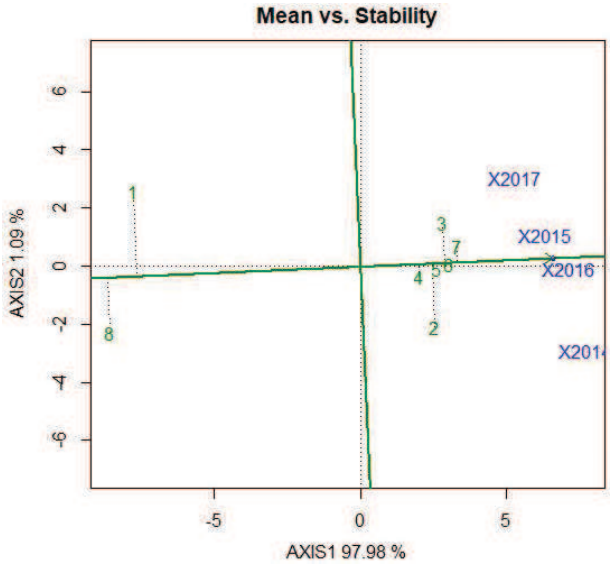

Fig. 4. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling groundnut genotypes evaluated for fresh seed dormancy at 21DAS during 2014-2017. (SVP=4, Centring=2, Scaling= 0.), (1 = Dh 86, 2 = PBS 12171, 3 = PBS 12187, 4 = PBS 12189, 5 = PBS 12190, 6 = PBS 12191, 7 = PBS 12192, 8 = TG 37A)

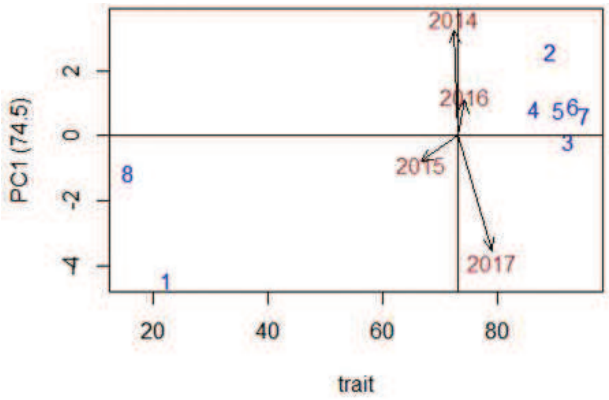

Fig. 5. AMMI biplot showing the main and IPCA 1 effects of both genotypes and environments on germination percentage at 21DAS during 2014-2017. 1 = Dh 86, 2 = PBS 12171, 3 = PBS 12187, 4 = PBS 12189, 5 = PBS 12190, 6 = PBS 12191, 7 = PBS 12192, 8 = TG 37A

best performing genotypes (highest dormancy). The axis of AEC ordinate is the line that passes through the biplot origin and is perpendicular to the AEC abscissa. The AEC ordinate approximates the genotypes contribution to the G×E interaction indicating the more the closest genotype to the AEC abscissa, the more is consistent or stable in the test environments (Yan 2001; Yan and Tinker 2006). Accordingly, Fig. 4 results indicated that advanced breeding lines *viz*., PBS 12192 (7), PBS 12191 (6), PBS 12187 (3), PBS 12190 (5), PBS 12171(2) and PBS 12189 (4) had highest intensity of fresh seed dormancy and stability across the environments while the cultivars TG 37A (8) followed by Dh 86 (1) had lowest fresh seed dormancy and stability at 21DAS over the years indicating had no dormancy which are not suitable for those areas where unexpected rainfall occurs at the time of maturity and rainfall prolonged till maturity period.

AMMI model analysis

The main and IPCA 1 effects of both G and E on germination percentage or fresh seed dormancy were shown in Fig. 5. For any G–E combination in the AMMI biplot, the additive part (main effects) of the AMMI model equals the G mean plus the E mean minus the grand mean, and the multiplicative part (interaction effect) is the product of G and E IPCA 1 scores Zobel et al. (1988). In AMMI biplots, the X-axes was the mean of germination per cent of genotypes over the environments or mean germination per cent of environments over genotypes and Y-axes was the genotypic or environmental IPCA1 mean scores on germination percent.

Genotypes with IPCA 1 scores >0 responded positively (adaptable) to environments that had IPCA scores >0 (i.e., their interaction is positive) but responded negatively to environments that had IPCA 1 <0; while genotypes having near zero/zero IPCA1 score indicates little or no interaction and indicates broad adaptability of genotype. The present study results showed that an advanced breeding line PBS 12171(2) had IPCA1 scores of >0 and was highly adaptable to the specific environments whereas advanced breeding lines *viz*., PBS 12187 (3), PBS 12189 (4), PBS 12190 (5), PBS 12191 (6) and PBS 12192 (7) with IPCA1 scores near to zero hence these advanced breeding lines were more stable and wider adaptability across the years for fresh seed dormancy. Cultivars, Dh 86 (1) and TG 37A (8) with IPCA1 scores <0, had no fresh seed dormancy and were less adaptable. The differences among cultivars in terms of direction and magnitude along the x-axis (trait) and y-axis (IPCA1 scores) were also important. The best genotype should be high fresh seed dormancy and stable across environments. Genotypes with lower

absolute IPCA1 scores will produce less GE interaction effect than the cultivar with higher absolute IPCA1 score hence these advanced breeding lines are considered as highly stable. Based on AMMI biplot analysis genotypes PBS 12187 (3), PBS 12192 (7), PBS 12190 (5), PBS 12189 (4), PBS 12191 (6) and PBS 12171 (2) were identified as most stable for fresh seed dormancy while the cultivars TG 37A (8) followed Dh 86 (1) had the highest variability in interaction (IPCA1 score) and these were less stable for fresh seed dormancy.

AMMI stability value (ASV)

AMMI model analysis does not allow quantification of stability measure which is essential to rank the genotypes according to their yield stability. Hence in order to overcome this problem, Purchase et al. (2000) proposed ASV measure it ranked genotypes based on stability and performance across the year. ASV is the distance of IPCA1 score against IPCA2 from zero. Proportional difference between IPCA1 and IPCA2 scores is used to calculate weight of IPCA1 score and to compensate for the relative contribution of IPCA1 and IPCA2 to total GE. Genotype with least ASV score is most stable. Accordingly, genotype PBS 12192 is the most stable followed by PBS 12187 and Dh 86 was least stable for fresh seed dormancy (Table 5).

Germination stability index (GSI)

Genotypes should not be selected based on stability alone because highly stable genotypes may be poor performers (Farshadfar et al. 2011). Hence it is necessary to include *per se* performance of a trait and stability in selection index. Dormancy and their stability are little fluctuating according to growing conditions of the environments. Therefore, stability analysis through various models provides meaningful conclusion regarding stability and performance of Spanish bunch genotypes across different environments. Among the different parameters of stability, Germination Stability Index (GSI) was used to select stable genotypes with fresh seed dormancy. In this method maximum variation explained by IPCA1 and IPCA2 in GE interaction were considered. ASV and mean of a trait is ranked in such a way that the lowest ASV takes the rank one and lowest germination percent (*i.e* high fresh seed dormancy) takes rank one and then the ranks are summed in a single simultaneous selection index named as germination stability index (GSI). The genotypes with lowest GSI values are considered as most stable with high fresh seed dormancy. Result showed that four advanced breeding line *viz*., PBS 12192, PBS 12187, PBS 12191 and PBS 12190 had low GSI score hence identified as most stable genotypes with high fresh seed dormancy whereas genotype Dh 86 had highest GSI value and hence is least stable with no fresh seed dormancy (Table 5). This stability parameter includes ASV and mean performance in a single non-parameric index hence the most desirable index for discriminating the most stable genotypes with high grain yield (Farshadfar et al. 2011).

Authors' contribution

Conceptualization of research (NK, BCA, MCD); Designing of the experiments (NK, BCA, MCD); Contribution of experimental materials (NK, ALR, CL, MYS, RKM, PM); Execution of field/lab experiments and data collection (NK, BCA, MCD); Analysis of data and interpretation (NK, BCA, ALR, TR); Preparation of manuscript (NK, BCA, ALR).

Declaration

The authors declare no conflict of interest.

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E r r a t u m

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