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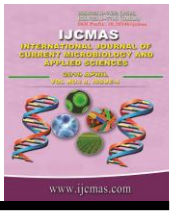

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Evaluation of Soybean Germplasm Lines for Agro-Morphological Traits and Terminal Drought Tolerance

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ABSTRACT

Keywords

Terminal, Germplasm accessions, Potassium Iodide (KI), Soybean, drought tolerance

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The occurrence of drought stress at seed filling stage is known to cause severe yield reduction in soybean especially where the crop is grown in rainfed conditions. Screening of large germplasm lines under natural drought conditions is extremely difficult to execute due to unusual rains. In the present study, about 328 germplasm lines are screened for terminal drought tolerance by spraying 0.2% of potassium iodide (KI) at R_5 stage and the tolerant lines were again retested under similar conditions in the subsequent year. The lines were classified as tolerant, moderately tolerant and susceptible based on the relative reduction in seed yield and 100-seed weight of treated over control conditions. The Shannon diversity index (SDI) indicated that genotypes were highly diverse for seed colour (H'= 1.20) and hilum colour (H'= 0.93). The PCA biplot analysis revealed that lines were more compactly and closely placed under controlled conditions as against treated. Four genotypes (TGX1835-3E, VSL-69, EC-105780 and PK-1243) were identified as relatively drought tolerant lines as they showed less reduction for number of pods per plant, seed yield and hundred seed weight under KI induced drought conditions. These lines were again validated next year and were found to be potential source for the development of drought tolerant varieties for the sustainable soybean production.

Introduction

Soybean (*Glycine max* L. (Merrill) is one of the leading oilseed crops grown for its edible oil and protein in India as well as world over. Soybean seed contains over 40% protein and 20% oil and 35% carbohydrate (Liu *et al.*, 1997) and its milk is considered as important source of food to infants in china. Recent studies have indicated that consumption of soybean reduces cancer, blood serum cholesterol, osteoporosis and heart disease

(Birt *et al.*, 2004). It is also a good source of minerals, vitamins, folic acid and iso-flavones which are credited with slow development of these diseases (Wilson *et al.*, 2004). In India more than 90% of soybean area is under rainfed conditions and the frequency of droughts is common phenomenon. Drought is one of the single most factors responsible for more than 50% reduction in soybean yields (Boyer *et al.*, 1982; Bray *et al.*, 2000). Soybean cultivation in India is overly dependent on seasonal monsoon rains which are erratic and uneven, causing termination of growth from germination to seed filling (Joshi and Bhatia, 2003). Drought is known to affect soybean yield by affecting all stages of plant growth and development; from germination to flowering, and seed filling to development as well as seed quality (Siddique *et al.*, 2001; Manavalan *et al.*, 2009). Occurrence of drought stress during vegetative stage can be compensated with rains during later part of crop growth, however drought at terminal growth stage especially during seed filling to seed maturity stage would cause severe yield loss which could not be recovered by any means (Sionit and Kramer, 1977; Hirasawa *et al.*, 1994; Saitoh *et al.*, 1999). Terminal drought stress in soybean causes gradual reduction in photosynthetic rate, followed by senescence of leaves and reduced seed size that finally results in reduced grain yields (Brevedan and Egli, 2003; Manavalan *et al.*, 2009). Reduced photosynthetic rate affects the synthesis and transportation of photosynthates from leaf to the seed causing reduction in seed size. However photosynthates stored in stem acts as reserves plays a pivotal role in substituting factor for seed filling and seed development in soybean (Constable and Hearn, 1978). Photosynthates stored in stem acts as an alternate source for seed development at times of terminal drought stress (Schnyder, 1993; Subbarao *et al.*, 1995). In soybean, it has been reported that about 25% of seed weight is obtained from stem reserves (Constable and Hearn, 1978).

One of the most sustainable ways to overcome the recurring and perennial problem of drought and to make soybean production more stable and sustainable is to develop climate resilient soybean genotypes with relatively drought tolerant to tide over short periods of drought stress at seed filling stage. Yield losses could be greatly reduced by identifying and adopting drought tolerant genotypes. However, no systematic breeding efforts for developing drought tolerant soybean genotypes are limiting due to the lack of proper and reliable field screening techniques. Field screening of large germplasm lines by withholding irrigation facility at particular stage is rather more cumbersome and time consuming as well as difficult execute due to monsoon rains. Few techniques were developed and standardized to stimulate drought like conditions under field conditions with the application of chemicals. Various indices/parameters have been adopted to quantify drought tolerance in soybean genotypes and other crops (Ku *et al.*, 2013). Potassium Iodide (KI) is known to mimic drought stress under natural conditions, it acts as desiccant on plants by reducing photosynthetic rate, chlorophyll content and senescence with increased content of sucrose and proline content (Sawhney and Singh, 2002) and the effect of drought stress on seed weight reduction could be compared with that of natural drought stress conditions. A single spray of KI at reproductive stage especially during seed filing stage (Blum *et al.*, 1983a; Bouslama *et al.*, 1984; Regan *et al.*, 1993) helps in differentiating genotypes based on their ability to form viable seeds and this method of screening is used to evaluate large number of germplasm lines for terminal drought tolerance traits in many crops (Nicolas and Turner, 1993; Royo and Blanco, 1998, Ashraf *et al.*, 2003; Singh *et al.*, 2012).

The present study was carried out to identify soybean lines tolerance to terminal drought tolerance.

Lack of progress in the development of drought tolerant varieties in soybean is mainly attributed to non-availability of proper screening facilities, poor understanding of physiological and biochemical responses of soybean varieties to drought (Bhatia *et al.*, 2014). Keeping these potential research gaps in view, the present investigation was formulated to evaluate the soybean germplasm for agro-morphological traits and terminal drought tolerance induced by KI under the field conditions. The main objectives of this study were (i) Evaluation of soybean germplasm lines for agro-morphological traits (ii) screening for terminal drought tolerance using KI (Potassium Iodide) and (iii) Identifying the soybean genotypes for drought tolerance.

Materials and Methods

Experimental site and weather conditions

The experiment was laid out at India Council of Agricultural Research-Indian Agricultural Research Institute (ICAR-IARI), New Delhi, India. The experimental farm has sandy loam to loamy soil with pH of 7.5 having semi-arid subtropical climate with an average temperature ranging from 19 to 32°C (July to November).

Experimental material and field evaluation

The experimental material consists of a 328 soybean germplasm lines (Table 1) selected randomly from Germplasm Management Unit at Division of Genetics, ICAR-IARI, Pusa Campus, New Delhi. Each accession was planted in two rows of three meter length, sown during 1st week of July 2014 in an augmented block design (Federer 1956) along with five checks varieties viz., Pusa 9712, SL 688, PS 1347 Ps 1092 and Bragg. The checks were replicated once after every 10 germplasm lines. The recommended row-to-row and plant-to-plant spacing of 45 and 5cm respectively was followed and all the agronomic practices were carried out timely to raise a healthy crop. The crop was raised by providing regular irrigation facilities without any biotic or abiotic stress symptoms until the seed filling stage (R_5). At R_5 stage the plants of one replication was sprayed/drenched completely with 0.2% of Potassium Iodide (KI) to mimic terminal drought stress (Bhatia *et al.*, 2014). Severity of terminal drought on germplasm lines was measured based on percent reduction of seed yield and 100-seed weight in treated as against normal was calculated and genotypes were grouped in to three different classes *viz.*, Tolerant (0 – 20%), Moderately susceptible (20.1 – 45%), susceptible (45.1 – 70%) as described by Bhatia *et al.*, (2014). The following traits were recorded from five randomly selected plants from each genotype of both control and treated plots and mean values were computed for analysis purposes. The quantitative traits were Days to 50 per cent flowering (DFF), Days to full maturity (DFM), Plant height (PH), Number of seeds per pod (NSP), Number of pods per plant (NPP), Hundred seed yield (HSW), Single plant yield (SPY) and Row yield (RY). Ten qualitative traits were recorded at flowering stage was growth habit, leaf shape, flower color, pod color, pod pubescence, pubescence color, seed shape, seed color, seed luster and hilum color. During second season (2015), 40 genotypes were chosen based on first year (2014) field screening results in such a way that equal number of lines from tolerant, moderately susceptible and susceptible lines for terminal drought tolerance trait and five check varieties were planted in a randomized block design consisting of two replications (Table 1b). One replication was imposed terminal drought stress at R_5 stage by drenching KI at 0.2% and the lines were screened for drought tolerance by recording seed yield and its contributing traits. Diversity parameters were calculated for qualitative traits by taking account of allelic richness (calculated from descriptor states) and allelic evenness through Shannon Diversity Index (SDI) (Shanon and Weaver, 1949) as follows:

$$\mathrm{SDIi} = \sum_{i=1}^{di} \mathrm{Pij}.\ \log \mathrm{Pij}$$

Where SDI_i = SDI for i^{th} descriptor, di = descriptor state for i^{th} descriptor, pij = the proportion of accessions for j^{th} descriptor states of i^{th} descriptor. Analysis of variances (ANOVA) was carried out using SAS 9.3 software (SAS Institute Inc., Cary, NC, USA). Estimate of co-efficient of variation (CV) was calculated as per the standard formulae (Burton 1952) and expressed in percent. Principal Components Analysis (PCA) was done using XL stat.

Results and Discussion

Diversity analysis

The Shannon diversity index (SDI) for 10 qualitative traits of the 328 germplasms lines were presented in Table 4. The highest SDI observed for seed colour (1.20) and lowest for pod pubescence (0.13) and with a mean of 0.57. This indicates that germplasms are highly diverse for seed colour (H’= 1.20) and hilum colour (H’= 0.93), whereas it is lowest for pod pubescence (H’= 0.13), pod colour (H’= 0.21) and leaf shape (H’= 0.25). Gangopadhyay *et al.*, (2016) reported high species diversity for intensity of stem colour, leaf shape, epicalyx shape, 13 quantitative characters and 3 biotic stress parameters between wild and cultivated species of *Okra* using SDI. In another study, Upadhyaya *et al.*, (2001) reported that SDI was used to classify chickpea core collection accessions into desi, intermediate and kabuli types based on 7 morphological descriptors and 15 agronomic characters.

Evaluation accessions for agro-morphological characters

Descriptive statistics for 328 genotypes under control and treated conditions were presented in Table 2c. The analysis of variance for control and treatment plots during 2014 season has revealed significant differences ($p<0.05$) for all morphological traits except for 100-seed weight (HSW) under control conditions and number of seeds per pod (NSPP) as well as single plant yield (SPY) under control and treated conditions (Table 2a&b). This indicates that there is sufficient quantity of variability present in the germplasm lines included in the present study for quantitative traits. The coefficient of variation ranged from 2.43% (days to 50% flowering) to 18.76% (row yield) under normal conditions where as under KI treated conditions it varied from 2.61% (days to 50% flowering) to 25.58% (single plant yield). Whereas during second season (2015) all the traits number of seeds per pod (NSPP) under control conditions, exhibited significant differences ($p<0.05$) for all quantitative traits. The random sample selected based on the first season results do possess much variability for all the characters. Coefficient of variation varied from 1.33 (Days to full maturity) to 47.62 (number of seeds per pod) under controlled conditions, whereas it was 5.31 (Plant height) to 24.55 (number of pods per plant) under KI treated conditions (Table 3a&b).

Principle component analysis

Terminal drought occurs when plants are exposed to water deficit during later stages of crop growth especially seed filling and seed development. The greatest loss occurs when the drought occurs during flowering stage (Frahm *et al.*, 2004). The effect of drought on the plant and its reactions depend also on duration and intensity of stress (Brar *et al.*, 1990). Principal components (PCs) and Eigen values of quantitative traits were analyzed to determine percent contribution of individual trait to the diversity under both the conditions is presented in Table 4a and b. Based on Eigen value of more than 1, PC1 and PC2 together explained 64.80% variation and 61.71% variation under controlled and treated conditions respectively. To be specific PC1 alone accounted 51.23% and 46.77% of variance under normal and treated conditions respectively. Remaining components contributed 35.20% under control and 38.23% under treated conditions to total diversity. The traits 100-seed weight, number of pods/plant, no of seeds/pod, row yield and single plant yield had major contributions towards PC1 and for PC2 the maximum variation contributed by plant height, number of seeds per plant, Days to 50% flowering, Days to full maturity, hundred seed weight and single plant yield under control conditions (Table 5c). Under KI treated conditions highest variation in PC1 was contributed by hundred seed weight, number of pods per plant, number of seeds per plant, row yield and single plant yield and in case of PC2, the main traits which contributed to maximum variation was days to 50% flowering, days to full maturity, plant height, single plant yield, number of seeds per pod and hundred seed weight. Thus under both conditions PC1 is mainly related to economic yield traits, whereas PC2 for other vegetative traits. Similar results were found by Deepika *et al.*, (2017) and Iqbal *et al.*, (2008) in Soybean and Gangopadhyay *et al.*, (2016) in okra. The PCA Biplot analysis indicated that genotypes were highly clustered and closely placed under control condition as compared with the treated conditions, they were loosely arranged due to the differential response of genotypes towards KI induced terminal drought stress (Fig. 1a & b). PC1 and PC2 having Eigen values higher than unity explained 82.55% of total variability among soybean genotypes attributed to seed yield (El-Hashash *et al.*, 2016). In another study, Kargar *et al.*, (2015) stated that, PC1, PC2 and PC3 contributed 32.57%, 27.20% and 15.02% to total variability and also explained 74.79% of traits variation with varimax rotation method under stress condition. Mahbub *et al.*, (2016) has indicated that, the PCA yield four of the Eigen values above unity accounted for 91.55% of the total variation. The first three principles accounted for 83.23% of the total variation. In the table 5a, PC1 has highest positive load from single plant yield (17.22), row yield (15.93), number of pods per plant (15.58), days to full maturity (15.39) and days to 50% flowering (14.06) under normal conditions, but under KI treated conditions (Table 5b) single plant yield (18.75), number of pods per plant (18.29), days to full maturity (17.17) and row yield (16.30) has highest contribution to the total diversity. Quantitative traits contributed positively to first three principal components and hence these could be given considerable importance for the genetic material under investigation by Iqbal *et al.*, (2008).

Screening of germplasm lines for terminal drought tolerance using KI

Presence of genetic variation for physiological traits is of the pivotal importance for the development of varieties for drought tolerance. Differential response of genotypes towards abiotic factors makes screening easy and effective in identification of drought tolerance genotypes. Lines expressing higher degree of tolerance towards terminal drought is characterized by their capacity in partition of photosynthates to the developing seeds after stress was imposed

(Nicolas and Turner, 1993; Ashraf *et al.,* 2003; Singh *et al.,* 2012). The faster rate of seed filling in few lines under KI treated conditions might have played a role in their ability to produce bigger seeds and higher seed yields that intern resulted in relative tolerance to terminal drought. In the present study, 328 germplasm lines were evaluated to identify terminal drought tolerant lines by the application of KI spray at R_5 stage to create drought like situation. The mean seed yield per row under control conditions was 175.57 g with a range of 6 to 634.0 g, whereas under KI treated conditions the mean yield was 67.88 g with the range of 2.0 to 308.0 g (Table 6). The mean seed yield reduction is 61.50% under KI treated drought conditions as compared to control. The seed yield reduction among the entries varies from 1.94% to a as high as 97.44%. For seed yield per plant, the average under control is 8.86 g, whereas under treated conditions it is 4.26 g, the reduction under treated conditions varies from 0.54% to the highest of 95. 01%. The mean hundred seed weight is 8.86 g and 4.26 g under control and treated conditions respectively. The average reduction for hundred seed weight is 33.41% under treated as compared with control conditions and the range of reduction varies from 0.62% to 96.67%. For pods per plant, the mean is 62.10% under control conditions, whereas it is 40.54% treated conditions. The average reduction for number of pods is 0.78% to 87.34%. The results have clearly indicated that there are large genotypic variations in response to KI spray induced drought stress in soybean germplasm lines. The lines were grouped into three different classes based on the percent reduction in seed yield and hundred seed weight of treated plots over control (Table 7). The genotypes,TGX1835-3E, VSL-61 and PK-1243 and EC-105790 has lowest (< 16.59%) reduction for seed yield and hundred seed weight under treated conditions and are considered as relatively tolerant to KI induced terminal drought stress, another group of lines consisting of G-2130, DS-9802, SL-633 and PKS-25 has a recorded 20.1 to 45% reduction for seed yield and hundred seed weight, whereas PK-1024, PK-1240, DS-2309 and UPSL-291 recorded the highest reduction (>50%) for seed yield and hundred seed weight under KI induced drought conditions.

Validation of identified drought tolerant lines for yield traits under field conditions

Performance of genotypes under KI induced terminal drought tolerance is verified further during next season (2015) by evaluating 40 genotypes based on first year results. Most genotypes showed consistent and similar responses like first year for all quantitative traits under KI induced terminal drought tolerance. Four terminal drought tolerant lines were identified during first year viz., TGX1835-3E, VSL-69, EC-105890 and PK-1243 were evaluated in second year for seed yield contributing traits under KI induced drought tolerance is discussed (Table 8). The average seed yield reduction ranged from 8.57% (EC-1055780) to 16.19% (PK-1243) under KI treated as compared to control. Seed yield per plant recorded 15.79% in EC-105780 to 19.59% in TRX1835-3E under treated over control. For hundred seed weight, the reduction is less than 10% across the four lines. From the above analysis, the lines (TGX1835-3E, VSL-69, EC-105780 and PK-1243) were identified as relatively drought tolerant in *Kharif*-2014 based on seed yield and hundred seed weight and had shown less than 20% reduction under treated conditions in the next season. The tolerant genotypes exhibited the capacity to produce healthy and normal seeds due to their ability to store the photosynthates in stem and translocate them to the developing seeds during drought like condition made them produce relatively good yields.

Table.1 List of soybean genotypes and their origin used for screening against terminal drought using KI during Kharif-2014

S. No	Genotype	origin	S. No	Genotype	Origin
1	BS-1	BIRSA, Ranchi	44	G-2132	AVRDC
2	BJJF-8	Unknown	45	IC-101449	Indigenous collection
3	DS 74	DS-Delhi	46	IC-141446	Indigenous collection
4	DS-76-1-3	DS-Delhi	47	JS-91-4	Jabalpur
5	DS-76-1-2-2	DS-Delhi	48	JS(SH)91-16	sehore,MP
6	DS-76-1-2-3	DS-Delhi	49	KALITUR	Indigenous collection
7	DS-MM-64	DS-Delhi	50	KG-83-1A	Kasbe-Digraj
8	DS-93-108A	DS-Delhi	51	KB-17	Kasbe-Digraj
9	DS-9703	DS-Delhi	52	L-377	AVRDC
10	DS-9802	DS-Delhi	53	L-416	AVRDC
11	EC-109514	EC-exotic	54	L-440	AVRDC
12	EC-109565	EC-exotic	55	L-587	AVRDC
13	EC-113396	EC-exotic	56	L-652	AVRDC
14	EC-114526	EC-exotic	57	L-680	AVRDC
15	EC-25720	EC-exotic	58	M-135	AVRDC
16	EC-76758	EC-exotic	59	M-53	AVRDC
17	EC-389148	EC-exotic	60	M-11913	AVRDC
18	EC-389179	EC-exotic	61	M-693	AVRDC
19	EC-389392	EC-exotic	62	MACS-57	Pune
20	EC-439618	EC-exotic	63	MAUS-71	Parbhani
21	EC-439619	EC-exotic	64	MAUS-311	Parbhani
22	EC-14436	EC-exotic	65	NRC 37	Indore
23	EC-39779	EC-exotic	66	PK-1162	Pantnagar
24	EC-39873	EC-exotic	67	PK-564	Pantnagar
25	EC-97351	EC-exotic	68	PK-1023	Pantnagar
26	EC-105790	EC-exotic	69	PK-1169	Pantnagar
27	EC-95299	EC-exotic	70	PK-1180	Pantnagar
28	G-395	AVRDC	71	PK-1223	Pantnagar
29	DS-12-13	DS-Delhi	72	PK-1240	Pantnagar
30	G-2253	AVRDC	73	PK-1243	Pantnagar
31	G-2265	AVRDC	74	PK-1250	Pantnagar
32	G-2344	AVRDC	75	PK-295	Pantnagar
33	G-2601	AVRDC	76	PLSO-6A	Pantnagar
34	G-2602	AVRDC	77	PLOS-91	Pantnagar
35	G-2603	AVRDC	78	SL-46	PAU, Ludhiana
36	G-2608	AVRDC	79	SL-432	PAU, Ludhiana
37	DS 2614	DS-Delhi	80	SL-443	PAU, Ludhiana
38	G-2631	AVRDC	81	SL-459	PAU, Ludhiana
39	G-2650	AVRDC	82	SL-284	PAU, Ludhiana
40	G-2651	AVRDC	83	TGX1828-4E	IITA, Nigeria
41	G-2656	AVRDC	84	TGX1831-32E	IITA, Nigeria
42	G-2670	AVRDC	85	TGX1864-25F	IITA, Nigeria
43	G-2130	AVRDC	86	TGX1835-3E	IITA, Nigeria

Table.1 List of soybean genotypes and their origin used for screening against terminal drought using KI during Kharif-2014

S. No	**Genotype**	**origin**	**S. No**	**Genotype**	**origin**
87	TGX1973-14	IITA, Nigeria	130	UPSV-22	Pantnagar
88	TGX1019-2FB	IITA, Nigeria	131	UPSV 24	Pantnagar
89	TAMS-38	BARC-amravati	132	UPSV-65A	Pantnagar
90	UGM-47	AVRDC	133	UPSV-72	Pantnagar
91	UGM-77	AVRDC	134	UPSV-19	Pantnagar
92	UPSL-19	Pantnagar	135	UPSV-31	Pantnagar
93	UPSL-34	Pantnagar	136	VLS-17	VPKS, Almora
94	UPSL-54	Pantnagar	137	EC-439597	EC-exotic
95	UPSL-62	Pantnagar	138	EC-439606	EC-exotic
96	UPSL-64	Pantnagar	139	EC-389170	EC-exotic
97	UPSL-92	Pantnagar	140	EC389116	EC-exotic
98	UPSL-152	Pantnagar	141	EC458355	EC-exotic
99	UPSL-156-B	Pantnagar	142	EC-458383	EC-exotic
100	UPSL-162	Pantnagar	143	EC-456525	EC-exotic
101	UPSL-163	Pantnagar	144	SL 525	PAU, Ludhiana
102	UPSL-180	Pantnagar	145	EC-456616	EC-exotic
103	UPSL-181	Pantnagar	146	EC-456639	EC-exotic
104	UPSL-211	Pantnagar	147	EC-457772	EC-exotic
105	SL-525	PAU, Ludhiana	148	EC-471315	EC-exotic
106	UPSL-291	Pantnagar	149	EC-471319	EC-exotic
107	UPSL-298	Pantnagar	150	EC-471851	EC-exotic
108	UPSL-309	Pantnagar	151	EC-471853	EC-exotic
109	UPSL-326	Pantnagar	152	EC-471870	EC-exotic
110	UPSL-332-B	Pantnagar	153	EC-471881	EC-exotic
111	UPSL-340-B	Pantnagar	154	EC-471882	EC-exotic
112	UPSL-343	Pantnagar	155	EC-471909	EC-exotic
113	UPSL-505	Pantnagar	156	EC-471910	EC-exotic
114	UPSL-652	Pantnagar	157	EC-471920	EC-exotic
115	UPSL-656	Pantnagar	158	EC-471921	EC-exotic
116	UPSL-706	Pantnagar	159	EC-471936	EC-exotic
117	UPSL-736	Pantnagar	160	EC-471-937	EC-exotic
118	UPSL-558	Pantnagar	161	EC-471956	EC-exotic
119	UPSL-769	Pantnagar	162	EC-471967	EC-exotic
120	UPSL-782	Pantnagar	163	EC-471969	EC-exotic
121	UPSL-784	Pantnagar	164	EC-471972	EC-exotic
122	UPSL-785	Pantnagar	165	EC-471979	EC-exotic
123	UPSL-786	Pantnagar	166	EC-471981	EC-exotic
124	UPSL-787	Pantnagar	167	EC-472119	EC-exotic
125	UPSL-57	Pantnagar	168	EC-472120	EC-exotic
126	UPSM-595	Pantnagar	169	EC-472162	EC-exotic
127	UPSV-2	Pantnagar	170	EC-472173	EC-exotic
128	UPSV-19	Pantnagar	171	EC-475184	EC-exotic
129	SL 525	PAU, Ludhiana	172	EC-472197	EC-exotic

Table.1 List of soybean genotypes and their origin used for screening against terminal drought using KI during Kharif-2014

S. No	Genotype	origin	S. No	Genotype	origin
173	EC-472199	EC-exotic	216	PK-1251	Pantnagar
174	EC-472202	EC-exotic	217	PK-1259	Pantnagar
175	EC-472203	EC-exotic	218	PK-1274	Pantnagar
176	EC-471720	EC-exotic	219	PK-1283	Pantnagar
177	EC-457191	EC-exotic	220	19-P3	Indore
178	RKS	Kota, Rajasthan	221	19-P3	Indore
179	SL-637	PAU, Ludhiana	222	JS-2000-20	Jabalpur
180	UGM-20075	Pantnagar	223	MRSB-352	Unknown
181	PK-1387	Pantnagar	224	NRC 65	Indore
182	HiMSO-1598	Palampur	225	PS-1370	Pantnagar
183	PK-1347	Pantnagar	226	RKS-15	Kota, Rajasthan
184	TS-148-22	BARC	227	TS-39	BARC
185	MACS-757	Pune	228	SL-518	PAU, Ludhiana
186	MACS-869	Pune	229	HiMSO-1602	Palampur
187	TS-3	BARC	230	HiMSO-24	Palampur
188	SL-633	PAU, Ludhiana	231	PS-1374	Pantnagar
189	DS-200	DS-Delhi	232	PS-1394	Pantnagar
190	DS-960	DS-Delhi	233	JS (SH)-40	Sehore, MP
191	PS-9813	Pantnagar	234	JS(SH)-40	Sehore, MP
192	PS-9816	Pantnagar	235	MRSB-345	Unknown
193	PS-9817	Pantnagar	236	VSL 61	PAU, Ludhiana
194	PS-9819	Pantnagar	237	SL 679	PAU, Ludhiana
195	PS-9820	Pantnagar	238	SL-710	PAU, Ludhiana
196	PS-9822	Pantnagar	239	PK-1347	Pantnagar
197	DS-9814	DS-Delhi	240	SL 637	PAU, Ludhiana
198	DS-9721	DS-Delhi	241	PS-633	Pantnagar
199	HiMSO-1563	Palampur	242	PS-1368	Pantnagar
200	HiMSO-1587	Palampur	243	SL-638	PAU, Ludhiana
201	JS-94-67	Jabalpur	244	AMS-99-22	Amravati
202	JS-(SH)-95-26	Sehore	245	SL-751	PAU, Ludhiana
203	KB-222	Kasbe-Digraj	246	PKS-25	Pantnagar
204	Lee	USA	247	AMS-353	Amravati
205	MAUS-62-2	Parbhani	248	SL-717	PAU, Ludhiana
206	MAUS-64-1	Parbhani	249	PKS-34	Pantnagar
207	MAUS-31	Parbhani	250	AMS-47	Amravati
208	NRC 45	Indore	251	PS-1403	Pantnagar
209	NRC 47	Indore	252	MAUS-231	Parbhani
210	NRC 51	Indore	253	NRC-72	Indore
211	NRC 53	Indore	254	MAUS-49-1-2	Parbhani
212	PK-1024	Pantnagar	255	PS-1410	Pantnagar
213	PK-1041	Pantnagar	256	TANUS-55	TNAU
214	PK-1060	Pantnagar	257	VLS-65	VPKS, Almora
215	PK-1081	Pantnagar	258	KDS-256	Kasbe-Digraj,

Table.1 List of soybean genotypes and their origin used for screening against terminal drought using KI during Kharif-2014

S. No	Genotype	origin	S. No	Genotype	origin
259	PS-1420	Pantnagar	302	NRC-89	Indore
260	PS-1415	Pantnagar	303	DSb-19	Dharwad
261	PKS-36	Pantnagar	304	JS-20-38	Jabalpur
262	SL-738	PAU, Ludhiana	305	KBS-2011	Kasbe-Digraj
263	MACS-1037	Pune	306	VLS-201	VPKS, Almora
264	NRC-24	Indore	307	KBS-2010	Kasbe-Digraj
265	DS-2309	DS-Delhi	308	DS-2706	DS-Delhi
266	SL-747	PAU, Ludhiana	309	PS-1499	Pantnagar
267	VLS-66	VPKS, Almora	310	RKS-66	Kota, Rajasthan
268	Dsb-9	Dharwad	311	NRC-89	Indore
269	AMS-99-33	Amravati	312	VLS 81	Almora
270	Dsb-10	Dharwad	313	AMS-56	Amravati
271	PS-1437	Pantnagar	314	JS 2038	Jabalpur
272	NSO-111	MAHYCO	315	PS 1503	Pantnagar
273	SL-452	PAU, Ludhiana	316	HiMSO 1681	Palampur
274	MACS-1126	Pune	317	MACS 1364	Pune
275	NSO-78	MAHYCO	318	KDS 701	Kasbe-Digraj
276	NRC-78	Indore	319	MAUS 608	Parbhani
277	MAUS-295	Parbhani	320	KBS 2011	Kasbe-Digraj
278	SL-790	PAU, Ludhiana	321	NRC-94	Indore
279	AMS-4-63	Amravati	322	RKS-115	Kota, Rajasthan
280	NRC-76	Indore	323	VLS-84	Almora
281	PS-1454	Pantnagar	324	NRC-93	Indore
282	MACS-1184	Pune	325	MACS-1416	Pune
283	PS-1450	Pantnagar	326	PS-1521	Pantnagar
284	DS-2614	IARI, Delhi	327	NRC-91	Indore
285	JS-20-05	Jabalpur	328	MACS-1394	Pune
286	JS-20-19	Jabalpur		**Checks**	
287	JS(SH)-2	Sehore	329	Pusa 9712	IARI, Delhi
288	Dsb-15	Dharwad	330	SL 688	PAU, Ludhiana
289	PS-1466	Pantnagar	331	PS 1347	Pantnagar
290	MACS-1259	Pune	332	PS 1092	Pantnagar
291	JS-20-21	Jabalpur	333	Bragg	USA
292	PS-1476	Pantnagar			
293	DS-12-5	DS-Delhi			
294	PS-1480	Pantnagar			
295	SL-871	PAU, Ludhiana			
296	DS-27-11	DS-Delhi			
297	MACS 1340	Pune			
298	JS 20-35	Jabalpur			
299	JS(SH)-93-37	Sehore			
300	KBS-2010	Kasbe-Digraj			
301	SL-900	PAU, Ludhiana			

Table.1a List of soybean genotypes used for screening against terminal drought using KI during Kharif-2015

S. No	Genotype	S. No	Genotype
1	DS-9802	24	VSL-61
2	EC-97351	25	SL-679
3	EC-105790	26	PK-1347
4	G-2130	27	PS-1368
5	PK-1169	28	SL-751
6	PK-1180	29	PKS-25
7	PK-1240	30	PKS-34
8	PK-1243	31	AMS-47
9	SL-46	32	KDS-256
10	SL-432	33	PS-1420
11	TGX1828-4E	34	PS-1415
12	TGX1835-3E	35	DS-2309
13	UPSL-291	36	MACS-1126
14	UPSL-298	37	NRC-78
15	EC-471979	38	KBS-2010
16	SL-633	39	AMS-56
17	HiMSO-1563	40	PS-9818
18	HiMSO-1587		
19	KB-222	1	Pusa-9712
20	PK-1024	2	SL-688
21	JS-2000-20	3	PS-1347
22	RKS-15	4	PS-1092
23	TS-39	5	Bragg

Table.2a Analysis of variance for growth and yield parameters of germplasm lines grown under control conditions Kharif-2014

Source of variation	**df**	**Days to 50% flowering**	**Days to full maturity**	**100-seed weight**	**No. of pods per plant**	**No. of seeds per pod**	**Plant height**	**Row yield**	**Single plant yield**
Block	6	5.86 ^{NS} (0.6715)	18.86 ^{NS} (0.068)	1.05^{NS} (0.4536)	77.18^{NS} (0.1635)	0.02 ^{NS} (0.4481)	57.90^{NS} (0.6581)	4983.62^{NS} (0.0031)	3.90^{NS} (0.1065)
Treatments	332	61.14** (<.0001)	47.38** (<.0001)	7.00** (<.0001)	807.63** (<.0001)	0.22** (<.0001)	173.38* (0.0175)	20047.16** (<.0001)	34.74** (<.0001)
Tests	327	52.54** (<.0001)	44.45** (<.0001)	6.59** (<.0001)	773.05** (<.0001)	0.20** (<.0001)	159.36* (0.0303)	12664.38** (<.0001)	28.60** (<.0001)
Among Checks	4	641.1** (<.0001)	233.33** (<.0001)	4.76 (0.0075)	1341.23** (<.0001)	0.020^{NS} (0.4269)	1240.74** (<.0001)	94343.21** (<.0001)	3.84^{NS} (0.1325)
Test V/s Checks	1	594.05** (<.0001)	271.78** (<.0001)	154.84** (<.0001)	10975.14** (<.0001)	5.70** (<.0001)	564.13* (0.0158)	2198899.89** (<.0001)	2363.53** (<.0001)
Error	24	8.70	8.21	1.06	45.32	0.02	83.66	1085.16	1.96
CD at 5% Among Test		9.43	9.16	3.29	21.52	0.54	29.24	105.32	4.47
CD at 5% Test Vs checks		6.97	6.78	2.43	15.92	0.399	21.64	77.32	3.31
CV (%)		5.41	2.43	11.99	10.83	6.54	12.63	18.76	15.77

NS: Non significant; ** highly significant; * significant; values in parenthesis indicate the Probability value (Pr>F).

Table.2b Analysis of variance for growth and yield parameters of germplasm lines sprayed with Potassium Iodide (KI) Kharif-2014

Source of variation	df	Days to 50% flowering	Days to full maturity	100-seed weight	No. of pods per plant	No. of seeds per pod	Plant height	Row yield	Single plant yield
Block	6	10.69^{NS} (0.5164)	14.38^{NS} (0.1622)	1.29^{NS} (0.30)	11.66^{NS} (0.940)	0.26^{NS} (0.0148)	108.15^{NS} (0.5410)	224.59^{NS} (0.5764)	0.86^{NS} (0.6345)
Treatments	332	63.49^{**} (<.0001)	44.32^{**} (<.0001)	5.09^{**} (<.0001)	486.82^{**} (<.0001)	0.27^{*} (0.0003)	112.18^{*} (0.004)	5489.24^{**} (<.0001)	11.17^{**} (<.0001)
Tests	327	54.97^{**} (<.0001)	42.05^{**} (<.0001)	4.63^{**} (<.0001)	409.94^{**} (<.0001)	0.26^{*} (0.0004)	97.68^{**} (<.0001)	3668.83^{**} (<.0001)	8.79^{**} (<.0001)
Among Checks	4	626.54^{**} (<.0001)	200.1^{**} (<.0001)	4.53^{*} (0.0076)	646.06^{**} (<.0001)	0.08^{NS} (0.3765)	1313.51^{**} (<.0001)	50311.19^{**} (<.0001)	1.65^{NS} 0.2706
Test V/s Checks	1	615.20^{**} (<.0001)	175.03^{**} (<.0001)	159.67^{**} (<.0001)	25616.84^{**} (<.0001)	5.38^{**} (<.0001)	49.43^{NS} (0.3002)	411856.43 ** (<.0001)	809.06^{**} (<.0001)
Error	24	11.99	8.41	1.01	41.28	0.07	44.08	279.23	1.2
CD at 5%Among Test		11.07	9.27	3.21	20.54	0.89	21.22	53.72	3.50
CD at 5%Test Vs Checks		8.19	6.86	2.38	15.20	0.66	15.71	39.53	2.59
CV (%)		6.31	2.61	18.18	16.26	13.79	10.94	22.68	25.58

NS: Non significant; ** highly significant; * Significant; Values in parenthesis indicate the Probability value (Pr> F).

Table.2c Descriptive statistics for quantitative characters of 328 genotypes screened for drought tolerance under control and KI treated conditions

Characters	Max.		Min.		Range		Mean		CV%		SE(d)		CD among tests (0.05)	
	C	T	C	T	C	T	C	T	C	T	C	T	C	T
Days to 50% flowering	68.80	68.77	36.6	34.17	32.2	34.6	54.92	55.17	5.41	6.31	0.469	0.484	9.43	11.07
Days to full maturity	147.4	124.74	99.94	98.34	47.46	26.4	118.16	110.04	2.43	2.61	0.398	0.388	9.16	9.27
100-seed weight	16.12	13.15	2.46	0.41	13.66	12.74	8.41	5.33	11.99	18.18	0.153	0.122	3.29	3.21
No. of pods per plant	174.48	145.11	13.39	4.6	161.09	140.5	60.86	37.1	10.83	16.26	1.724	1.225	21.52	20.54
No. of seeds per pod	3.32	2.97	1.97	0.88	1.35	2.08	2.56	1.99	6.54	13.79	0.027	0.029	0.54	0.89
Plant height	110.06	96.83	32.44	32.4	77.62	64.43	72.96	60.66	12.63	10.94	0.705	0.554	29.24	21.22
Row yield	636.57	351.37	1.47	0.17	635.09	351.2	158.45	62.38	18.76	22.68	7.292	3.400	105.32	53.72
Single plant yield	37.37	15.02	0.22	0.11	37.15	15.02	8.2	3.86	15.77	25.58	0.353	0.175	4.47	3.5

C: control, T: treatment

Table.3a Analysis of variance for growth and yield parameters of germplasm lines grown under control conditions Kharif-2015

Source of variation	df	Days to 50% flowering	Days to full maturity	100-seed weight	No. of pods per plant	No. of seeds per pod	Plant height	Row yield	Single plant yield
Block	1	1.60^{NS} (0.662)	1.877^{NS} (0.350)	0.215NS (0.0018)	187.06^{NS} (0.058)	0.072 ^{NS} (0.467)	7.91^{NS} (0.135)	0.008^{NS} (0.921)	3.66^{NS} (0.126)
Treatments	44	95.26** (<.0001)	131.64** (<.0001)	2.57** (<.0006)	292.11** (<.0001)	0.2082^{NS} (<.0736)	188.24** (<.0001)	11668.13** (<.0001)	12.86** (<.0001)
Error	44	8.25	2.10	0.94	49.61	0.134	3.41	105.55	1.50
CD at 5%		5.79	2.92	1.95	14.19	NS	3.72	20.70	2.47
CV (%)		5.58	1.33	12.36	17.02	47.62	3.69	9.15	16.79

Table.3b Analysis of variance for growth and yield parameters of germplasm lines grown under KI treated conditions Kharif-2015

Source of variation	df	Days to 50% flowering	Days to full maturity	100-seed weight	No. of pods per plant	No. of seeds per pod	Plant height	Row yield	Single plant yield
Block	1	30.04^{NS} (0.306)	6.94 ^{NS} (0.691)	0.105^{NS} (0.6108)	4.32^{NS} (0.712)	0.0393 ^{NS} (0.2737)	153.83^{NS} (0.0848)	19.40463^{NS} (0.7116)	0.0003^{NS} (0.982)
Treatments	44	98.29** (<.0001)	140.45** (<.0001)	2.92** (<.0001)	126.74** (<.0001)	0.0913** (<.0001)	85.83** (0.0356)	4414.41** (<.0001)	6.233** (<.0001)
Error	44	28.08	43.53	0.399	31.47	0.032	49.49	43.11	0.659
CD at 5%		10.68	13.29	1.27	11.30	0.36	5.18	13.23	1.63
CV (%)		10.32	10.67	12.72	24.55	8.08	5.21	9.15	20.00

Table.4 Shannon-Weaver diversity indices for qualitative traits of the 328 germplasm accessions

Sl. No.	Character	H^I
1	Growth habit	0.69
2	Leaf shape	0.25
3	Flower colour	0.67
4	Pod colour	0.21
5	Pod pubescence	0.13
6	Pubescence colour	0.26
7	Seed Shape	0.69
8	Seed colour	1.2
9	Seed lustre	0.69
10	Hilum colour	0.93
	Average	0.57

Table.4a Estimation of Principal component, Eigen value, proportional and cumulative percent variation for control block

Component	Eigen Values	Variability %	Cumulative %
P_1	4.0985	51.2307	51.2307
P_2	1.0853	13.5662	64.7969
P_3	0.7750	9.6879	74.4848
P_4	0.6151	7.6885	82.1733
P_5	0.5142	6.4275	88.6008
P_6	0.3798	4.7471	93.3479
P_7	0.2868	3.5847	96.9325
P_8	0.2454	3.0675	100.0000

Table.4b Estimation of Principal component, Eigen value, proportional and cumulative percent variation for Treatment block

Component	Eigen Values	Variability %	Cumulative %
P_1	3.7417	46.7711	46.7711
P_2	1.1953	14.9408	61.7119
P_3	0.7926	9.9073	71.6193
P_4	0.7169	8.9615	80.5808
P_5	0.5665	7.0812	87.6620
P_6	0.4199	5.2489	92.9109
P_7	0.2989	3.7357	96.6466
P_8	0.2683	3.3534	100.0000

Table.5a Estimation of percent contribution of traits for principal component in control block

Characters	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8
Days to 50%	14.06	9.52	2.65	26.09	2.06	0.31	40.04	5.26
Days to full	15.39	1.93	7.83	22.96	0.00	1.70	40.06	10.12
100-seed weight	13.35	1.93	2.46	0.00	77.96	1.17	0.02	3.11
No. of pods per	15.58	1.09	14.52	1.56	7.79	29.77	3.43	26.27
No. of seeds per	8.11	3.57	60.42	23.89	0.00	2.40	1.09	0.51
Plant height	0.36	80.12	0.27	16.95	1.23	0.02	1.05	0.00
Row yield	15.93	0.87	1.41	3.61	10.23	62.26	3.90	1.78
Single plant yield	17.22	0.96	10.43	4.93	0.72	2.38	10.40	52.95

Table.5b Estimation of percent contribution of traits for principal component in treatment block

Characters	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8
Days to 50%	12.87	18.08	0.00	13.90	13.22	3.63	32.26	6.04
Days to full	17.17	3.68	1.20	2.56	22.88	1.03	44.28	7.20
100-seed weight	10.14	2.05	2.17	68.43	13.64	0.36	3.09	0.13
No. of pods per	18.29	1.31	1.37	0.47	14.85	19.94	2.12	41.66
No. of seeds per	6.42	8.87	80.53	0.05	0.69	0.96	2.00	0.49
Plant height	0.06	64.08	4.75	13.69	16.20	0.60	0.51	0.12
Row yield	16.30	0.59	7.43	0.83	5.42	66.00	3.24	0.18
Single plant yield	18.75	1.34	2.55	0.07	13.10	7.48	12.50	44.20

Table.5c Loadings of principle component for PC1 and PC2

Loadings	Control		Treatment	
	P_1	P_2	P_1	P_2
Days to 50%	-0.759	0.321	-0.694	0.465
Days to full maturity	-0.794	0.145	-0.802	0.210
100-seed weight	0.740	0.145	0.616	0.157
No. of pods per plant	0.799	0.109	0.827	0.125
No. of seeds per pod	0.577	0.197	0.490	0.326
Plant height	-0.121	0.933	-0.046	0.875
Row yield	0.808	0.097	0.781	0.084
Single plant yield	0.840	0.102	0.838	0.127

Table.6 Seed yield, seeds per plant, 100-seed weight and pods per plant of 328 soybean genotypes evaluated for terminal drought tolerance during Kharif-2014

Characters	**Control**			**Treatment**			**Percent reduction due to KI spray**	
	Mean	**Range**	**CV%**	**Mean**	**Range**	**CV%**	**Mean**	**Range**
Seed yield (g/row)	175.57	6.00 – 634.00	18.76	67.88	2.00 – 308.00	22.68	61.34	1.94 – 97.44
Seed yield (g/plant)	8.86	1.60 – 36.13	15.77	4.26	0 – 15.18	25.58	51.92	0.54 – 95.01
100-seed weight(g)	8.59	2.50 – 16.20	11.99	5.72	0.35 – 12.56	18.18	33.41	0.62 – 96.67
No. of pods/plant	62.10	11.00 – 180.00	10.83	40.54	4.00 – 120.66	16.26	34.72	0.78 – 87.34

Table.7 classification of germplasm lines based on the effect of KI spray on row yield and 100-seed weight under control and KI treated conditions during Kharif-2014

Sl No.	**Group**	**Germplasms**	**Row yield (g)**		**100-seed weight(g)**	
			Control	**KI treated**	**Control**	**KI treated**
1	Tolerant (0 – 20%)	TGX1835-3E	216.17	197.28 (8.74%)	10.54	9.72 (7.76%)
		VSL-61	246.77	218.84(11.32%)	9.06	8.82 (2.65%)
		EC-105790	248.37	223.74(9.92%)	10.33	9.24 (10.53%)
		PK-1243	262.31	228.61 (12.85%)	9.09	7.58 (16.59%)
2	Moderately tolerant (20.1 – 45%)	G-2130	90.17	53.47 (40.70%)	12.48	7.34 (41.17%)
		DS-9802	122.17	83.74 (31.70%)	9.28	6.42(30.80%)
		SL-633	176.32	120.42 (31.70%)	10.69	6.71 (37.21%)
		PKS-25	216.20	146.27 (32.35%)	11.37	8.11 (28.65%)
3	Susceptible (45.1 – 85%)	PK-1024	76.21	28.92 (62.04%)	12.97	6.25 (51.84%)
		PK-1240	86.34	43.38 (49.76%)	7.79	2.35 (69.83%)
		DS-2309	64.57	29.25 (54.70%)	12.86	4.01 (68.85%)
		UPSL-291	81.54	33.81 (63.90%)	8.78	3.07 (65.08%)

Table.8 Seed yield, seeds per plant, 100-seed weight and pods per plant of four identified soybean genotypes evaluated for terminal drought tolerance using KI Kharif-2015

Sl No.	Characters	TGX1835-3E		VSL-69		EC-105780		PK-1243	
		Control	KI	Control	KI	Control	KI	Control	KI
1	Seed yield (g/row)	101.64	86.65 (14.75%)	108.45	93.46 (13.83%)	98.78	90.31 (8.57%)	109.73	91.96 (16.19%)
2	Seed yield (g/plant)	8.80	7.08 (19.59%)	7.78	6.34 (18.49%)	9.13	7.68 (15.79%)	10.47	8.46 (19.22%)
3	100-seed weight(g)	7.45	7.10 (4.70%)	5.20	4.90 (5.77%)	7.40	6.75 (8.78%)	6.40	5.78 (9.69%)
4	No. of pods/plant	65.25	53.68 (17.73%)	61.10	51.37 (15.92%)	50.92	40.95 (19.57%)	51.70	42.72 (17.38%)

KI=potassium iodide

Fig.1a Biplot of 328 soybean germplasm lines on PC1 and PC2 under controlled conditions Kharif-2014

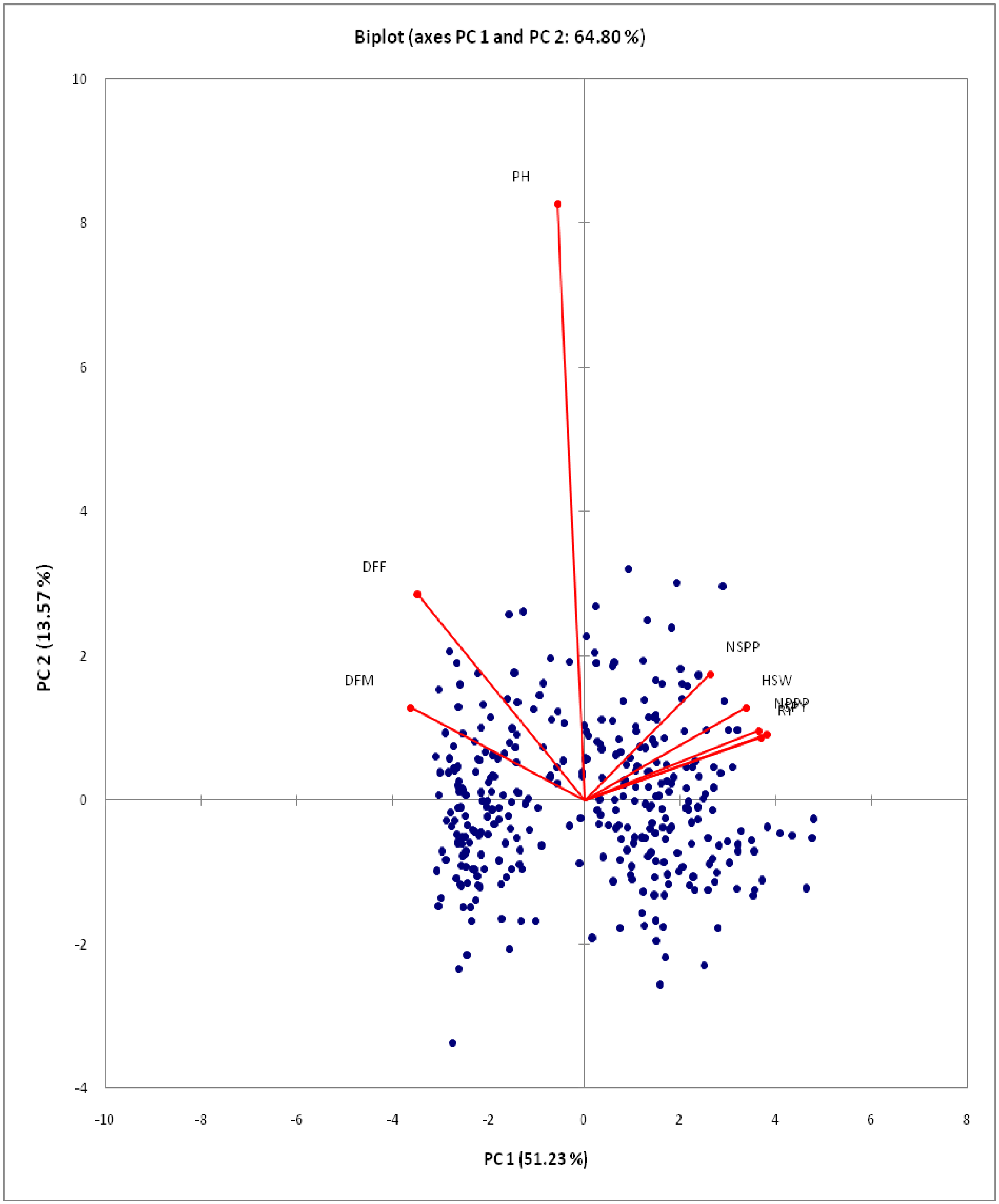
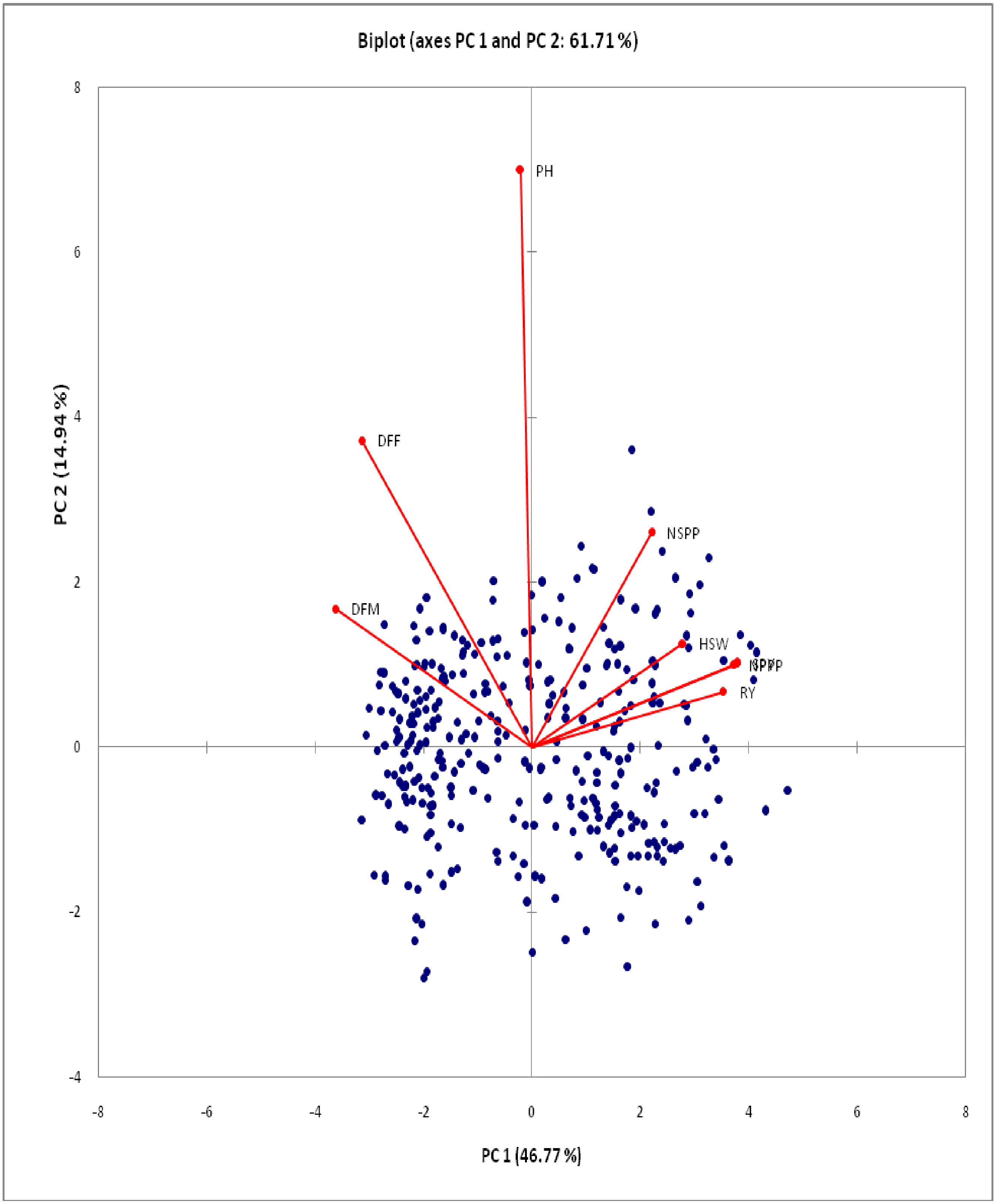


Fig.1b Biplot of 328 soybean germplasm lines on PC1 and PC2 under treated conditions Kharif-2014



In conclusion, drought is one of the most important factors responsible for the reduction of more than 50% seed yield in soybean. The occurrence of drought at terminal stage especially at seed filling to seed development in soybean is reported to cause severe yield loss. Drought tolerant genotypes have an inherent ability to increase source to sink mobilization of photosynthates under terminal drought conditions. KI spray at R_5 stage would imitate the terminal drought conditions and which is extensively tested in cereals and pulses as a defoliant and also mimics near drought like conditions under field conditions. Under KI treated conditions, the genotypes are placed well apart on a Biplot analysis and thus most lines have diverse expression towards KI spray, which shows that the lines were very divers in nature. In the present study, potassium iodide was applied at R_5 (seed filling) stage on a 328 germplasm lines to screen for terminal drought tolerance. Four genotypes (TGX1835-3E, VSL-69, EC-105780 and PK-1243) were identified as relatively tolerant as they showed least reduction for hundred seed weight and seed yield under KI induced drought over control. The identified genotypes were re-tested under similar conditions in next season. Based on two years testing, genotypes showing consistent behavior for drought tolerance were identified. Further studies by the authors will focus the molecular and physiological mechanisms involved in the drought tolerance in these lines for better utilization in breeding programmes.

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