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Pattern analysis for genotype by environment effects for seed weight and grain yield in pigeonpea hybrids

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Abstract

Genotype by environment interaction effects (GE) were assessed for seed weight and grain yield of 12 pigeonpea genotypes tested in 11 environments. Pattern analysis was applied to identify the grouping of genotypes and environments. For seed weight the genotype grouping was mostly based on the genetic make up of the hybrid or pure line. The environments did not reflect any specific pattern. For grain yield the hybrids and pure lines responded differently as separate groups and hierarchical separations reflected mean performance of genotypes. Environmental and genotype grouping revealed distinct pattern of GE interaction based on soil types. Black and non-black soil environments emerged as two distinct groups discriminating genotypes differently. Hybrids and controls showed specific adaptation to particular environments emphasizing the need to breed for location specific hybrids and select the testing sites and controls carefully.

Key words : Pigeonpea, GE interaction, pattern analysis, hybrid group

Introduction

One of the prerequisites of any breeding program is the assessment of genotypes, hybrids or pure lines over locations, to assess their performance in a given environment and their stability. Seed weight and grain yield of pigeonpea are highly affected by environment. Analysis of multilocation data for these traits can help to dissect the Genotype × Environment (GE) interactions into different components for assessing the genetic worth of genotypes for specific environments. Techniques for GE analysis based on linear regression [1, 2] can be informative when GE interaction has high linear association with the environmental index but when the non-linear component is also significant, they may not be useful and in many cases non-linear component has been found to be significant [3, 4].

With the advancement in statistical techniques, methods are available for analysis of GE interactions into components due to specific and broad adaptations. Pattern analysis, which consists of complementary procedures of classification and ordination [5, 6], can cluster the genotypes according to their response in different environments and also cluster the environments which are similar in the way in which they discriminate among genotypes. The patterns generated by these methods can reflect the specific adaptation of particular hybrid or pure line. The present study was attempted to assess the pattern of GE interactions for seed weight and grain yield.

Materials and methods

Eight hybrids involving the male sterile lines ms Prabhat DT, ms Prabhat NDT and ms T21 as female parents were tested along with four pure line varieties as checks. The details about the genotypes are given in Table 1. There were 11 testing environments which

Table 1. Important agronomic characters and grouping details of 12 pigeonpea genotypes, tested in 11 environments

Genotypes and code*	Days to 50% flowering	Days to maturity	Seed weight (g)	Yield (kg/ha)	Grouping	
A. Hybrids					SWT	GYDH
ICPH 8 (G1)	85	130	7.44	1438	G_1	G_1
ICPH 11 (G2)	88	133	7.24	1201	G_1	G_3
ICPH 13 (G3)	92	138	7.67	1246	G_4	G_4
ICPH 15 (G4)	94	139	7.80	1286	G_5	G_4
ICPH 16 (G5)	88	133	7.01	1346	G_3	G_6
ICPH 22 (G6)	92	139	7.68	1204	G_4	G_5
ICPH 149 (G7)	92	138	7.55	1203	G_7	G_5
ICPH 328 (G8)	94	141	7.36	1144	G_2	G_3
B. Checks (Pure lines)						
UPAS 120 (G9)	78	125	7.61	1287	G_8	G_7
Manak (G10)	77	124	7.06	1151	G_3	G_7
Pusa 33 (G11)	82	127	7.59	1293	G_8	G_6
CO 5 (G12)	87	136	7.90	1353	G_6	G_2

*Code in parenthesis

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differed in latitude from 10°N to 29°N. The soil type also differed from red to medium black and deep black. In two environments no irrigation was provided through out the crop period. The environments also differed in the date of planting, ranging from 24th June to 13th September. The agronomic data and other details of 11 environments are given in Table 2. At each location the genotypes were tested in three replications and the net plot size for each entry was 6.84 sq.m. Data were recorded on days to flowering and maturity, 100-seed weight (g) and grain yield per plot (reported as yield kg/ha).

Table 2. Grouping and other details of 11 testing environments

Location Abbrev.*, name and code*		Latitude	Precip-itation	Soil type	Days to 50% flowering	Days to maturity	Seed weight (g)	Yield (kg/ha)	Sowing time	Grouping	
										SWT	GYD
SEC- Secunderabad	E 1	17°N	120	Alfisol	79	112	7.42	1545	Sept.	E_1	E_1
PATB-Patancheru	E 2	17°N	NR	Vertisol	96	141	7.11	1140	June	E_4	E_6
PATR-Patancheru	E 3	17°N	NR	Alfisol	83	125	7.90	1654	June	E_4	E_3
AKL - Akola	E 4	23°N	1021,N.I♦	Vertisol	102	136	8.09	696	June	E_5	E_7
DHAR-Dharwar	E 5	15°N	624	Vertisol	76	136	8.16	657	July	E_4	E_8
AUR - Aurangabad	E 6	20°N	931	Vertisol	98	147	8.33	1868	July	E_2	E_2
HISN-Hissar	E 7	29°N	NR	Entisol	88	134	7.86	1556	June	E_6	E_5
PUD - Puddukotai	E 8	10°N	518	Vertisol	69	100	5.91	758	June	E_3	E_8
GW-Gwalior	E 9	26°N	NR	Entisol	97	144	7.18	1743	June	E_7	E_3
KAR-Karad	E 10	22oN	685,N.I.♦	Vertisol	99	154	7.51	801	June	E_5	E_6
HISD - Hissar	E 11	29°N		Entisol	74	138	6.96	1471	July	E_5	E_4

*as mentioned in dendrograms and biplots; ♦ no irrigation, all others had two irrigations; NR: Not reported

The mean values for seed weight and grain yield of genotypes from three replications at each location were used for analysis. Prior to Pattern analysis, REML (Residual Maximum Likelihood) analysis was performed for standardizing data at each location, giving each environment a mean of zero. This removes environment main effects, allowing GE interaction to determine the clustering. Pattern analysis [7] was applied to environment standardized data matrix. For classification agglomerative hierarchical procedure [7] with an incremental sum of squares grouping strategy was followed. Biplots, using first and second Principal components, were used to assess the pattern of relations among genotypes and environments. The GEBEI package [8] was used to generate these analyses.

Results and discussion

Seed weight

The mean 100-seed weight of genotypes across environments varied from 7.018 g (ICPH 16) to 7.906 g (CO5), (Tables 1 and 3). The environment mean seed weight across genotypes varied from 5.91 g (PUD) to 8.33 g (AUR) (Table 2). The partitioning of total sum of squares indicated that genotypes, environments and GE interactions accounted respectively for 5.51%, 33.99% and 21.50% of the total variation. The fact that environments accounted for maximum proportion of variation followed by GE interaction and genotypes agrees with similar findings of Byth *et al.*, [5]; De Lacy *et al.*, [9] and Cooper *et al.*, [10].

The results of Pattern analysis are presented in dendrogram for genotypes (Fig. 1) and environments (Fig. 2). The number of genotype and environment groups were decided on the basis of a minimum 50% sum of squares retained in the reduced GE matrix. Genotypes were classified into eight and environments into seven groups. This retained 73.69% of the GE sum of squares. The genotype dendrogram reflected two broad groups. The first to separate were UPAS 120 and Pusa 33, the two check varieties with almost equal mean seed weight. The next were two hybrids ICPH 13 and 22, which had the same mean seed weight and the same female parent, ms T21. The third group had a single member, the hybrid ICPH 15 with mean seed weight of 7.80 g. In the next separation were hybrids ICPH 8 and 11 with seed weights of 7.44 g and 7.24 g and the common female parent, ms Prabhat DT. Next in the hierarchy were the hybrid ICPH 16 and the check variety Manak, with the lowest seed weights. The variety CO5 with the highest seed weight (7.90 g) fell into a single member group which separated at a higher level of hierarchy in the dendrogram. The results indicated that for seed weight the genotype grouping was mostly based on the genetic make up of the hybrid/pure line, specifically in case of hybrids the male sterile line involved as female parent did influence the grouping pattern.

The environment dendrogram for seed weight also showed two broad groups with further classification into seven groups. Although classification was based

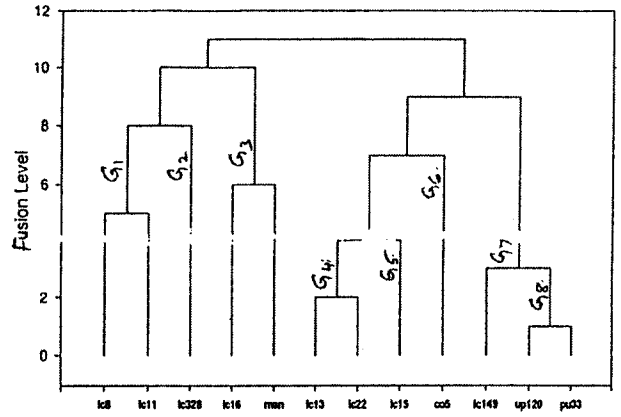

Fig. 1. Genotype dendrogram for 100 seed weight

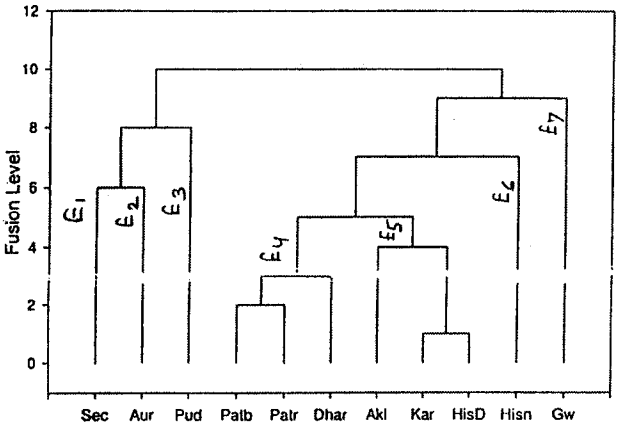

Fig. 2. Environmental dendrogram for 100 seed weight

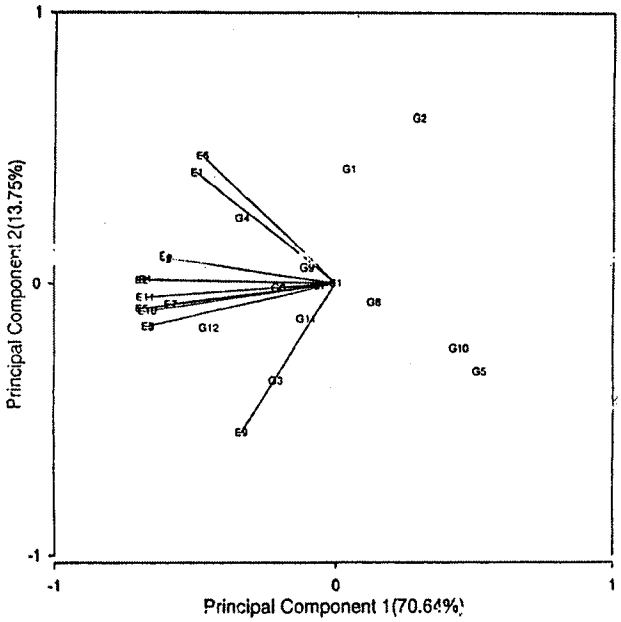

Fig. 3. Biplot for 100 seed weight

on seed weight, the grouping did not reflect any specific pattern. However it may be noted that the environment AUR with the highest (8.33 g) and PUD with the lowest (5.91 g) seed weights stood as single member groups and were separated at a much higher level of hierarchy in the dendrogram.

The results of ordination analysis for seed weight are presented in the Biplot (Fig. 3). The first two vectors in the biplot explained 84.39% of the total sum of squares of the GE. The interpretation of the biplot was based on the fact that size of angle between vectors determines the similarities between environments-the more acute the angle, the more strong correlation it denotes [11]. The biplot for seed weight showed that most of the environments were similar in discriminating among genotypes except AUR and GW which made an angle of more than 90^{o} between them.

However, AUR was more similar to SEC as the angle between them was more acute. The genotypes ICPH 22, ICPH 149, UPAS 120 and Pusa 33, which were close to the origin point were average in performance in all the environments and can be adjudged as stable. The position and perpendicular projection of genotype points onto an environmental vector can be used to identify a genotype having specific adaptation in that environment [12]. ICPH 15 was a good performer in almost all the environments and ICPH 13 was best in GW; ICPH 8 and 11 were also good in all the environments except GW.

The check CO5 belonging to a separate group was also an average to good performer in most of the environments. The remaining hybrids and check variety Manak were poorly adapted to the environments studied.

Grain yield

The mean yield of genotypes across environments varied from 1144 kg/ha (ICPH 328) to 1438 kg/ha (ICPH 8) (Tables 1 and 4). The environment mean grain yield across genotypes varied from 657 kg/ha (DHAR) to 1868 kg/ha (AUR) (Table 2).

The partitioning of total sum of squares indicated that genotypes, environments and GE interactions accounted respectively for 2.13%, 57.82% and 20.42% of the total variation. Evidently, GE interaction was almost ten times that of contribution of genotypes. Significant GE interaction for seed weight and grain yield in germplasm lines of pigeonpea has earlier been reported by some workers [3, 4, 13].

The results of Pattern analysis are presented in dendrograms for genotypes (Fig 4) and for environments (Fig. 5). Genotypes and environments were classified into seven and eight groups, respectively. This retained 71.53% of the GE sum of squares. The genotype dendrogram indicated two broad groups, one

Table 3. Genotype x environment data for 100-seed weight (g) of 12 pigeonpea genotypes tested in 11 environments

Genotypes \ Environments	SEC	PATB	PATR	AKL	DHAR	AUR	HISN	PUD	GW	KAR	HISD	MEAN
ICPH 8	7.670	7.033	7.500	8.367	8.067	9.000	8.133	6.000	6.370	6.967	6.833	7.44
ICPH 11	9.000	6.933	7.300	7.700	7.167	9.000	7.100	6.000	6.300	6.933	6.233	7.24
ICPH 13	6.000	6.967	8.333	8.267	8.867	8.000	8.200	6.667	7.630	8.000	7.467	7.67
ICPH 15	8.000	7.067	7.867	8.633	8.867	8.667	7.867	7.000	6.700	7.667	7.467	7.80
ICPH 16	5.670	6.467	7.100	7.767	7.367	8.333	6.900	6.000	8.530	6.900	6.167	7.01
ICPH 22	7.670	7.333	8.033	8.233	8.667	8.333	7.233	6.333	7.270	7.800	7.600	7.68
ICPH 149	7.670	7.067	8.000	7.833	7.767	8.333	8.333	5.333	7.100	8.033	7.653	7.35
ICPH 328	7.330	7.300	8.000	8.100	7.900	8.000	7.100	5.000	7.000	8.100	7.200	7.36
UPAS 120	9.000	7.200	7.933	7.567	8.467	8.333	8.200	6.000	7.430	7.267	6.400	7.61
Manak	5.330	6.867	8.200	7.200	7.933	8.333	8.333	5.000	7.500	6.633	6.333	7.06
Pusa 33	7.670	7.367	8.033	8.333	8.333	8.000	8.667	5.667	7.330	7.433	6.733	7.59
CO 5	8.000	7.833	8.533	9.167	8.567	7.667	8.300	6.000	6.970	8.400	7.533	7.90
Mean	7.420	7.119	7.903	8.097	8.164	8.333	7.864	5.917	7.18	7.511	6.967	7.49
S.E.	2.211	0.236	0.297	0.552	0.527	0.500	0.449	0.301	1.239	0.542	0.366	0.85

Table 4. Genotype x environment data for mean grain yield (kg/ha) of 12 pigeonpea genotypes tested in 11 environments

Genotypes \ Environments	SEC	PATB	PATR	AKL	DHAR	AUR	HISN	PUD	GW	KAR	HISD	MEAN
ICPH 8	1978	1175	2111	624	833	1886	1628	1077	1927	906	1677	1438
ICPH 11	1511	1043	1280	804	502	1806	1555	592	1877	565	1680	1201
ICPH 13	1642	1341	1341	443	707	2071	1707	655	1445	860	1495	1246
ICPH 15	1374	1557	1395	741	560	2271	1333	882	1835	880	1314	1286
ICPH 16	1608	947	2200	658	638	1998	1706	616	1882	833	1723	1346
ICPH 22	979	1731	1296	931	863	1820	1222	877	1386	901	1239	1204
ICPH 49	1357	1506	1542	833	680	1389	1822	816	1035	1028	1225	1203
ICPH 328	1793	1213	1211	916	638	1801	1019	660	1122	809	1402	1144
UPAS 120	1569	633	2073	487	658	1718	1993	685	2310	521	1512	1287
Manak	902	658	1656	448	473	1616	1913	563	2353	595	1485	1151
Pusa 33	1852	588	2003	400	614	2403	1625	687	1924	565	1558	1293
CO 5	1974	1288	1741	1072	721	1640	1155	987	1819	1145	1341	1353
Mean	1545	1140	1654	696	657	1868	1556	758	1743	801	1471	1263
S.E.	549.7	284.1	321.7	185.9	79.9	455.3	373.1	180.4	198.0	157.3	276.2	308.3

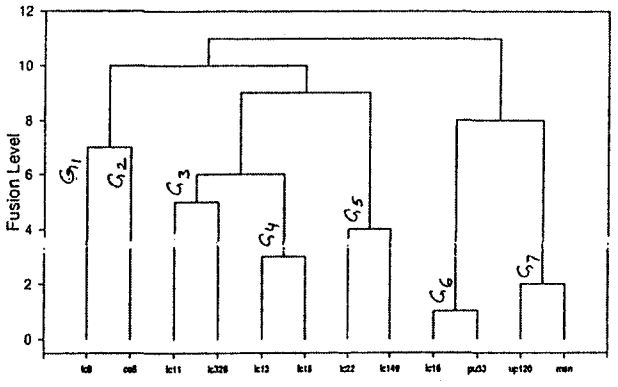

Fig. 4. Genotype dendrogram for grain yield H

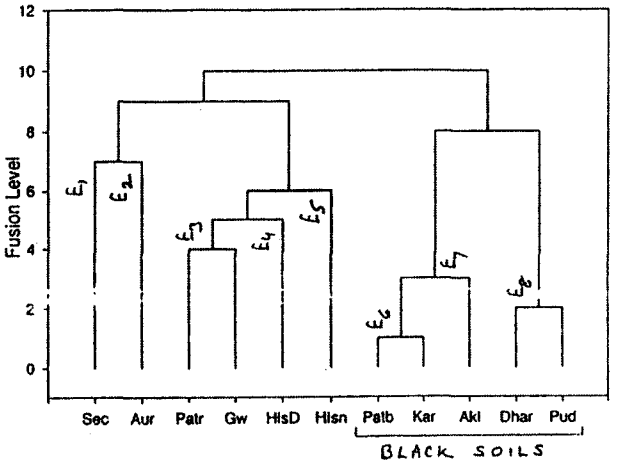

Fig. 5. Environmental dendrogram for grain yield H

represented by hybrids and the other by pure lines, with one exception. The first to separate were ICPH 16 and the check Pusa 33 with mean grain yield of 1346 and 1293 kg/ha, respectively. In the next split the two checks UPAS 120 (1287 kg/ha) and Manak (1151 kg/ha) were separated. The third group comprised

two hybrids ICPH 13 and 15 with grain yield of 1246 and 1286 kg/ha, respectively. The next to separate were ICPH 22 and ICPH 149, both with similar mean values for grain yield.

The genotypes with higher grain yields-ICPH 8 with 1438 kg/ha and CO5 with 1353 kg/ha separated as two single member groups. As is evident, in contrast to the results obtained for seed weight, for grain yield the genotypes did not show any grouping based on the male sterile line in their genetic make up. However, the pure lines used as checks did behave as a separate group and the hierarchical separations did reflect mean performance of genotypes. The environment dendrogram for grain yield also showed two broad groups. With one exception of AUR, the environments were separated on the basis of soil types viz. black and others. This is in contrast to what was observed for seed weight where no such distinction was indicated.

In general, the grain yield in non-black environments varied from 1471 kg/ha to 1743 kg/ha. However, in black soil environments it varied from 657 kg/ha to 1868 kg/ha with a mean value of 986 kg/ha. This finding is in agreement with earlier report of Chauhan *et al.*, [14], wherein they reported that yield of extra short duration pigeonpea cultivars was about twice as high on Alfisols as on Vertisols.

The first to separate on the dendrogram were PAT B and KAR, though their mean yield levels were quite different. The next split comprised of DHAR and PUD followed by AKL. Subsequently, the non-black soil environments separated with the exception of AUR which separated from SEC at a higher level. It may be noted that though in latitude the black soil type environments varied from 10°N to 23°N and in days to maturity from 100 to 154 days, they formed a distinct group and separated at a very low level of hierarchy. This emphasizes the need to test the genotypes in similar soil types to minimize the GE interaction effects.

The first two vectors in the biplot (Fig. 6) explained 64.37% of the total sum of squares of GE. The biplot revealed that the vectors for environments with black soil formed angles of more than 90° with the other environments. This indicated that based on soil types there are two distinctly independent groups of environments which discriminate among genotypes. To mention the extreme case the environment vector for PAT B made an angle of approximately 180° with the environment vector for HIS N showing that genotype discrimination in these two environments is opposite in direction. Among the black soil environments, PAT B and AKL on one hand and PUD and DHAR on the other hand, were almost overlapping and hence showed great similarity in discrimination among genotypes. The

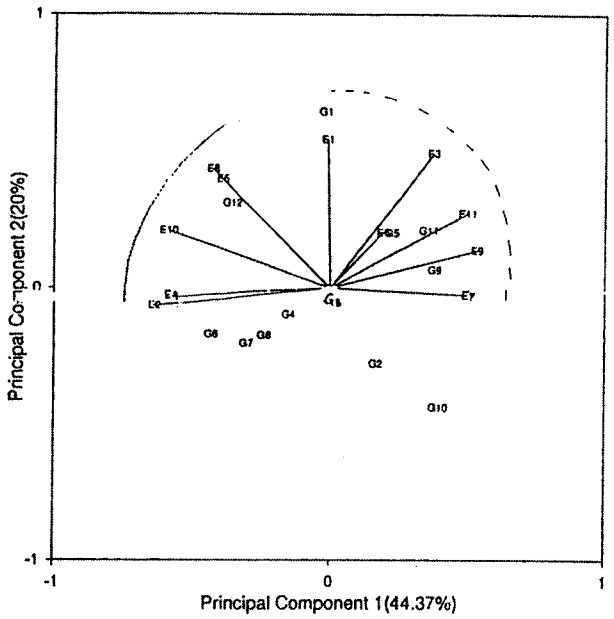

Fig. 6. Biplot for grain yield H

hybrid ICPH 13, being close to the origin point, was an average performer in all the environments. In black soil environments the good performers were ICPH 22, 149, 328 and CO5. All other genotypes were either very poor performers or not adapted to these environments. In the non-black soil environments PAT R and AUR (though with black soil) made a very narrow angle indicating that they were similar whereas SEC and HIS N were at 90° indicating that these environments tended to discriminate genotypes differently. In the non-black soil environments the best genotypes were ICPH 16, UPAS 120, Manak and Pusa 33. The highest yielding hybrid ICPH 8 was best performer in SEC and PAT R, in all other environments it did not show good adaptation.

The above results have clearly indicated that among the pure lines used as checks, three were adapted to non-black soil environments whereas CO5 was good in black soils. Contrary to the belief that hybrids show wider adaptation than pure lines, they showed adaptation to specific environments. This indicates the need to breed for location specific hybrids. Further, while selecting the testing sites for experimental hybrids, greater emphasis should be placed on soil type to minimize the GE effects.

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