GENOTYPE BY ENVIRONMENT INTERACTION IN SOYBEANS GROWN IN DIVERSE LOCATIONS IN OKLAHOMA (USA) AND IN NORTH WEST FRONTIER PROVINCE (PAKISTAN)

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CHAPTER I

INTRODUCTION

The difference in the relative performance of genotypes across environments is termed genotype by environment (GE) interaction. 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.

GE interactions are an important concern to all plant breeders. The presence of GE interactions can hinder progress from selection by masking genotypic effects. The agronomic and/or economic value of a cultivar across environments may be considered the general or overall utility of the cultivar. Breeders often make selections based on the ranking of genotypes at one or more environments (13).

The impact of GE interactions on the ranking of breeding lines at different environments is of interest and importance. GE interactions always must be considered in applied plant breeding programs; however, the importance of these interactions and their implications are often difficult to measure on a routine basis (10). Large GE interactions may compel the breeder to test in several environments. However, it is only feasible to test in several environments if there are few genotypes. 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 a GE interaction. This is especially true if the high yielding sector of the population of genotypes contributes proportionally different to the interactions present (1).

The existence of GE interactions and their effects on progress from selection are widely recognized. Genotype by year interactions (GY) are always of importance in developing improved cultivars. Genotype by 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 (50). If no GE 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.

Pakistan is deficient in edible oil and protein. Domestic edible oil production meets only 20 percent 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 N.W.F.P (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.

CHAPTER II

LITERATURE REVIEW

Allard and Bradshaw (1) classified GE interaction into predictable and unpredictable types. They suggested that GL interactions were predictable while GY and GYL interactions were not. They also suggested that GYL interactions are more important to the breeders, but they are more difficult to evaluate and use.

Schutz and Bernard (50) considered GE interactions as two parts. They reported that one part is due to the difference in genetic correlations from one environment to another and the second part is due to the difference in genotypic variances. If the breeder is interested in selecting superior genotypes, the differences in genotypic variances are of relatively less importance.

Lin et al. (29) classified genotypic stability parameters into three types. 1) The variance across environments.2) the genotype interaction effect squared and summed across environments and 3) the residual mean square of deviations from the regression of a genotype on an environmental index. They indicated that the three concepts represent different aspects of stability and individually do not always provide a complete picture of response. They concluded that the nonparametric approach may be advantageous because a cultivar's response characteristics can be assessed qualitatively.

Simmonds (55) reported that decisions for the selection of cultivars for yield and/or some other important agronomic characteristics are not valid if based only on mean yields or percentages in the presence of substantial GE effects. He listed two potentially advantageous effects of transferring emphasis from means to regression :1) more accurate assessment of the kind of environment to which a new cultivar might be adapted, 2) and to enforce closer attention to site choice.

Several authors have proposed reducing the contribution of GE interactions to variance among variety mean by subdividing the testing area into homogeneous subareas [Horner and Frey (22)], but this procedure does not reduce the number of tests. Finlay and Wilkinson (18) and Eberhart and Russsell (16) proposed stability parameters to measure consistency of performance over environments. However, the stability parameter analysis is not feasible in a preliminary testing program.

Lin and Binns (28) proposed a new stability parameter to analyze cultivar by location by year experiments which they classified as Type 4. This parameter is defined as years within location mean squares, averaged over all locations. Using three sets of data for two crops (two for wheat and one for oats) they compared Type 3 and 4 stability parameters and found Type 4 to be more consistent and therefore potentially more useful as a genetic parameter.

Borojevic and Williams (8) studied GE interactions for yield components and their effects on wheat yield. They tested three cultivars over a ten year period at two locations. They used analysis of variance and regression analysis to estimate GE interactions and stability parameters. They found a significant GY interaction for the parameters studied (plant height and yield), which is indicative of inconsistent ranking among genotypes and requires testing genotypes over years.

Eskridge et al. (17) studied 18 wheat genotypes across 14 environments for flour protein concentration and kernel hardness in 1988 and 1989. They used univariate and multivariate approaches to measure the genotypic consistency of wheat quality trials based on the probability of traits falling within acceptable limits. They suggested that a probability based approach provides a simple and flexible decision making tool to identify genotypes with high probability of providing acceptable quality when grown across diverse environments.

Bassett et al. (4) investigated four soft white winter wheat cultivars at 21 diverse locations in Washington and Idaho from 1983 through 1985 for six quality traits. Cultivar and environmental effects were found significant for all the traits (flour yield, cookie diameter and hardness). Genotype x environment interactions were small, but significant. Among the variance components, year contributed most to total variance. The LY component was greatest for flour yield, cookie diameter and hardness. These findings also agree with those of Baenziger et al. (5), who found highly significant differences among environments and cultivars and their interactions for flour yield and protein content among several soft red wheat cultivars.

Vogel et al. (60) studied intermediate wheatgrass grown at two locations in 1980 and 1981. Analyses of variance were used to evaluate results at each location for each year, over years for a single location, over locations for a single year and over years for both locations. The over year analysis of variance was analyzed as a split plot. Treatment means were used in the combined analyses over years and locations to determine significance of the main effects of genotypes, locations, years and their interactions. They reported significant differences among genotypes for forage yield and quality. GL and GY interaction effects were significant for first cut forage yield but not for second cut. These results were similar to those reported by Lamb et al. (27).

Lamb et al. (27) studied 42 crested wheatgrass genotypes at two locations for two years. Analysis of variance procedures were used to evaluate results at each location for each year, over years for a single location, over locations for a single year, and over years for both locations. They reported significant differences among genotypes for all traits (heading, maturity, yield) except for second cut and proteins in all four single years and at two locations. They concluded that there are definite genetic differences among crested wheatgrass genotypes within locations for the traits evaluated, and that these differences are consistent over years. They suggested that within a location, a single year of sampling should be sufficient to identify crested wheat grass genotypes differing in first cut IVDMD (in vitro dry matter digestibility), but for selecting among the high yielding lines additional testing may be needed.

Yates and Cochran (64) tested five barley cultivars at six locations for two years. A significant GL interaction was detected for yield which indicates an inconsistent ranking among genotypes and requires testing genotypes over several locations.

Sharma et al. (54) studied the effect of GE interaction in triticale in two different environments (stress and non-stress environments). Analysis of variance was performed for each environment for all the characters as well as over the two environments to assess the genotype x environment interaction. They concluded that genotypic variance was larger than GE interaction variance. The ratio of these variances suggested that grain yield was highly influenced by GE interactions. They also concluded that very high GE interactions for yield in triticale might be less stable due to their narrow genetic base and that the breeding material should be tested under different locations and environments to select for genotypes which really demonstrate higher stability.

Dobhal and Gautam (15) tested 11 genotypes of ricebean during 1988-91. They found a significant genotype x environment interaction for pods/plant, pod length, and yield/plant. Analysis of variance revealed significant differences among genotypes under each environment for all the characters under study. The pooled analysis of variance also revealed significant differences among genotypes and environments, indicating the presence of genetic variability among the genotypes. Highly significant mean squares due to environments and GE interactions suggested that the genotypes interacted considerably with environmental conditions.

Reedy (45) investigated 25 genotypes of short duration rice in six different environments from 1987 through 1989. They conducted pooled analysis of variance in which mean squares due to GE interaction were found highly significant indicating differential behavior of genotypes to different environments for grain yield. Ganesh and Soundarpandian (19) reported similar results for grain yield in short duration varieties of rice.

Sharma and Godawat (51) evaluated 30 high yielding varieties of foxtail millet at four locations in 1985 and 1986. They used stability analysis proposed by Eberhart and Russell (16) to identify ideal genotypes. They reported a significant difference among genotypes and genotype x location interaction for spike weight, spike length, biological yield and grain yield. They concluded that genotypes differ in their performance at all locations over the period of years.

Mahajan et al. (31) investigated 20 genotypes of finger millet (Eleusine coracana) from 1987 through 1989. Stability analyses were carried out following Eberhart and Russell (16). The parameters of stability , i.e. regression coefficient and deviation from regression were used to identify the best genotypes for acid soils in mid-altitudes of Meghalaya. They reported that the GE interaction was significant only for grain yield. GE interactions for ear length, 100-seed weight and plant height were nonsignificant. They concluded that all the genotypes perform differently over the period of years for seed yield, but no differences were found for ear length, 100-seed weight, and plant height.

Saeed et al. (47) studied the GE interaction in grain sorghum at five locations across Nebraska and Kansas in 1978 and 1979. They evaluated 46 hybrids and five lines of sorghum. The stability analysis of variance and stability parameter: linear regression coefficient and deviation from regression of genotypic means over environmental index were computed as suggested by Eberhart and Russell (16). Hybrids and lines showed significant interaction with environments for seed weight and yield.

Mohammad et al. (34) evaluated 54 genotypes of sorghum at three locations in Kansas during 1986 and 1987. A combined analysis of variance was conducted using SAS procedure for mean separation. They reported a significant GE interaction for forage and grain yield. GY interactions were found significant for forage yield, grain yield, crude protein, but were notsignificant for acid detergent fiber. The variance components of all traits except for forage yield were comparatively smaller than the second order interaction of GYL. Large significant second order interactions indicated differential response of genotypes grown under diverse environmental conditions. The significant GL interactions observed for grain and forage yield indicated that Kansas could be divided into subareas for selection and production of sorghum cultivars.

Naidu et al. (37) conducted an experiment during 1987-1989 to study the stability of seed yield of 20 genotypes of mungbeans (Phaseolus radiatus) in six diverse environments. Analysis of variance revealed significant differences among the genotypes and environments. Environmental variance was higher than genotypic variance indicating its greater contribution to the total estimated variance. GE interactions were significant when tested against pooled deviation.

Reddy et al. (46) investigated 11 genotypes of mungbeans for stability of yield and its component characters in 1986 and 1987. Regression analysis was used to evaluate the performance of genotypes across the environments. Genotypes showed significant differences for plant height, pods/plant, pod length, and seed yield. The highly significant environmental effects proved the importance of additive environmental variance, confirming that the environments had different effects on the performance of genotypes (for plant height and seed yield). The study confirm the findings of Kandaswamy et al. (26).

Muduli and Hati (35) tested 22 genotypes of mungbeans and eight genotypes of blackgram in a period of four years. Pooled analysis of variance indicated significant differences among genotypes and environments for seed yield, indicating the presence of genetic variability in the material for both the pulses. The GE interactions were also significant indicating considerable interaction of genotypes with the environment in the expression of this trait. These results confirms the findings of Gupta et al. (20) and Sarma et al. (49).

Murray and Verhalen (36) tested 62 breeding lines of cotton for two years at two locations in Oklahoma. They concluded that testing over years, locations, or both would provide more precise differentiation among lines for yield. They also concluded that estimates of the relative efficiency of two vs. one year's testing before selection indicated that it should be practiced after each year for maximizing selection progress per unit of time.

Patel et al. (42) tested 13 promising genotypes of cotton from 1986 through 1988. They reported a significant GE interaction for boll number and seed cotton yield, indicating that the genotypes behaved differently under different environments.

Dani (14) investigated ten cotton cultivars and five experimental hybrids for a period of three years. He conducted a combined analysis of variance and found GY, year x harvest date and genotype x harvest date interactions highly significant for oil content. The only significant interaction found in case of protein was yield x harvest date. The conclusion from this study was to keep harvest time under consideration for efficient sampling and evaluation of genotypes for oil and protein content.

Campbell and Kern (9) investigated ten sugarbeet cultivars at five locations for four years. They used the combined analysis of variances procedure for statistical evaluation. GY interactions were significant for all the traits studied (root yield, % sucrose, sodium and potassium contents). GL interaction was significant only for root yield. GLY interactions were significant for all traits except for potassium concentration.

Nandanwar et al. (38) studied eight genotypes of alfalfa for a period of three years.

Pooled analysis of variance and regression analyses were utilized for the identification of desirable genotypes. They found a significant GE interaction for green and dry matter yields of alfalfa, which indicates a considerable difference among the genotypes for their fodder and dry matter yield performance across environments.

Birari et al. (7) conducted an experiment during 1987-1989 to assess the stability of yield and its component characters in seven genotypes of cowpea. They used the Eberhart and Russell (16) approach to identify the genotypes with desirable performance. They reported an inconsistency in the performance of genotypes in different environments, for plant height, 100-seed weight, harvest index and seed yield.

Casler and Hovin (10) studied the GE interactions for spring and summer forage yield of reed canarygrass in 48 genotypes during a three year period at four diverse Minnesota locations. They used mean yield response to environments and regression analysis to determine the performance of genotypes across environments. Variance among genetic entries and the GE interactions were significant for spring and summer dry matter yield.

Link et al. (30) investigated 48 inbred lines of faba beans grown at 17 locations for a period of two years. Estimates of variance components for the effect of genotypes and GY interaction were highly significant. Significant interactions were also found among locations and for GLY. They suggested that by choice of an appropriate location, degree of cross fertilization can be increased considerably.

Sarma and Roy (48) evaluated 14 genotypes of toria (Brassica rapa) and eight of indian mustard from 1990 through 1992, at Diphu (India). Pooled analysis of variance showed significant differences among the genotypes of toria and indian mustard for seed yield and maturity. The significant pooled deviations for yield and maturity indicate the presence of nonlinear, unpredictable components of GE interaction showing differences among the genotypes.

Verma et al. (59) tested 13 promising genotypes of toria (Brassica rapa) from 1989 through 1992 in three diverse environments. The pooled analysis of variance showed a significant GE interaction for yield, which indicates that genotypes perform differently in different environments.

Shafii et al. (52) evaluated 32,26 and 60 commercial cultivars of winter rapeseed for yield and oil percentage from 1986 through 1988 at 12, 16 and 17 locations. They used the Additive Main effects and Multiplicative Interaction (AMMI) statistical model and reported that significant GE interaction influenced the relative ranking of cultivars across environment for both seed yield and oil content.

Norden et al. (40) studied the stability of four peanut multiline populations with their component lines from 1980 through 1983 at two locations in Florida. They used linear regression techniques to characterize genotypic stability through the use of two stability parameters: regression coefficient and deviation from regression. They reported a significant GE interaction for pod yield, 100-seed weight and seed yield. Though multilines did not have greater stability in all cases, the differences between each multiline and its least stable component line was generally greater then the differences between the multiline and its most stable component line. This suggests that the chance of improving the yield stability of peanut cultivars is increased when the multiline approach is used.

Raut et al. (43) studied five bunch-erect genotypes of peanut in three different seasons, i.e. winter (rabi)-summer of 1987-88, rainy season of 1988 and winter (rabi)-

summer of 1988-89, for plant height, 100-seed weight and seed yield. Two regression techniques were utilized to determine the stability of the peanut genotypes. They found significant difference in magnitude of GE interaction for all the traits.

Cramer and Beversdorf (13) tested five soybean genotypes at two locations in 1980 and 1981 to determine the effect of GE interaction on selection for low linolenic acid soybeans. They conducted analysis of variance procedures and reported significant GLY interactions at the 1% level of significance in the Ontario Soybean Variety Trials. However, GL and GY interactions were nonsignificant. In another study in which ten genotypes were tested at three locations over a period of two years, they reported significant GL and GY interactions while GLY interaction was nonsignificant.

Matzinger (32) in a review of GE interactions of various crops found that the three way interactions were usually of greater importance. He suggested that GL interactions are not common since soybeans are bred for a narrow range of adaptability.

Whitehead and Allen (63) tested eight soybean lines in two high and two low stress environments from 1982 through 1986. They reported significant differences in genotypes across locations over a period of years. However, when low stress tests or high stress tests were combined over years for the two locations, there were no significant differences among genotypes. However, there were significant GE interactions when the low and high stress environments were combined over years and locations. The first order GE interactions were significant when the low stress tests were combined, but GLY interactions were not. When high stress sites were combined over years and locations, the second order interactions were significant but the first order interactions were not.

Panter and Allen (41) tested 17 high yielding soybean lines at 16 location-year combinations in a randomized complete block design with three replications from 1982 to 1986. An analysis of variance of seed yield was performed to determine the effect of locations, nursery environment, line, replications and all interactions. Regression analyses were also used to determine if yield was related to height, maturity and lodging. They concluded that the soybean lines responded differently under different environmental conditions. They also found significant relationships between yield and maturity, yield and lodging and yield and height.

Cianzio et al. (12) studied the effect of a tropical environment (Puerto Rico) on the protein and oil percentage of temperate soybean genotypes. Analysis of variance and rank correlations were calculated for protein, oil and protein + oil percentage. They found no major differences in the performance of genotypes. However, the genotype x planting date and GY interactions were significant for the oil percentage of genotypes from cross 1 (Wells x PI 153269). The genotype x year x planting date interactions were significant for the three traits for genotypes from cross 2 (Woodworth x Pando).

Hawkins et al. (21) also studied the effect of a tropical environment on the oil composition of soybean genotypes adapted to a temperate climate. They reported significant GE interactions for linolenic acid. They also reported changes in ranking of 20 lines of maturity groups I to III grown in Iowa and Puerto Rico. They concluded that the differences would not hinder selection in a tropical environment for low linolenic acid soybeans adapted to the Northern USA.

Weaver and Wilcox (62) studied the differences among soybean group II and group III genotypes grown in wide and narrow rows for maturity, lodging, height and seed yield over a period of two years. GY interactions were significant for all characters except plant height in both maturity groups in wide rows. In narrow rows, the year effect was large but nonsignificant. There was almost a total absence of GY interaction for seed yield in the two groups. They concluded that yield testing in narrow rows would be more efficient in identifying high yielding genotypes, especially when selection is based on one year evaluation. When the combined analysis of variance procedure was performed, they found no significant row width x genotype interaction for any character studied, which indicated that genotypes did not respond differently to row spacings.

Mayers et al. (33) studied eight soybean genotypes in three tropical dry season environments to evaluate the genotypic and environmental effects on growth and seed yield per plant. Multiple linear regression analyses were conducted on genotypic, environmental and GE means to evaluate the magnitudes of the respective effects on the relationships. They found that early maturing lines produced consistently less biomass when compared with other lines in the three environments. However in the late maturing genotypes the relative ranking within environments were different. They found large differences in seed yield per plant, averaged over genotypes and sowing dates, between KRS and WRS (Kimberley Research Station and Walkmin Research Station).

Sinclair et al. (57) studied genotypic variations in soybean nodule number and weight. They studied 100 soybean genotypes from 1983 through 1985 at two locations in Florida. An analysis of variance and environmental stability measure was used to determine the performance of the genotypes. 'Hardee', 'Centennial' and 'F81-7313' ranked among the genotypes with the greatest nodule weight and number. Their rankings were consistent across years and locations tested.

Hugie and Orf (23) studied genotypic interactions of 276 early maturing soybean genotypes with row spacings. They were evaluated in six yield tests at two locations over a period of two years. Analyses of variance were conducted for yield, plant height and 100-seed weight. They reported a significant GYL interaction for all the characters measured, which indicates fluctuations in ranking of genotypes associated with individual location-year combinations and requires testing genotypes over both locations and years.

Johnson et al. (25) estimated the genetic and environmental variability in soybeans for yield, plant height, 100-seed weight and percent oil at four locations in two years. They concluded that estimates of genetic variance obtained in different environments were less consistent and the estimates of GE interactions were higher for yield than for the other characters.

Baikhaki et al. (2) studied the association of GE interactions with performance level of soybean lines in preliminary yield tests. They evaluated 44 soybean lines and four cultivars at four locations in 1973 and 1974. Pooled analysis of variance was conducted to evaluate the performance of genotypes. GY and GL interactions were not significant, however they found a significant GYL interaction for yield.

Nigam et al. (39) evaluated nine soybean varieties for a period of five years in different rainfed situations. Regression analysis was performed to evaluate the performance of genotypes. They reported a significant GE interaction for yield, suggesting an inconsistency in the performance of varieties in different environments.

Sharma et al. (53) tested 28 promising soybean genotypes for stability of performance for days to first flowering, days to maturity, and seed yield in 1977 and 1978. They conducted a statistical analysis proposed by Eberhart and Russell (16) and reported a highly significant GE interaction for all three characters concluding that the characters are highly influenced by change in the environments. They also reported a highly significant difference in the variance due to environment, indicating that the response to environments was genetically controlled.

Jagtap et al. (24) tested three soybean and three pigeonpea genotypes from 1988 through 1990. The variance due to genotypes and environments were significant for all traits (100-seed weight, pods/plant, and seed yield) which suggests a significant influence of environments on these characters. They also conducted the Finlay and Wilkinson (18) method of analysis and found that none of the soybean and pigeonpea genotypes had any adaptability and that the genotypes showed average stability for all the characters understudy.

Baisakh and Dash (3) studied the performance of 46 genotypes of soybean in north eastern region of Orissa from 1988 through 1990.. The analysis of mean data for both years separately and when pooled showed significant genotype and GY interactions for plant height, pods/plant, 100-seed weight, and seed yield, which indicates differential response of genotypes to the environments. These results confirm the findings of Chaudhry and Singh (11) and Nigam et al. (39).

Taware et al. (59) investigated six soybean varieties during the rainy seasons of 1986 and 1987 at four locations in India. They conducted pooled analyses of variance and found significant differences between varieties for plant height, 100-seed weight and seed yield. The mean squares for environments differed significantly for the characters under study, which indicates a considerable influence of locations on all the characters. These results confirm the findings of Sharma et al. (53), Singh and Choudhary (56), Patil et al. (42), Bhatnagar and Tiwari (6), and Raut et al. (44).

Weaver et al. (61) studied the stability parameters for maturity group VI through group VIII of soybean cultivars over a three years period in 28 environments in central and southern Alabama. Joint regression analysis revealed that a major part of GE interaction could be accounted for by the differences between the fitted regression lines. They reported that when adapted cultivars are being compared in a stability analysis, the ideal cultivar should have high seed yield, a regression coefficient of zero and minimum deviation from regression. They also stated that a positive regression coefficient would seem more desirable, which usually results in lower than average seed yields in unfavorable environments. A cultivar with positive regression coefficient would be better adapted to high yield environments, but would lack the wide adaptations of the ideal cultivars.

CHAPTER III

MATERIALS AND METHODS

Fifteen genotypes (Table 2) of group IV and group V soybeans from the Oklahoma Soybean Variety Test were used in this study. These genotypes were grown from 1991 through 1994 at four Oklahoman locations (Bixby, Haskell, Chickasha and Goodwell). In 1994 four Pakistani locations (Malakandher, Tarnab, Mansehra and Swat) were added to the study.

Data from these 20 tests (1991-1994) were used to estimate GE interactions (GL, GY, GLY) for plant height, 100-seed weight and seed yield. Plant height data were not available at the Goodwell location in any of the years, therefore data from three locations were utilized. A Randomized Complete Block Design with three replications was used for this study. Plot size was 3m x 7m with row spacing of 75cm. There were four seven meter rows in each plot. The central two rows were used to collect data. Plant height was measured from ground level to the tallest part of the plant. A sample of seeds from one of the central rows were counted and weighed to get 100-seed weight. Seed yield was measured from one of the two central rows. The plantings in Oklahoma were accomplished with the help of a research plot planter. Weeding was done manually and with recommended chemicals. At two locations (Goodwell and Chickasha) limited irrigations were applied for plant survival. Tests at Bixby and Haskell were dependent on rainfall. Harvesting and threshing were done with the help of research equipment.

In Pakistan at all four locations, manual power was used from planting to threshing. At the time of seedbed preparation, fertilizer was applied at the rate of 25:50:50 (NPK) kg/ha. Lines were drawn with the help of a hand hoe and seeds mixed with inoculum were spread in these lines and then covered with a layer of soil (3cm -5cm). Weeding at different stages was done manually (no chemicals were used). At all four locations irrigations were applied at different stages of plant growth (flood irrigation method was used). Six to seven irrigations were applied when: 1. The plants had three to four leaves, 2. Plants began to flower, 3. Pods were filling, 4. Seeds were maturing. Harvesting was done manually and each plant row was threshed separately by beating with sticks.

In Oklahoma, Chickasha represents a moderate rainfall area and has a Reinach silt loam soil, a member of the coarse, silty, mixed, thermic Pachic Haplustolls. Haskell receives a higher average rainfall and has Taloka silt loam soil, a member of the fine, mixed, thermic Mollic Albaqualfs. Goodwell receives very little rainfall and has a Richfield clay loam soil, a member of the fine, montmorillonitic, mesic Aridid Argiustoll. Bixby receives higher average rainfall and has Okemah silt loam soil type classified as fine, mixed, thermic Acquic Paleudolls.

In Pakistan Mansehra and Swat receive higher average rainfall compared to the Malakandher and Tarnab locations. Malakandher represents a Dennis soil type classified as fine, mixed, thermic Acquic Paleudolls. Tarnab represents an Enders soil type classified as clayey, mixed, thermic Typic Hapludults. Mansehra represents a Choska soil type classified as coarse silty, mixed termic Fluventic Hapludolls. Swat represents an Okay soil type classified as fine, silt loam, mixed, thermic Typic Argiudolls.

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 (1980), using genotypes, locations, and years as main effects. Genotypes and Years were considered random and locations as fixed effects. In the ANOVA, if the second order interaction (GLY) was found significant for seed yield, seed weight and plant height, the data were further analyzed to test how genotypes performed at each location, separately over the years. LSD (least significant difference) procedures were 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 combinations did not exhibit GL interactions. There were a total of 16 location combinations and only seed yield was evaluated.

Regression analyses were also used to determine stability parameters as defined by Eberhart and Russell (16). Every location within a year was considered one environment. In this method the individual genotype response to changing environment was determined by regressing the individual genotypic mean on the environmental index (environmental index = location mean minus the grand mean).

Eberhart and Russell (16) procedures also permit the partitioning of GE interaction mean square into a component due to heterogeneity between the slopes of regression and a component due to residual or remainder which measures the scatter of points about the regression lines. If the heterogeneity mean square alone is significant, we can predict all the GE interaction for each genotype from the linear regression on environmental index.

If the remainder mean square alone is significant, there is either no relationship or no simple relationship between the GE interaction and the environmental index, and there are genotypes present in the test that are unstable or unpredictable in performance. If heterogeneity and residual mean squares both are significant, then heterogeneity mean squares should be tested against the residual mean square to determine whether a significant portion of the variation in the interactions can be explained by the regression.

Two stability parameter were used to determine the stability of each genotype. The regression coefficient (b) serves as the first stability parameter. Genotypes with b values greater than one are considered responsive or better adapted to increasingly favorable conditions but are considered unstable in performance over environments. Genotypes with b values of one are less responsive but will perform in a more predictable or stable manner, and those genotypes with b value less than one will be relatively better adapted to less favorable growing conditions.

To determine which genotypes contribute to this instability, the second stability parameter is calculated. This consists of individual genotypes residual mean squares being tested over the pooled error of the regression ANOVA. The residual mean square is a measure of consistency in performance of a genotype over varying environments. Genotypes with significant residual mean squares are considered unstable and their performance tends to be unpredictable. The ideal genotype is one with a high mean yield, a regression coefficient equal to one and a nonsignificant residual mean square.

CHAPTER IV

RESULTS AND DISCUSSION

The genotype by location (GL) interaction measures the consistency of performance among genotypes at different locations. A significant GL interaction suggests wide fluctuations in the ranking of genotypes across locations and requires testing of genotypes over a range of locations. Conversely, the absence of a GL interaction suggests that a particular genotype performs similarly compared to other genotypes at the multiple test locations. Therefore, multiple location testing may not be required or may be reduced. Also, a superior genotype selected at one location should perform well compared to other genotypes at alternate locations.

The genotype by year (GY) interaction indicates variable performance of genotypes in different years. A significant GY interaction indicates inconsistency in ranking among genotypes and requires testing genotypes over a period of years. Conversely, the absence of a GY interaction suggests that multiple year testing may not be needed.

The genotype by location by year (GLY) interaction measures the stability among genotypes for each combination of year and location. A significant GLY interaction is indicative of fluctuations in ranking of genotypes associated with individual location year combinations and requires testing of genotypes across locations over years. The absence of significant interactions of genotypes with locations, years , or LY indicates that a test at one location during one year may be sufficient to identify genotypes with superior genetic potential.

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 through 1994 (Table 1). This significant interaction 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. 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/h and 3369 kg/ha. According to the average data, 'Hartwig' (3369 kg/ha), 'OK 885409' (3236 kg/ha), 'HSC 591' (3208 kg/ha) and 'Hutcheson' (3173 kg/ha) were in the top-yielding significance group (i.e. OK 885409, HSC 591, and Hutcheson were not significantly different from the highest yielding genotype, Hartwig). In 1991, these same genotypes were in the top-yielding significance group. However, Hutcheson was not in the top group in 1992. OK 885409 and HSC 591 were not in the top-yielding group in 1993. HSC 591 was not in the top group in 1994. Hartwig was the only genotype which was in the top-yielding group every year at the Bixby location.

At the Haskell location (Table 3) the yield range among genotypes was from 2206 kg/ha ('Sparks') to 2933 kg/ha (Hutcheson). According to the average data, Hutcheson (2933 kg/ha), OK 885409 (2750 kg/ha) and 'Manokin' (2746 kg/ha) were in the top-yielding significance group. The same three genotypes were in the top-yielding group in every year at this location. Three additional genotypes (HSC 591, 'Forrest' and Hartwig) were in the top-yielding group in 1991, 1992 and 1993.

Genotypes at the Chickasha location (Table 4) yielded on the average between 1939 kg/ha (Douglas) and 2907 kg/ha (OK 885409). The top-yielding significance group of genotypes (according to the average data) were identified as OK 885409 (2907 kg/ha), 'Bay' (2852 kg/ha), Manokin (2829 kg/ha), 'OK 885420' (2751 kg/ha), 'Walters' (2673 kg/ha), 'Stafford' (2671 kg/ha), and Hutcheson (2642 kg/ha). 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 1994. OK 885420 and Stafford were in the top significance group in 1993 and 1994. Hutcheson and Walters were in the top group in 1991, 1993 and 1994.

The mean seed yield of genotypes over four years at the Goodwell location (Table 5) ranged from 1560 kg/ha (Forrest) to 3268 kg/ha ('CX 458'). According to the average data the top-yielding significance group of genotypes included CX 458 (3268 kg/ha), followed by 'HSC 401' (3215 kg/ha), Douglas (3149 kg/ha), Stafford (2867 kg/ha), Sparks (2834 kg/ha), Crawford (2831 kg/ha), OK 885409 (2561 kg/ha), Manokin (2480 kg/ha), and Hutcheson (2448 kg/ha). CX 458 was the only genotype in the top-yielding group in all the four years. HSC 401 and Douglas were in the top group in 1991, 1992 and 1994.

Sparks and Crawford were in the top group in 1991 and 1992. Stafford was included in the top group in 1991, 1994 and Hutcheson was in the top group only in 1993.

The genotypes which performed well at Bixby, Haskell and Chickasha did not perform well at Goodwell. Perhaps it might be due to the late maturing genotypes (mostly Group V) which yielded high at the Bixby, Haskell and Chickasha locations, but low at the Goodwell location. Conversely, the early maturing genotypes (mostly Group IV) yielded best at the Goodwell location. According to the average data the genotype 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 Haskelll. It might be appropriate to conclude that this genotype will perform well at all these locations. Hartwig was in the top group in each of the four years at Bixby, but not at any other location or in any year. The genotype Hutcheson was in the top group according to the average data and in 1991, 1993 and 1994 at Bixby, and in all years at Haskell but only in 1991, 1993 and 1994 at Chickasha. It might be appropriate then to conclude that Hartwig will perform well at Bixby. Hutcheson appears to perform well at all locations.

A combined analysis of variance (Table 6) was performed to estimate the GE interaction for seed yield utilizing all eight locations (in Pakistan and USA) and 15 genotypes in 1994. 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. Out of the 16 location combinations only two showed a nonsignificant GL interaction.

Haskell-Mansehra:

The GL was nonsignificant for seed yield at this location combination (Table 7). At the Haskell-Mansehra locations all genotypes tested performed in a similar way on the average relative to each other. If genotypes are selected at one of the locations we may be able to predict their performances at the other location. Also, we may be able to select genotypes at one location which will perform well at the alternate location. The location and genotypic components were also nonsignificant. However, the genotypic component was the largest of all the components.

Chickasha-Mansehra:

The GL interaction was nonsignificant for seed yield at the Chickasha-Mansehra combination (Table 8). The nonsignificant interaction indicates that all the genotypes performed similarly on the average relative to each other at these locations. Genotypes selected at Chickasha may perform in a similar way when grown at Mansehra and vice versa. Genotype and location components were also nonsignificant. The genotypic component was largest of all the components; therefore, the major contribution to the nonsignificant GL interaction was due to genotypes.

Table 9 shows the mean seed yield of soybean genotypes at Haskell, Chickasha, Mansehra, (Haskell-Mansehra) and (Chickasha-Mansehra) in 1994. The top-yielding significance group according to the average data at the Haskell-Mansehra combination included Hutcheson (3221 kg/ha), Manokin (3118 kg/ha), Stafford (2998 kg/ha), CX 458 (2986 kg/ha), Douglas (2895 kg/ha) and OK 885409 (2891 kg/ha).

At the Chickasha-Mansehra combination genotypes in the top-yielding significance group were the same except for Douglas. At Haskell, Hutcheson, Manokin and OK 885409 were in the top group while at Chickasha all the six genotypes which make up the top group at the Haskell-Mansehra combination (except Douglas) were in the top-yielding significance group. At Mansehra the same six genotypes were in the top-yielding group. Genotypes selected at any of the these locations should perform similarly at the alternate locations.

The nonsignificant GL interactions at Haskell-Mansehra and Chickasha-Mansehra indicate that genotypes developed at the two locations in the US may perform well at Mansehra. On the other hand, high yielding genotypes selected at Mansehra may perform well at Chickasha and/or Haskell. This would be a tremendous opportunity for both countries soybean breeding programs. Since genotypes developed at any of the locations could be used at other locations.

The mean seed yields (kg/ha) of soybean genotypes at three Pakistani locations are reported in Table 10. Genotypes at Malakandher yielded on the average between 257 kg/ha (Douglas) and 3567 kg/ha (HSC 591). HSC 591 was the top yielding genotype. At the Tarnab location, genotypes yielded between 1140 kg/ha (Douglas) and 3107 kg/ha (HSC 591). At Swat genotypes yielded between 2149 kg/ha (OK 885420) and 3475 kg/ha (Crawford). HSC 591 was the top yielding genotype at all three locations, however at Swat Crawford, CX 458, and Walters were included in the top significance group.

A combined regression analysis for seed yield (Table 11) was conducted to test the significance of the GE interactions. 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. As heterogeneity between regression was nonsignificant and residual mean square was significant, we could not predict the GE interaction for each genotype from the linear regression on environmental index. There are certain genotypes in the test whose performance is not predictable or they are unstable; therefore, the second stability parameter was calculated. The individual genotype residual mean squares were tested against the pooled error in the combined ANOVA.

Except for HSC 591 and OK 885420 all the residual mean squares were nonsignificant (Table 12). The residual mean square is the measure of consistency in performance of genotypes over different environments and a significant residual mean square means that the genotypes are unstable and their performance is unpredictable. 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 manner. Also, their mean yields were greater than the grand mean (2531 kg/ha). 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. 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 Walter had b value less than one which suggests that these genotypes will perform better in less favorable environments. The genotypes Hartwig and Manokin also had a mean yield greater than grand mean, which implies that these genotypes will be slightly better than rest of the genotypes in the group.

A significant GLY interaction (Table 13) was observed in the combined analysis for 100-seed weight from 1991 through 1994 at four locations in the USA. The genotypes in this study performed differently over locations and years. The GL interaction was also significant for 100-seed weight, which suggests wide fluctuations in ranking of genotypes. Genotypes should be tested at multiple locations. The GY interaction was also significant indicating a differential response of genotypes and requires testing of genotypes over a period of years. YL interaction was also significant which suggests that testing should be done at various locations in more than one year to identify high performance genotypes. Since the GLY interaction was significant, further analyses were conducted to check the performance of genotypes at each of the locations separately over the years (1991-94).

Genotypes at the Bixby location (Table 14) ranged between 12 and 19 gm/100 seeds. The top significance group of genotypes with large 100-seed weights were Crawford and Douglas (19gm/100 seeds) . The low 100-seed weight group of genotypes (12-14 gm/100 seeds) included Forrest, HSC 591, Hartwig, Walter and OK 885409. At Haskell (Table 15), genotypes ranged between 13 and 20gm/100 seeds. The group of genotypes with higher 100-seed weights included Douglas (20 gm/100 seeds), followed by Crawford, Sparks and Bay (19gm/100 seeds). The low 100-seed weight group of genotypes (13-14 gm/100 seeds) included Walters, Hartwig, Forrest, HSC 591 and OK 885409. Genotypes at the Chickasha location (Table 16) ranged from 13 to 20gm/100 seeds. The genotype with the highest 100-seed weight was Bay (20 gm/100 seeds), followed by OK 885420, and Douglas (17gm/100 seeds). At the Goodwell location (Table 17) genotypes ranged from 12 to 18 gm/100 seeds. The significance group of genotypes with the largest 100-seed weights were identified as Douglas and Crawford (18 gm/100 seeds). The lower 100-seed weight group (12-14 gm/100 seeds) consisted of Forrest, Hartwig, OK 885409, Manokin, OK 885420, Walters, Hutcheson, HSC 591 and Stafford.

A combined regression analysis for 100-seed weight (Table 18) revealed significant genotype, environment and GE interactions. Significant heterogeneity mean square and residual mean square indicated that the relationship between the overall mean of genotypes and environmental index was not strictly linear. The genotype HSC 401 had nonsignificant residual mean square (when tested against the pooled error) with regression coefficients close to one (0.97) (Table 19) and mean 100-seed weight equal to the grand mean. This genotype should be considered stable over all environments and less responsive to favorable growing conditions. The genotype Stafford with a nonsignificant residual mean square and b value of 1.33 should be highly responsive to increasingly favorable conditions but should not be considered a stable genotype. The genotypes Walters and Forrest also had nonsignificant residual mean squares, with b values of 0.75 and 0.47, respectively. They should be relatively better adapted to less favorable growing conditions. The genotypes which show significant residual mean square are considered to be unstable and those genotypes with b value greater than one would be considered responsive and would perform better in favorable environments. These genotypes with b value less than one are better adapted to less favorable growing conditions.

A significant GLY interaction was obtained for plant height in the combined analysis over four years and three locations in the USA from 1991 through 1994 (Table 20). This indicates the presence of fluctuations in ranking of genotypes associated with individual location-year combinations and requires testing of genotypes across locations over years. The GL interaction was nonsignificant, which means that a particular genotype performs about the same compared to the other genotypes at various test locations. Since the three way interaction was significant, further analyses were conducted to check the performance of genotypes at each locations over the years (1991-94).

At the Bixby location (Table 21), plant height ranged from 20 inches to 37 inches. The tallest genotype was HSC 401 followed by Crawford, HSC 591 and Sparks. At the Haskell location (Table 22) plant height of genotypes ranged between 24 and 34 inches. The tallest genotypes identified were HSC 591 and HSC 401. At the Chickasha location (Table 23) plant height ranged from 23 to 39 inches. The tallest genotype identified was HSC 591 followed by Crawford.

A combined regression analysis for plant height (Table 24) revealed significant genotype, environment and GE interactions. The heterogeneity mean square and residual mean square were also significant, which indicates that the relationship between the overall mean of genotype and environmental index was not strictly linear. In Table 25 mean plant heights, regression coefficients and residual mean squares of individual genotypes with appropriate F tests are reported.

Genotypes HSC 401, Hutcheson and Walters showed nonsignificant residual mean squares. HSC 401 and Walters with b values of 1.1 and 1.22 and plant heights of 37 and

30 inches, respectively, would be considered relatively better genotypes in favorable environments. The genotype Hutcheson, on the other hand, with b value of 0.8 and plant height of 24", would be considered relatively better in less favorable environments.

CHAPTER V

SUMMARY AND CONCLUSIONS

Genotype by environment (GE) interactions are an important concern to all plant breeders. The presence of GE interactions can hinder the progress from selection by masking genotypic effects. Fifteen genotypes of group IV and group V soybeans from the Oklahoma Soybean Variety Test were used in this study. These genotypes were grown from 1991 through 1994 at four Oklahoma locations (Bixby, Haskell, Chickasha and Goodwell). In 1994 four Pakistani locations (Malakandher, Tarnab, Mansehra and Swat) were added to the study.

A randomized complete block design (RCBD) with three replications was used in this study and data were collected on seed yield, plant height and 100-seed weight. Two statistical procedures (analysis of variance and linear regression) were used to analyze the data. The objective of this study was to determine if any GE interactions were present when the same 15 genotypes were grown at different locations in the USA and to identify high yielding stable genotypes at specific locations in Oklahoma. This study was also designed 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.

A significant GLY interaction was observed for seed yield, plant height and 100-seed weight in the combined analysis of variance for four years and four locations in

Oklahoma from 1991 through 1994. Genotypes were inconsistent in their performance for all the characters when tested across locations and years. Because of the significant second order interactions further analyses were performed to evaluate genotypic performance at each location (Oklahoma) over years.

The top-yielding significance group of genotypes at Bixby were Hartwig, OK 885409, HSC 591 and Hutcheson. Hartwig was the only genotype in the top group in all four years. At Haskell the top-yielding significance group of genotypes included Hutcheson, OK 885409 and Manokin. The same three genotypes were in the top group in all the years. At Chickasha the first seven genotypes were in the top-yielding significance group over four years, none of these seven genotype were in the top group consistently over the four years. However, Bay and Manokin were in the top group in 1992, 1993, 1994 and OK 885409, Walters and Hutcheson were in the top group in 1991, 1993 and 1994. At Goodwell nine genotypes were in the top-yielding group. CX 458 was the only genotype in the top group in all the four years.

OK 885409 was in the top-yielding group in 1991, 1992 and 1994 at Bixby, in 1991, 1993 and 1994 at Chickasha, in all four years at Haskell. It might be appropriate to conclude that OK 885409 will perform well at all these locations. The genotypes which performed well at Bixby, Haskell and Chickasha did not perform well at Goodwell. Perhaps it might be due to late maturing genotypes (mostly Group V) which yielded high at Bixby, Haskell and Chickasha, but low at Goodwell. Conversely, the early maturing genotypes (mostly Group IV) yielded best at Goodwell.

A significant GL interaction was observed for seed yield in the combined ANOVA when all eight locations (in Pakistan and the USA) were studied in 1994. The significant interaction indicated that the genotypes yielded differently across locations. All the location combination (16 location combinations in all) were analyzed. Only two (Haskell-Mansehra and Chickasha-Mansehra) combinations showed nonsignificant GL interactions. Genotypes at these locations may perform in a similar manner.

A combined regression analysis proposed by Eberhart and Russell (16) was conducted to test the significance of the GE interactions for seed yield, 100-seed weight and plant height. Genotype, environment, and GE interactions were significant in each analysis. The GE interaction was partitioned into heterogeneity and residual mean squares. Since the residual mean square alone was significant for seed yield, we could not explain the GE interaction completely by linear regression. There were some genotypes in the group whose performance was unpredictable. To identify which genotypes were causing this instability, individual genotype residual mean squares were tested against the pooled error.

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, with 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. A significant GE interaction was observed for 100-seed weight and plant height in the combined regression analysis. The GE interaction was partitioned into heterogeneity and residual mean squares, as both of them were significant when tested against pooled error. Heterogeneity mean squares were then tested against pooled deviation, which also came out to be significant. Therefore the linear regression can explain most of the interaction.

Both stability parameters, b value and residual mean square of individual genotypes, were tested against the pooled error to identify the performance of genotypes over all the environments.

HSC 401 had a nonsignificant residual mean square for 100-seed weight, with regression coefficient close to one and mean 100-seed weight equal to the grand mean. This genotype should be considered stable over all environments and less responsive to favorable growing conditions.

HSC 401, Hutcheson and Walters showed nonsignificant residual mean squares for plant height. HSC 401 and Walters with b value of 1.1 and 1.22 would be considered more desirable genotypes in favorable environments. Hutcheson with a b value of 0.8 should be relatively better adapted in less favorable environments.

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Table 1. Analysis of variances over four years (1991-94), four locations (Oklahoma) and fifteen genotypes for seed yield (kg/ha).

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	24.9	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 $\alpha = 0.01$

Table 2. Mean seed yield (kg/ha) of soybean genotypes at Bixby from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Hartwig	3409	3424	2562	4080	3369 a
OK 885409	3534	3617	1572	4219	3236 ab
HSC 591	3807	3398	2026	3599	3208 ab
Hutcheson	3798	2574	2402	3917	3173 abc
Manokin	3236	3258	2169	3634	3074 bc
OK 885420	3333	3144	1967	3723	3042 bc
Bay	3483	3250	1877	3498	3027 bc
Walters	3791	3179	1650	3448	3017 bc
Forrest	3750	2818	2071	3120	2940 cd
Stafford	2899	3082	1879	3186	2762 d
Crawford	2294	2941	1472	3201	2477 e
CX 458	1945	2953	1020	3786	2426 e
HSC 401	2231	2830	1547	2935	2386 e
Douglas	2003	2641	1059	3771	2369 e
Sparks	2288	2579	1011	3113	2248 e
LSD 0.05	544	527	486	591	239
CV%	10.69	10.37	16.62	9.99	10.35

Means with the same letter are not significantly different.

Table 3. Mean seed yield (kg/ha) of soybean genotypes at Haskell from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Hutcheson	2492	3437	2163	3641	2933 a
OK 885409	2417	3414	2008	3161	2750 ab
Manokin	2321	3142	2155	3368	2746 ab
HSC 591	2469	3388	2202	2727	2697 b
Forrest	2607	3225	2163	2767	2690 b
Hartwig	2296	3389	2108	2778	2643 b
OK 885420	2111	3451	2011	2862	2609 bc
Stafford	2196	3125	1824	2972	2529 bcd
Bay	2300	3256	1872	2674	2526 bcd
Walters	2319	2691	2219	2313	2385 cde
Crawford	1800	3230	1765	2663	2365 de
HSC 401	2072	3109	1519	2706	2352 de
Douglas	1934	2880	1549	3004	2342 de
CX 458	1630	3142	1275	3026	2269 e
Sparks	1610	2996	1519	2700	2206 e
LSD 0.05	254	682	358	505	232
CV%	7.00	12.81	11.36	10.47	11.3

Means with the same letter are not significantly different.

Table 4. Mean seed yield (kg/ha) of soybean genotypes at Chickasha from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
OK 885409	2292	2593	3193	3549	2907 a
Bay	1950	3268	2713	3478	2852 ab
Manokin	1646	3211	2726	3735	2829 abc
OK 885420	1608	2619	3036	3743	2751 abcd
Walters	2196	2495	3024	2976	2673 abcd
Stafford	1468	2353	3286	3583	2671 abcd
Hutcheson	2047	2349	2821	3353	2642 abcde
Hartwig	2009	2470	2560	3200	2560 bcdef
CX 458	1204	2125	3408	3467	2551 cdef
HSC 591	2045	1939	2984	3057	2506 def
HSC 401	1256	2315	2821	3032	2356 efg
Sparks	1226	2247	2880	2831	2296 fg
Forrest	1022	2078	3057	2911	2267 fg
Crawford	1038	2237	2768	2614	2164 gh
Douglas	625	2095	2546	2489	1939 h
LSD 0.05	282	547	714	824	294
CV%	10.72	13.53	14.66	15.43	14.36

Means with the same letter are not significantly different.

Table 5. Mean seed yield (kg/ha) of soybean genotypes at Goodwell from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
CX 458	3405	3674	2973	3018	3268 a
HSC 401	3890	3777	2237	2959	3215 ab
Douglas	3599	3543	2067	3389	3149 ab
Stafford	3381	3086	1999	3000	2867 abc
Sparks	3478	3322	2075	2460	2834 abc
Crawford	3406	3183	2332	2403	2831 abc
OK 885409	2706	3596	2653	1292	2561 abcd
Manokin	2705	3003	2004	2207	2480 abcde
Hutcheson	3140	2985	2579	1086	2448 abcde
Bay	2536	3266	2443	1195	2360 bcdef
OK 885420	2633	3016	1964	1166	2195 cdef
Hartwig	2740	2559	2231	1088	2154 cdef
Walters	2053	2104	1750	1025	1733 def
HSC 591	1595	2646	1582	771	1649 ef
Forrest	1392	2437	1612	800	1560 f
LSD 0.05	486	654	429	467	868
CV %	10.26	12.73	11.86	15.08	41.9

Means with the same letter are not significantly different.

Table 6. Analysis of variance for seed yield (kg/ha) at eight locations (USA and Pakistan) and fifteen genotypes in 1994.

Source	df	SS	MS	F Value	Pr > F	
LOC	7	143498516	20499788	13.25	0.0001	**
REP (LOC)	16	12422844	776428	1.21	0.2617	
GENO	14	13482110	963008	0.68	0.7872	
GENO*LOC	98	138463719	1412895	2.2	0.0001	**
ERROR	224	143776558	641860			

** denotes significance at $\alpha = 0.01$

Table 7. Analysis of variance for seed yield (kg/h) at Haskell and Mansehra in 1994.

Source	DF	SS	MS	F Value	Pr > F
LOC	1	574401.11	574401.11	9.46	0.0856
REP(LOC)	4	148469.38	37117.34	0.35	0.8432
GENO	14	3876725.29	276908.95	2.13	0.0842
GENO*LOC	14	1816539.56	129752.83	1.22	0.286
ERROR	56	5944774.62	106156.69		

** denotes significance at $\alpha = 0.01$

Table 8. Analysis of variance for seed yield (kg/h) at Chickasha and Mansehra in 1994.

Source	DF	SS	MS	F Value	Pr > F
LOC	1	4970250	4970250	14.48	0.0119
REP(LOC)	4	1074897.87	268724.47	1.57	0.1951
GENO	14	4438403.73	317028.84	1.29	0.3197
GENO*LOC	14	3438610.67	245615.05	1.43	0.1682
ERROR	56	9587246.1	171200.8		

** denotes significance at $\alpha = 0.01$

Table 9. Mean seed yield (kg/ha) of soybean genotypes at Haskell, Chickasha, Mansehra, Haskell-Mansehraand Chickasha-Mansehra combinations.

GENOTYPES	Haskell	Chickasha	Mansehra	Haskell Mansehra	Chickasha Mansehra
Hutcheson	3641 a	3353 abc	2800 ab	3221 a	3077 abcd
Manokin	3368 ab	3735 a	2868 ab	3118 ab	3302 a
Stafford	2972 bc	3583 ab	3023 a	2998 abc	3303 a
CX 458	3026 bc	3467 ab	2946 a	2986 abc	3206 ab
Douglas	3004 bc	2489 d	2785 ab	2895 abc	2637 d
OK 885409	3161 abc	3549 ab	2621 ab	2891 abc	3085 abcd
HSC 401	2706 cd	3032 abcd	2832 ab	2769 bc	2932 abcd
Bay	2674 cd	3478 ab	2859 ab	2766 bc	3168 ab
HSC 591	2727 cd	3057 abcd	2726 ab	2727 c	2892 abcd
Sparks	2700 cd	2831 bcd	2736 ab	2718 cd	2783 bcd
Forrest	2767 cd	2911 bcd	2660 ab	2713 cd	2785 bcd
Crawford	2663 cd	2614 cd	2743 ab	2703 cd	2679 cd
OK 885420	2862 c	3743 a	2512 ab	2687 cd	3128 abc
Hartwig	2778 cd	3200 abcd	2475 ab	2627 cd	2837 abcd
Walters	2313	2976 abcd	2381 b	2347 d	2679 cd
LSD 0.05	505	824	557	377	479
CV%	10.47	14.66	12.22	11.59	13.95

Means with the same letter within the same column are not significantly different.

Table 10. Mean seed yield (kg/ha) of soybean genotypes at three Pakistani locations in 1994.

GENOTYPES	Malakandher	Tarnab	Swat
HSC 591	3567 a	3107 a	3458 a
Hartwig	2721 b	2463 bc	2753 fg
Forrest	2574 bc	2519 b	2411 i
OK 885409	2463 bc	2482 bc	2546 ghi
Walters	2169 bc	2096 bcd	3317 ab
Manokin	1986 cd	2059 bcde	2804 ef
Hutcheson	1544 de	1949 cdef	3101 cd
OK 885420	1471 de	1838 def	2149 j
Bay	1287 ef	1691 defg	3129 bcd
CX 458	993 efg	1508 efg	3284 abc
Sparks	772 fgh	1397 fg	2690 fgh
Crawford	735 fgh	1453 fg	3475 a
HSC 401	662 gh	1434 fg	3192 bcd
Stafford	588 gh	1269 g	3015 de
Douglas	257 h	1140 g	2481 hi
LSD 0.05	597	563	214

Means with the same letter within the same column are not significantly different.

Table 11. Combined regression analysis of variance for seed yield (kg/ha) over four years (1991-94), at 20 locations (USA and Pakistan).

Source	df	MS	F
ENV	19	16499041	18.85 **
GENO	14	1586099	1.81 **
ENV x GENO	266	875343	2.75 **
HETEROGENEITY	14	473963	1.41
RESIDUAL	252	897642	2.82 **
ERROR	600	317943	

** denotes significance at $\alpha = 0.01$

Table 12. Estimates of mean ($\bar{x}$), regression coefficient (b) and residual mean squares for seed yield (kg/ha), over four years (1991-94) at 20 Locations (USA and Pakistan).

Genotypes	($\bar{x}$)	b	Res. M.S.	F
Bay	2601	1.09	106554	0.34 NS
Crawford	2387	1.12	166979	0.53 NS
Cx 458	2539	1.28	329112	1.04 NS
Douglas	2279	1.22	438049	1.38 NS
Forrest	2400	0.76	357557	1.12 NS
HSC 401	2468	1.09	289794	0.91 NS
HSC 591	2655	0.67	522011	1.64 *
Hartwig	2666	0.76	193442	0.61 NS
Hutcheson	2673	1.04	149453	0.47 NS
Manokin	2712	0.9	66436	0.21 NS
OK 885409	2796	1.02	154184	0.49 NS
OK 885420	2517	0.71	788892	2.48 **
Sparks	2297	1.12	161357	0.51 NS
Stafford	2561	1.13	192511	0.61 NS
Walters	2410	0.76	242800	0.76 NS
Error			317943	

Table 13. Analysis of variances over four years (1991-94), four locations (Oklahoma) and fifteen genotypes for 100-seed weight (gm).

Source	df	SS	MS	F Value	Pr > F
YEAR	3	110.01	36.67	0.83	0.5041
LOC	3	296.38	98.79	2.01	0.1624
YEAR*LOC	9	365.07	40.56	9.26	0.0001 **
REP (YEAR*LOC)	32	30.67	0.96	1.21	0.2027
GENO	14	2487.31	177.67	10.98	0.0001 **
GENO*YEAR	42	535.87	12.76	1.81	0.0062 **
GENO*LOC	42	320.414	7.63	3.03	0.0001 **
GENO*LOC*YEAR	126	530.68	4.21	5.32	0.0001 **
ERROR	448	354.67	0.792		

** denotes significance at $\alpha = 0.01$

Table 14. 100-seed weight (gm) of soybean genotypes at Bixby from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Crawford	19	20	17	19	19 a
Douglas	20	20	16	21	19 a
Sparks	19	19	13	21	18 b
OK 885420	19	17	15	19	18 b
Bay	17	19	18	19	18 b
CX 458	16	18	13	20	17 c
HSC 401	17	17	14	17	16 d
Manokin	16	16	13	14	15 e
Stafford	15	15	14	14	15 e
Hutcheson	13	16	14	17	15 e
Forrest	13	14	13	14	14 f
HSC 591	15	13	13	14	14 f
Hartwig	12	16	11	15	14 f
Walters	15	14	13	14	14 f
OK 885409	12	13	11	13	12 g
LSD 0.05	1.4	1.3	1.3	1.2	0.7
CV%	5.39	4.7	5.59	5.52	5.18

Means with the same letter are not significantly different.

Table 15. Mean 100-seed weight (gm) of soybean genotypes at Haskell from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Douglas	19	19	18	22	20 a
Crawford	19	18	21	19	19 b
Sparks	18	19	17	21	19 b
Bay	21	17	20	18	19 b
OK 885420	19	17	17	17	18 c
HSC 401	17	16	17	18	17 d
CX 458	16	17	14	19	17 d
Hutcheson	17	16	15	16	16 e
Stafford	16	13	14	15	15 f
Manokin	16	15	15	15	15 f
Walters	16	13	13	13	14 g
Hartwig	14	14	13	15	14 g
Forrest	15	13	13	14	14 g
HSC 591	14	12	13	14	13 h
OK 885409	13	12	13	13	13 h
LSD 0.05	1.1	1.1	1.5	1.6	0.7
CV%	3.79	4.44	5.59	5.72	5.03

Means with the same letter are not significantly different.

Table 16. Mean 100-seed weight (gm) of soybean genotypes at Chickasha from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Bay	20	20	19	20	20 a
OK 885420	17	16	16	17	17 b
Douglas	13	18	18	18	17 b
Crawford	13	16	17	18	16 c
Sparks	12	15	17	20	16 c
Hutcheson	17	14	16	18	16 c
CX 458	12	14	15	17	15 d
Forrest	15	12	13	15	14 e
HSC 401	13	13	15	16	14 e
HSC 591	15	11	13	15	14 e
Hartwig	14	12	13	15	14 e
Walters	15	12	13	15	14 e
Manokin	15	12	14	15	14 e
OK 885409	13	13	12	13	13 f
Stafford	12	11	15	15	13 f
LSD 0.05	1.4	1.4	1.3	1.3	0.6
CV%	5.95	6.15	5.23	5.49	5.3

Means with the same letter are not significantly different.

Table 17. Mean 100-seed weight (gm) of soybean genotypes at Goodwell from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
Douglas	17	18	17	18	18 a
Crawford	18	17	19	16	18 a
Sparks	17	18	16	17	17 b
HSC 401	17	16	18	14	16 c
CX 458	17	16	17	15	16 c
Bay	14	17	13	15	15 d
Forrest	13	13	15	14	14 e
Hartwig	15	13	13	14	14 e
OK 885409	14	11	16	14	14 e
Manokin	14	13	16	10	13 f
OK 885420	13	14	13	11	13 f
Walters	13	12	13	13	13 f
Hutcheson	13	14	11	13	13 f
HSC 591	12	11	12	12	12 g
Stafford	12	12	14	11	12 g
LSD 0.05	2.6	1.4	1.3	1.5	0.9
CV%	10.71	5.78	5.31	6.42	7.68

Means with the same letter are not significantly different.

Table 18. Combined regression analysis of variance for 100-seed weight (gm) over four years (1991-94), at 20 locations (USA and Pakistan).

Source	df	MS	F	
ENV	19	94.32	13.30	**
GENO	14	178.65	25.21	**
ENV x GENO	266	7.09	6.10	**
HETEROGENEITY	14	10.02	8.64	**
RESIDUAL	252	6.93	5.97	**
ERROR	600	1.16		

** denotes significance at $\alpha = 0.01$

Table 19. Estimates of mean $(\bar{x})$, regression coefficient (b) and residual mean squares for 100-seed weight (gm), over four years (1991-94), at 20 locations (USA and Pakistan).

Genotypes	$(\bar{x})$	b	Res. M.S.	F
Bay	18	0.43	4.24	3.66 **
Crawford	18	0.76	2.23	1.92 **
Cx 458	16	0.8	2.57	2.22 **
Douglas	18	0.88	2.38	2.05 **
Forrest	14	0.47	1.47	1.27 NS
HSC 401	16	0.97	1.12	0.97 NS
HSC 591	14	0.94	1.48	1.28 NS
Hartwig	14	1.12	1.94	1.67 *
Hutcheson	16	1.27	3.32	2.86 **
Manokin	15	1.43	2.09	1.80 **
OK 885409	14	0.74	2.19	1.89 **
OK 885420	16	1.05	3.27	2.82 **
Sparks	18	1.08	3.09	2.66 **
Stafford	14	1.33	0.99	0.85 NS
Walters	14	0.75	1.05	0.91 NS
Error			1.16	

Table 20. Analysis of variances over four years (1991-94) , three locations (Oklahoma) and fifteen genotypes for plant height (inches).

Source	df	SS	MS	F Value	Pr > F
YEAR	3	9345.16	3115.05	15.74	0.0026 **
LOC	2	790.33	395.16	1.92	0.2194
YEAR*LOC	6	1160.41	193.41	5.69	0.0001 **
REP (YEAR*LOC)	24	66.81	2.78	0.69	0.8648
GENO	14	7675.21	548.23	10.48	0.0001 **
GENO*YEAR	42	1669.67	39.82	1.13	0.3159
GENO*LOC	28	1339.01	47.82	1.37	0.1451
GENO*LOC*YEAR	84	2962.25	35.26	8.71	0.0001 **
ERROR	336	1361.87	4.05		

** denotes significance at $\alpha = 0.01$

Table 21. Mean plant height (inches) of soybean genotypes at Bixby from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
HSC 401	37	37	28	45	37 a
Crawford	36	29	29	47	35 b
HSC 591	34	36	24	39	33 c
Sparks	37	22	23	45	32 d
Bay	20	29	24	39	28 e
Douglas	27	27	19	39	28 e
Hartwig	21	35	21	36	28 e
OK 885420	29	24	20	39	28 e
CX 458	26	27	21	34	27 ef
Stafford	29	28	18	35	27 ef
Walters	20	27	22	36	26 f
Manokin	29	19	19	30	24 g
Forrest	17	27	18	33	24 g
OK 885409	12	27	17	32	22 h
Hutcheson	12	23	18	27	20 i
LSD 0.05	2.6	2.4	2.2	2.2	1.2
CV%	5.96	5.17	6.08	6.53	5.37

Means with the same letter are not significantly different.

Table 22. Mean plant height (inches) of soybean genotypes at Haskell from 1991 through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
HSC 591	33	36	26	39	34 a
HSC 401	30	39	28	39	34 a
Sparks	24	39	26	39	32 b
Bay	31	29	26	42	32 b
Hartwig	26	35	25	37	31 bc
Crawford	28	36	25	34	31 bc
Forrest	31	24	27	39	30 cd
Walters	25	28	24	38	29 de
Douglas	21	31	24	35	28 ef
Stafford	25	30	26	30	28 ef
CX 458	24	28	21	34	27 fg
OK 885420	22	24	23	36	26 gh
OK 885409	23	28	18	31	25 hi
Hutcheson	22	24	20	32	25 hi
Manokin	26	21	23	27	24 ij
LSD 0.05	3.3	4.3	3.3	3.1	1.8
CV%	7.66	8.65	7.66	6.59	7.62

Means with the same letter are not significantly different.

Table 23. Mean plant height (inches) of soybean genotypes at Chickasha from 1991through 1994.

GENOTYPES	1991	1992	1993	1994	AVERAGE
HSC 591	34	44	32	45	39 a
Crawford	35	39	34	45	38 ab
HSC 401	36	35	35	40	37 bc
Sparks	33	36	30	41	35 d
Forrest	34	34	33	36	34 de
Hartwig	33	33	24	34	31 f
CX 458	28	29	27	35	30 fg
Walters	31	29	26	34	30 fg
OK 885420	30	27	24	34	29 gh
Douglas	30	27	26	31	29 gh
Bay	33	24	23	33	28 hi
OK 885409	29	33	22	25	27 ij
Manokin	33	26	19	30	27 ij
Stafford	29	29	23	27	27 ij
Hutcheson	25	22	19	25	23 k
LSD 0.05	3.7	4.6	3.6	4.3	1.8
CV%	6.97	8.9	8.21	7.31	7.28

Means with the same letters are not significantly differently.

Table 24. Combined regression analysis of variance for plant height (inches) over four years (1991-94), at 16 locations (USA and Pakistan).

Source	df	MS	F
ENV	15	1941.33	30.92 **
GENO	14	630.01	10.03 **
ENV x GENO	210	62.79	10.08 **
HETEROGENEITY	14	143.6	23.05 **
RESIDUAL	196	57.02	9.15 **
ERROR	480	6.23	

** denotes significance at $\alpha = 0.01$

Table 25. Estimates of mean ($\bar{x}$), regression coefficient (b) and residual mean squares for plant height (inches), over four years (1991-94) at 20 locations (USA and Pakistan).

Genotypes	($\bar{x}$)	b	Res. M.S.	F
Bay	29	0.9	21.05	3.38 **
Crawford	35	0.98	15.65	2.51 **
Cx 458	30	1.26	32.07	5.15 **
Douglas	29	0.6	12.45	2.01 **
Forrest	31	1.28	25.97	4.17 **
HSC 401	37	1.1	7.2	1.16 NS
HSC 591	34	0.55	31.25	5.02 **
Hartwig	30	0.92	16.79	2.71 **
Hutcheson	24	0.8	9.64	1.55 NS
Manokin	26	0.61	11.77	1.89 **
OK 885409	25	0.84	17.91	2.87 **
OK 885420	30	1.47	11.16	1.79 **
Sparks	33	1.04	22.21	3.57 **
Stafford	30	1.19	20.95	3.36 **
Walters	30	1.22	8.46	1.35 NS
Error			6.23	

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VITA

Fazle Subhan

Candidate for the Degree of

Doctor of Philosophy

Thesis: GENOTYPE BY ENVIRONMENT INTERACTION IN SOYBEANS GROWN IN DIVERSE LOCATIONS IN OKLAHOMA (USA) AND IN NORTH WEST FRONTIER PROVINCE (PAKISTAN)

Major Field: Crop Science

Biographical:

Personal Data: Born in Dir, NWFP, Pakistan, June 7, 1962, the son of Fazli Hanan and Mehmooda Begum; married Farida Khatoon on June 1, 1990; and father of two children, Faiza and Hinnah.

Education: Graduated from Pakistan Air Force Shaheen High School, Peshawar, Pakistan, in 1978; received Fellow of Science Degree from Fedral Government Degree College at Peshawar, in 1980; received Bachelor of Science with Honors in Agronomy from NWFP Agricultural University Peshawar in 1985; received Master of Science with Honors in Agronomy from NWFP Agricultural University Peshawar in 1987; completed requirements for the Doctor of Philosophy Degree at Oklahoma State University in December, 1996.

Professional Experience: Served as Agricultural Credit Officer in Habib Bank Limited at Karachi, Quetta, Loralai and Turbat from July 1986 to February 1987; Research Officer at Cereal Crops Research Institute Pirsabak, Nowshera, Pakistan, July 1987 to May 1991.

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