

Genotype X Environment Interaction in Soybeans Grown in Oklahoma (USA) and in NWFP (Pakistan)

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Abstract: Fifteen genotypes of group IV and group V soybeans from the Oklahoma Soybean Variety Test were grown from 1991 to 1994 at four Oklahoma (USA) locations and in 1994 four NWFP (Pakistan) locations to investigate Genotype x Environment (GE) interactions and genotypic stability. Significant Genotype x Locations and Genotype x Location x Year (GLY) interactions were observed for seed yield. The top-yielding genotypes at Bixby were Hartwig, OK 885409, HSC 591 and Hutcheson. At Haskell the top-yielding genotypes included Hutcheson, OK 885409 and Manokin. At Chickasha and Goodwell 7 and 9 genotypes were in the top yielding group; respectively. OK 885409 was in the top-yielding group in 1991, 1992 and 1994 at Bixby, in 1991, 1993 and 1994 at Chickasha, and in all four years at Haskell. A significant Genotype x Location (GL) interaction was observed for seed yield when all eight locations (in Pakistan and the USA) were studied in 1994. Only Haskell-Mansehra and Chickasha-Mansehra showed nonsignificant Genotype x Location interactions. Combined regression analysis was also used. Genotypes OK 885409, Hutcheson, HSC 401 and Bay had nonsignificant residual mean squares but only OK 885409 and Hutcheson had b value close to one and a mean yield higher than the grand mean. These genotypes are less responsive to favorable environments, but should perform in a more predictable or stable manner.

Key words: Soybeans, Genotype x Environment interaction, Pakistan, USA

Introduction

In most plant breeding programs, selection of the best commercially suitable cultivars for a target group of environments is based on the information obtained from evaluation of cultivars grown in a sample of environments. This information can be approximate and consequently selection of the best cultivars involves choosing among cultivars that may respond uncertainly in many other environments. In preliminary stages when there are a large number of lines, the breeder can test them at only one or two locations. The breeder may discard superior genotypes if he restricts the number of locations because of GE interaction, (Sharma *et al.*, 1980). This is especially true if the high yielding sector of the population of genotypes contributes proportionally different to the interactions present, (Nigam *et al.*, 1990).

The existence of GE interactions and their effects on progress from selection are widely recognized, (Baisakh and Dash, 1992). Genotype x year interactions (GY) are always of importance in developing improved cultivars. Genotype x location interactions (GL) are of relatively less importance when selection is done for local adaptation but often assume a dominant role in selecting for wide adaptation. If no Genotype x Environment interactions occur when data from two or more locations are analyzed, selections could be made at one location that should perform well at the other locations (Virk *et al.*, 1985). Pakistan is deficient in edible oil and protein. Domestic edible oil production meets only 20 % of the total edible oil requirement of the country. To fill the gap between domestic production and total consumption the government has to import a large quantity of oil and spends huge amounts of foreign exchange (Agricultural Statistics of Pakistan, 1994).

The principal indigenous oilseed crops that contribute to the production of edible oil include cotton, rape, mustard and peanuts. Soybeans and sunflower were added to the list of oilseed crops for commercial cultivation in the late 1970's. However, due to its satisfactory oil and high protein content soybeans are preferred to sunflower (PARC, 1990). Soybeans have a high production potential on research fields both as a spring and summer crop. Since being recommended for commercial production in the late 1970's, the area in soybean production is close to 4000 hectares in NWFP (North West

Frontier Province).

The exchange of research information and ideas between Pakistan and the USA should improve soybean improvement programs in both the countries. We may find that we can develop cultivars at one of four locations in the USA which performs well at one or more locations in Pakistan. The present study was designed to determine if any genotype x environment interactions were present when the same 15 soybean genotypes were grown at different locations in the USA and to identify high yielding and stable genotypes for specific locations in Oklahoma. Characters studied included plant height, 100-seed weight and seed yield. A second objective was to identify one or more locations in the USA which produced no GE interactions for yield when paired with one or more locations in Pakistan.

Materials and Methods

Fifteen genotypes (Table 2) of group IV and group V soybeans from the Oklahoma Soybean Variety Test were used. These genotypes were grown from 1991 to 1994 at four Oklahoman locations (Bixby, Haskell, Chickasha and Goodwell). In 1994 four Pakistani locations (Malakandher, Tarnab, Mansehra and Swat) were added. Data from these 20 tests (1991-1994) were used to estimate GE interactions (Genotype x Location, Genotype x Year, Genotype x Location x Year) for seed yield.

Table 1: Analysis of variances over four year (1991-94) four locations (Oklahoma) and fifteen genotypes for seed yield (kg ha⁻¹)

Source	df	SS	MS	F value	Pr>F
Year	3	79723907	26574636	1.59	0.2574
Loc	3	12835817	4278606	0.24	0.8674
Year*Loc	9	148576279	16508475	24.90	0.0001**
Rep(Year*Loc)	32	16668140	520879	1.43	0.062
Geno	14	21169044	1512075	0.72	0.7468
Geno*year	42	29576579	704204	1.39	0.0825
Geno*loc	42	80347312	1913031	3.78	0.0001**
Geno*loc*year	126	63690736	505482	1.39	0.008**
Error	448	162796793	363386		

**denotes significance at $\alpha=0.01$

A Randomized Complete Block Design was used and plot size was 3x7 m² with row spacing of 75 cm. There were four rows (7 m long) in each plot. The central two rows were used

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to collect data.

Statistical procedures for the analyses of the data included: 1. An analysis of variance (ANOVA), according to the split plot design proposed by Steel and Torrie (1984) using genotypes, locations, and years as main effects. Genotypes and Years were considered random and locations as fixed effects. If the second order interaction (GLY) was found significant for seed yield, the data were further analyzed to test how genotypes performed at each location each year. LSD test was performed to differentiate genotypes with significant statistical differences in their means. In 1994 four Pakistani locations were added to the test sites and two location analyses were conducted to determine which location combinations did not exhibit GL interactions.

Regression analyses were also used to determine stability parameters as defined by Eberhart and Russell (1966). Every location within a year was considered one environment. In this method the individual genotype response to changing environments was determined by regressing the individual genotypic mean on the environmental index (environmental index = location mean minus the grand mean). Two stability parameter were used to determine the stability of each genotype. The regression coefficient (b) serves as the 1st stability parameter and the 2nd one is individual genotypes residual mean squares being tested over the pooled error of the regression ANOVA. Genotypes with significant residual mean squares were considered unstable and their performance unpredictable. The ideal genotype should be one with a high mean yield, a regression coefficient equal to one and a nonsignificant residual mean square.

Results and Discussion

A significant GLY interaction was observed for seed yield in the combined analysis of variance for four years and four locations in Oklahoma from 1991 to 1994 (Table 1) which indicates that the genotypes were inconsistent in their performance for yield when tested across locations and years. The GL interaction was also significant which suggests fluctuations in genotypic ranking and requires testing of genotypes over a range of locations (Sharma *et al.*, 1980). All three main effects (Genotypes, Locations and Years) were nonsignificant. Since the three-way interaction was significant, further analyses were performed to test how genotypes performed at each of the locations separately over the years (1991-1994) and an LSD test was conducted to identify genotypes which differed in their performance. Genotypes at the Bixby location (Table 2) yielded between 2248 kg ha⁻¹ and 3369 kg ha⁻¹. 'Hartwig' (3369 kg ha⁻¹), 'OK 885409' (3236 kg ha⁻¹), 'HSC 591' (3208 kg ha⁻¹) and 'Hutcheson' (3173 kg ha⁻¹) were in the top-yielding.

At the Haskell location the yield range among genotypes was from 2206 kg ha⁻¹ ('Sparks') to 2933 kg ha⁻¹ (Hutcheson). Hutcheson (2933 kg ha⁻¹), OK 885409 (2750 kg ha⁻¹) and 'Manokin' (2746 kg ha⁻¹) were in the top-yielding significance group. The same three genotypes were in the top-yielding group in every year at this location. Genotypes at the Chickasha location yielded on the average between 1939 kg ha⁻¹ (Douglas) and 2907 kg ha⁻¹ (OK 885409). The top-yielding significance group of genotypes were identified as OK 885409 (2907 kg ha⁻¹), 'Bay' (2852 kg ha⁻¹), Manokin (2829 kg ha⁻¹), 'OK 885420' (2751 kg ha⁻¹), 'Walters' (2673 kg ha⁻¹), 'Stafford' (2671 kg ha⁻¹), and Hutcheson (2642 kg ha⁻¹). None of the genotype was in the top group consistently in all the four years. However, OK 885409 was in the top significant group in 1991, 1993 and 1994. The genotypes Bay and Manokin were in the top group in 1992, 1993 and

Table 2: Mean seed yield (kg ha⁻¹) of soybean genotypes at Bixby, Haskell, Chickasha and Goodwell averaged over four years from 1991 to 1994.

Genotypes	Bixby	Haskell	Chickasha	Goodwell
Hartwig	3369a	2643b	2560bcdef	2154cdef
Ok885409	3236ab	2750ab	2907a	2561abcd
Hsc591	3208ab	2697b	2506def	1649ef
Hutcheson	3173abc	2933a	2642abcde	2448abcde
Manokin	3074bc	2746ab	2829abc	2480abcde
Ok885420	3042bc	2609bc	2751abcd	2195cdef
Bay	3027bc	2526bcd	2852ab	2360bcdef
Walters	3017bc	2385cde	2673abcd	1733def
Forrest	2940cd	2690b	2267fg	1560f
Stafford	2762d	2529bcd	2671abcd	2867abc
Crawford	2477e	2365de	2164gh	2831abc
CX458	2426e	2269e	2551cdef	3268a
Hsc401	2386e	2352de	2356egf	3215ab
Douglas	2369e	2342de	1939h	3149ab
Sparks	2248e	2206e	2296fg	2834abc
Lsd0.05	23.85	23.2	29.4	8.28
Cv%	10.35	11.3	14.36	41.9

Table 3: Mean squares for seed yield (kg ha⁻¹) for eight location (USA and Pakistan), Haskell, Mansehra and Chickasha-Mansehra combination

Source	USA and Pakistan	Haskell-Mansehra	Chickasha-Mansehra
Loc	20499788**	574401	4970250
Rep(Loc)	776428	37117	268724
Geno	963008	276909	317029
Geno*Loc	1412895**	129753	245615
Error	641860	106157	171201

** denotes significance at α = 0.01

Table 4: Combine regression analysis of variance for seed yield (Kg ha⁻¹) over four year 1991-94 at 20 location (USA and Pakistan)

Source	df	MS	F
Env	19	16499041	18.85**
Geno	14	1586099	1.81**
Env*	266	875343	2.75**
Heterogeneity	14	473963	1.41
Residual	252	897642	2.82**
Error	600	317943	

** denotes significance at α = 0.01

Table 5: Estimate of mean (x), regression coefficient (b) and residual mean squares for seed yield (kg ha⁻¹)

Genotypes	(x)	b	Res.M.S	F
Bay	2601	1.09	106554	0.34NS
Crawford	2387	1.12	166979	0.53NS
Cx458	2539	1.28	329112	1.04NS
Douglas	2279	1.22	438049	1.38NS
Forrest	2400	0.76	357557	1.12NS
Hsc401	2468	1.09	289794	0.91NS
Hsc591	2655	0.67	522011	1.64*
Hartwig	2666	0.76	193442	0.61NS
Hutcheson	2673	1.04	149453	0.47NS
Manokin	2712	0.9	66436	0.21NS
Ok885409	2796	1.02	154184	0.49NS
Ok885420	2517	0.71	788892	2.48**
Sparks	2297	1.12	161357	0.51NS
Stafford	2561	1.13	192511	0.61NS
Walters	2410	0.76	242800	0.76NS
Errors			317943	

NS = Non-significant

1994. The mean seed yield of genotypes over four years at the Goodwell location ranged from 1560 kg ha⁻¹ (Forrest) to 3268 kg ha⁻¹ ('CX 458'). The top-yielding significance group of genotypes included CX 458 (3268 kg ha⁻¹), followed by 'HSC 401' (3215 kg ha⁻¹), Douglas (3149 kg ha⁻¹), Stafford

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(2867 kg ha⁻¹), Sparks (2834 kg ha⁻¹), Crawford (2831 kg ha⁻¹), OK 885409 (2561 kg ha⁻¹), Manokin (2480 kg ha⁻¹), and Hutcheson (2448 kg ha⁻¹). CX 458 was the only genotype in the top-yielding group in all the four years.

The genotypes which performed well at Bixby, Haskell and Chickasha did not perform well at Goodwell due to the late maturing genotypes (mostly Group V). Conversely, the early maturing genotypes (mostly Group IV) yielded best at the Goodwell location. A combined analysis of variance (Table 3) was performed to estimate the GE interaction for seed yield utilizing all eight locations (in Pakistan and USA) and 16 genotypes in 1994. The result was in consistence with those of Eberhart and Russell (1966). The GL interaction was highly significant, which indicates that the genotypes yielded differently across locations. The location component was also found highly significant and was the largest of all the components. Since one objective of this study was to identify one or more locations in the USA which produces no GE interaction for yield when paired with one or more locations in Pakistan, every combination of two locations was analyzed. Only two locations (Haskell-Mansehra and Chickasha-Mansehra) showed a nonsignificant GL interaction.

Pakistan (NWFP):Malakandher, Tarnab, Mansehra and Swat. USA(Oklahoma):Bixby, Haskell, Chickasha and Goodwell.

The location and genotypic components were also nonsignificant. However, the genotypic component was the largest of all the components.

The nonsignificant GL interactions at Haskell-Mansehra and Chickasha-Mansehra indicate that genotypes developed at the two locations in the USA may perform well at Mansehra. On the other hand, high yielding genotypes selected at Mansehra may perform well at Chickasha and/or Haskell. Since genotypes developed at any of the locations could be used at other locations.

A combined regression analysis for seed yield (Table 4) was conducted to test the significance of the GE interactions as proposed by Eberhart and Russell, (1966). Genotype, environment and GE interactions were all significant.

The GE interaction was partitioned into heterogeneity and residual mean squares. Both were tested against the pooled error. Heterogeneity between regression was nonsignificant and the residual mean square was significant. There were certain genotypes in the test whose performance was not predictable or they were unstable. Therefore, the second stability parameter was calculated as proposed by Raut *et al.* (1990). The individual genotype residual mean squares were tested against the pooled error in the combined ANOVA. The results are in confirmation of the findings of Reedy *et al.* (1990).

Except for HSC 591 and OK 885420 all the residual mean squares were nonsignificant (Table 5). A significant residual mean square means that the genotypes are unstable and their performance is unpredictable. Raut *et al.* (1990) revealed same results. Genotypes OK 885409 and Hutcheson showed a regression coefficient close to one (1.02, 1.04) which means that these genotypes are less responsive to favorable environments but should perform well in more predictable and stable man ner. Also, their mean yields were greater than the grand mean (2531 kg ha⁻¹). The genotypes Bay, Crawford,

CX 458, Douglas, HSC 401, Sparks and Stafford had b value greater than one, which implies that these genotypes should perform better in increasingly favorable environments.

The results confirms the findings of Taware *et al.* (1990). Moreover, except for Crawford, Douglas, HSC 401 and Sparks all the above mentioned genotypes had a mean yield higher than the grand mean. The genotypes Forrest, Hartwig, Manokin and Walters had a b value less than one which suggests that these genotypes will perform better in less favourable environments. The genotypes Hartwig and Manokin also had a mean yield greater than the grand mean, which implies that these genotypes will be slightly better than rest of the genotypes in the group. Genotypes were inconsistent in their performance for all the characters when tested across locations and years. This confirms the findings of Baisakh and Dash (1992). A significant Genotype x Location interaction was observed for seed yield when all eight locations (in Pakistan and the USA) were studied in 1994. Out of the 16 location combinations only Haskell-Mansehra and Chickasha-Mansehra showed nonsignificant interaction, which implies that genotypes at these locations may perform in a similar way. The results of the combined regression analyses revealed that genotypes 885409, Hutcheson, HSC 401 and Bay has nonsignificant residual mean squares but only Ok 885409 and Hutcheson had b values close to 1 with mean yield higher than the grand mean. This implies that these genotypes are less responsive to favourable environments but should perform in a more predictable manner.

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