Indian Journal of Agricultural Sciences **82** (9): 759–67, September 2012

Application of GGE biplot analyses for characterizing diverse sesame (*Sesamum indicum)* germplasm for yield and yield-contributing traits

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Received: 30 December 2010; Revised accepted: 22 April 2012

ABSTRACT

A representative sample of 146 diverse sesame accessions, originating from 26 countries and assigned into six groups on the basis of their eco- geographical origin, was characterized for yield and yield-contributing traits using "GGE biplot analyses". 'Which-won-where' application of GGE biplot was used to rank accessions of each group on the basis of collective trait contributions to individual accession. Eighteen promising accessions having combination of positive traits (PI 202722$^{\text{Myanmar}}$, PI 223713$^{\text{India}}$, PI 220664$^{\text{Afghanistan}}$, PI 285173$^{\text{Israel}}$, PI 165021$^{\text{Turkey}}$, PI 170711$^{\text{Turkey}}$, PI 490063$^{\text{South Korea}}$, PI 490033$^{\text{South Korea}}$, PI 345669$^{\text{Soviet Union}}$, PI 561705$^{\text{Mexico}}$, PI 594909$^{\text{Mexico}}$, PI 280790$^{\text{United States}}$, PI 198155$^{\text{Egypt}}$, PI 189081$^{\text{Cameroon}}$, PI 246386$^{\text{Zaire}}$, Pragati $^{\text{India}}$, SVPR 1$^{\text{India}}$, ACHBB 97$^{\text{India}}$) were identified. Correlation coefficient analysis (GGE biplot) as carried out over two years, revealed that total pods/plant (r=0.453**, 0.24**), pods on main shoot (r=0.337**, 0.492**) and seeds/pod (r=0.268**, 0.254**) were the main yield-contributing traits in sesame. Per cent oil content/protein content had no inverse relationship with yield which makes it possible to combine high yield and high oil content in sesame cultivars. A select group of accessions (24) were also compared for stability of performance over two years. Altogether changed ranking was observed for majority of the accessions during second year indicating their differential genonotype × environment response; however one accession PI 223713 was identified which was stable for high yield and yield contributing traits across two years.

Key words: Germplasm characterization, GGE biplot analyses, Stability, Trait inter-relationships, Yield-contributing traits

Morphological characterizations are often useful indicators to evaluate the agronomic worth of a genotype of any crop species. Systematic characterization of available germplasm and quantification of variability therein is essential to exploit its breeding potential. Although varietal trials are routinely conducted to compare a large number of genotypes in multiple environments (years and locations), analysis is mostly limited to yield without taking into account information on other traits. Analysis of genotype by environment data is mostly limited to genotype evaluation based on genotype main effect (G). GGE biplot was proposed (Yan *et al.* 2000, Yan 2001) to address situations relative to genotype by environment data. In GGE biplot analysis, genotype (G) and its interaction with the environment (GE) are the two sources of variation that are relevant for genotype evaluation in a given environment and are considered simultaneously for appropriate genotype assessment: it ranks genotypes on the basis of collective contributions of all the traits. Over the years GGE biplot has been modified to analyses of other type of breeding related data, including genotype by trait tables, character associations, stability analysis etc. 'Which-won-where' is one such application which is used to rank genotypes in a given environment.

Sesame (*Sesamum indicum* L.) is an important oilseed crop in India but it has low productivity. Much phenotypic variation has been reported in different sesame germplasm collections (Mahajan *et al.* 2007, Ashri 2007). The present studies were undertaken to evaluate representative sample (146) of sesame germplasm (458) of Indian and exotic origin available at PAU, Ludhiana India, for yield and yield-contributing traits using GGE biplot methodologies for its effective utilization in breeding programmes for productivity enhancement. Germplasm had been categorized for growth habit, plant height, capsule type, no. of capsules per axil, maturity and seed size for three years prior to the conduct of this study, and morphologically diverse material was selected to be part of 146 accessions.

Based on a part of Ph D thesis of the first author submitted to PAU during 2010

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MATERIALS AND METHODS

A total of 146 accessions of sesame germplasm collection of Indian (53) and exotic (93) origin representing different eco-geographic regions formed the basic plant material. Indian germplasm was represented by 16 promising genotypes and 37 released varieties (including two check varieties) identified for commercial cultivation since 1959. Exotic germplasm, comprising 93 genotypes of 25 sesame-growing countries across the world was procured from United States Department of Agriculture, Agricultural Research Service, Plant Genetic Resources Conservation Unit (USDA, ARS, PGRCU), Griffin, GA, USA in 2003. The material along with checks Pb-Til-1 and TC-289 was evaluated for two years (2007 and 2008) in the research fields of Punjab Agricultural University, Ludhiana in augmented design with 24 blocks. Each block was allotted six test genotypes and two repeat check varieties (Pb-Til-1 and TC 289). Each genotype in a block, whether test or check, was assigned randomly to a paired row plot of 3 m length and row-to-row distance of 30 cm. Recommended plant-to-plant distance of 10–15 cm was maintained after 15 days of sowing and need based irrigation was applied to avoid water stress. The data were recorded on 15 morpho-physiological traits. These were: days to 50% flowering, days to 100% flowering, days to complete flowering, days to maturity, number of primary branches, plant height (cm), main shoot length (cm), pods on main shoot, total pods/plant, seeds/pod, pod length (cm), seed size (1000-seed wt in g), seed yield/plant (g), per cent protein content and per cent oil content. To avoid yield losses due to shattering, mature plants per test genotype were harvested and collected in nylon net bags (45 cm × 60 cm) for drying. Data with respect to check varieties were subjected to analysis of variance as per augmented design using statistical package for augmented design (SPAD) to obtain adjusted trait values for checks and test genotypes. The adjusted trait values were subjected to analysis of variance and used for germplasm characterization using 'which-won-where' analysis of GGE biplot. The test genotypes were assigned into six arbitrary groups (A-F) based on their geographical origin (Table 1). Biplot graphs on all six groups were generated by using the "GGE biplot" software (Yan 2001). The 'which won where' view of biplot analysis was used to identify the genotypes with the highest value for one or more characters or the one with package of desirable characters in each group. In this analysis, a polygon is drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then starting from the biplot origin, perpendicular lines to each side of the polygon are drawn, thus dividing the biplot into different sectors, each sector having its own best/poor performing genotypes. Accessions at the vertex of the polygon are either the best or the poorest for one or more traits (Yan and Tinker 2007). Data of the various characters over 146 genotypes were also subjected to the study of association relationships using GGE biplot software (Yan 2001), and to stability analysis on the basis of select group of genotypes (24) over two years (Yan 2001).

RESULTS AND DISCUSSIONS

The adjusted estimates of means along with other parametric values for evaluated 15 traits over 146 genotypes as obtained during 2007 and 2008 crop seasons are presented in Table 2. Different estimates for trait values as evident from range and means were obtained for each year. Much differences were observed for days to flowering, days to maturity and plant vigour related traits. This may be attributed to differential rain pattern for the two years. During the first year, well distributed rains over the entire growing period were observed which proved very conducive for the normal growth of the crop. During the second year, rainfall was erratic; almost daily rains during the vegetative phase of the crop lead to delay in flowering, and very few rainy days during reproductive phase precipitated high temperatures and consequently early maturity. Sesame being very sensitive to growing conditions, responded differently during two years. This was reflected in different mean values, decrease in range estimates and trait variation. The results of analysis of variance as carried out per augmented design for 2007, 2008 and also pooled over two years considering years as replications as per RBD, are presented in Table 3. Significant variation was observed for almost all the traits among the test genotypes during both the years. Data of first year only was considered for various GGE biplot analyses as maximum trait variability (Table 2) was observed during first year of evaluation.

Table 1 Grouping of germplasm on the basis of eco-geographical origin

Geographical distribution	Number of genotypes	Identity	Region/countries
Group A	18	Germplasm collection	China, India, Myanmar, Afghanistan
Group B	25	Germplasm collection	Turkey, Iraq, Iran, Israel, Greece, Syria
Group C	15	Germplasm collection	Former Soviet Union, Korea, Korea South, Japan
Group D	22	Germplasm collection	Venezuela, México, United States, Argentina
Group E	13	Germplasm collection	Egypt, Libya, Mozambique, Sudan, Somalia, Cameroon, Zaire,
Group F	53	Released varieties (37), Promising genotypes (16)	India

Table 2 Basic statistics of the morpho-physiological characters of 146 sesame accessions as observed during 2007 and 2008 crop seasons

Character	Character value						CV (%)			
	Min		Max		Range		Mean±SE			
	2007	2008	2007	2008	2007	2008	2007	2008	2007	2008
Days to 50% flowering	22.7	30.9	58.2	52.4	35.5	21.5	34.7±0.43	38.2±0.3	14.6	9.6
Days to 100 % flowering	28.0	33.0	68.6	57.0	40.5	24.0	38.7±0.49	42.1±0.3	15.3	8.8
Days to complete flowering	58.3	53.4	97.8	74.4	39.5	21.0	66.8±0.39	63.0±0.3	7.1	6.6
Days to maturity	69.9	79.3	124.0	97.3	54.0	21.0	85.4±0.44	87.1±0.3	6.2	4.7
Primary branches	1.00	1.2	7.2	5.7	6.50	4.5	3.3±0.09	3.3±0.07	32.2	26.0
Plant height (cm)	84.8	75.6	191.3	145.0	106.5	70.2	146.2±1.49	111.6±1.0	12.3	11.5
Main shoot length (cm)	5.4	38.1	120.2	89.4	114.8	51.3	84.6±1.22	68.2±0.7	17.4	13.3
Pods on main shoot	4.1	13.3	61.1	48.8	57.0	35.5	29.6±0.61	24.8±0.4	24.9	23.4
Pods/plant	18.1	23.4	124.1	100.9	106.0	77.5	69.7±1.64	57.1±1.3	27.0	28.4
Pod length (cm)	2.0	2.16	3.4	3.4	1.4	1.3	2.6±0.02	2.6±0.01	8.7	6.5
Seed yield per plant(g)	2.2	1.3	20.3	16.7	18.1	15.4	9.2±0.30	8.3±0.2	38.8	34.5
Seeds/pod	28.6	35.0	79.6	74.0	51.0	39.0	56.5±0.78	55.9±0.6	16.8	13.7
Seed size (g)	2.2	1.9	4.91	3.9	2.7	2.0	3.3±0.04	2.9±0.03	15.0	14.2
Per cent oil content	36.1	38. 5	53.1	53.2	17.0	14.7	47.0±0.26	47.3±0.2	6.7	5.8
Per cent protein content	20.9	20.3	30.1	29.2	9.2	8.9	25.7±0.15	25.6±0.1	7.3	6.2

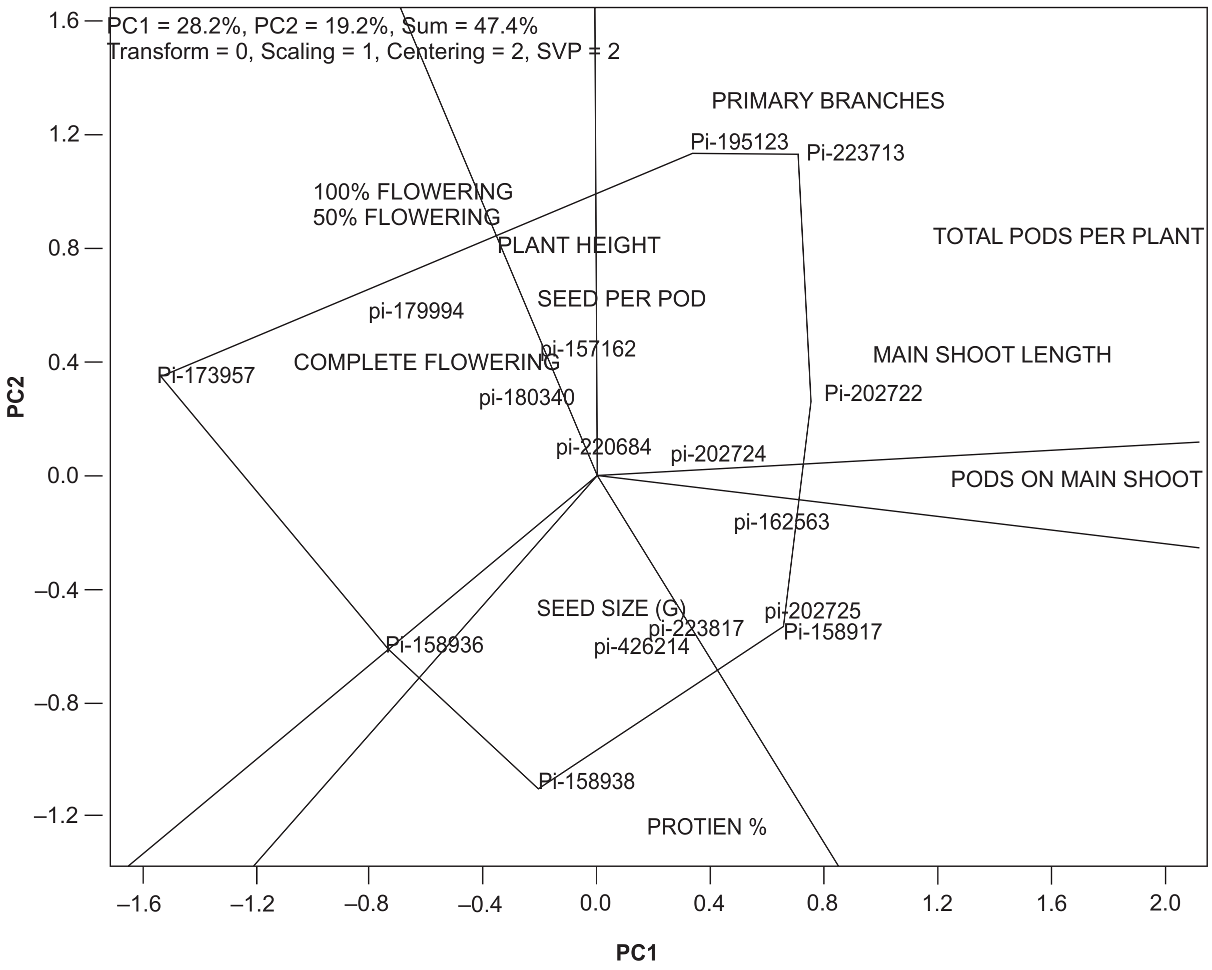

Fig 1 Polygon view of the genotype by trait biplot of Group A accessions

Table 3 Analysis of variance (ANOVA) for the 15 morpho- physiological traits in sesame

Source	d f	50% FL	100% FL	C F	MAT	PB	PH	MSL	PMS	TP	PL	SYP	SP	POC	1000 SW	PPC
Analysis of variance (2007)																
Block (Adj.)	23	2.4**	2.7**	2.9	6.5	0.38	222.9*	88.9	16.5	150.4	0.03	13.7**	30.05	3.3**	0.11	1.82
Treatments (Adj.)	145	21.1**	27.4**	17.5**	22.3**	0.86	242.9**	144.3	47.7**	359.3	0.04**	10.9**	79.5**	9.1**	0.2**	2.91
Error	23	1.0	1.0	1.6	3.9	0.59	85.5	82.3	10.6	241.8	0.01	4.5	16.32	0.92	0.07	1.62
Analysis of variance (2008)																
Block (Adj.)	23	2.5	1.3	10.6*	3.37*	0.29	132.9	144.58**	13.12	221.3*	0.42**	9.35*	24.67	2.99**	0.34	1.06
Treatments (Adj.)	145	10.9**	9.52**	14.77**	14.37**	0.57	128.3**	68.15	29.36**	240.9**	0.23*	7.30*	45.71**	8.85**	1.3**	2.93*
Error	23	2.2		4.10	1.43	0.25	41.09	41.59	10.78	89.6	0.15	3.98	16.78	0.44	0.3	1.8
Pooled analysis (over 2007 and 2008)																
Replication	1	943.9**	833.8**	1030.4**	238.9**	.26	83619.1**	20765**	1857.0**	9078**	.10	146.9**	290.9**	7.85**	10.0**	.39
Treatments	145	32.0	37.7	28.5	27.5	1.2	340.7	137.3	49.3	344.9	.81	12.0	96.02	17.27**	.28	5.6**
Error	145	10.3	11.3	11.4	17.9	.63	161.7	124.0	37.7	343.2	.74	7.4	30.9	.36	.10	.48

* $P = 0.05$, ** $P = 0.01$

50% FL, Days to 50% flowering; 100% FL, days to 50% flowering; C F, days to complete flowering; MAT, days to maturity; PB, primary branches; MSL, main shoot length; PMS, pods on main shoot; TP, total pods per plant; PL, pod length; SP, seeds per pod; 1000 SW, seed size; SYP, seed yield per plant; POC, per cent oil content; PPC, per cent protein content

Morphological characterization using 'which-won-where' GGE biplot analysis

The first two principle components PC I and PC II together which makeup biplot explained 40.8 to 60% of total variation of the standardized data within all six groups. The vertex accessions along with their trait specificity were identified in each group. Some of these had maximum contribution for positive traits, e g high yield, number of pods/plant, bigger pods, etc., whereas others had high values for negative traits, e g more days to flowering and maturity, more plant height etc. Genotypes identified for positive traits in each group, in general are being discussed herein.

Group A (China, India, Myanmar, Afghanistan)

This group comprised 18 accessions of which seven (PI 195123, PI 223713, PI 202722, PI 158917, PI 158938, PI 158936, and PI 173957) were identified as the vertex accessions (Fig 1). Accession PI 223713 was identified for high yield (14g), whereas PI 202722 was package for pods on main shoot (32), main shoot length (86 cm), total pods/plant (95) and pod length (3 cm). PI 285173 had the maximum pods on main shoot (40); accession PI 195123 had maximum primary branches (5).

Group B (Turkey, Iraq, Iran, Israel, Greece, Syria)

Nine accessions out of the 25 of group B were the vertex accessions (Fig 2) of which four were identified for desirable traits. Accession PI 165021 was the package for three desirable traits, viz. maximum seeds per pod (68), total pods/plant (114) and seed yield/plant (11.00 g). Accession PI 170711 was identified for main shoot length (118 cm), seed size (3.60 g) and pod length (2.61 cm). Accession PI 285173 had the maximum pods on main shoot (40), whereas PI 238473 had the highest value for days to 50 per cent flowering (47), days to 100% flowering (51) and complete flowering (71).

Group C (Former Soviet Union, Korea, Korea South, Japan)

In the biplot graph of group C, six of the15 accessions formed the vertex points (Fig 3). The genotype PI-345669 was identified to be desirable for seed yield/plant (12.54 g), per cent oil content (50.10), total pods/plant (115), primary branches (3), days to 50% flowering (35), days to 100% flowering (40), complete flowering (69), plant height (166 cm), and seed size (3.45 g). The accession PI 490063 was desirable for pods on main shoot (25), main shoot length (78 cm), and days to maturity (87), the accession PI 282740 was desirable for per cent protein content (27.45), whereas PI 490033 had maximum pod length (3.44 cm) and seeds/d (63).

Group D (Venezuela, Mexico, United States, Argentina)

In this group (Fig 4), accession PI 594909 was identified for pod length (3.40 cm) and seeds/pod (71), while accession PI 561705 was identified for pods on main shoot (42), seed

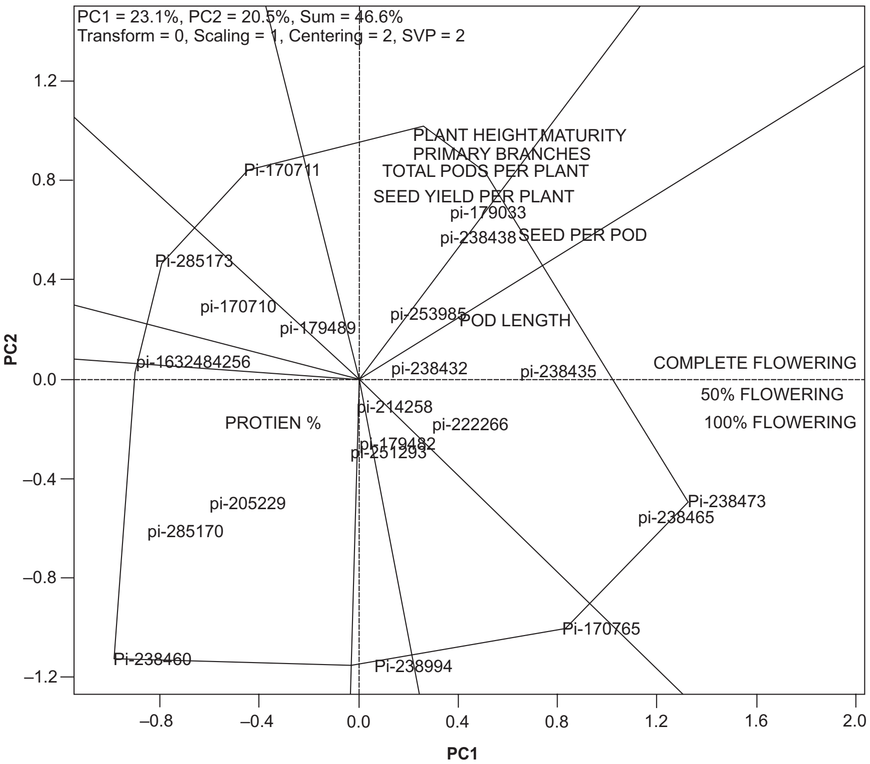

Fig 2 Polygon view of the genotype by trait biplot of Group B accessions

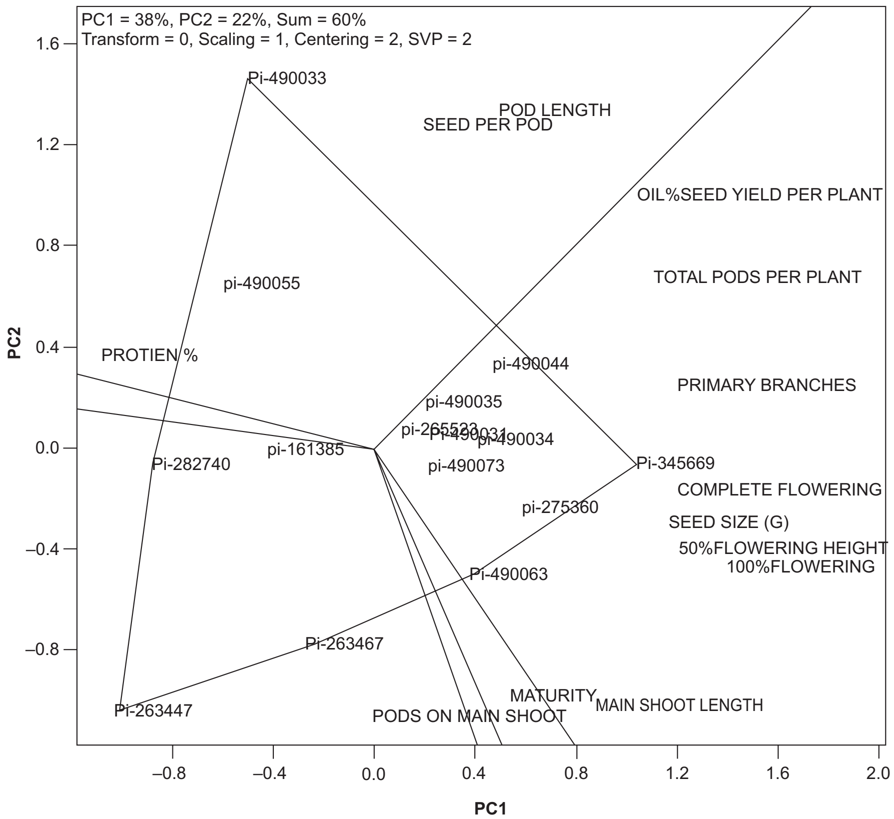

Fig 3 Polygon view of the genotype by trait biplot of Group C accessions

yield/plant (13.67 g), and total pods/plant (109) main shoot length (100 cm). The accession PI 254708 was the best for per cent oil content (52.50) and PI 280790 had the highest value for seed size (3.52 g). The Accession PI 153514 had the maximum value for days to 50% flowering (40), days to 100% flowering (46), complete flowering (68), primary branches (4) and plant height (158 cm) while PI 153517 took maximum days to maturity (89).

Group E (Egypt, Libya, Mozambique, Sudan, Somalia, Cameroon, Zaire)

In this group six genotypes, PI 189081, PI 490103, PI 210687, PI 224663, PI 231034 and PI 198155 were identified to be vertex genotypes (Fig 5). Accession PI 189081 was a package for five desirable traits, viz. seeds/pod (75), seed size (3.73 g), per cent oil content (52.70), main shoot length (97 cm) and pod length (2.82 cm). The accession PI 490103 had the maximum value for per cent protein content (28) and days to maturity (92), whereas accession PI 198155 was desirable for pods on main shoot (36) and total pods/plant (84).

Group F (India)

The evaluated 53 Indian genotypes were assigned into six sectors with ACHBB 97, Brijeshwari, Pragati, SVPR 1, RMT 256 and Stiff-stem as the vertex genotypes. The genotype ACHBB 97 had highest value for seed size (3.94 g) among the evaluated cultivars. National check variety Pragati was the best for pods on main shoot (47) and seed yield/plant (20.29 g), whereas SVPR 1 was the best for total pods/plant (121) and maximum primary branches (7). Stiff-stem had maximum trait values for –ve traits.

GGE biplot studies as conducted on representative sample of sesame genotypes of six eco-geographic groups in the present study led to the identification of eighteen {PI 202722 (Myanmar), PI 223713 (India), PI 220664 (Afghanistan), PI 285173 (Israel), PI-165021 (Turkey), PI 170711 (Turkey), PI 490063 (Korea South), PI 490033 (Korea South), PI 345669 (Former Soviet Union), PI 561705 (Mexico), PI 594909 (Mexico), PI-280790 (United States), PI 198155 (Egypt), PI 189081 (Cameroon), PI 246386 (Zaire), Pragati (India), SVPR 1 (India) and ACHBB 97 (India)} promising accessions on the basis of their collective trait contribution. These are presented along with their trait contribution and eco-geographic origin in Table 4.

Interrelationships among phenotypic characters

Interrelationship/correlation information is required to obtain the expected response of other characters on yield when selection is applied to the character of interest in a breeding programme. In the biplot for correlations (Table 5), the lines that connect the biplot origin and characters are called character vectors and the cosines of the angles between the vectors of the two traits approximate the extent of correlation between them (Kroonenberg 1995, Yan 2002). In the present analyses as conducted over two years, yield was found to be significantly and positively correlated with three traits, viz. total number of pods/plant (r=0.453**, 0.24**), pods on main shoot (r=0.337**, 0.492**) and seeds/pod (r=0.268**, 0.254**) during both the years, whereas with all other traits it had non-significant positive or negative values. Positive correlation of seed yield/plant with pods/plant was previously reported by Tomar *et al.* (1999). In the present study, seed size had very weak correlation (r=0.120, 0.107) with seed yield, whereas Onginjo and Ayiecho (2009) found a positive significant correlation of seed yield with seed size. Highly significant and positive correlations among maturity related (50%, 100%, CF and days to maturity) and plant vigour related traits (number of primary branches, plant height) were observed, however, none of these were found to

Table 4 Best sesame accession identified for different yield contributing traits*, ** in each geographical group using genotype by trait GGE biplot analysis

Geographical distributions	Seed yield	Pods on main shoot	Pods per plant	Seeds per pod	Seed size
Group A	PI 223713 (14.34 g)	PI 202722 (31)	PI 202722 (95)	PI 223713 (73)	PI 220664 (3.65 g)
Group B	PI 165021 (11.03 g)	PI 285173 (40)	PI 165021 (114)	PI 165021 (68)	PI 170711 (3.65 g)
Group C	PI 345669 (12.54 g)	PI 490063 (25)	PI 345669 (115)	PI 490033 (63)	PI 345669 (3.45 g)
Group D	PI 561705 (13.67 g)	PI 561705 (42)	PI 561705 (109)	PI 594909 (71)	PI 280790 (3.52 g)
Group E	PI 246386 (13.85 g)	PI 198155 (36)	PI 198155 (84)	PI 189081 (75)	PI 189081 (3.72 g)
Group F	Pragati (20.29 g)	Pragati (47)	SVPR 1 (121)	ACHBB 97 (73)	ACHBB 97 (3.94 g)

*trait value in parentheses, ** bold seed size was not found to be yield-contributing trait but it is a preferred trait

Table 5 Correlation coefficients among different characters studied in the evaluated germplasm (2007)

Character	50%FL	100%FL	C F	MAT	PB	PH	MSL	PMS	TP	PL	SYP	SP	POC	1000 SW	PPC
50% FL	1.000	0.941**	0.657**	0.483**	0.306**	0.484**	–0.111	–0.389	–0.047	–0.078	–0.031	0.060	–0.175	–0.014	–0.181
100% FL		1.000	0.715**	0.537**	0.290**	0.503**	–0.137	–0.425	–0.063	–0.110	–0.104	0.046	–0.146	–0.070	–0.173
CF			1.000	0.659**	0.276**	0.524**	0.055	–0.359	–0.102	–0.036	–0.063	0.118	–0.07	–0.061	–0.145
MAT				1.000	0.164	0.349**	0.045	–0.389	–0.231	–0.142	–0.146	0.003	–0.111	0.153	–0.011
PB					1.000	0.387**	0.007	0.004	0.429**	0.102	0.083	0.002	–0.068	0.027	–0.235
PH						1.000	0.222**	–0.095	0.040	–0.120	0.126	0.133	–0.143	0.163	–0.198
MSL							1.000	0.363**	0.317**	0.062	0.148	0.194*	0.115	0.206*	–0.071
PMS								1.000	0.446**	0.001	0.337**	0.091	–0.018	–0.097	–0.011
TP									1.000	0.231**	0.453**	0.002	0.049	–0.046	–0.056
PL										1.000	0.092	0.188*	0.198**	0.044	–0.041
SYP											1.000	0.268**	0.049	0.120	–0.031
SP												1.000	0.123	0.020	–0.102
POC													1.000	0.101	0.100
1000 SW														1.000	0.023
PPC															1.000

* $P = 0.05$, ** $P = 0.01$

have correlation with yield.

Most of the correlation studies in oilseed crops indicate yield to be inversely related with seed oil content/protein content. No such relationship in the present study was observed during analyses of two years which indicates that either source was not the limiting factor or both these traits are influenced by other factors. For example, seed colour which in sesame is associated with thickness of the seed coat, has been found to be determining factor for oil content (Banga *et al.* 2008) as all white seeded (thinner seed coat) sesame genotypes have high (~50%) oil content, whereas most of the dark seeded genotypes have low estimates (~40%). Moisture stress during reproductive phase (Banga *et al.* 2008) has also been found to be associated with low oil content. Thus in sesame an independent breeding programme can be successfully formulated for combining high yield and high oil content.

Correlation between two or more characters may result from linkage of genes governing two or more characteristics or pleiotropic effects of genes (Falconer 1989). Many studies are available on seed yield components and their relative contribution in sesame which indicate number of branches/plant, number of pods/plant, main shoot length, plant height, pod length, number of locules/pod, number of seeds/pod and seed size to be main yield contributors. Few detailed studies (Kang 1994, Beech and Imrie 2001, Morris 2009) have also been conducted to determine the ideal sesame plant type. It was concluded that it is difficult to draw optimal ideotype in sesame as it is grown under a wide range of conditions which affect character expression, their interaction among themselves and with environment.

Stability of the genotypes across the years

Over the years, it has been observed that sesame cultivars do not perform consistently over locations or over years. In the present study also, same set of genotypes (146) was evaluated for two years at same location but different results were obtained with respect to trait parameters (Table 2) and analysis of variance (Table 3). Pooled analysis considering years as replications indicated significant differences between years for almost all the traits, whereas treatment effects became non-significant (Table 3). Therefore, it was thought to identify stable genotypes among a select group (24) of sesame test genotypes for stability over two years using GGE biplot wherein years were considered as environments. Based on the performance during first year (2007) two best yielders and two poor yielders were identified from each geographic group. Thus 12 genotypes, namely Pragati (India), PI 223713, PI 202722, PI 238473, PI 285170, ACHBB 97, PI 246386, PI 224662, PI 594909, PI 561705, PI 490044 and PI 345669 were identified to be best yielders, whereas PI 158936, PI 158938, PI 205229, PI 214256, Stiff-Stem, TKG 22, PI 210687, PI 490103, PI 229667, PI 280790, PI 263447 and PI 263467

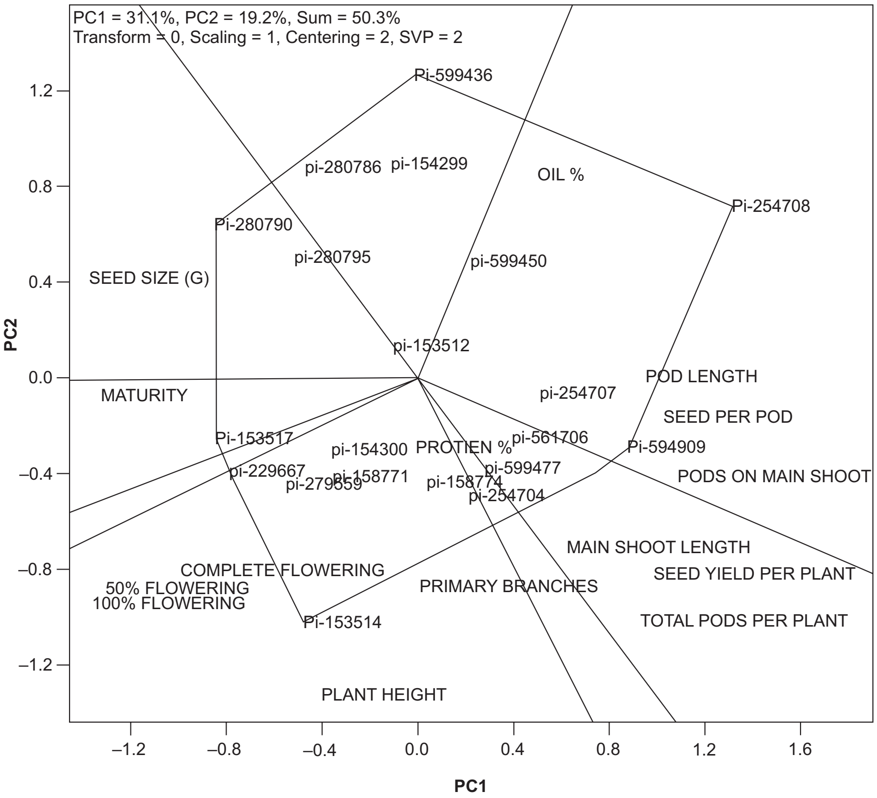

Fig. 4 Polygon view of the genotype by trait biplot of Group D accessions

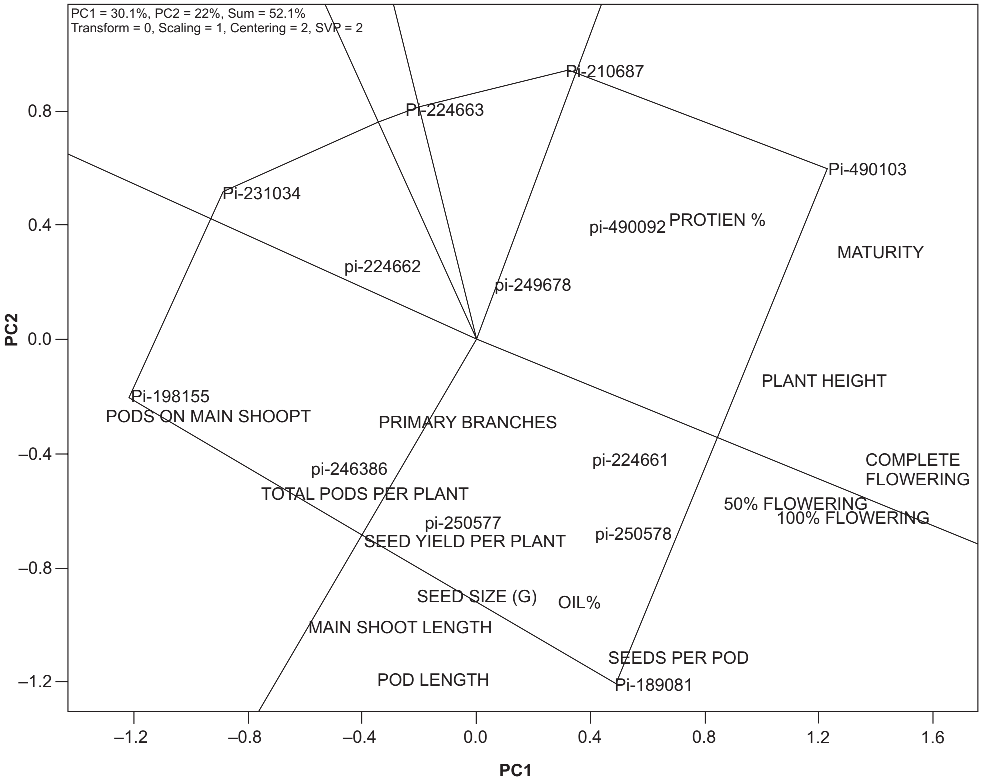

Fig 5 Polygon view of the genotype by trait biplot of Group E accessions

were identified to be low yielders. These were compared diagrammatically for their performance during two years using GGE biplot methodology of ranking genotypes based on performance in one environment. To rank a genotype based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis of this environment, and along this axis falls the ranking of the genotypes. Comparison of the diagrammatic GGE biplot analyses indicated that the ranking of majority of the 24 genotypes, except for PI 223713 (1st and 2nd), PI 246386 (7th and 6th.) and PI 263447 (24th and 24th), was not the same during two years. Even the national check Pragati, the second best genotype of 2007 was placed among poor performing genotypes at overall rank of 18th during 2008, whereas PI 280790 which ranked as poor 23rd during first year was the third best yielding genotype during second year.

The present study led to the identification of geographically diverse sesame genotypes which carry desirable traits for productivity enhancement. Association studies indicated three traits, viz. total number of pods/plant, pods on main shoot and seeds/pod to be main determinants of seed yield. High oil content had no adverse effect on yield. Yield performance was not consistent for most of the evaluated genotypes over the evaluated two years; even the national check variety Pragati was not high yielding during both the years. Study led to the identification of one genotype (PI 223713) having stable performance.

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