THESIS

MICHIGAN STATE UNIVERSITY LIBRARIES
3 1293 01055 0220

This is to certify that the

dissertation entitled

EFFECTS OF DENSE PUBESCENCE ON

QUANTITATIVE TRAITS IN SOYBEAN

presented by

Ram Pratap Sah

has been accepted towards fulfillment
of the requirements for

Ph.D. degree in Plant Breeding & Genetics

James D. Kelly

Major professor
Dr. James D. Kelly

Date February 27, 1992

MSU is an Affirmative Action/Equal Opportunity Institution

O-12771

LIBRARY
Michigan State
University

PLACE IN RETURN BOX to remove this checkout from your record.
TO AVOID FINES return on or before date due.

DATE DUE	DATE DUE	DATE DUE

MSU is An Affirmative Action/Equal Opportunity Institution
c:\circ\datedue.pm3-p.1

EFFECTS OF DENSE PUBESCENCE ON QUANTITATIVE TRAITS IN SOYBEAN

By

Ram Pratap Sah

A DISSERTATION

Submitted to
Michigan State University
in partial fulfillment of the requirements
for the degree of

DOCTOR OF PHILOSOPHY

Department of Crop and Soil Sciences
(Plant Breeding and Genetics Program)

1992

615 1364

ABSTRACT

EFFECTS OF DENSE PUBESCENCE ON QUANTITATIVE TRAITS IN SOYBEAN

By

Ram Pratap Sah

Pubescence density in soybean has previously been found to affect plant vigor and resistance to insects and drought. There is inadequate information on how they affect quantitative traits and their genetic variance. The objective of this research was to study the effect of dense pubescence on the quantitative traits of economic importance, their genetic variance, heritability, and correlation coefficients, and to discuss implications of findings to soybean breeding.

Wells II with normal pubescence and Harosoy with dense pubescence were crossed and progenies for normal and dense pubescence types were developed in a nested design, and were evaluated for two years in F_6 and F_7 generations at two locations in Michigan. The genotypic differences were significant for all traits. Trait means were affected by pubescence density, year, location and their interactions. Pubescence density affected all traits except seed size and protein. The interaction effect of year x location x pubescence density revealed that effects of pubescence density were not persistent for most traits except height. Pubescence density did not exhibit main effects on any trait, but interaction effects were present with all traits indicating situations where pubescence density could be useful in breeding.

In general, the variances due to pubescence density and its interactions were low compared with additive and additive x additive variances for all the traits except height. Pubescence density did not influence heritability. Heritability estimates were high for maturity, height and lodging (>0.50); moderate for seed size and protein (0.35-0.49); and low for yield and oil (0.24-0.34). The correlation coefficients were affected by year, location, pubescence density and their interactions. Certain correlations, like yield with seed size and protein; maturity with height and lodging; and height with lodging were strongly positive and stable across factors. Protein and oil exhibited a strong negative correlation. Stepwise regression was used to select variables for predicting yield, protein and oil. The implications of these findings to soybean breeding for quantitative traits are discussed.

DEDICATED TO
MY GRANDMOTHER

ACKNOWLEDGMENTS

I wish to express my sincere thanks and gratitude to my major professor, Dr. James D. Kelly for his encouragement, advice and help. To my other committee members, Drs. Dale D. Harpstead, Charles Cress and Amy Iezzoni, I extend my obligation and appreciation for their valuable comments and critiques. Also, I feel indebted to Dr. Thomas G. Isleib, my former major professor, who initiated and guided this research. I appreciate his help on analytical procedures even after he moved to N.C. State University.

I am obliged to the National Agricultural Research Council (NARC) and to ARPP/USAID, Nepal for providing the opportunity and financial support to accomplish this study. Financial support received from the Department of Crop and Soil Sciences, Michigan State University, is also acknowledged.

To all the friends in soybean and drybean programs of this Department, I offer my appreciation for their help. I thank Ms Betsy Bricker for her advice in final document printing. I take this opportunity to thank Mr. Bharat P. Upadhyay and his family for providing friendship and support in joys and agonies. Last but not least, I am thankful to my wife, Shanti, and to my sons, Shashi, Sanjeev and Sujeet, who have always been very inspiring and supportive.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

ARPP	- Agricultural Research and Production Project.
AVRDC	- Asian Vegetable Research and Development Center.
FAO	- Food and Agriculture Organization.
IITA	- International Institute of Tropical Agriculture.
IRRI	- International Rice Research Institute.
INTSOY	- International Soybean Program.
NGLIP	- National Grain Legume Improvement Program.
USAID	- United States Agency for International Development.

INTRODUCTION

Soybean (*Glycine max* L. Merr.) is an important legume as a source of human food, animal feed, and materials for many industrial uses. As a source of protein and oil, it complements the contribution of most cereal crops. Currently, the crop is grown on 58.2 million hectares with a production of 107.3 million tons worldwide (FAO, 1989). The major producing countries are the USA, Brazil, China and Argentina accounting for nearly 87 % of the world's production. However, the importance of this crop as a rich source of protein and oil, and role in soil improvement through nitrogen-fixation has recently been recognized in developing countries including Nepal, where its area and production are considerably increasing. Although soybean has been a traditional crop in Nepal, its commercial cultivation is recently being realised with the development of new high yielding varieties, production technologies and processing industries (NGLIP, 1988).

Soybean is considered to have originated in China, where this has been cultivated for over 4,500 years (Probst and Judd, 1973) with its introduction into the USA in the 1800's. It was only after early 1900's, that the importance of this crop as a rich source of protein and oil was recognized. Concerted efforts have been made since 1960's towards the improvement of this crop worldwide (Caldwell,1973). The USA is the leading soybean producer contributing about 41.2 and 48.8 percent to the world's area and production respectively. Michigan is one of the important soybean producing states in the USA with an area of 0.44 million hectares and a production of 1.05 million tons (Agri. Stat., USDA,1990).

Considerable progress has been made in the past toward the genetic improvement of soybean for increased yield and other agronomic traits. Currently, in addition to the national programs, several international centers, INTSOY, IITA, IRRI and AVRDC have a mandate to further improve soybean for yield, protein, oil, and other agronomic traits in addition to resistance to major pest, diseases and stress factors. The significance of

germplasm in crop improvement as a source of elite genes is great. The USDA maintains nearly 10,000 accessions of the world soybean germplasm which represents extensive genetic diversity for the various morphological, physiological and isozyme characters (Palmer and Kilen, 1987). One of the characteristic features of varieties grown in the US is rather a dense covering of the erect hairs or the trichomes on the stem, leaf, calyx, and pod (Carlson,1973). An individual trichome has a diameter of about 20-40 μm and a length of about 0.5 -3.0 mm. However, considerable genetic variation in trichome size, form, density, durability, and color occurs in the exotic germplasm (Bernard and Weiss, 1973). Many of the pubescence variants have been genetically characterized, and most are controlled by single dominant or recessive gene (Bernard, 1975; Bernard and Weiss, 1973). Bernard and Singh (1969) reported the existence of five independent genes controlling the different pubescence types in soybeans. Pubescence density has been found to increase plant vigor, reduce damage from insect (*Empoasca spp.*), and reduce transpiration rate, providing this crop with better adaptation particularly under drought (Hartung et al., 1980). Cooper and Waranyuwat (1985) observed that densely pubescent indeterminate plants exhibited increased lodging. A differential response of the *Pd*-gene (dense pubescence) in the determinate and indeterminate genotypes has been observed, with an yield decrease in the later. However, densely pubescent genotypes tend to yield slightly higher than those with normal pubescence (Hartwig and Edwards,1970; Singh et al., 1971).

Most of the traits of economic importance in soybean are quantitative in nature and exhibit continuous variation. Currently used breeding methods for manipulating the quantitative traits have their origin or rationale in quantitative genetics. The development of a more efficient breeding procedure is dependent upon a better understanding of the types of genetic variance and gene action underlying the inheritance of the quantitative traits. Johnson and Bernard (1963) reported that only additive component of genetic variance has so far been exploited in soybean breeding for the quantitative traits such as yield.

Information on the various types of gene action and their relative importance in the inheritance of traits of interest have been obtained in only a few populations of soybeans (Brim, 1973). Hanson et al.(1967) observed additive x additive epistasis for seed yield, maturity and percent seed mottling accounting for more than 50% of the total genetic variance. Significant dominance variance has also been reported for economic traits such as plant height, seed weight, and lodging (Crossiant and Torrie,1971). Since quantitative traits are controlled by a large number of loci, linkage effects may become important in interpreting these variances (Gates et al., 1960).

A clear understanding of the nature of gene action controlling quantitative traits is crucial for the effective breeding of soybean. Also, the type and magnitude of gene action are greatly influenced by the nature of the population, character studied, sample size chosen, and the genetic models and analysis procedures used. Though additive variance is the primary component for the genetic variance of quantitative traits in soybean, evidence of non-additive variance for certain traits indicate the need for modification of the breeding procedure for manipulation of such traits (Brim, 1973). Heterosis or inbreeding depression may not adequately reflect non-additive gene action for self-fertilizing species since dominance and epistasis deviations may be both positive and negative and will tend to cancel out when averaged over loci. Many practical decisions in breeding program are based on the magnitude of heritable variation. Estimates of heritability and their role in predicting gains from selection have been done extensively in soybeans (Johnson and Bernard, 1963). Most of these estimates are broad-sense heritability, which include dominance and epistatic components of genetic variance. Since these components are not fixed in the self-pollinated crops like soybeans, such estimates may not be very useful in predicting gains from selection. However, heritability in narrow sense(h^2) is more important to the breeder because effectiveness of selection depends on the additive portion of the variance in relation to the total variance (Falconer, 1960).

Correlation and regression estimates are also important to the breeders for use in indirect selection , particularly when heritability of the economic traits is lower compared to the associated traits. The correlated response studied to date do not appear to provide useful selection criteria for increased yield. The results are inconsistent from cross to cross, and over environments (Brim,1973). It appears that the usefulness of correlated responses in selection for yield will depend on recognizing attributes other than those usually measured and which are more closely related to physiological processes associated with productivity (Brim,1973).

A knowledge of kind and amount of variability affecting important agronomic traits is essential for a successful breeding program (Croissant and Torrie, 1971). The isolation of single genetic factors affecting quantitative traits is of great interest to plant breeders as they can easily manipulated through breeding (Powell et al., 1985). Though there are some reports exhibiting the effects of pubescence on quantitative traits in soybean, there is inadequate information available to date on how dense pubescence affects genetic components of variance of quantitative traits like yield, maturity, height, lodging, seed size, protein and oil in soybeans; and how it (pubescence) affects correlation and heritability estimates. Therefore, a more reliable information on these is essential to drawing valid inferences and planning an effective breeding procedure for soybeans. Also, these are crucial to the understanding of the underlying genetic phenomenon, used to design an effective breeding program incorporating dense pubescence as a desirable trait for the improvement of the quantitative traits like yield, maturity, height, lodging, seed size, protein and oil in soybean. Breeding for the quantitative traits is difficult and time taking because of their polygenic inheritance. If the effects of pubescence density on these traits are significant, it can be used for indirect selection in breeding for these quantitative traits.

Research Objectives :

1. To study the effects of dense pubescence on quantitative traits such as grain yield, maturity, plant height, lodging, seed size, protein, and oil.
2. To estimate the genetic components of variance (additive, dominance, additive x additive) for these quantitative traits under the different genetic models.
3. To estimate genotype x environment interactions affecting the components of genetic variances.
4. To estimate narrow-sense and broad-sense heritability of these quantitative traits, and gain from selection.
5. To determine correlation and regression coefficients of the quantitative traits under study.
6. To discuss the significance of the findings in relation to breeding for quantitative traits in soybean.

2 LITERATURE REVIEW

2.1 Morphology of Pubescence

Considerable variation exists among soybean genotypes with respect to size, shape, durability, and distribution of plant hairs or trichomes. Singh et al. (1971) studied the morphology of five different pubescent types: normal, dense, sparse, curly, and glabrous; and their effects on the agronomic traits in soybean. They developed near isogenic lines through backcrossing in 'Harosoy' and 'Clark' for the different pubescent types. They found that hairs of normal, dense and sparse types were morphologically similar, each consisting of a very long (1-3 mm) cylindrical cell with one, two or three basal cells. Hairs of curly pubescence were similar to normal type initially, but then became flat, curled and tended to fall off. Glabrous plants had a hair stub made up of 1-7 nearly isometric cells. Puberulent plant hairs consisted of a single elongate (0.1 mm) apical cell with 1-3 basal cells. They found significant difference for number of hairs in different pubescence types. Normal and curly had 6-8 hairs /mm^2 , sparse 2-3 hairs/mm^2, while dense had 30-31 hairs/ mm^2. These number of hairs were also highly positively correlated with leafhopper resistance. In addition, they found that dense pubescent plants grew tallest followed in descending order by normal, sparse, curly, and glabrous plants. Grain yields of lines with normal, dense, and sparse pubescence were similar, and superior to the curly and glabrous lines. However, they did not find much difference for seed weight, protein and oil composition of the seeds due to pubescence, except that the extreme damage to the glabrous lines caused a reduction in seed size, and an increase in seed protein in some environments.

Wolley (1964) found that hairs on the upper surface of mature 'Hawkeye' soybean leaves were about 1 mm in length, and spaced about 1 mm apart, accounting for 10% of the total leaf surface. Each hair consists of a long distal cell, 0.5-1.5 mm in length, which is

surrounded by a cushion of epidermal cells. The hairs are slanted slightly towards the tip and edge of the leaflet. Mature hairs dry out and become air filled or flattened (Dzikowski, 1937). In addition to these elongated uniceriate trichomes, small five-celled club shaped trichomes are abundant on all young organs. These trichomes persists, but gradually senesce in the mature leaves.

Franceschi and Giaquinta (1983) reported that the cuticle over the distal two cells becomes distended, indicating that a secretory product accumulates beneath it. They speculated from ultrastructural evidence that a volatile terpenoid compound is secreted which helps to protect the developing leaflets against foraging insects.

2.2 Inheritance of Pubescence

2.2.1 Pubescence Types

Several workers have reported inheritance of pubescence in soybean. Nagai and Saito (1923) reported a single gene difference between glabrous (*P*-) and pubescent (*pp*) plants, with glabrous being dominant. They also gave evidence for a linkage of *'Pp'* (Pubescence gene) and *'Mm'* loci with 18% cross-over measured on a large population. *'M'* was a gene for black stripes (mottling) on a brown or buff seed coat, and the allelic *'m'* produced self brown or buff.

Owen (1927) also reported a single gene control of pubescence, with glabrous being dominant. He used a glabrous mutant and a Japanese glabrous variety, crossed with a pubescent type, and found that the inheritance was the same in both. He reported a linkage of P_1p_1 with *Rr* (black vs brown seed coat) in both the crosses, and suggested that both glabrous lines carried the same gene for glabrousness. Woodworth and Veatch (1929) obtained a glabrous mutant from Wentz (1926) and a dominant glabrous Japanese variety from W.J. Morse of the USDA, and crossed them. The F_1 was glabrous, the F_2 segregated 13 glabrous : 3 pubescent plants, and the F_3 segregation supported the

hypothesis of two unlinked gene pairs P_1p_1 and P_2p_2.. Due to the apparent but very short pubescence of the p_2 plants they were designated 'puberulent' type. Another distinct pubescence type has been reported among Japanese varieties. Takahashi and Fukuyama (1919) described that in addition to glabrous variety, two other varieties had hairs which flattened, curled, and eventually fell off. However, they reported no genetic work with this trait.

Piper and Morse (1923) observed segregation for amount of pubescence in a cross between a pubescent and a nearly smooth Japanese variety. Johnson and Hollowell (1953) called this type "appressed hairy" in a report on insect damage study with 27 introductions of this type, and 7 glabrous ones. William (1950) reported that appressed pubescence types was found in several introductions from Japan and Korea. He found that the F_2's between appressed and normal pubescence types were all intermediate, and that the F_3's gave a 1:2:1 ratio for appressed: intermediate : normal types. Kawahara (1963) studied F_2 populations from crosses of a glabrous variety 'Mizukuguri' with pubescent varieties, *'Odate-1'* and 'Tansentanryoku' and found that a single dominant gene produced glabrousness, presumably the P_1 of the earlier workers. He also reported a gene pair *'Wewe'* for strongly shiny versus weakly shiny leaves. However, since *'We'* was 100% linked to P_1, this apparent leaf shine was probably due to the absence of pubescence, and therefore, explainable by P_1 .

Bernard and Singh (1969) studied the inheritance of pubescence in great detail. They crossed normal type with glabrous (P_1) , curly (*Pc*), dense (*Pd*), sparse (*Ps*), and puberulent (P_2), and studied the F_2 and F_3 data. They found that each of these five pubescence types differed from the normal by a single gene pair. The normal was dominant to puberulent, but recessive to glabrous, dense and sparse, and intermediate with curly pubescence. Four of these types (P_1, *Pc, Pd, Ps*) occur in varieties from eastern Asia, and the fifth (P_2) originated as a mutant found in Iowa in 1924. They also studied linkage and

allelism among P_1, *Pc,Pd,* and *Ps* by crossing their isogenic lines in 'Clark' and 'Harosoy' genetic backgrounds with a puberulent line(T-31). The F_2 results showed that the genes P_1, *Pc, Pd,* and *Ps* are separate, unlinked or not closely linked loci. The F_2 data of the crosses combining T-31 with the 'Harosoy' isogenic lines, each carrying one of the four other pubescence genes, also showed that P_2 was also a distinct unlinked locus. They observed that glabrous (P_1) appeared to be epistatic to the other types, although *Pd* and *Ps* affected the density of the hair stubs visible on close inspection of the glabrous plants. The genes *pc* and p_2 and *pc* affect the form of hairs independently of the density effects of *Pd* and *Ps*. *Pd* and *Ps* interact with each other in an additive fashion in controlling hair density. They crossed T- 145 (glabrous , P_1 *r*) and Clark (normal p_1R) and studied the F_2 ratio to estimate the linkage of these two loci. The F_2 data gave a maximum likelihood estimate of 0.20.+/- 0.46 crossing over between P_1- and *R*- loci, which does not deviate significantly from the 0.18 estimate of Nagai and Saito (1923), ie, the two loci are linked.

2.2.2 Pubescence Color

Tawny (brown) and gray pubescence colors are equally frequent among the most plant introductions and cultivars of soybean in the USA. Woodworth (1921) reported that pubescence color is controlled by a single gene pair, with tawny *(T)* being dominant over gray *(t)*. He also observed that this gene interact with *Ii* (light/dark hilum), W_1w_1 (purple/white flower), and *Rr* (black/brown seed coat) genes to give a new hilum color. Their interaction with the allele *'T'* produces only gray or black pigments in the seed, while *'t'* produces imperfect black or buff pigment.

Genetic combination	Pigmentation in seed
I_R_T_w_1w_1	Gray
I_R_tt w_1w_1	Buff
ii R_T_W_1_	Black
ii R_tt W_1_	Imperfect black
ii R_T_w_1 w_1	Black
ii R_tt w_1w_1	Buff
ii rr T-	Brown
ii rr tt	Buff

In tawny pubescent genotypes, the trichomes on the young plants are colorless, but after several weeks of growth, the trichomes on the stems, pods, and leaves develop brown pigments (Palmer and Kilen, 1987). This pigment is retained in the plant and facilitates classification of tawny and gray pubescent genotypes. Among gray pubescent genotypes, most trichomes are without brown pigment, giving a distinct phenotype to the plants. The *'T'* allele has a major effect on the production or regulation of an enzyme necessary for the formation of quercetin from kaempherol. Cultivars with *'T'* allele have free quercetin (the aglycone) in the pubescence and those with *'t'* have free kaempherol (Buttery and Buzzell, 1973). Bernard (1975) described another major gene pair affecting pubescence color. The alleles *'Td'* produces dark-tawny, and *'td'* light tawny in presence of *'T'* allele. In contrast to *'T'* allele, which affects the hilum color in seed and flavonol glycosides, *'Td'* affects only pubescence color. In presence of *'tdtd'*, there is no or markedly less flavonol in the pubescence (Buttery and Buzzell, 1973).

2.3 Effects of Pubescence on Insects Resistance

Pubescence density in soybean has been found to affect insects resistance. Poos (1929) reported that among 15 species of Homoptera, only *Empoasca fabae* could cause injury to soybean, and that the extent of injury was related to the amount and kind of hairs present. Glabrous cultivars were injured much more than the pubescent ones. Poos and Smith (1931) reported that a glabrous soybean variety showed a greater infestation and oviposition of leafhoppers (*Empoasca fabae*) than the pubescent varieties. A number of introduced soybean varieties were studied at Arlington, Virginia, by Johnson and Hollowell (1935), where they found severe potato leafhopper infestation and damage to the glabrous types. The damage were less in curly types, while the normal pubescent varieties were undamaged or slightly infested. They also studied the F_3, F_4, and F_5 generations from a cross between pubescent and glabrous soybeans and observed that glabrous plants were damaged by leafhopper. Genetic linkage between P_1 (glabrous) and genes for leafhopper susceptibility was ruled out since no cross-over types were detected in a large population. However, Morse and Carter (1937) reported that Japanese investigators have found glabrous soybeans to be highly resistant to soybean pod-borer (*Laspeyresia glycinivorella Mats.*), while pubescent types are highly susceptible. Both insects are present in Japan, but only leafhoppers in the USA.

Wolfenbarger and Sleesman (1963) obtained seeds of several pubescent types from the USA soybean laboratory and studied their reaction to leafhopper at two sites in Ohio. They observed that dense and normal lines had high resistance to leafhopper, sparse had only low resistance, while the glabrous and curly types showed severe stunting and hopper burn. Hartwig and Edwards (1970) reported that seed yield of the glabrous type was significantly lower than the normal types in three of the six years of testing. In those years, glabrous lines had higher leafhopper damage. They also found that curly lines had lower leafhopper resistance than the normal ones.

Singh et al. (1971) studied the effect of near isogenic lines of the pubescent types in 'Harosoy' and 'Clark' genetic backgrounds to compare leafhopper injury. They found that the trend was similar in both, but differed considerably with the pubescent types. Dense pubescent types showed significantly the lowest hopper number followed by normal and sparse which did not differ significantly. The hopper numbers were highest in curly and glabrous, but they did not differ significantly among themselves. Broersma et al. (1972) developed isogenic lines of pubescent types into 'Clark' and 'Wayne' backgrounds and studied their effects on leafhopper injury. They found that the orientation of hairs was more important than the number of hairs for resistance. Glabrous lines had more damage than others. They believed that orientation and perhaps the size and other hair characteristics were significant factors in determining leafhopper resistance. Also, they observed that glabrous strains had significant increase in yield, number of pods/node, pods/main stem, and weight of 100 seeds when the leafhoppers were controlled with an insecticide.

2.4 Effects of pubescence on Agronomic Traits

Pubescence type and density have been found to affect plant vigor, insect resistance, agronomic and physiological traits. Hartwig and Edwards (1970) measured the effects of several morphological traits on seed yield in soybeans by transferring each of the trait into a common background through backcrossing. The only traits that influenced yield were indeterminate growth and glabrousness. The lower yield of indeterminate types was considered due to lodging and that of glabrous types was due to increased damage by the potato leafhoppers. The seed yield of the glabrous type was significantly lower than the normal isogenic line particularly in the year when leafhopper damage was severe. However, yield differences were not significant in the isogenic lines of curly-normal or dense-normal. The pubescence color had no effect on yield.

Singh et al. (1971) studied the effect of different pubescence types on different agronomic traits under different environments. They developed near isogenic lines of normal, dense, sparse, curly, and glabrous pubescence types in 'Harosoy' and 'Clark' genetic backgrounds. Effects were found to be similar in both the genetic backgrounds. Dense pubescent plants grew tallest, followed in descending order by normal, sparse, curly, and glabrous. Yields of lines with normal, dense and sparse pubescence were similar, and superior to curly and glabrous lines. In 'Clark' background, dense lines yielded significantly lower than normal , which may be due to lodging of dense lines during the grain filling stage. The maturity didn't differ among the pubescence types in 'Clark' background, while in 'Harosoy', glabrous was significantly later than other types. The difference was not significant among normal, dense, sparse, and curly types. The traits, 100 seed weight, and percent protein and oil in seed were not affected by the pubescence types . They indicated that the growth differences possibly reflect the action of genes closely linked with the pubescence genes, or they might result from pleiotropic effects of the pubescence genes themselves.

Broersma et al. (1972) studied the effects of pubescence types in 'Harosoy' and 'Clark' backgrounds on leafhopper incidence and yield. They found that glabrous and curly types had significantly higher hopper number and generally lower yields than other types. However, when leafhopper incidence was only in the early stage, glabrous and curly types regained growth , and the yields were identical to the other types. Also, they studied the effects of leafhopper control with an insecticide, dimethiate in 'Harosoy' background. They found that yield, number of pods/node, and 100 seed weight increased significantly in the glabrous lines when insects were controlled. However, there were no significant difference among curly and normal lines for these traits. Hartung et al. (1980) studied the effect of various alleles including those for pubescence types in 'Clark' and 'Harosoy' backgrounds. They found that the *Pd* (dense pubescence) allele had no

significant effect on yield averaged over cultivars. However, there was a significant yield increase in 'Harosoy', but it decreased nonsignificantly in 'Clark' with a decrease in pubescence density. The *Pd* allele resulted in more vigorous plants, that were significantly taller, more prone to lodging, and later in maturity. The increase in yield of 'Harosoy', but decrease in 'Clark' indicated a significant *Pd* allele x genotype interaction. Based on their observation, a synergistic effect of *Pd* and *t* (gray pubescence) was present. Sparse (*Ps*) had no effect on yield , but significantly reduced plant height and seed weight. The allele causes a loss in vigor perhaps of the opposite effects of reduced pubescence as described for *Pd*. Semi-sparse (Ps^s) allele, however, significantly reduced yields, hastened maturity, and deceased plant height. The complementary recessive alleles *pa1* and *pa2* (appressed pubescence) slightly increased yields. However, the influence of the genetic background was evident, since they significantly increased yields in 'Clark', and decreased yields in 'Harosoy'. Maturity was also hastened, plant height was decreased slightly, lodging was increased, and seed quality improved. Again these overall effects arose as a result of the major effect of these alleles in 'Harosoy' and negligible effects in 'Clark'. Apparently, the effects of *pa1pa2* gene in the 'Harosoy' genetic background is not clear.

Cooper and Waranyuwat (1985) studied the effects of three genes *Pd* (dense pubescence), Rps_1 (Phytophthora root rot resistance), and *ln* (narrow leaflet) in near isogenic lines of 'Harosoy' and 'Clark'. In all these comparisons, the addition of the *Pd* gene to the indeterminate isolines resulted in a significant increase in plant height and lodging, and a significant decrease in yield. In absence of lodging, the height of the determinate isolines was significantly increased in two of the three comparisons, and the yield was either increased (Harosoy) or the difference was not significant(Clark). This differential response of the *Pd* gene in determinate and indeterminate isolines strongly supports the hypothesis that failure to obtain a significant yield increase, or in this case,

getting a yield decrease by addition of the *Pd* gene to the indeterminate isolines was mainly due the increased lodging.

Specht et al. (1985) reported that pubescence morphology could be altered by the various qualitative genes, and that such alteration might improve adaptation to unique production environment. They evaluated near isogenic lines of 'Clark' and 'Harosoy', which possessed genes singly or in combination for pubescence morphology'(*pa1, pa2, Pb, Pc,* Pd_1, Pd_2, *Ps* , and P_1) for their agronomic performance. They found that *pa1pa2* (appressed pubescence) consistently increased seed yield in 'Clark' genetic background , but not in 'Harosoy'. The Pd_1 allele (dense) had little effect on seed yield in 'Harosoy', but reduced yield in 'Clark'. All other alleles were either deleterious or neutral in their effects on yield. Only Pd_1 and Pd_2 alleles resulted in greater plant height; while the other alleles had either no effect or reduced plant height. Thus the Pd_1, Pd_2, *pa1* and *pa2* alleles may thus offer an adaptive advantage in cultivars for certain production environments.

The morphological change which affects the environment of leaf and may benefit crop productivity is increased leaf pubescence. Gausman and Cardenas (1973) found that leaf pubescence on detached soybean leaves decreased the reflectance of near infrared radiation , but had no effect on the reflectance of photosynthetically active radiation. The resultant effect of additional leaf pubescence has been reported to be a reduction in transpiration (Woolley,1964; Ghorashy et al.,1971; Ehleringer and Mooney, 1978) by reducing the radiation load on leaf. Ghorashy et al. (1971) studied the effect of leaf pubescence on transpiration, photosynthesis, and seed yield of three near isogenic lines of soybeans, and found that photosynthetic rates and yields were not affected significantly by pubescence types (normal, dense, glabrous). The transpiration rates of normal and glabrous lines were the same, and were significantly higher than the dense type. The isolines differed in vegetative characteristics, shoot weight, root weight, leaf area and plant height, which may have influenced transpiration rate. According to Waggoner (1966), leaf

hair should reduce diffusion of water more than CO_2, since the boundary layer resistance constitutes a greater proportion of total resistance to water vapor diffusion than to CO_2 diffusion. These findings suggests that water use might be reduced without reducing photosynthetic rate or yield of soybean by increasing pubescence.

Baldocchi et al. (1983) studied the effect of leaf pubescence on mass and energy exchange between soybean canopies and atmosphere. They found that additional pubescence in an isoline of 'Harosoy' decreased latent heat flux (LE) and increased sensible heat flux from the crop. The net radiation (Rn), turbulent mixing, and CO_2 exchange over normal and dense lines were similar. No differences were found in internal plant water potential or stomatal resistance. They suggested that differential partitioning of Rn by isolines was due to differential penetration of solar radiation into the canopies- -more solar radiation penetrated into the Hypersoy dense pubescence (HPD) canopy. The CO_2 water flux ratio (CWFR) was greater in the HPD isoline since additional pubescence reduced LE. This observation suggests that increasing pubescence density improves water use efficiency.

2.5 Variance Components

A number of agronomic traits in crop plants are influenced by genes at many loci, causing a variation in the segregating generation to be continuous or quantitative in nature. When quantitative factors are involved, linkage may affect the inheritance of a trait. Knowledge of type and amount of gene action, and degree of linkage influencing the quantitatively inherited traits is important to plant breeders in selecting a suitable breeding procedure. Most of the currently used breeding methods for manipulating metric traits have their origin or rationale in quantitative genetics. The development of a more efficient breeding procedure for quantitative traits is dependent upon a better understanding of the nature of gene action underlying the inheritance of the quantitative traits (Burton,1987). In

soybean, hereditary variance has been partitioned through experiments using materials generated by nested (hierarchic) or diallel designs. Relationship among these progenies are equated with components of variance and covariance among generations. This permits Least Square estimation of genotypic variance into additive, dominance, epistasis and linkage effects. The magnitude of genetic variance component is unique to the population from which the components are obtained. These variance components are influenced by degree of dominance and allele frequency (Falconer, 1981).

Gates et al. (1960) reported linkage of genes controlling quantitative traits in soybean. They found that linkage was significant for flowering time, height, and yield, but not for maturity, period from flowering to maturity, seed weight, percent oil, and lodging. Linkage in components related in form to additive variances was found in all these characters, while linkage in components related in form to dominance variance was demonstrated only for plant height. Repulsion linkages predominated for height and yield, while coupling linkages predominated for flowering time. Brim and Cockerham (1961) reported that additive component of variance was significant for all the characters studied. Dominance effect was too little as was expected for the self-fertilizing species. However, there was considerable amount of additive x additive epistasis. Cockerham (1963) found a significant dominance variance for seed size and plant height. However, Hanson et al. (1967) reported a considerable additive x additive epistasis for seed yield, maturity, and percent seed coat mottling, accounting for more than 50% of the total genetic variance.

Croissant and Torrie (1971) reported evidence of non-additive effects and linkage in two hybrid populations of soybeans. They studied F_4, F_5, F_6, and F_7 generations in the first year, and their respective F_5, F_6, F_7, and F_8 generations in the second year. Their nested design allowed an estimation of genotypic variance and covariance. Based on multiple and partial regression analysis, they found that additive genetic variance was the major component of the genotypic variance for all the character studied. However, they

also found dominance variance for plant height, seed weight, and lodging, but there were relatively small. Linkage components appeared to be important for days to flowering, plant height, seed weight, and lodging. Brim(1973) mentioned that additive variance is the primary component of the genotypic variance for the traits of economic importance in soybeans. Dominance and epistasis may be present with positive and negative signs, which will tend to cancel out when averaged over loci. However, hybrid vigor and inbreeding depression have been observed in soybeans, indicating that it may be worthwhile to look for heterozygous gene combinations. When additive x additive effects are important, early generation testing may not be an appropriate selection approach, since an opportunity must be provided for unique gene combinations to come together.

Cockerham (1983) modified the procedures for interpreting the covariances of self-fertilizing relatives by using several identity by descent measures in addition to the inbreeding coefficient (F). This has permitted the development of genetic models with additive and dominance effects that are general for all gene frequencies. VandeLogt et al. (1984) studied the components of genetic variance and the effects of linkage for the quantitative traits in barley. They studied F_4, F_5, F_6, and F_7 generations from two crosses in the first year, and their F_5, F_6, F_7, and F_8 generations in the second year. Least Square analysis was used to calculate additive, dominance and linkage effects. Additive genetic variance was important for all the traits in both the crosses. However, dominance variance was also present for heading date, kernel brightness, test weight, and grain yield, but the estimates of dominance variance may have been inflated by linkage effects. There was coupling phase linkage for grain yield in both the crosses, and for heading date in one. The results indicated that breeding procedures which keep linked blocks of favorable genes intact should be utilized in crosses among adapted barley genotypes. Powell et al. (1985) reported the effect of two major genes, *'denso'*(dwarfing) and a locus determining *'daylength'* gene on quantitative traits in barley. They developed

inbred lines with and without these traits (isolines) and found that the contribution of these loci to the estimates of additive genetic variance decreased in following rounds of recombinations(selfing). This demonstrated that in these cases the association between major genes and quantitative characters was due to linkage disequilibria.

2.6 Heterosis

While additive variance is the primary component of hereditary variance, non-additive types of genetic effects can contribute significantly to the variation in some traits of soybean populations (Brim,1973). Though several workers reported heterosis for yield in soybean , it is quite difficult to produce large scale F_1 seed in practice. Brim and Cockerham (1961) evaluated F_1's from two crosses and estimated means of F_2 to F_5 generations. The F_1's were significantly greater than the high parent for yield, height, and total weight in one cross, and for yield only in the other cross. Heterosis above high parent averaged 20% percent. Inbreeding depression was neither very consistent nor very great for the advanced generations.

Weber et al. (1970) measured heterotic response in a large number of crosses (3-24 plants/cross). Seed yield of F_1 hybrids averaged 13.4% greater than the high parent of the cross. More than 75% of the hybrids exceeded the high parent of the respective cross. Likewise, Hillsman and Carter (1981) found a 12.9% and 6.2% heterosis for yield over the midparent and high parent respectively. Nelson and Bernard (1984) studied 37 F_1's over two years and locations in a replicated test and observed a 7.9% and 3.3% heterosis for yield over the mid parent and high parent respectively. Evidence clearly shows that given the proper genetic combinations, high parent heterosis occurs. However, it is not yet clear how much of this is due to dominance, and how much due to dominance x dominance , dominance x additive or due to additive x additive epistasis.

2.7 Heritability

In soybean breeding, most of the heritability estimates are made by evaluating a set of lines in one or more environments, and then from analysis of variance, genotypic and phenotypic variances are estimated and used to calculate the heritability (Johnson et al., 1955). Two other methods involve single plant evaluation are:

i) Estimation of genotypic variance in a single environment by subtraction of non-segregating generations(parent or F_1) from segregating generations F_2 , F_3 etc.(Powers,1955).

i) Parent-offspring regression (Falconer,1960): single plant based on means of progeny.

Yet another type of estimate is the realized heritability, which is a narrow sense estimate based on the ratio of selection response to selection differential.

Byth and Caldwell (1969) studied the heritability of yield, maturity, lodging, seed size, protein, oil, phenotypic score, and early lodging in F_6 and F_7 generations in three different environments. They concluded that heritability was relatively consistent across environments for all the traits except for yield. For yield, it was highest under favorable growth conditions and lowest in poor environments (drought). Brim (1973) presented a representative sample of heritability estimates from eight populations, and for nine quantitative traits that are commonly measured in soybean breeding populations. Heritability was the lowest (0.03-0.58) for seed yield, and relatively higher for other traits. These estimates were in close agreement as suggested by Johnson and Bernard(1963). Shannon et al.(1972) estimated heritability for yield, percent protein, and protein yield in six populations of F_3 lines from crosses between high and low protein lines. The heritabilities for percent protein were higher than those for yield. Protein yield and seed yield heritabilities were similar. Predicted progress as a percentage of population mean from selecting the highest 10% of each population (k=1.76) ranged from 3.3 - 4.7% for

percent protein, 0.0 - 10.7% for yield, and 0.0 - 10.7% for protein yield. Shorter et al. (1976) found heritability for percent protein to be 0.70 and 0.86 for protein yield 0.55 and 0.72, and for percent oil 0.84 and 0.83 respectively in two populations of soybeans.

In two recurrent selection experiments, Brim and Burton (1979) calculated realized heritability estimates for percent protein of 0.29 and 0.34 over six cycles of selections, and response per cycle of selection was 0.7 and 1.6% respectively of the base population mean. In a recurrent mass selection experiment Burton and Brim (1981) estimated realized heritability for percent oil to be 0.21. Openshaw and Hadley (1984) estimated heritability in two populations in F_3 or F_4 generations. They also found a similar result, with heritabilities of percent protein 0.90 to 0.75, percent oil 0.93 to 0.73, and of yield 0.78 to 0.68 respectively in the two populations. In addition, heritability estimates have been done for a variety of other traits by several workers (Brim, 1973). Most of these estimates are broad-sense heritabilities (H), which may have some degree of dominance , and additive x dominance and / or dominance x dominance interaction components in the genetic component of variance. In self-pollinated crops like soybean, these non-additive components of variances are not fixable, and thus the heritability estimates based on genotypic variance are not very predictable.

Kelly and Bliss (1975) estimated heritabilities of percent seed protein and available methionine in drybean, and found that the broad-sense heritability ranged from 0.32-0.71 for percent protein, 0.43--0.56 for percent available methionine, and 0.38-0.60 for available methionine as percent of protein. However, narrow-sense heritability calculated by the standard unit regression analysis of F_3 and F_4 family means on F_2 and F_3 parental values ranged from 0.63-0.79 , 0.82-0.89, and 0.82- 0.85 in the F_3 generation; and from 0.32-0.61, 0.52-0.87, 0.51-0.81 in the F_4 generation for the above three traits respectively. This clearly indicates that the components non-additive genetic variance decreases in later generations on selfing. Yiran et al.(1990) calculated the components of

genetic variance and heritability in the Davis population of gerbera. They found that the estimates of narrow sense heritability for flowering time was 0.5 while that of broad-sense was 0.77. Estimates of component of variance indicated that the major genetic effects controlling flowering time is additive. However, the dominance component accounted for 28% of the total variance, and the environmental component was 23 percent.

Anderson et al.(1991) reported the heritability and early generation selection response for resistance to early and late leaf spot in peanut. Selection based on F_2 family means in the F_3 generation via defoliation, infection and sporulation was performed for early and late leaf spot. They calculated broad-sense, narrow-sense, and realized heritabilities in the two populations for early and late leaf spot disease for lesion number, infection rating and defoliation. The estimates were significantly different from one to another type. In most cases realized estimates were higher than narrow sense heritability obtained via parent-offspring regression, and in most cases were comparable or higher than broad-sense estimates. This also indicates the presence of non-additive components of genetic variance causing higher estimates of heritabilities when calculated on broad-sense.

2.8 Correlation Among Traits

Correlated variation of two characters may be due to the similar genetic causes or due to similar response to environmental influence (Brim, 1973). The two components of correlated response may be separated statistically. If genetic correlations are high, attempts to obtain a response in one character by selecting for an associated character may be worthwhile. This is especially true , when a character of high economic importance has low heritability compared with the associated character. Soybean breeders have utilized correlated response to some degree in selection procedure.

Johnson and Bernard (1963) reported genotypic correlations of a few traits with yield. Yield had a correlation coefficient of 0.4 with maturity, followed in decreasing

order by plant height (0.3), seed weight (0.2), percent protein seed(0.2), oil (0.1), and exhibited no correlation lodging & days to flower. Anand and Torrie (1963), and Kwon and Torrie (1964) obtained genotypic and phenotypic correlations of these traits with yield. Their results showed that increased plant height, late maturity, and high lodging were positively correlated with yield both genotypically and phenotypically. On the other hand, Byth et al. (1969) found that short plant height and resistance to lodging were associated with yield in crosses involving indeterminate types. They also found that the association of yield and maturity varied with the environments. However, the correlation coefficients of protein and oil with yield varied considerably from cross to cross. In general, correlation of protein and yield was better than oil and yield. The association of several morphological characters with yield was investigated by Hartwig and Edwards (1970). They transferred these characters into a common genetic background by backcrossing. Only two characters, indeterminate growth and glabrousness were associated with yield. Both affected yield adversely; the former was due to early season lodging, the latter was due to injury by the potato leafhopper(*Empoasca fabae* Harris).

Brim (1973) summarized phenotypic and genotypic correlations between yield and eight commonly measured traits in soybean. It is evident from the differences among the correlation coefficients from any particular pair of trait, that significance as well as direction of correlation depend upon the population in which the traits are measured. Simpson and Wilcox(1983) also studied phenotypic correlations of yield with other traits and reported that it was significant and positive with height, lodging and maturity in all the four populations they studied.

There has been interest in the study of correlations between yield and yield components traits, and between yield and physiological traits. Johnson et al. (1955) found that genetic correlations between yield and pod number were 0.28 and 0.14, and between yield and seed size were 0.66 and 0.43 respectively in the two populations they studied. In

a group of seven cultivars, Pandey and Torrie (1973) found average correlation of 0.5 between yield and pods per unit area, 0.35 between yield and number of seeds/pod, and 0.04 between yield and seed size. On the other hand, Ecochard and Ravelomanantsoa (1982) found a genetic correlation of 0.95 between pod number and total yield in a segregating population of spaced plants.

Buzzell and Buttery (1977) found correlations -0.44 and -0.19 between harvest index and yield in two populations, while Buttery et al.(1981) reported a positive relationship between photosynthetic rate per unit leaf area (PA) and yield when measured 40-50 days after planting. However, Ford et al. (1983) found no significant correlation between yield and photosynthesis (rate of CO_2 uptake per unit leaf area). The negative relationship between percent seed protein and percent seed oil is well established (Hanson et al., 1961; Shorter et al.,1976; Brim and Burton, 1979; Burton and Brim, 1981). Burton et al. (1982) have shown that percent protein in seed, and methionine content of protein are not correlated. However, Openshaw and Hadley (1981) found that the correlation between percent oil and percent sugar in the seed was positive and significant, and the correlation between percent protein and percent sugar was significant and negative. Also, the correlations between sugar content and yield were non-significant. In the selection experiment, increase in the oleic acid fraction of soybean oil led to a correlated decrease in the linoleic and linolenic acid fractions (Burton et al., 1983).

3 MATERIALS AND METHODS

3.1 Development of Experimental Material

Wells II, a soybean cultivar with normal pubescence (++) was crossed to L62-0801, a near isogenic variant of Harosoy with dense pubescence (*PdPd*). The parentage and characteristics of the two parents are given below:

Characteristics	Harosoy (*PdPd*)	Wells II(++)
Parentage	HSY #6/ T 207(*Pd*)	WLS #3/ ARK(RPSIC)
Maturity group	2	2
Growth habit	indeterminate	indeterminate
Flower color	pink	pink
Pod color	gray	gray
Pubescence	dense	normal
Pubescence color	gray	gray
Seed color	yellow	yellow
Hilum	yellow	intermediate

The cross was made in 1983 and the F_1's were grown in1984 to produce the F_2 seeds. The F_2's were grown in 1985 space planted, and plants with dense pubescence *(PdPd, Pd+)* were selected. Rows of selfed progenies of F_2 selected plants ($F_{2,3}$ families) were grown in 1986. The F_3 rows segregating for Pubescence (progeny of *Pd+*) were identified, and dense pubescence plants *(PdPd, Pd+)* were again selected from those rows ($F_{3,4}$). These F_3 , families were grown in 1987 and individual plants from the segregating families($F_{3,4}$) were threshed separately (*PdPD, Pd+*, ++ plants). These $F_{3,5}$ plant rows were grown in 1988 and families were classified as uniform dense pubescence (PdPd),

segregating for pubescence *(PdPd, Pd+, ++)*, and uniform normal pubescence(++). Uniform rows of dense and normal families were bulked separately. Fifteen F_2 dense plants were selected, and within each F_2 , two F_3 plants were selected, and within each F_3 one normal and one dense pubescence family were finally bulked Thus a total of 60 lines were generated (30 normal and 30 dense) in a hierarchical design (Figure 1). These 60 families can be classified as 15 F_2-derived, times 2 F_3 (F_2)- derived, times the 2-pubescence density within each F_3 progeny.

3.2 Field Evaluation

3.2.1 Experimental Design and Procedure

The experimental material consisted of 62 entries including 60 lines developed for pubescence, and the two parents Harosoy and Wells II. These lines were evaluated in 1989 and 1990 at East Lansing (Ingham) and Britton (Lenawee). In the first year, the pubescent lines were F_6 generation while in the second year they were F_7 generation. The experiments were conducted in Randomized Complete Block Design (RCBD) with two replications. Each plot consisted of two rows of 3.3 m length 51 cm apart. Seed rate was maintained at 33 per meter of row length. Seeding was done with a soybean planter.

The two sites E. Lansing and Britton differ considerably for soil types. Britton has a characteristic clay loam soil, while E. Lansing has loam to Capac loam soils. Fertilizers were applied @ 134 kg /ha NPK (0:0:60) at Britton and @ 179 kg /ha NPK (6:24:24) at E. Lansing. In order to control weeds herbicides Scancor @ 0.5 kg /ha + Dual @ 6.5 l /ha were pre-plant incorporated during tillage.

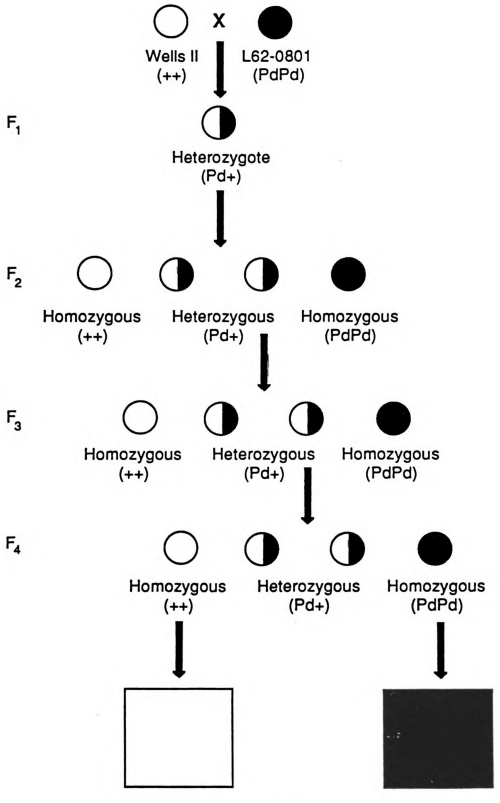

Figure 1. Development of family structure.

The experiments were planted and harvested on the following dates at each site:

Site	1989 planting	1989 harvesting	1990 planting	1990 harvesting
E. Lansing	May 24	Oct.18	May 23	Oct. 29
Britton	May 12	Oct. 9	May 11	Oct. 16

In the 1989 growing season, there was heavy rainfall in the late May and early June. However, little damage was done due to timely drainage of rain water out the field. The 1990 growing season was normal at both the sites. There were no major pest or disease problems except for a few Phytophthora affected plants in 1989 at E. Lansing in some of the entries. Bacterial pustules was common in most of the late maturing lines, but the incidence was very low without any significant effect on yield.

3.2.2 Data Recorded

Observations were taken for plant height, maturity, lodging, seed, yield, seed size, and percentage protein and oil in the seed for the individual plot. The description of measurements are as follows:

Plant height	Height of the randomly selected plants in centimeters measured from the ground level to the tip of the main stem.
Maturity	Number of days after August 31 to reach complete maturity of all he plants,indicated by senescence of leaves and drying of pods and stem.
Lodging	Recorded on a 1-4 scale, 1 = all plants complete erect at 90^0 angle

	2 = plants between $>60^0$ to $<90^0$ angles
	3 = plants between $>45^0$ to $<60^0$ angles
	4 = plants at $< 45^0$ angles or completely flat on the ground
Seed yield	Weight of cleaned beans adjusted to 14.5% moisture in ton /ha
Seed size	Weight in grams of randomly selected 100 seeds adjusted to 14.5% moisture
% Protein	Percent of protein in the seed using NMR (Nuclear magnetic rasonance) technique
% Oil	Percent of oil in the seed using NMR technique

3.3 Statistical Analysis

The data recorded over years and locations were used for various types of analysis to draw inferences about the materials, estimate components of variances, correlation among traits, regression coefficients , and heritability of the various traits under different models. Various SAS (1985) procedures were used to derive these information.

3.3.1 Means Comparison

SAS TTEST procedure was used to estimate mean, standard deviation, range, and variances for the various components like year, location, density, entry, and their interactions for the various characters studied. Also, this procedure provided estimates of 'T' to compare these statistics and drawing inferences about the populations. Proc Means procedure was also used to compute mean, range, variance, CV, of the data by entry, F_2, F_3 (F_2) , density, location, and their interactions.

3.3.2 Analysis of Variance

The analysis of variance was done using PROC ANOVA procedure of SAS, 1985. Two models were used to estimate the variance components.

3.3.2.1 General Model ANOVA

Here the total variance was partitioned into year (Y), location (L), Y x L, rep (YL), entry (E), Y x E, L x E, Y x L x E, and error. These estimates were used to calculate broad-sense heritability and Genetic advance as compared with the nested model.

Statistical Model:

$$Yijklm = u + Ai + Bj + (AB)ij + R(AB)ijk + Tl + (AT)il + (BT)jl + (ABT)ijl + Eijklm$$

Where, u = general mean

Ai = year effect (Y)

Bj = location effect (L)

$(AB)ij$ = Y x L effect

$R(AB)ijk$ = rep effect

Tl = treatment effect (T)

$(AT)il$ = effect of Y x T

$(BT)jl$ = effect of L x T

$(ABT)ijl$ = effect of Y x L x E

$Eijklm$ = Environmental or error effects

3.3.2.2 Nested Model ANOVA

Here the analysis of variance was performed in the nested design model, where the total variance was partitioned into the following variance components:

Y, L, R (Y xL), F_2, F_3 (F_2), Density (D), F_2xD, F_3 (F_2) x D, L x F_2, L x F_3 (F_2), L x D, Y x F_2, Y x F_3 (F_2), Y x D, Y xF_2 x D, Y x F_3 (F_2) x D, Y x L x F_2, Y x L x F 3 (F_2), Y x L x D, L x F_2 x D, L x F_3 (F_2) x D, Y xL x F_2 x D, Y x L x F 3 (F_2) x D, Error.

Where, Y = year, L = location, D = Pub. density, R = replication

F_2 = F_2 derived progenies, and F_3 (F_2) = F_3 derived progenies within the F_2.

3.3.2.3 Correction for F-test

The 'F' values produced by the SAS in both the models used only the final error mean square (MS) to estimate F values for each component line. Since each component line consists of many more items in addition to the error term (Table 1 & 2) in each model, the F-values produced by the SAS are not correct and need to be corrected. Based on the items included in each component line, the error term for each line was recalculated by addition and subtraction of MS of different lines in the Nested model (Table 3). Also, a corrected error degree of freedom (dfe) was calculated for each component line to test the significance of 'F' values. Approximate dfe was calculated using the following equation:

Example:

$$MSe = MS\ F_2 + MS\ LD - MS\ LF_2D$$

Where, MSe is the estimated error MS for a line to calculate the corrected F value.

MS on the right are the Mean Squares of respective line in the ANOVA

$$dfe = \frac{MSe^2}{\frac{MS\ F_2^2}{df\ F_2} + \frac{MS\ LD^2}{df\ LD} + \frac{MS\ LF_2D^2}{df\ LF_2D}}$$

Where, dfe = estimated error df for testing the significance of corrected F values.

Table 1. Expected mean squares(EMS) from General Model ANOVA

Source	df	EMS
1. Year(Y)	y-1	$\sigma^2 e + r\sigma^2 ylg + rg\,\sigma^2 yl + rgl\,\sigma^2 y$
2. Location(L)	l-1	$\sigma^2 e + r\sigma^2 ylg + rg\,\sigma^2 yl + rgy\sigma^2 l$
3. Y x L	(y-1)(l-1)	$\sigma^2 e + r\sigma^2 ylg + rg\,\sigma^2 yl$
4. Rep(YL)	yl(r-1)	$\sigma^2 e + \sigma^2 r(yl)$
5. Genotype(G)	g-1	$\sigma^2 e + r\sigma^2 ylg + ry\sigma^2 lg + rl\sigma^2 yg + ryl\sigma^2 g$
6. G x Y	(g-1)(y-1)	$\sigma^2 e + r\,\sigma^2 ylg + rl\sigma^2 yg$
7. G x L	(g-1)(l-1)	$\sigma^2 e + r\,\sigma^2 ylg + ry\sigma^2 lg$
8. G x Y x L	(g-1)(y-1)(l-1)	$\sigma^2 e + r\,\sigma^2 ylg$
9. Error	subtraction	$\sigma^2 e$

Table 2. Expected mean squares (EMS) from the Nested Model ANOVA.

# Source	df	EMS
1. Year(Y)	(y-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdf_3\sigma^2ylf_2 + rdlf_2\sigma^2yf_3 + rdlf_3\sigma^2yf_2 + df_2f_3\sigma^2r(yl) + rdf_2f_3\sigma^2yl + rdlf_2f_3\sigma^2y$
2. Location(L)	(l-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdf_3\sigma^2ylf_2 + rdyf_2\sigma^2lf_3 + rdyf_3\sigma^2lf_2 + df_2f_3\sigma^2r(yl) + rdf_2f_3\sigma^2yl + rdy_2f_3\sigma^2l$
3. Y x L	(y-1)(l-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdf_3\sigma^2ylf_2 + df_2f_3\sigma^2r(yl) + rdf_2f_3\sigma^2yl$
4. Rep(YL)	yl(r-1)	$\sigma^2e + df_2f_3\sigma^2r(yl)$
5. F_2	(f_2-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdf_3\sigma^2ylf_2 + rdlf_2\sigma^2yf_3 + rdlf_3\sigma^2yf_2 + rdyf_2\sigma^2lf_3 + rdyf_3\sigma^2lf_2 + rdyl\ f_2\sigma^2f_3 + rdyl\ f_3\sigma^2f_2$
6. $F_3(F_2)$	$f_2(f_3$-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdlf_2\sigma^2yf_3 + rdyf_2\sigma^2lf_3 + rdyl\ f_2\sigma^2f_3$
7. Pub Density(D)	(d-1)	$\sigma^2e + rf_2\sigma^2ylf_3d + rf_3\sigma^2ylf_2d + rf_2f_3\sigma^2yld + ryf_2\sigma^2lf_3d + ryf_3\sigma^2lf_2d + ryf_2f_3\sigma^2ld + rlf_2\sigma^2yf_3d + rlf_3\sigma^2yf_2d + rlf_2f_3\sigma^2yd + ryl\ f_2\sigma^2f_3d + ryl\ f_3\sigma^2f_2d + rlyf_2f_3\sigma^2d$
8. F_2 x D	(f_2-1)(d-1)	$\sigma^2e + rf_2\sigma^2ylf_3d + rf_3\sigma^2ylf_2d + ryf_2\sigma^2lf_3d + ryf_3\sigma^2lf_2d + rlf_2\sigma^2yf_3d + rlf_3\sigma^2yf_2d + ryl\ f_2\sigma^2f_3d + ryl\ f_3\sigma^2f_2d$
9. $F_3(F_2)$ x D	$f_2(f_3$-1)(d-1)	$\sigma^2e + rf_2\sigma^2ylf_3d + ryf_2\sigma^2lf_3d + rlf_2\sigma^2yf_3d + ryl\ f_2\sigma^2f_3d$
10. L x F_2	(l-1)(f_2-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdf_3\sigma^2ylf_2 + rdyf_2\sigma^2lf_3 + rdyf_3\sigma^2lf_2$
11. L x $F_3(F_2)$	(l-1)$f_2(f_3$-1)	$\sigma^2e + rdf_2\sigma^2ylf_3 + rdyf_2\sigma^2lf_3$
12. L xD	(l-1)(d-1)	$\sigma^2e + rf_2\sigma^2ylf_3d + rf_3\sigma^2ylf_2d + rf_2f_3\sigma^2yld + ryf_2\sigma^2lf_3d + ryf_3\sigma^2lf_2d + ryf_2f_3\sigma^2ld$

Table 2. Cont'd..

# Source	df	EMS
13. Y x F_2	$(y-1)(f_2-1)$	$\sigma^2 e + rdf_2\sigma^2 ylf_3 + rdf_3\,\sigma^2\, ylf_2 + rdlf_2\sigma^2\, yf_3 + rdlf_3\sigma^2 y\, f_2$
14. Y x $F_3(F_2)$	$(y-1)f_2(f_3-1)$	$\sigma^2 e + rdf_2\sigma^2 ylf_3 + rdlf_2\sigma^2\, yf_3$
15. Y x D	$(y-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rf_3\,\sigma^2\, ylf_2 d + rf_2f_3\,\sigma^2\, yld + rlf_2\sigma^2\, yf_3 d + rlf_3\sigma^2 y\, f_2 d + rlf_2f_3\,\sigma^2 yd$
16. Y x F_2 x D	$(y-1)(f_2-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rf_3\,\sigma^2\, ylf_2 d + rlf_2\sigma^2\, yf_3 d + rlf_3\sigma^2 y\, f_2 d$
17. Y x $F_3(F_2)$ x D	$(y-1)f_2(f_3-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rlf_2\sigma^2\, yf_3 d$
18. Y x L x F_2	$(y-1)(l-1)(f_2-1)$	$\sigma^2 e + rdf_2\sigma^2 ylf_3 + rdf_3\,\sigma^2\, ylf_2$
19. Y x L x $F_3(F_2)$	$(y-1)(l-1)(f_2-1)$	$\sigma^2 e + rdf_2\sigma^2 ylf_3$
20. Y x L x D	$(y-1)(l-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rf_3\,\sigma^2\, ylf_2 d + rf_2f_3\,\sigma^2 yld$
21. L x F_2 x D	$(l-1)(f_2-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rf_3\,\sigma^2\, ylf_2 d + ryf_2\sigma^2 lf_3 d + ryf_3\sigma^2 lf_2 d$
22. L x $F_3(F_2)$ x D	$(l-1)f_2(f_3-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + ryf_2\sigma^2 lf_3 d$
23. Y x L x F_2 x D	$(y-1)(l-1)(f_2-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d + rf_3\,\sigma^2\, ylf_2 d$
24. Yx L x $F_3(F_2)$x D	$(y-1)(l-1)f_2(f_3-1)(d-1)$	$\sigma^2 e + rf_2\sigma^2 ylf_3\, d$
25. Error	subtraction	$\sigma^2 e$

Table 3. Estimation of the Error MS (MSe) for the individual component line in the Nested Design Model.

#	Source	MS term used
1.	Year(Y)	13 +3 - 18
2.	Location(L)	10 + 3- 18
3.	Y x L	18 + 4 - 25
4.	Rep(YL)	25
5.	F_2	10 + 6 -11 + 13 - 14 - 18 + 19
6.	$F_3(F_2)$	11 + 14 -19
7.	Pub. Density(D)	8 + 15 - 16 + 12- 21 - 20 + 23
8.	F_2 x D	21 + 16 -23 + 9 -22 - 17 +24
9	$F_3(F_2)$ x D	22 + 17 - 24
10.	L x F_2	18 + 11 - 19
11.	L x $F_3(F_2)$	19
12.	L x D	20 + 21 - 23
13.	Y x F_2	14
14.	Y x $F_3(F_2)$	18
15.	Y x D	20 + 16 -23
16	Y x F_2 x D	23 + 17 -24
17.	Y x $F_3(F_2)$ x D	24
18.	Y x L x F_2	19
19.	Y x L x $F_3(F_2)$	25
20.	Y x L x D	23
21.	L x F_2 x D	22 + 23 -24
22.	L x $F_3(F_2)$ x D	25
23.	Y x L x F_2 x D	24
24	Y x $F_3(F_2)$ x D	25
25	Error	from Anova

From the corrected F tests in the two models, the effects of genotype, F_2,$F_3(F_2)$, Density, and their interactions with year and locations on the various quantitative traits were determined.

3.3.3 Estimation of Genetic Components of Variances

The nested design components of variances was used to estimate genetic components of variances (additive, dominance, additive x additive) following the procedure of Cockerham (1983). Because pubescence density is a factor crossed with the random effects of F_2 and F_3 -derived families, the effects of *Pd*-gene on genetic variance of the quantitative traits were calculated. Cockerham (1983) used covariance of relatives from self-fertilization and calculated coefficients of the quadratic components for the various covariances. He developed the following equations to calculate the coefficients for the genetic terms:

i) **F_g (inbreeding coefficient)** = $1- (1/2)^g$

It is the probability that the two alleles of 'g'(individual) are identical by descent.

ii) **θ_{tgg} (coancestory coefficient)** = $(1+ F_t)/2$

It is the probability that a random allele from g is identical by descent to a random allele from g'.

iii) **$\gamma_{tgg'}$ (three gene identity measure)** = $(F_g+ F_t)/2$

It is the probability that the two alleles of g and a random allele of g' are identical by descent.

iv) **$\Delta_{tgg'}$ (two gene pair identity)** = $F_t + [(F_g - F_t) (F_{g'} - F_t)]/ (1- F_t)$

It is the probability that two alleles of g and two alleles of g' are identical by descent.

v) **$\delta_{tgg'}$ (four gene probability)** = $F_t+ [(F_g - F_t) (F_{g'} - F_t)] / [2(1- F_t)]$

It is the probability that all the four alleles of g and g' are identical by descent.

vi) $\delta_{tg + g'} = [(1- F_g)(1- F_{g'})]/[2(1- F_t)]$

It is the probability that neither of the two alleles of g, nor g' are identical by descent, and a random one of two possible gene pairs between g and g' has both pairs identical by descent.

The genotypic variances can be partitioned into the following genetic terms:

$$Gijk = m + aij + aik + dijk$$

Where, *Gijk* = genotypic value for an individual with jth and kth allele at ith locus.

m = population mean

a's = additive effects of alleles

d's = dominance effects of alleles

Based on these, the covariance among relatives can be equated into the genetic terms (Cockerham,1983):

$$C_{tgg'} = 2\theta_{tgg'} s^2 A + 2\delta_{tg + g'} \sigma^2 D + 2(\gamma_{tgg'} + \gamma_{tgg'}) D_1 + \delta_{tgg'} D_2 + (\Delta_{tg.g'} - F_g F_{g'}) H$$

Where, $C_{tgg'}$ = Covariance of g and g'progenies both originating from t- th generation

$\sigma^2 A$ = Additive variance over loci

$\sigma^2 D$ = Dominance variance over loci

D_1 = covariance of a_j and d_{ji}

D_2 = Variance of $d_{ij's}$

H = Inbreeding depression over loci

With two alleles at each locus, $H = \sigma^2 D$, and with all gene frequencies being one-half, $D_1 = 0$, $D_2 = 0$.

When translated into formulas for the identity measures, the coefficients for the quadratic components of $C_{tgg'}$ are :

Component	Coefficient
$\sigma^2 A$	$1 + F_t$
$\sigma^2 D$	$\frac{(1+F_g)(1+F_{g'})}{1-F_t}$
D_1	$F_g + F_{g'} + 2F_t$
D_2	$\frac{F_t + (F_g - F_t)(F_{g'} - F_t)}{2(1-F_t)}$
H	$\frac{F_t(1-F_g)(1-F_{g'})}{1-F_t}$

Accordingly, Cockerham (1983) developed the coefficients of the quadratic components of various covariances(Table 4).

The test materials were developed in a nested (hierarchical) design with the common ancestors in F_2 and F_3 (F_2)- derived families. Nested designs are appropriate for self-fertilizing species. Initial estimates of nested design components of variance or covariance are linear functions of covariances of relatives. In 1989 the test materials were F_2 and F_3 (F_2) derived lines evaluated in F_6 , and in 1990 they were in F_7 generation. Accordingly, their respective covariances, F_t , F_g and coefficients of genetic variances were calculated. The coefficients for σ^2 F_2 and $\sigma^2 F_3$ (F_2) were calculated by averaging their respective genetic variances in F_6 and F_7 generations as follows:

Table 4. Coefficients for quadratic components for various covariances for the F_2 and F_3 derived lines in F_6 and F_7 generations.

tgg'	t	g	F_t	F_g	σ^2A	σ^2D	σ^2AA
044($F_{2,6}$)	0	4	0	15/16	1	1/256	1
144($F_{3,6}$)	1	4	1/2	15/16	3/2	3/256	9/4
055($F_{2,7}$)	0	5	0	31/32	1	1/1024	1
155($F_{3,7}$)	1	5	1/2	31/32	3/2	3/ 1024	9/4

Average σ^2F_2:

$$= [\sigma^2(F_{2,6}) + \sigma^2(F_{2,7})] / 2$$

$$= (\sigma^2A + 1/256\,\sigma^2D + \sigma^2AA \text{ in } F_6) + (\sigma^2A + 1/1024\sigma^2D + \sigma^2AA \text{ in } F_7) / 2$$

$$= \sigma^2A + 5/2048\,\sigma^2D + \sigma^2AA$$

Average σ^2F_3:

$$= [\sigma^2(F_{3,6}) + \sigma^2(F_{3,7})] / 2$$

$$= (3/2\,\sigma^2A + 3/256\,\sigma^2D + 9/4\,\sigma^2AA \text{ in } F_6) + (3/2\,\sigma^2A + 3/1024\,\sigma^2D + 9/4\,\sigma^2AA \text{ in } F_7) /2$$

$$= 3/2\,\sigma^2A + 15/2048\,\sigma^2D + 9/4\,\sigma^2AA$$

Average σ^2F_3 (F_2):

$$= [(\sigma^2F_3 - \sigma^2F_2 \text{ in } F_6) + (\sigma^2F_3 - \sigma^2F_2 \text{ in} F_7)/ 2$$

$$= \quad (1/2\ \sigma^2A + 1/128\ \sigma^2D + 5/4\ \sigma^2AA \text{ in } F_6) + (1/2$$

$$\sigma^2A + 1/512\ \sigma^2D + 5/4\ \sigma^2AA \text{ in } F_7)/2$$

$$= \quad 1/2\ \sigma^2A + 5/1024\ \sigma^2D + 5/4\ \sigma^2AA$$

Using these coefficients, a matrix of coefficients for the genetic variances for the various component lines was developed (Table 5).

3.3.4 Least Square Analysis

Least Square Analysis was performed to estimate the components of genetic variance. PROC REG procedure of SAS (1985) was used for the estimation. The assumptions are:

i) Errors are normally distributed

ii) Errors are independent of random variables

iii) Errors have a common variance(no heterogeneity of variance)

Regression Model:

$$\gamma = C\beta$$

$$\gamma C' = CC'\beta$$

$$(CC')^{-1}C'\gamma = (CC')^{-1}CC'\beta$$

$$\beta = (C'C)^{-1}C'\gamma$$

Where, β = column vector (25 x 1) of genetic components of variance

C = matrix (25 x 25) of coefficients

γ = column vector (25 x1) of Mean Square (MS) values from the ANOVA of nested design

Weighted Least Square Analysis was done to see the variation in the estimates of genetic components due to models. The principles underlying Weighted Least Square is that each observation in 'γ' is divided by the proportionality factor and the rescaled

Table 5. Matrix of Coefficients of the Variances for the different component lines in the Nested Design Model.

#	Source	df	x1	x2	x3	x4	x5	x6	x7	x8	x9	x10	x11	x12	x13	x14	x15	x16
1.	Year (Y)	1	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	20
2.	Location(L)	1	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	0
3.	Yx L	1	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	0
4.	Rep(YL)	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5.	F_2	14	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	20
6.	$F_3(F_2)$	15	1	0	0	0	0	0	0	0	2	0.019	5	0	0	0	0	4
7.	Pub. Density(D)	1	1	5	0.019	6.5	10	0.039	13	60	0	0	0	10	0.039	13	120	0
8.	F_2 x D	14	1	5	0.019	6.5	10	0.039	13	0	0	0	0	10	0.039	13	0	0
9.	$F_3(F_2)$ x D	15	1	1	0.009	2.5	2	0.019	5	0	0	0	0	2	0.019	5	0	0
10.	L x F_2	14	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	0
11.	L x $F_3(F_2)$	15	1	0	0	0	0	0	0	0	2	0.019	5	0	0	0	0	0
12.	L x D	1	1	5	0.019	6.5	10	0.039	13	60	0	0	0	0	0	0	0	0
13.	Y x F_2	14	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	20
14	Y x $F_3(F_2)$	15	1	0	0	0	0	0	0	0	2	0.019	5	0	0	0	0	4
15.	Y x D	1	1	5	0.019	6.5	0	0	0	60	0	0	0	10	0.039	13	120	0
16.	Y x F_2 x D	14	1	5	0.019	6.5	0	0	0	0	0	0	0	10	0.039	13	0	0
17.	$F_3(F_2)$ x D	15	1	1	0.009	2.5	0	0	0	0	0	0	0	2	0.019	5	0	0
18.	Y xL x F_2	14	1	0	0	0	0	0	0	0	10	0.039	13	0	0	0	0	0
19.	Y xL x $F_3(F_2)$	15	1	0	0	0	0	0	0	0	2	0.019	5	0	0	0	0	0
20.	Y x L x D	1	1	5	0.019	6.5	0	0	0	60	0	0	0	0	0	0	0	0
21.	L x F_2 x D	14	1	5	0.019	6.5	10	0.039	13	0	0	0	0	0	0	0	0	0
22.	L x $F_3(F_2)$ x D	15	1	1	0.009	2.5	2	0.019	5	0	0	0	0	0	0	0	0	0
23.	Yx L x F_2 x D	14	1	5	0.019	6.5	0	0	0	0	0	0	0	0	0	0	0	0
24.	Y x L x $F_3(F_2)$ x D	15	1	1	0.009	2.5	0	0	0	0	0	0	0	0	0	0	0	0
25.	Error	236	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Where,

x1= $\sigma^2 e$ x2 = σ^2yld A x3 = σ^2yld D x4 = σ^2yld AA x5 = σ^2 ld A x6 = σ^2 ld D x7 = σ^2 ld AA x8 = σ^2 yld

x9 = σ^2ylA x10 = σ^2yl D x11 = σ^2ylAA x12 = σ^2ydA x13= σ^2yd D x14 = σ^2ydA A x15 = σ^2yd x16 = σ^2y A

Table 5. Continued.....

#	Source	df	X17	x18	x19	x20	x21	x22	x23	x24	x25	x26	x27	x28	x29	x30	x31	x32	x33
1.	Year (Y)	1	0.078	26	0	0	0	0	0	0	0	0	0	0	0	240	120	0	240
2.	Location(L)	1	0	0	0	20	0.078	26	0	0	0	0	0	0	0	240	120	240	0
3.	Yx L	1	0	0	0	0	0	0	0	0	0	0	0	0	0	240	120	0	0
4.	Rep(YL)	4	0	0	0	0	0	0	0	0	0	0	0	0	0	240	0	0	0
5.	F_2	14	0.078	26	0	20	0.078	26	0	0	0	0	40	0.157	52	0	0	0	0
6.	$F_3(F_2)$	15	0.039	10	0	4	0.039	10	0	0	0	0	8	0.078	20	0	0	0	0
7.	Pub. Density(D)	1	0	0	120	0	0	0	20	0.078	26	240	0	0	0	0	0	0	0
8.	F_2 x D	14	0	0	0	0	0	0	20	0.078	26	0	0	0	0	0	0	0	0
9.	$F_3(F_2)$ x D	15	0	0	0	0	0	0	4	0.039	10	0	0	0	0	0	0	0	0
10.	L x F_2	14	0	0	0	20	0.078	26	0	0	0	0	0	0	0	0	0	0	0
11.	L x $F_3(F_2)$	15	0	0	0	4	0.039	10	0	0	0	0	0	0	0	0	0	0	0
12.	L x D	1	0	0	120	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13.	Y x F_2	14	0.078	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	Y x $F_3(F_2)$	15	0.039	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15.	Y x D	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16.	Y x F_2 x D	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17.	$F_3(F_2)$ x D	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18.	Y xL x F_2	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19.	Y xL x $F_3(F_2)$	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20.	Y x L x D	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21.	L x F_2 x D	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22.	L x $F_3(F_2)$ x D	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23.	Yx L x F_2 x D	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24.	Y x L x $F_3(F_2)$ x D	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25.	Error	236	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Where,

$x17 = \sigma^2 y\ D$ $x18 = \sigma^2 y\ AA$ $x19 = \sigma^2 ld$ $x20 = \sigma^2 l\ A$ $x21 = \sigma^2 l\ D$ $x22 = \sigma^2 l\ AA$ $x23 = \sigma^2 d\ A$ $x24 = \sigma^2 d\ D$ $x25 = \sigma^2 d\ AA$

$x26 = \sigma^2 d$ $x27 = \sigma^2 A$ $x28 = \sigma^2 D$ $x29 = \sigma^2 AA$ $x30 = \sigma^2 R(YL)$ $x31 = \sigma^2 YL$ $x32 = \sigma^2 L$ $x33 = \sigma^2 Y$

dependent variables will have equal variance. Rescaling gives weight to each observation proportional to the reciprocal of its standard deviation. The estimates were the same under weighted and unweighted Least Square analysis. This might be due to the large number (25) of variables included in the regression model used. Hence, Principal component Analysis was done to select the important variables from the matrix of coefficients. PRINCOMP procedure of SAS (1985) was used for this purpose, and the important variables were selected. Weighted Least Square analysis for each trait studied was then applied with the selected variables under the following models:

Model 1: Additive components only

Model 2: Additive and additive x additive components only

Model 3: Additive and dominance components only

3.3.5 Estimation of Heritability

The effectiveness of selection for a trait depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among genotypes in a population, a concept referred to as heritability. The heritability of a character has a major impact on the methods chosen for population improvement, inbreeding and other aspects of selection. Single plant selection may be effective for a trait with high heritability, and relatively less effective for one with low heritability. The extent to which replicated testing is required over years, locations or environments will greatly depend on the type and amount of heritability of the traits under consideration. The two following types of heritability are most often estimated and used by breeders in deciding breeding procedure and predicting genetic advance:

$$\text{Broad sense heritability}(H) = \sigma^2 G / \sigma^2 P$$

$$\text{Narrow sense heritability } (h^2) = \sigma^2 A / \sigma^2 P$$

Where, $\sigma^2 P = \sigma^2 G + \sigma^2 E$

$\sigma^2 G = \sigma^2 A + \sigma^2 D + \sigma^2 I + \sigma^2 E$

$\sigma^2 P$ is the phenotypic variance

$\sigma^2 G$ is the genotypic variance

$\sigma^2 E$ is the error variance

$\sigma^2 A$ is the additive variance

$\sigma^2 D$ is the dominance variance

$\sigma^2 I$ is the interaction or epistatic variance

($\sigma^2 AxA$, $\sigma^2 AxD$, $\sigma^2 DxD$, $\sigma^2 AxAxA$.....)

In the present study, heritability estimates were done according to Rasmusson and Glass (1967). Only broad sense estimates were done using genotypic and phenotypic variances from the General ANOVA, and the estimates were compared with the heritability obtained in different models in the Nested ANOVA. Using the components of genetic variances obtained from Least Square Analysis narrow sense heritability estimates were done for model-1 (only additive) and model-2 (additive, additive x additive), and broad sense estimates were done for model-3 (additive, dominance). Also, the estimates were compared under full and selected variables conditions in models-2 and 3. The heritability estimates were used to predict gains from selection (Gs). Since the materials were evaluated over two years and two locations, following formula was used to calculate the heritability.

$$\text{Broad sense heritability}(H) = \sigma^2 G/\sigma^2 P$$

$$= \frac{\sigma^2 G}{\sigma^2 E/RLY+\sigma^2 LYG/LY+\sigma^2 LG/L+\sigma^2 YG/Y+\sigma^2 G}$$

Where, R,L,Y represent replication, location and year respectively.

Narrow sense heritability (h^2) = $\sigma^2A/\sigma^2 P$ or $\sigma^2A + \sigma^2AA / \sigma^2 P$

Where, σ^2A will involve all additive and its interaction with the additive variances, and $\sigma^2 P$ will involve all variances included in the respective model and the error variance. Here too the respective variance was divided with the components involved like in broad sense estimate to calculate the phenotypic variance.

Also, Parent-offspring regression procedure as proposed by Lush (1940) was used to compute heritability. The model used was:

$$Yi = a + bXi + ei$$

Where, *Yi* = performance of offspring on parent

a = mean performance of parents evaluated

b = linear regression coefficient

Xi = performance of *ith* parent

ei = experimental error associated with measurement of *Xi*

The heritability estimate was adjusted for inbreeding as suggested by Smith and Kinman(1965) as follows:

$$\text{Heritability} = b/ 2\, rxy$$

Where, *rxy* is the coefficient of parentage (63/64 between F_6 and F_7 generations)

Gain from selection was calculated according to Sprague and Federer (1951) using the following formula:

Gain from Selection (Gs)

$$Gs = K\, \sigma P\, H$$

Where, K= Constant based on selection intensity (2.06 at 5% selection)

σP = Phenotypic standard deviation

H = Heritability of the trait

Gain from Selection as percent of Mean (Gs %)

Gs % = Gs / Mean x 100

3.3.6 Estimation of Correlation and Regression Coefficients

The estimates of correlation coefficients among traits are useful for indirect selection. The character of ultimate importance in a selection program is referred to as the primary character and those which influence primary character are referred to as the secondary characters. For example, yield may be considered as a primary character, and plant height, lodging, maturity etc. as the secondary characters. The potential value of indirect selection for secondary character that is quantitatively inherited was summarized by Falconer(1981):

$$CRx = rA \frac{iy\ hy}{ix\ hx}$$

Where, CRx = amount of improvement in the primary character

obtained by indirect selection for secondary character

Rx = amount of improvement obtained by direct selection for

primary character

rA = genetic correlation between primary character(x) and

secondary character(y)

iy = selection intensity for secondary character

ix = selection intensity for primary character

hy = square-root of narrow sense h^2 of secondary character

hx = square-root of narrow sense h^2 of primary character

The selection for morphological or physiological characters is of no value if the characters' performance is not correlated with the primary character.

In the present study, PROC CORR procedure of SAS was used to estimate Pearson's correlation coefficients. The multiple correlation coefficients among seven characters studied were calculated by overall genotypic means (AVE), year (Y), location (L), year x location, pubescence density(D), year x D, location x D, and year x location x D. The effects of year, location, pubescence density and their interactions on correlation coefficients were compared.

Regression coefficients also reflects the relationship between the dependent variable and the independent variables. It is the measure of dependence of the dependent variable on the independent variable. Thus, an unit change in the independent variable will bring a change in the dependent variable. Based on the nature and degree of regression coefficients, the dependent variable can be manipulated in a positive or negative direction. This information can be used as a tool in manipulating of the traits of interest by the breeders. The model is:

$$Y = a + b1x1 + b2x2 + b3x3 + ...$$

Where, Y = performance of dependent variable

a = point of intercept

$b1$ = regression coefficient of $x1$ independent variable

$b2$ = regression coefficient of $x2$ independent variable

$b3$ = regression coefficient of $x3$ independent variable

$x1$, $x2$ and $x3$ are the values of respective variables

SAS (1985) Stepwise REG procedure was used to calculate the regression coefficients for the dependent variables yield, protein, and oil. Using these coefficients, prediction equations were developed for the above characters.

4 RESULTS

4.1 Comparison of Treatment Means

The overall mean, range, variance and C.V. of the progenies for the seven characters studied are presented in Table 6. The overall mean for yield was 3.36 t/ha with a range 0.99-5.03 t/ha, and a C.V. of 22.0 percent. Maturity had an overall mean of 30.3 days (after 8/31) with a C.V. of 20.7 percent. Plant height exhibited a large variance with a mean of 103.0 cm and a C.V. of 15.3 percent. Lodging scored on a 1-4 scale had a mean of 2.2 with the highest C.V. of 39.2 percent. Seed size showed a mean of 19.2 g(100 seeds) with arrange of 13.2-26.1 g and a C.V. of 11.9 percent. The means for protein and oil were 39.2 and 19.2 % respectively with very low variance and C.V. values. These statistics for the parents, Wells II and Harosoy also exhibited a similar trend. Wells II had higher means than Harosoy for yield, while lower for other traits. The C.V. were high for yield, maturity in both, for lodging in Harosoy (Table 6).

The variable means and other statistics when computed by year showed a considerable variation, and their means were compared using TTEST (Table 7). The magnitude and range of difference differed with the characters and year. In general, the means were higher in 1990 than in 1989. However, variance and C.V. showed a mixed trend. The C.V. were higher for lodging (approx. 40%), moderate for seed size, maturity, plant height and yield (8-24%), and very low for protein and oil (<3.0%). When the means were compared using TTEST, the differences were significant for all the characters except for height.

The means and other statistics computed by location, showed a considerable effect of location on the performance of these characters (Table 8). In general, the estimates were higher at Lenawee than at Ingham . The mean yield at Lenawee was 3.75 t/ha which was almost a ton higher than at Ingham when averaged over years. Though the difference for maturity, lodging, and size were not great, TTEST showed a significant difference.

Table 6. Overall mean, range, variance, Variance as percent of mean (Var %) and Coefficient of variance (C.V.) of the characters.

#	Character	N	Mean	Range	Variance	Var %	C.V.
Progeny (F_6 & F_7)							
1.	Yield (t/ha)	480	3.35	0.99-5.03	0.546	16.26	22.0
2.	Maturity (days 8/30)	480	30.3	21.0-45.0	39.501	130.36	20.7
3.	Height (cm)	480	103.0	56.0-168.	248.560	241.20	15.3
4.	Lodging (1-4)	480	2.3	1.0-4.0	0.963	43.28	44.1
5.	Seed Size (g/100)	480	19.3	13.2-26.1	5.289	27.48	11.9
6.	Protein (%)	480	39.2	33.4-44.9	12.103	30.90	8.9
7.	Oil (%)	480	19.3	17.8-22.1	0.514	2.67	3.7
Parent : Wells II(++)							
1.	Yield (t/ha)	8	3.75	2.75-4.58	0.431	11.49	17.5
2.	Maturity (days 8/30)	8	27.4	22.0-35.0	25.410	92.82	18.4
3.	Height (cm)	8	88.2	76.0-99.0	61.839	70.17	8.9
4.	Lodging (1-4)	8	1.0	1.0-1.0	0.00	0.00	0.0
5.	Seed Size (g/100)	8	17.5	14.6-20.7	3.659	20.90	10.9
6.	Protein (%)	8	39.0	35.2-42.1	17.785	45.63	8.4
7.	Oil (%)	8	19.6	18.8-20.5	0.597	3.05	3.9
Parent : Harosoy (PdPd)							
1.	Yield(t/ha)	8	3.11	2.00-4.26	0.806	25.91	28.9
2.	Maturity (days 8/30)	8	28.1	20.0-37.0	31.553	112.18	19.9
3.	Height (cm)	8	103.1	86.0-127.0	176.69	171.34	12.9
4.	Lodging(1-4)	8	2.1	1.0-3.0	0.410	19.29	30.2
5.	Seed Size (g/100)	8	20.4	16.3-24.6	8.194	40.14	14.0
6.	Protein (%)	8	39.5	34.7-43.0	16.27	41.24	10.2
7.	Oil (%)	8	19.3	18.8-19.8	0.142	0.74	2.0

N = sample size Var % = Var / Mean x 100

Table 7. Comparison of means and other statistics of the characters by Year.

Year	Variable	N	Mean	Range	Variance	C.V.	ITI	P>ITI
'89	Yield	240	3.24	0.99-5.03	0.61	24.0	-3.44	0.0006
'90	Yield	240	3.47 *	1.35-4.75	0.46	19.6		
'89	Maturity	240	27.1	21.0-35.0	9.95	11.6	-12.18	0.0001
'90	Maturity	240	33.5 *	22.0-45.0	48.96	20.9		
'89	Height	240	103.8	56.0-168.0	287.5	16.3	0.978	0.3283
'90	Height	240	102.4	76.0-147.0	209.6	14.1		
'89	Lodging	240	1.9	1.0-4.0	0.724	44.5	-7.34	0.0001
'90	Lodging	240	2.5 *	1.0-4.0	1.011	39.6		
'89	Seed Size	240	17.6	13.2-22.0	2.269	8.6	-22.9	0.0001
'90	Seed Size	240	20.9 *	17.7-26.0	2.775	8.0		
'89	Protein	240	35.8	33.4-38.3	0.787	2.5	-86.2	0.0001
'90	Protein	240	42.5 *	40.7-44.9	0.678	1.9		
'89	Oil	240	18.7	17.8-19.7	0.134	2.0	-22.5	0.0001
'90	Oil	240	19.7 *	18.3-22.1	0.365	3.1		

N = Number of sample. ITI = Estimates of 't'. * = Significantly higher by t-test.

Table 8. Comparison of means and other statistics of the characters by Location.

Location	Variable	N	Mean	Range	Variance	C.V.	ITI	P>ITI
ING	Yield	240	2.95	1.05-4.29	0.301	18.8	-14.05	0.0001
LEN	Yield	240	3.75 *	0.99-5.03	0.465	18.2		
ING	Maturity	240	28.0	22.0-42.0	23.71	17.4	-8.553	0.0001
LEN	Maturity	240	32.6 *	21.0-45.0	44.94	20.6		
ING	Height	240	107.1 *	61.0-150.0	196.8	13.1	5.927	0.0001
LEN	Height	240	98.9	56.0-168.0	267.2	16.5		
ING	Lodging	240	2.4 *	1.0-4.0	0.942	41.2	3.000	0.0028
LEN	Lodging	240	2.1	1.0-4.0	0.953	46.7		
ING	Seed Size	240	18.9	13.1-24.1	3.961	10.6	-3.694	0.0002
LEN	Seed Size	240	19.6 *	14.4-26.0	6.344	12.8		
ING	Protein	240	39.0	33.4-43.8	12.791	9.2	-1.278	0.2016
LEN	Protein	240	39.4	34.0-44.9	11.383	8.6		
ING	Oil	240	19.2	18.0-20.8	0.415	3.4	-0.808	0.4192
LEN	Oil	240	19.3	17.8-22.1	0.612	4.1		

N = Number of samples. ING = Ingham, LEN = Lenawee
* = Significantly higher by t-test. ITI = Estimate of 't'.

However, the means were not significantly different for protein and oil over the locations. Likewise, when effects of pubescence density on means and other statistics of the characters were computed (Table 9), pubescence appeared to affect some of the traits. However, the degree of difference was not very high. Dense pubescence had higher mean for maturity, height, lodging and size; almost identical for protein and oil; but lower for yield than the normal pubescence type. When tested with the TTEST, the means were significantly different for yield, maturity, height, lodging and oil, but non-significant for size and protein.

The mean and other statistics were further computed on year x location, year x location x pub. density, pub. density x year , and pub. density x location to see the effects of these interactions on the performance of the characters. Only the significance of their mean difference are presented for comparison (Table 10-13). A comparative evaluation of significance of mean differences due to year, location, and density is presented in Table 10. It is evident that the means were significantly different for yield, maturity and lodging over year, location and pubescence density. However, for height the means were not significantly different over year, but different over location and density. Likewise, seed size exhibited a significant difference over year and location, but non-significant over density. Protein means were significantly different only for year, while oil means differed over year and density.

When the variable means were compared by year x location interaction, the TTEST significance were quite interesting. The means were significantly different over locations both in 1989 and 1990 for yield, height and lodging (Table 11). However, the differences were non-significant for maturity and seed size in 1989, and for protein in 1990. Mean of oil percentage did not show significant difference over locations in either of the years. However, the trend was different when compared over years within the location. For example, the means were different over years at both locations for maturity, lodging, seed size, protein and oil, and non-significant over years for yield at Ingham, and for height at

Table 9. Comparison of means and other statistics of the characters by Pubescence Density.

Pub.Density	Variable	N	Mean	Range	Variance	C.V.	ITI	P>ITI
Dense	Yield	240	3.26	1.05-4.73	0.50	21.7	-2.78	0.0055
Normal	Yield	240	3.44 *	0.99-5.03	0.57	22.0		
Dense	Maturity	240	31.2 *	21.0-45.0	41.81	20.7	3.253	0.0012
Normal	Maturity	240	29.4	21.0-45.0	35.61	20.3		
Dense	Height	240	109.3 *	66.0-168.0	226.5	13.2	9.507	0.0001
Normal	Height	240	96.7	56.0-132.0	192.3	14.3		
Dense	Lodging	240	2.5 *	1.0-4.0	0.891	38.3	5.535	0.0001
Normal	Lodging	240	2.0	1.0-4.0	0.924	48.5		
Dense	Seed Size	240	19.3	13.3-26.0	5.56	12.2	0.895	0.3714
Normal	Seed Size	240	19.2	14.1-24.7	5.01	11.7		
Dense	Protein	240	39.2	33.4-44.9	12.32	8.9	0.129	0.8970
Normal	Protein	240	39.1	33.5-44.0	11.93	8.8		
Dense	Oil	240	19.2	18.0-22.1	0.455	3.5	-2.31	0.0211
Normal	Oil	240	19.3 *	17.8-21.4	0.562	3.9		

N= Number of samples. ITI = Estimates of 't'. * = Significantly higher by t-test.

Table 10. Effects of Year, Location and Pubescence Density on the the significance of variable means using TTEST.

#	Variables	Year	Location	Pub.density
1.	Yield	*	*	*
2.	Maturity	*	*	*
3.	Height	ns	*	*
4.	Lodging	*	*	*
5.	Seed size	*	*	ns
6.	Protein	*	ns	ns
7.	Oil	*	ns	*

* = Means significantly different, ns = Means not significantly different.

Table 11. Effects of Year x Location on the significance of variable means using TTEST.

#	Variables	'89	'90	ING	LEN
1.	Yield	*	*	ns	*
2.	Maturity	ns	*	*	*
3.	Height	*	*	*	ns
4.	Lodging	*	*	*	*
5.	Seed size	ns	*	*	*
6.	Protein	*	ns	*	*
7.	Oil	ns	ns	*	*

* = Means significantly different. ns= Means not significantly different.

Lenawee. When the effects of density on variable means were compared within year and location, the differences were non-significant in most cases (Table 12). However, the differences were significant for yield at Ingham in 1989, for maturity at Ingham and Lenawee in 1990, and for oil at Ingham and Lenawee in 1990. Height was the only character that exhibited a significant difference over years and location due to pubescence density.

Similarly, the significance of the effects of density x year and density x location on the treatment means are presented in Table 13. When the effects of year on density were compared, the differences were significant over years both in dense and normal types for maturity, lodging, seed size, protein and oil, but only in dense pubescence affected yield. Year effects were non-significant for height both in dense and normal types. Similarly, when the effects of locations were compared in dense and normal types, the variable means differed significantly in both types over locations for yield, maturity, height and seed size, but only for lodging in normal type. However, location effects were non-significant both in dense and normal types for protein and oil.

4.2 Analysis of variance

4.2.1 General Model ANOVA

The ANOVA for General Model for the seven characters studied are presented in Table 14 & 15 . Here in this model the total variance was partitioned into year, location, replication, genotype and their interactions. In order to have a more reliable F-test, mean square for error (MSe) and degree of freedom for error (dfe) for the respective component line was recalculated (as described in materials and methods) and used to calculate the corrected 'F' values. With the respective MS and F-significance, C.V., LSD, and grand mean are also presented in the tables.

The analysis of variance for yield showed a non-significant effect due to year (Y), location (L) and interaction of genotype (G) with year and location. However, the effects

Table 12. Effects of Year x Location x Pub. Density on the significance of variable means using TTEST.

#	Variable	89		90	
		ING	LEN	ING	LEN
1.	Yield	*	ns	ns	ns
2.	Maturity	ns	ns	*	*
3.	Height	*	*	*	*
4.	Lodging	*	*	ns	*
5.	Seed size	ns	ns	ns	ns
6.	Protein	ns	ns	ns	ns
7.	Oil	ns	ns	*	*

* = Means significantly different. ns= Means not significantly different.

Table 13. Effects of Density x Year, and Density x Location on the significance of variable means using TTEST.

#Variable	Density x Year		Density x Location	
	Dense	Normal	Dense	Normal
1.Yield	*	ns	*	*
2.Maturity	*	*	*	*
3.Height	ns	ns	*	*
4.Lodging	*	*	ns	*
5.Seed size	*	*	*	*
6.Protein	*	*	ns	ns
7.Oil	*	*	ns	ns

* = Means significantly different. ns= Means not significantly different.

of genotype , Y x L and Y x L x G were significant (Table 14). The C.V. was 13.3% which shows that the error variance was not very high for these measurements. Likewise, the ANOVA for maturity showed a significant F-test for Genotype (G), Y x L, Y x G, and Y x L x G. The C.V. was 5.8 % which indicated a reliable results produced by the ANOVA (Table 14). Height exhibited a significant F-test due to Genotype, Y x L, and Y x G. However, the F-test results were different for lodging. In this case, the effects of year, location, genotype, L x G, and Y x L x G were all significant. The C.V. was slightly higher (26.5%) for this. The analysis of variance for seed size, protein and oil are presented in Table 15. Seed size produced a different F-test . The differences were non-significant for year, location, genotype, Y x G, and L x G; and significant for Y x L and Y x L x G. However, a significant effect due to year, genotype, Y x L, Y x G, L x G, and Y x L x G were observed in case of protein . The F-test for oil also indicated a significant effect of year, genotype, and Y x L x G.

4.2.2 Nested Model ANOVA

In the Nested Model ANOVA, the design partitioned the total variance into 25 components involving year, location, replication (YL), F_2, F_3 (F_2), pubescence density (D), and their respective interactions (Table 16-17). Since PROC ANOVA procedure of SAS (1985) produced the F- values using a common error variance and df, the corrected error variance (MSe) and degree of freedom for error (dfe) for each component line was recalculated to compute the corrected F-values and their significance (explained in Materials & Methods). The analysis of variance showed a differential F-values and their significance for the seven traits studied (Table 16-17).

The ANOVA for yield, maturity, height and lodging are presented in Table 16. The F-test for yield showed a significant effect due to Y x F_2, Y x F_3 (F_2) x D, Y x L x F_3 (F_2), and Y x L x D, and all other main and interaction effects were non-significant. Though, density had no main effect, it exhibited interaction effect in some cases. The

Table 14. Estimates of Mean Squares (MS) and F-tests significance of the characters in the General Model ANOVA.

#	Source	df	Yield	Maturity	Height	Lodging
1.	Year(Y)	1	6.03	4931.6	285.0	44.76*
2.	Location(L)	1	82.02	2620.2	8210.3	8.00**
3.	Y x L	1	3.72**	2729.3 **	1128.0**	0.00
4.	Rep(YL)	4	2.71**	28.7 **	2504.3**	9.71**
5.	Genotype(G)	61	0.89**	101.1**	1137.4**	3.49**
6.	Y x G	61	0.40	14.9*	137.6**	0.45
7.	L x G	61	0.35	9.4	64.9	0.70*
8.	Y x L x G	61	0.32 **	9.6**	68.0	0.42*
9.	Error	244	0.20	3.1	69.5	0.34
	Mean		3.35 t/ha	30.2 days	102.8 cm	2.2
	C.V(%)		13.3	5.8	8.1	26.5
	LSD(0.05)		0.87	3.4	16.3	1.1
	LSD(0.01)		1.15	4.5	21.5	1.5

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

Table 15. Estimates of Mean Squares (MS) and F-tests significance of the characters in the General Model ANOVA.

#	Source	df	Seed size	Protein	oil
1.	Year(Y)	1	1379.1	5628.1**	130.20**
2.	Location(L)	1	73.4	22.0	0.26
3.	Y x L	1	69.8**	8.6**	0.41
4.	Rep(YL)	4	22.8**	0.1	0.00
5.	Genotype(G)	61	9.6**	3.2**	0.94*
6.	Y x G	61	1.0	0.7*	0.51**
7.	L x G	61	1.4	0.9*	0.27
8.	Y x L x G	61	2.6**	0.5**	0.24**
9.	Error	244	0.62	0.006	0.006
	Mean		19.2 gm	39.2 %	19.2 %
	C.V.(%)		4.1	0.2	0.4
	LSD(0.05)		1.5	0.15	0.15
	LSD(0.01)		2.0	0.19	0.20

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

Table 16. Estimates of Mean Squares (MS) and F-tests significance of the characters in the Nested Model ANOVA.

#	Source	df	Yield	Maturity	Height	Lodging
1.	Year(Y)	1	6.323	4838.7	238.0	48.133*
2.	Location(L)	1	76.501	2511.6	8151.0	9.075*
3.	Y x L	1	3.413	2660.2	1267.5	0.000
4.	Rep(YL)	4	2.543	26.0**	2410.5	7.762
5.	F_2	14	2.021	242.5*	1904.5*	7.104
6.	$F_3(F_2)$	15	0.858	74.4*	662.4*	3.105*
7.	Pub. Density(D)	1	4.193	409.6	18924.2	28.783
8.	F_2 x D	14	0.255	32.8	338.3	0.954
9.	$F_3(F_2)$ x D	15	0.265	45.4**	491.1**	1.090
10.	L x F_2	14	0.609	20.2	81.1	1.313
11.	L x $F_3(F_2)$	15	0.447	9.6	70.7	0.498
12.	L x D	1	0.834	0.0	168.6	0.796
13.	Y x F_2	14	0.878*	30.5	201.0	0.605
14.	Y x $F_3(F_2)$	15	0.319	13.6	176.3	0.585
15.	Y x D	1	0.961	121.7	18.0	1.453
16.	Y x F_2 x D	14	0.174	4.1	98.6	0.274
17.	Y x $F_3(F_2)$ x D	15	0.251*	4.8	96.6	0.191
18.	Y x L x F_2	14	0.544	22.8	49.8	0.587
19.	Y x L x $F_3(F_2)$	15	0.440**	11.1**	95.5	0.532*
20.	Y x L x D	1	1.003*	3.37	453.3**	0.000
21.	L x F_2 x D	14	0.125	4.3	53.3	0.383
22.	L x $F_3(F_2)$ x D	15	0.159	4.5	48.8	0.545
23.	Y x L x F_2 x D	14	0.185	3.1	31.6	0.201
24	YxLx$F_3(F_2)$xD	15	0.095	3.5	49.0	0.386
25.	Error	236	0.205	3.1	68.6	0.328
Mean			3.35	30.3	103.1	2.2
C.V.(%)			13.5	5.8	8.1	26.2

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

estimates for C.V.(13.5%) which indicated that the experimental error with this trait was very low. The F-test for maturity showed a significant effects due to F_2, F_3 (F_2), and highly significant effects due to Y x L, F_3 (F_2) x D, and Y x L x F_3 (F_2). Pubescence density did not show much effect on maturity. The estimates of C.V.(5.8%) was within acceptable range. The F-tests for height, however, showed non-significant effects due to most of the main and interaction effects (Table 16). The effects were significant for F_2, F_3 (F_2), F_3 (F_2) x D and Y x L x D. In case of lodging, however, the effects of year, location, F_3 (F_2), and Y x L x F_3 (F_2) were significant. Pubescence density did not show either the main or interaction effect for lodging. The ANOVA for seed size, protein and oil are presented in Table 17. Seed size exhibited non-significant F-tests for most of the components. There were no significant effect of year and location on seed size. However, the effects of F_3 (F_2), F_3 (F_2) x D, Y x L x F_2, Y x L x F_3 (F_2) and Y x L x F_2 x D were significant. Here too, pub. density did not show any direct effect on seed size. The analysis of variance for protein, however, showed more significant F-tests than other variables (Table 17). The effects of year (Y), Y x L, F_2, L x F_3 (F_2), Y x F_3 (F_2) x D, L x F_3 (F_2) x D and Y x L x F_2 x D were significant at 0.05 probability, and those of Y x L x F_2 and Y x L x F_3 (F_2) x D were significant at 0.01 probability. Though pubescence density had no main effect in this case, it had considerable interaction effects. The year effect for oil was significant, and interactions of Y x D, Y x L x F_3 (F_2), and Y x L x F_3 (F_2) x D were also significant. The estimates of C.V. in all these cases were within the acceptable range indicating the reliability of the results.

4.3 Estimation of the Components of Variance

4.3.1 General Model ANOVA

Using the Expected Mean Square (EMS) from Table 1 and the Mean Square (MS) from the ANOVA (Tables 14-15) of the respective component line was used to estimate σ^2G, σ^2GY, σ^2GL, σ^2GLY , σ^2e and σ^2P for the traits studied (Table 18). The

Table 17. Estimates of Mean Squares (MS) and F-tests significance of the characters in the Nested Model ANOVA.

#	Source	df	Seed size	Protein	Oil
1.	Year(Y)	1	1327.5	5447.26*	126.58
2.	Location(L)	1	70.3	19.76	0.33
3.	Y x L	1	63.8	6.96*	0.35
4.	Rep(YL)	4	21.1	0.012	0.003
5.	F_2	14	15.8	9.49*	2.15
6.	$F_3(F_2)$	15	8.7*	1.80	0.93
7.	Pub. Density(D)	1	4.2	3.48	2.72
8.	F_2 x D	14	7.1	1.47	0.29
9.	$F_3(F_2)$ x D	15	6.2*	0.91	0.38
10.	L x F_2	14	1.7	1.73	0.55
11.	L x $F_3(F_2)$	15	1.3	0.89*	0.20
12.	L x D	1	6.9	0.00	0.40
13.	Y x F_2	14	1.4	0.74	1.05
14.	Y x $F_3(F_2)$	15	0.8	0.76	0.43
15.	Y x D	1	2.2	0.00	3.88**
16.	Y x F_2 x D	14	0.7	0.74	0.19
17.	Y x $F_3(F_2)$ x D	15	0.8	0.62*	0.18
18.	Y x L x F_2	14	6.3*	1.12**	0.36
19.	Y x L x $F_3(F_2)$	15	2.1**	0.02**	0.20**
20.	Y x L x D	1	0.42	2.03	0.03
21.	L x F_2 x D	14	0.95	0.51	0.20
22.	L x $F_3(F_2)$ x D	15	1.33	0.72*	0.20
23.	Y x L x F_2 x D	14	1.73*	0.68*	0.25
24	YxLx$F_3(F_2)$xD	15	0.66	0.21**	0.17**
25.	Error	236	0.60	0.006	0.006
Mean			19.2	39.2	19.2
C.V.			4.0	0.2	0.4

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

Table 18. Estimates of components of variance from the General Model ANOVA.

#	Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1.	σ^2G	0.065	10.735	996.76	0.4140	0.931	0.360	0.058
2.	σ^2GY	0.020	1.337	17.39	0.0083	-0.404	0.045	0.068
3.	σ^2GL	0.007	-0.061	-0.78	0.0718	-0.302	0.098	0.009
4.	σ^2GYL	0.062	3.260	-0.75	0.0375	0.980	0.262	0.117
5.	σ^2e	0.025	0.385	8.69	0.0426	0.077	0.001	0.001
6.	σ^2P	0.097	12.26	1006.54	0.469	1.186	0.497	0.126

G = Genotype, Y = Year, L = Location, P = Phenotype, e = Error, and σ^2 = Variance.

estimates of σ^2G was highest for height, moderate for maturity, seed size, lodging and protein, and relatively low for yield and oil. The trend was nearly similar for the interaction variance of genotype with year and location. The estimates were negative for σ^2GL for maturity, for σ^2GL and σ^2GLY for height, and for σ^2GY and σ^2GL for seed size. The estimates of σ^2e were low in most cases except for height. In computing the phenotypic variance, negative estimates of components were assumed to be zero.

4.3.2 Nested Model ANOVA

The Least Square analysis of SAS produced the estimates of various components included in the respective models. Three models, Additive (A), Additive & Additive x Additive (A & AxA), and Additive & Dominance (A&D) were used to estimate the components of variance under Weighted and Unweighted Least Square analysis. The SAS output produced a different estimates for the component lines under additive model for Weighted and Unweighted analysis. Hence, the Weighted variance estimates were used and presented here. However, in case of the other two models(A & AxA, A&D) the computer output did not show any difference in the estimates of variance components under Weighted and Unweighted analysis. Therefore, Principal Component Analysis (PCA) was performed for each character for the two models. Based on PCA, important component of variance were selected for each case to include in Weighted Least Square analysis. When the selected components were used, the computer results were different for Weighted and Unweighted analysis. Therefore, for these models the estimates for components of variance are presented for both full and selected models for comparison and estimates of heritability. Some of the components of variance produced negative estimates. They were assumed to be zero while computing the phenotypic variance and heritability.

4.3.2.1 Additive Model

The estimates of components of variance for the Additive model are presented in Table 19. The estimates differed considerably with the characters and also with the

Table 19. Estimates of components of variance in Additive(A)-Weighted Model.

#	X#	Variance	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1	X1	σ^2_e	0.19118	3.17649	68.30531	0.32711	0.61961	0.00600	0.00603
2	X3	σ^2_{yldA}	-0.01143	-0.00436	-7.53916	-0.02407	0.18262	0.15612	0.05848
3	X5	σ^2_{ldA}	0.00040	0.13314	1.87523	0.01975	-0.05036	-0.02126	-0.00668
4	X8	σ^2 yld	0.01473	0.00358	7.04534	-0.43059	-0.01841	0.02072	-0.00447
5	X9	σ^2_{ylA}	0.04080	2.26807	-1.66760	0.02983	0.62010	0.00777	0.04284
6	X12	σ^2_{ydA}	0.00611	0.12399	7.27783	0.00172	-0.07662	0.00867	-0.00774
7	X15	σ^2_{yd}	-0.00086	0.97641	-4.23398	0.22779	0.00789	-0.01755	0.03064
8	X16	σ^2_{yA}	0.01338	0.45293	8.53472	0.00120	-0.26761	0.03869	0.04164
9	X19	σ^2_{ld}	-0.00144	2.12815	-2.52835	0.22082	0.04443	-0.01472	0.00155
10	X20	σ^2_{lA}	0.00367	-0.16362	1.47087	0.03293	-0.24511	0.10096	0.01095
11	X23	σ^2_{dA}	0.00413	1.55548	12.63528	0.03169	0.40195	0.05571	0.00870
12	X26	σ^2_d	0.01382	-0.00928	78.90910	0.00000	-0.03851	0.00439	-0.00501
13	X27	σ^2_A	0.03419	6.18078	48.69436	0.17726	0.55953	0.15836	0.02804
14	X30	$\sigma^2_{r(yl)}$	0.00980	0.09526	9.75922	0.03098	0.08518	0.00002	-0.00001
15	X31	σ^2_{yl}	0.00385	21.76241	-9.31119	0.33373	0.30451	0.05725	-0.00068
16	X32	σ^2_l	0.30422	-0.60523	28.52121	-0.16538	0.04757	0.04492	-0.00099
17	X33	σ^2_y	0.01100	9.03929	-5.03826	0.00000	5.28791	22.66469	0.52248
F-test			9.62	12.62	12.11	12.25	11.40	3.75	4.20
Prob>IFI			0.0014	0.0006	0.0006	0.0006	0.0008	0.0315	0.0224

y = year, l = location, d = pubescence density, A = additive, e = error, and σ^2 = variance.

component lines. The value of σ^2A were higher than σ^2e for maturity, protein and oil, and lower for yield, height, lodging and size. The estimates for σ^2d (Pub. Density) were generally very low or negative compared to σ^2A for all the characters except height. The interaction variances of additive (A) with year (Y), location (L), and pub. density (d) were lower than their main effects. The estimates of 'F' and their probabilities are presented for each for interpretation. The F-tests were also significant for the Weighted Least Square Regression model used to estimate the components of variance.

4.3.2.2 Additive & Additive x Additive Model

The estimates of variances of the full model are presented in Table 20. The values were higher for σ^2AA (Additive x Additive) than σ^2A (Additive) for all the characters except protein. The estimates of σ^2A under this model were either very low or even negative. When compared with σ^2e (Error), the estimates of σ^2e were higher than σ^2AA for all except oil. However, when compared with σ^2d(Pub.density), the estimates of σ^2AA were higher for yield, maturity, lodging, size and oil, and lower for height and protein. The comparison of year and location variances showed a mixed trend. The estimates were higher for σ^2l (Location) than σ^2y (Year) for yield and height, while lower for maturity, lodging, size, protein and oil. The interaction variances were lower than their respective main effects.

The estimates of components of variances under the selected model based on PCA are presented in Table 21. When PCA was applied to select the important components, the number and the component line deleted from the full model differed considerably with the characters. A minimum of two (seed size) and maximum of seven (lodging) components were deleted in the selected model. The F-test for the Weighted Regression analysis were all significant. In this model, the estimates of σ^2A increased compared to the full model, and were nearly identical for some of the traits like yield, maturity and height. However, the estimates were negative for lodging, size and oil for σ^2A, and for protein in the case of

Table 20. Estimates of components of variance in Additive, Additive x Additive (A,AxA)- Full Model.

#	X#	Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1	X1	σ^2_e	0.20570	3.05000	68.69000	0.32890	0.60280	0.00600	0.00600
2	X2	σ^2_{yldA}	0.11155	-0.46666	5.87583	-0.11488	0.40895	0.05983	-0.07600
3	X4	σ^2_{yldAA}	-0.08890	0.36666	-10.21833	0.06883	-0.13990	0.05766	0.09600
4	X5	σ^2_{ldA}	-0.04760	-0.30666	4.58291	-0.04850	-0.52861	-0.31166	-0.02666
5	X7	σ^2_{ldAA}	0.03200	0.32666	-1.85916	0.05124	0.34672	0.22666	0.01666
6	X8	σ^2_{yld}	0.01362	0.00450	7.02800	-0.43726	-0.02184	0.02250	-0.00366
7	X9	σ^2_{ylA}	-0.05630	-0.21250	-18.46666	-0.05612	0.37078	0.22450	-0.03133
8	X11	σ^2_{ylAA}	0.06940	1.68500	12.75666	0.06309	0.15516	-0.08700	0.05133
9	X12	σ^2_{ydA}	-0.08705	-0.50833	-12.01333	0.12084	-0.28643	-0.20958	-0.01791
10	X14	σ^2_{ydAA}	0.06608	0.47333	14.39333	0.08735	0.14343	0.16583	0.00916
11	X15	σ^2_{yd}	-0.00025	0.97783	-4.18566	0.22846	0.00984	-0.01733	0.03050
12	X16	σ^2_{yA}	0.06732	0.10708	-6.14770	-0.01248	-0.15934	-0.24000	0.00958
13	X18	σ^2_{yAA}	-0.03897	0.21416	10.54208	0.01028	-0.06532	0.17000	0.01916
14	X19	σ^2_{ld}	-0.00090	2.15925	-2.55258	0.22208	0.04672	-0.01508	0.00141
15	X20	σ^2_{lA}	0.00489	0.96666	9.95958	0.08471	-0.25977	-0.17208	0.01979
16	X22	σ^2_{lAA}	-0.00126	-0.17666	-6.46083	-0.03724	0.02387	0.15583	-0.00791
17	X23	σ^2_{dA}	0.02831	-7.83833	-84.08000	-0.14846	-0.53691	0.15333	-0.03041
18	X25	σ^2_{dAA}	-0.01634	7.08833	73.06500	0.13339	0.68990	-0.08333	0.02916
19	X26	σ^2_{d}	0.01358	0.00000	79.05333	-0.02140	-0.03501	0.00529	-0.00491
20	X27	σ^2_{A}	-0.01594	2.76322	17.92041	-0.04512	-0.19783	0.15187	-0.02031
21	X29	σ^2_{AA}	0.03299	2.00270	18.37583	0.14573	0.51701	0.00003	0.03312
22	X30	$\sigma^2_{r(yl)}$	0.00974	0.09579	9.75762	0.03097	0.08525	0.00002	-0.00001
23	X31	σ^2_{yl}	0.00442	21.78658	-9.29325	0.33411	0.30848	0.04861	-0.00006
24	X32	σ^2_{l}	0.30425	-0.60779	28.51375	-0.16569	0.04621	0.05079	-0.00087
25	X33	σ^2_{y}	0.01073	9.04491	-4.95760	0.01599	5.28597	22.66950	0.52308

y = year, l = location, d = pubescence density, A = additive, AA = additive x additive, e = error, and σ^2 = variance.

Table 21. Estimates of components of variance in Additive, Additive x Additive (A, AxA)-selected Model based on Principal Component Analysis (PCA).

#	X#	Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1	X1	σ^2_e	0.20570	3.05794	68.69000	0.32923	0.60280	0.00600	0.00572
2	X2	σ^2_{yldA}	0.11372	-0.46136	9.34367	0.04498	0.16505	0.02556	-0.07993
3	X4	σ^2_{yldAA}	-0.08976	0.36136	-13.08931	-0.04660	-0.04234	0.08825	0.08968
4	X5	σ^2_{ldA}	-0.04876	-0.30666	1.86026	x	-0.40041	-0.29453	-0.03164
5	X7	σ^2_{ldAA}	0.03246	0.32666	0.70891	x	0.29544	0.21137	0.02819
6	X8	σ^2_{yld}	x	0.00450	x	0.02004	-0.00893	0.011623	-0.00260
7	X9	σ^2_{ylA}	0.00572	-0.09776	-8.01870	-0.05601	0.37078	0.16911	-0.03142
8	X11	σ^2_{ylAA}	0.02880	1.48121	5.37865	0.06297	0.15516	-0.06474	0.05142
9	X12	σ^2_{ydA}	-0.08829	-0.50833	-18.15146	x	-0.14617	x	-0.02505
10	X14	σ^2_{ydAA}	0.06657	0.47333	20.49318	x	0.08732	x	0.02050
11	X15	σ^2_{yd}	0.00754	0.97783	-0.80995	x	x	x	0.02984
12	X16	σ^2_{yA}	x	0.05104	-11.37168	-0.01248	-0.15934	x	0.00958
13	X18	σ^2_{yAA}	x	0.31473	14.23109	0.01028	-0.06532	x	0.01916
14	X19	σ^2_{ld}	0.00664	x	0.92101	-0.00547	x	0.00197	x
15	X20	σ^2_{lA}	-0.02612	x	x	0.08471	-0.25977	-0.14439	0.01979
16	X22	σ^2_{lAA}	0.01902	x	x	-0.03724	0.02387	0.14470	-0.00791
17	X23	σ^2_{dA}	0.02913	-7.83833	x	-0.15220	-0.61016	0.0485	x
18	X25	σ^2_{dAA}	-0.01667	7.08833	x	0.14414	0.71920	-0.00041	x
19	X26	σ^2_{d}	x	1.07962	78.19953	0.11368	-0.00995	-0.00337	-0.00400
20	X27	σ^2_{A}	0.01771	2.81156	22.90020	-0.04513	-0.19783	0.28093	-0.02031
21	X29	σ^2_{AA}	0.01351	1.91437	15.14541	0.14573	0.51701	-0.06687	0.03312
22	X30	$\sigma^2_{r(yl)}$	0.00974	x	9.75762	x	0.08525	0.00003	x
23	X31	σ^2_{yl}	0.00365	21.99061	-9.36462	0.39605	0.30848	0.05089	-0.00008
24	X32	σ^2_{l}	0.30465	-0.61887	28.64379	-0.16569	0.04621	0.04965	-0.00087
25	X33	σ^2_{y}	0.01212	9.03869	-4.92110	x	5.28597	x	0.52308
F-test			18.44	15.04	5.95	8.19	7.62	5.24	9.91
Prob>IFI			0.0059	0.0229	0.0287	0.0143	0.1223	0.0244	0.019

y = year, l = location, d = pubescence density, A = additive, AA = additive x additive, e = error, and σ^2 = variance.

σ^2AA. The estimates of σ^2e were identical in both the models, and were higher than σ^2A and σ^2AA in most cases. Here again the estimates of σ^2d were low, but were positive for maturity, height and lodging, and negative for size, protein and oil. The variances due to year and location showed a mixed trend, being positive for some and negative for others. However, σ^2l was high for yield and height, and low for size and protein, and negative for maturity, lodging and oil. Year variances were high for maturity, size and oil, and low for yield.

4.3.2.3 Additive & Dominance Model

The estimates of components of variances of this model are presented in Table 22. The estimates of σ^2D (Dominance) were much higher than σ^2A (Additive) for all the traits except protein. Likewise, σ^2D were too high compared to σ^2e for all the traits studied. However, the estimates of σ^2d (Pub. density) were either very low or negative for all the traits except height. The estimates of σ^2l (Location) were high for yield, height, and low for size and protein, and negative for maturity, lodging and oil. The estimates of σ^2y (Year) were high for protein, maturity and oil, and low for yield, and negative for height. The interaction variances were high where dominance (D) was involved. However, this showed plus and minus effects, and differed considerably with the characters and component lines. In the selected model (Table 23), the number and type of component lines deleted from the full model differed considerably with the characters. A minimum of three and a maximum of eight lines were deleted from the full model. Also, the estimates of F-test were significant for all the traits. The estimates of components of variances changed in the selected models compared to the respective full models. However, σ^2e (Error) remained the same. Here also, the σ^2D were higher than the estimates of σ^2A for all characters. The estimate were negative for σ^2A in case of seed size and oil. Here again, the estimates of σ^2d(Pub. Density) were either very low or negative for most of the traits. In this case, year variances were not very high for maturity, lodging and protein, and hence not included in the selected model. However, σ^2y were high for seed size and

Table 22. Estimates of components of variance in Additive & Dominance (A & D)-Full Model.

#	X#	Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1	X1	σ^2_e	0.20570	3.05000	68.69000	0.32890	0.60280	0.00600	0.00600
2	X2	σ^2_{yldA}	0.06833	-0.28840	0.90809	-0.08141	0.34093	0.08786	-0.02932
3	X3	σ^2_{yldD}	-18.45674	76.12456	-2121.453	14.29065	-29.04498	11.97231	19.93079
4	X5	σ^2_{ldA}	-0.03181	-0.14557	3.66608	-0.02323	-0.35762	-0.19988	-0.01847
5	X6	σ^2_{ldD}	6.58662	67.23842	-382.6758	10.54716	71.36706	46.65523	3.43053
6	X8	σ^2_{yld}	0.01362	0.00450	7.02800	-0.43704	-0.02184	0.02250	-0.00366
7	X9	σ^2_{ylA}	-0.02207	0.61843	-12.17585	-0.02501	0.44730	0.18159	-0.00601
8	X10	σ^2_{ylD}	14.28473	346.84676	2625.7289	12.98627	31.93825	-17.90737	10.56603
9	X12	σ^2_{ydA}	-0.05447	-0.27491	-4.91542	0.07776	-0.21570	-0.12780	-0.01339
10	X13	σ^2_{ydD}	13.60205	97.42710	2962.6072	-17.98113	29.52315	34.13379	1.88679
11	X15	σ^2_{yd}	-0.00025	0.97783	-4.18566	0.22834	0.00984	-0.01733	0.03050
12	X16	σ^2_{yA}	0.04816	0.21232	-0.96715	-0.00742	-0.19144	-0.15645	0.01900
13	X17	σ^2_{yD}	-8.03004	44.12017	2171.7596	2.11845	13.45665	35.02145	3.94849
14	X19	σ^2_{ld}	-0.00091	2.15319	-2.55258	0.22196	0.04672	-0.01508	0.00141
15	X20	σ^2_{lA}	0.00426	0.00984	6.78462	0.06641	-0.24803	-0.09550	0.01590
16	X21	σ^2_{lD}	-0.26094	-36.39484	-1330.987	-7.67296	4.91931	32.10300	-1.630901
17	X23	σ^2_{dA}	0.02014	-4.29416	-47.54750	-0.08176	-0.19195	0.11166	-0.01583
18	X24	σ^2_{dD}	-3.35299	1454.0170	14987.692	27.36324	141.51880	-17.09402	5.98290
19	X26	σ^2_{d}	0.01359	0.00000	79.02210	0.00000	-0.03530	0.00532	-0.00493
20	X27	σ^2_{A}	0.00032	3.75086	26.98241	0.02673	0.05712	0.32604	-0.00397
21	X28	σ^2_{D}	6.78329	411.69165	3777.4732	29.95760	106.28051	13.22055	6.80942
22	X30	$\sigma^2_{r(yl)}$	0.00974	0.09579	9.75762	0.03097	0.08525	0.00003	-0.00001
23	X31	σ^2_{yl}	0.00442	21.78658	-9.29325	0.33411	0.30848	0.04681	-0.00006
24	X32	σ^2_{l}	0.30425	-0.60779	28.51375	-0.16569	0.04621	0.05079	-0.00087
25	X33	σ^2_{y}	0.01073	9.04491	-4.95679	0.00000	5028597	22.66950	0.52308

y = year, l = location, d = pubescence density, A = additive, D = dominance, e = error, and σ^2 = variance.

Table 23. Estimates of components of variance in Additive & Dominance (A & D)- selected Model based on Principal Component Analysis (PCA).

#	X#	Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
1	X1	σ^2_e	0.20570	3.05794	68.6900	0.32890	0.60322	0.00600	0.00450
2	X2	σ^2_{yldA}	0.04294	-0.56523	x	0.02221	0.01256	0.31442	-0.04410
3	X3	σ^2_{yldD}	-14.09533	142.42842	x	-9.62933	10.75451	-11.38408	21.60899
4	X5	σ^2_{ldA}	x	-0.00693	2.18939	x	-0.18919	-0.31277	-0.00423
5	X6	σ^2_{ldD}	x	33.825457	-579.5404	x	51.11211	58.23327	1.97255
6	X8	σ^2_{yld}	0.01369	0.00727	6.56154	-0.43443	-0.00614	x	-0.00225
7	X9	σ^2_{ylA}	0.01994	0.68533	x	-0.03163	0.04700	0.01393	0.00048
8	X10	σ^2_{ylD}	5.93000	337.64839	x	14.89305	15.57588	19.66893	9.03945
9	X12	σ^2_{ydA}	-0.04187	0.12852	-7.93421	x	x	-0.30173	-0.00628
10	X13	σ^2_{ydD}	11.43999	x	3499.3121	x	x	51.97255	1.15780
11	X15	σ^2_{yd}	x	x	-4.10942	0.22723	x	x	0.02979
12	X16	σ^2_{yA}	x	x	x	x	x	x	0.01561
13	X17	σ^2_{yD}	x	x	x	x	x	x	4.76394
14	X19	σ^2_{ld}	-0.00001	3.12943	-2.36521	0.22176	x	-0.00383	x
15	X20	σ^2_{lA}	-0.01677	x	0.08161	0.06972	-0.04792	x	0.00913
16	X21	σ^2_{lD}	3.92001	x	293.81769	-8.62716	13.09301	10.71161	x
17	X23	σ^2_{dA}	0.00452	-4.49426	x	-0.08013	-0.30173	0.19833	-0.02291
18	X24	σ^2_{dD}	-0.08736	1502.5641	x	29.56741	156.4775	-25.98290	6.70940
19	X26	σ^2_{d}	x	0.00000	79.96204	0.00000	-0.01098	-0.00322	-0.00422
20	X27	σ^2_{A}	0.02437	3.84559	26.50796	0.02303	-0.03865	0.24221	-0.00060
21	X28	σ^2_{D}	2.77687	417.70152	4861.0278	31.01456	99.56659	12.45653	5.99571
22	X30	$\sigma^2_{r(yl)}$	0.00974	x	9.79534	0.03097	x	0.00002	x
23	X31	σ^2_{yl}	0.00365	26.18191	-9.45016	0.33419	0.51768	22.71823	-0.00011
24	X32	σ^2_{l}	0.30464	-2.72567	28.55448	-0.16573	0.02685	-11.28412	-0.00084
25	X33	σ^2_{y}	0.01212	x	-4.32704	x	5.26561	x	0.52309
F-test			22.12	23.96	4.10	15.38	7.08	3.95	9.19
Prob>IFI			0.0005	0.0001	0.024	0.0014	0.0068	0.0480	0.0460

y = year, l = location, d = pubescence density, A = additive, D = dominance, e = error, and σ^2 = variance.

oil. The estimates of σ^2l were high and positive for height and yield, low for seed size, while negative for rest of the characters.

4.4 Estimates of Heritability and Gain from Selection

4.4.1 Additive Model

The estimates of heritability (h^2, H), Gain from selection(Gs) at 5 % selection intensity and Gain from selection as percent of mean (Gs %) of the seven characters under the different models are presented in Tables 24-28. The estimates from the Additive model are in Table 24 . In this case the heritability estimates are narrow -sense (h^2) which were computed as the ratio of σ^2A/σ^2P . The phenotypic variance was calculated as explained in the chapter materials and methods.

The heritability estimate was highest for maturity (0.86) and lowest for oil (0.36). For yield h^2 was 0.50, and those for protein and seed size were 0.57 each, while for height and lodging were 0.73 each. The gain from selection showed a similar trend. The Gs % was highest (33.6 %) for lodging and lowest for oil (1.1%). Yield showed a response of 8.0 % , seed size 6.1 % , while maturity and height had 16.4 % and 11.9 % respectively.

4.4.2 Additive & Additive x Additive Model

The estimates of heritability, Gs and Gs % calculated from this model are presented in Table 25 . Here also the trend was nearly similar to the Additive model. However, the estimates were comparatively much lower. Yield showed the lowest heritability (0.24) followed by protein and oil. Maturity exhibited the highest estimate of h^2 (0.49) and those of height, lodging and seed size were around 0.40. The Gs and Gs % also showed the similar trends. The gain from selection for yield was 0.2 t/ha, and 0.4 % and 0.2 % for protein and oil respectively. When compared at Gs %, lodging exhibited the highest gain of 22.2 %, followed by maturity, height, yield, seed size, and protein and oil.

Table 24. Estimates of Heritability, Gain from Selection(Gs) and Gs as percentage of mean(Gs %) in Additive Model.

#	Character	h^2	Gs	Gs %
1.	Yield	0.50	0.3	8.0
2.	Maturity	0.86	5.0	16.4
3.	Height	0.73	12.3	11.9
4.	Lodging	0.73	0.7	33.6
5.	Seed size	0.57	1.2	6.1
6.	Protein	0.57	0.6	1.6
7.	Oil	0.36	0.2	1.1

h^2 = narrow sense heritability.

Table 25. Estimates of Heritability, Gain from Selection(Gs) and Gs as percentage of mean(Gs %) in Additive and Additive x Additive Model.

#	Character	h^2	Gs	Gs %
Full Model:				
1.	Yield	0.24	0.2	5.4
2.	Maturity	0.49	3.1	10.4
3.	Height	0.38	7.6	7.4
4.	Lodging	0.39	0.5	22.2
5.	Seed size	0.43	1.0	5.0
6.	Protein	0.27	0.4	1.1
7.	Oil	0.33	0.2	1.1
Selected Model:				
1.	Yield	0.27	0.2	5.0
2.	Maturity	0.48	3.1	10.2
3.	Height	0.66	10.3	10.0
4.	Lodging	0.47	0.5	24.6
5.	Seed size	0.30	0.7	3.5
6.	Protein	0.58	0.8	2.1
7.	Oil	0.31	0.2	1.1

h^2 = narrow sense heritability.

When these estimates were calculated from the A & AxA selected model (Table 25), there were some changes in the estimates. In this case, height exhibited the highest heritability (0.60) followed by protein (0.58), maturity (0.48), lodging (0.47), oil (0.31) seed size (0.30), and yield (0.27). Here the heritability for protein increased considerably compared to the Additive model (0.27). Yield, however, had the lowest heritability in this case also.

The estimates of Gs and Gs % were influenced accordingly. The Gs for yield was 0.2 t / ha, while for protein and oil were 0.8 % and 0.2% respectively. Height showed a very high response (10.3 cm). The Gs % showed a response of 24.6 % for lodging, followed by maturity (10.2 %), height (10.0 %), yield (5.6 %), seed size (3.5 %), protein (2.1 %) and oil (1.1 %).

4.4.3 Additive and Dominance Model

The estimates of heritability, Gs and Gs % of the characters in full model are presented in Table 26. Since the estimates of σ^2A were very low in this model, only broad sense heritability (H) were computed. Also, the Gs and Gs % were calculated using the broad sense heritability.

The estimates of heritability were moderate for most of the traits (Table 26). Lodging exhibited the highest heritability (0.57), followed by seed size (0.45), yield (0.44), oil (0.37), maturity (0.32), height (0.28) and protein (0.24). The Gs and Gs % were accordingly influenced. However, these estimates were very high (above 100 %) for some traits . Also, in the selected model, (Table 26), the trend was almost similar. However, height had the highest heritability (0.83), followed by lodging (0.63), seed size (0.49), oil (0.34), protein and maturity (0.33), and yield (0.31). The estimates of Gs and Gs % were were again very high for lodging, height, seed size, yield and maturity.

Table 26. Estimates of Heritability, Gain from Selection(Gs) and Gs as percentage of mean(Gs %) in Additive and Dominance Model.

#	Character	H	Gs	Gs %
Full Model:				
1.	Yield	0.44	3.6	106.1
2.	Maturity	0.32	23.7	78.3
3.	Height	0.28	66.8	64.8
4.	Lodging	0.57	8.5	387.9
5.	Seed size	0.45	14.8	77.0
6.	Protein	0.24	3.7	9.4
7.	Oil	0.37	0.3	17.1
Selected Model:				
1.	Yield	0.31	1.9	56.9
2.	Maturity	0.33	11.8	38.8
3.	Height	0.83	130.8	126.9
4.	Lodging	0.63	9.1	412.1
5.	Seed size	0.49	14.4	75.1
6.	Protein	0.33	4.2	10.7
7.	Oil	0.34	3.0	15.4

H = broad sense heritability.

4.4.4 General Model ANOVA

Also, the estimates of broad-sense heritability (H), Gs and Gs% were computed using the variances from the General ANOVA Model (Table 27). These estimates were similar to the Additive model. The heritability was highest for height (0.99), followed by maturity and lodging (0.88 each), seed size (0.79), protein (0.72), yield (0.62), and oil (0.46). The estimates of Gs showed a 0.43 t /ha response for yield at 5 % selection intensity. When compared on the basis of Gs%, it was highest for height (62.7 %), followed by lodging (56.4 %), while for yield, maturity and seed size it ranged 10-20 %, and protein and oil exhibited a low response (2-3 %).

4.4.5 Parent-Offspring Regression

Parent-offspring regression analysis was also used to compute heritability and to compare the results with the other models. Here the regression of '90 means on '89 means was done by PROC REG of SAS (1985). Further, the adjustments for inbreeding of parents was done as suggested by Smith and Kinman (1965). The estimates of F-test, C.V., b, and h^2 are presented in Table 28. The regression model was adequate to estimate reg-coefficient (b). The heritability computed in this way showed a different trend. The estimates were very low for yield and lodging (0.02 & 0.01 respectively), and moderately high for height (0.77).

4.5 Estimates of Correlation Coefficients

4.5.1 Average Means Correlation

The estimates of Pearson's correlation coefficients (Genotypic) with their significance are presented in Tables 29-33. The r-coefficients of variables using overall genotypic means (AVE) are given in Table 29. Yield showed a significant positive correlation with maturity, seed size and protein, and non-significant with height, lodging and oil. The estimates, however, was negative with height. Maturity had a significant

Table 27. Estimates of Heritability, Gain from Selection(Gs) and Gs as percentage of mean(Gs %) in General Model ANOVA.

#Character		H	Gs	Gs %
1.	Yield	0.67	0.43	12.8
2.	Maturity	0.88	6.3	20.8
3.	Height	0.99	64.7	62.7
4.	Lodging	0.88	1.3	56.4
5.	Seed size	0.79	1.8	9.2
6.	Protein	0.72	1.1	2.7
7.	Oil	0.46	0.3	1.8

Table 28. Estimates of Heritability by Parent-Offspring Regression (Regression of 1990 on 1989).

#	Character	F	P>IFI	C.V.	b	h^2
1.	Yield	9974.1	0.0001	21.9	0.037	0.02
2.	Maturity	11473.7	0.0001	20.5	0.338	0.17
3.	Height	20414.3	0.0001	15.3	1.151	0.77
4.	Lodging	2488.8	0.0001	43.9	0.024	0.01
5.	Seed size	36006.8	0.0001	11.6	0.215	0.11
6.	Protein	69019.8	0.0001	8.3	0.437	0.22
7.	Oil	428691.7	0.0001	3.3	0.215	0.11

$h^2 = b/2\ rxy$
$= b \times 32/63$
$= 0.51\ b$

Table 29. Estimates of correlation coefficients and their respective significance among variables using average genotypic means(AVE).

Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield	___	0.27**	-0.06	0.01	0.38**	0.24**	0.03
Maturity		___	0.28**	0.45**	0.44**	0.45**	0.32**
Height			___	0.55**	-0.11*	-0.09	-0.14**
Lodging				___	0.26**	0.28**	0.17**
Seed size					___	0.75**	0.50**
Protein						___	0.59**
Oil							____

*,** Significant at $p<0.05$ and $p<0.01$, respectively.

positive correlation with all other characters. On the contrary, lodging exhibited a very poor correlation with yield, but significant positive with all other traits. Seed size and protein also showed a significant positive correlation with all other traits. Oil also had a positive association with all except yield. These correlation estimates have been used as AVE in the text and tables.

4.5.2 Effects of Pubescence Density, Year and Location on Correlation

In order to study the effects of pubescence density on the estimates of r-coefficients, the correlations were generated for pubescence density and the estimates were compared with the overall or average (AVE) coefficients (Table 30). Here the estimates in general were in agreement with the overall (AVE) estimates of Table 29. The association of yield with maturity, seed size, and protein were significant and positive in all cases; while correlations with lodging and oil were not significant. However, the association of yield with height were not strong being significant negative in dense, and significant positive in the normal type. The r-coefficients of maturity with height, lodging, seed size, protein and oil were significant and positive in all the cases. However, height showed a strong positive association with lodging, and a weakly negative association with seed size, protein and oil. The association of lodging with seed size and protein were significant positive both in dense and normal types, and were in agreement with the AVE estimates. Moreover, with oil, the correlation was significant positive in normal , and very weak in the dense type. Likewise, the association of seed size with protein and oil, and of protein with oil were all highly significant positive in all the cases.

The correlation coefficients were also computed by year and location, and the estimates were compared to see how these factors affect the coefficients. The correlation coefficients by year are presented in (Appendix D.1). Here most of the correlation coefficients were identical to the overall (AVE) estimates of Table 29 with some exceptions. The association between yield and maturity was negative in '89, but

Table 30. Estimates of correlation coefficients and their respective significance among variables by Pubescence Density.

Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield							
D	____	0.28**	-0.16*	0.04	0.50**	0.31**	0.08
N	____	0.31**	0.15*	0.04	0.28**	0.17**	0.04
AVE	**____**	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity							
D		____	0.29**	0.47**	0.42**	0.49**	0.35**
N		____	0.20**	0.39**	0.46**	0.42**	0.34**
AVE		**____**	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height							
D			____	0.58**	-0.24**	-0.12	-0.12
N			____	0.42**	-0.01	-0.08	-0.10
AVE			**____**	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging							
D				____	0.14*	0.23**	0.08
N				____	0.38**	0.36**	0.31**
AVE				**____**	**0.26****	**0.28****	**0.17****
Seed size							
D					____	0.74**	0.46**
N					____	0.74**	0.56**
AVE					**____**	**0.75****	**0.50****
Protein							
D						____	0.50**
N						____	0.69**
AVE						**____**	**0.59****
Oil							
D		D= Dense Pub.					____
N		N= Normal Pub.					____
AVE		*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively					**____**

significant positive in '90. Likewise, between yield and height was non-significant in '89, but significant negative in '90. However, with lodging, the association was not significant. The r-coefficient with seed size and protein were significant and positive, while with oil it showed significant negative in '89. These coefficients were in full agreement with the AVE for seed size, protein and lodging, but partial for rest of the characters. The estimates of maturity with other variables were similar to AVE in most cases and differed for some. The association of maturity with protein showed a negative correlation in both the years, however, the AVE had significant positive. Likewise, for oil, the estimates were positive in one and negative in another year. The correlations of lodging with other variables were mostly in agreement to the AVE estimates. The r-coefficients were very high between height and lodging. The association of seed size with other variables were similar in some and variable in others. Seed size had a strong positive correlation with yield in '90, but showed a significant negative association in '89. There was almost a negative association between height and seed size, and also the r-coefficient were non-significant with lodging and protein in either year. It also showed a negative correlation with oil in '90. Protein on the other hand showed a positive association with yield and seed size in all cases, however, negative in both years with maturity, height and oil, and no association with lodging. The association of protein and oil were strongly negative in both the years in contrast to the overall estimates of Table 29.

The effects of location on the estimates of r-coefficients are presented in Appendix D.2. The trend was agreeable to the overall estimates (AVE) in some cases, while different in others. The association of yield and maturity negative at ING and positive at LEN, with height it was significant positive at LEN and negative at ING. Yield had a positive association with lodging at LEN. However, the correlation coefficients of yield with seed size, protein and oil were almost stable and in agreement with the AVE estimates. Seed size showed a strong positive association with yield, and protein had a significant positive association at LEN. The association of yield and oil was very low and negative.

However, the association of maturity with height were significant and positive in all cases. Here too, the association of maturity and lodging was very strong and positive. However, with seed size, protein and oil the r-coefficients were poor and non-significant at ING, and significant positive in other cases. The correlation of height with lodging were very strong and positive in all cases, and non-significant with seed size, protein and oil at LEN, and significant negative in all other cases. Lodging on the other hand, had a positive association with seed size, protein and oil. Seed size exhibited a strong positive correlation with protein and oil in all cases. Also, the association of protein and oil was significant and positive in all cases, contradictory to the year estimates.

4.5.3 Effects of Interactions of Year, Location & Pubescence Density on Correlation

In addition to the main effects, the interaction effects of Y x L, Y x D, L x D and Y x L x D on the estimates of r-coefficients were also computed and compared to have a better understanding of the association among characters, and how they are influenced by these factors. These estimates were also compared with the overall (AVE) estimates of Table 29. The effects of Y x D on the estimates of r-coefficients are presented in Table 31. In this case, the estimates were stable for some and variable for others. For example, yield showed a strong positive association with seed size and protein, poor or negative with height, lodging and oil, but variable with maturity. It showed a negative association with in '89 and positive in '90 both with dense and normal types. The association of maturity with height and lodging were significant positive and stable in all cases and variable for seed size, protein and oil. Height also showed a strong positive correlation with lodging, and those with seed size, protein and oil were weakly negative in general. The association of lodging with seed size and oil were weak and variable, and nonsignificant (negative) with protein. The relationship of seed size with protein were mostly significant positive, and with oil were weak and negative. It was interesting to note that the AVE r- coefficient

Table 31. Estimates of correlation coefficients and their respective significance among variables by Year x Pubescence Density.

Variable		Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield								
'89	D	____	-0.30**	-0.15	-0.03	0.51**	0.57**	-0.29**
	N	____	-0.18*	0.35**	0.14	0.26**	0.39**	-0.25**
'90	D	____	0.48**	-0.16	-0.02	0.50**	0.15	0.03
	N	____	0.59**	-0.15	-0.11	0.37**	0.27**	-0.14
	AVE	____	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity								
'89	D		____	0.52**	0.40**	-0.43**	-0.57**	0.33**
	N		____	0.35**	0.26**	-0.14	-0.33**	0.13
'90	D		____	0.35**	0.43**	0.21*	-0.16*	-0.14
	N		____	0.26**	0.27**	0.38**	0.06	-0.08
	AVE		____	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height								
'89	D			____	0.56**	-0.28**	-0.34**	0.06
	N			____	0.55**	0.22*	-0.12	-0.12
'90	D			____	0.68**	-0.32**	-0.22*	-0.23*
	N			____	0.48**	-0.18*	-0.17*	-0.08
	AVE			____	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging								
'89	D				____	-0.07	-0.12	0.06
	N				____	0.21*	-0.14	0.18*
'90	D				____	-0.09	-0.10	-0.21*
	N				____	0.12	-0.10	-0.10
	AVE				____	**0.26****	**0.28****	**0.17****
Seed size								
'89	D					____	0.41**	-0.15
	N					____	0.13	-0.03
'90	D					____	0.28**	0.07
	N					____	0.34**	-0.07
	AVE					____	**0.75****	**0.50****
Protein								
'89	D						____	-0.62**
	N						____	-0.65**
'90	D						____	-0.58**
	N						____	-0.66**
	AVE						____	**0.59****
Oil								
'89	D							____
	N		D = Dense Pub.					____
'90	D		N= Normal Pub.					____
	N		*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.					____
	AVE							____

of seed size and protein with oil were strongly positive. However, when compared by year and density, the estimates were significant negative with protein , and non-significant negative with seed size in all the cases.

Likewise, the estimates of L x D also showed an interesting trend(Table 32). Here the coefficients were in agreement with the overall (AVE) in most cases. However, association of yield with seed size and protein, maturity with height and lodging, lodging with seed size, protein and oil, seed size with protein and oil, and protein with oil, were all fairly stable and positive. It was interesting to note that association of oil with seed size and protein were very high and positive here in all the cases.

The estimates were further computed by density within location and year (Table 33) and compared with the overall (AVE) estimates of Table 29. Here again, some of the combinations were stable, while others varied due to interactions of year, location and pubescence density. As is evident, the association of yield with seed size and protein, and of maturity with height and lodging were stable in most cases. Also, the r-coefficient between maturity and protein were almost negative. Similarly, the estimate of height with lodging were high and significantly positive, and not very stable with seed size, protein and oil. In this case lodging did not show a strong association with seed size, protein and oil. The correlation of seed size and protein were fairly high and positive in most cases, and weak or negative with oil. Here again, the correlation of protein and oil were very strong and negative in all cases contradictory to the overall (AVE) estimate in Table 29.

The r-coefficients by year x location are presented in Appendix D.3. It is evident that the estimates were stable for some combinations and variable for others. For example, the association of yield with height and lodging were very weak and negative in all cases, and significant positive with seed size in all cases except one. However, the estimates showed Y x L interaction effects for maturity, protein and oil. The correlation of maturity with height and lodging were strong and positive in all cases except '89-ING for lodging. However, it showed a mixed trend for seed size, protein and oil. It was interesting to note

Table 32. Estimates of Correlation Coefficients and their respective significance among variables by Location x Pubescence Density.

Variable		Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield								
ING	D	___	-0.10	-0.17	0.13	0.55**	0.31**	0.08
	N	___	-0.10	0.15	-0.07	0.07	-0.06	-0.17
LEN	D	___	0.23**	0.13	0.12	0.44**	0.41**	0.02
	N	___	0.28**	0.49**	0.34**	0.36**	0.32**	0.03
	AVE	____	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity								
ING	D		___	0.61**	0.49**	0.04	0.23**	0.05
	N		___	0.59**	0.42**	-0.03	0.04	-0.02
LEN	D		___	0.28**	0.57**	0.59**	0.74**	0.51**
	N		___	0.27**	0.63**	0.70**	0.78**	0.59**
	AVE		____	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height								
ING	D			___	0.45**	-0.31**	-0.16	-0.15
	N			___	0.24**	-0.27**	-0.31**	-0.33**
LEN	D			___	0.68**	-0.12	-0.06	-0.07
	N			___	0.55**	0.22**	0.13	0.07
	AVE			___	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging								
ING	D				___	0.28**	0.28**	0.05
	N				___	0.45**	0.37**	0.30**
LEN	D				___	0.07	0.19*	0.12
	N				___	0.40**	0.39**	0.34**
	AVE				____	**0.26****	**0.28****	**0.17****
Seed size								
ING	D					___	0.73**	0.39**
	N					___	0.67**	0.50**
LEN	D					___	0.82**	0.50**
	N					___	0.81**	0.60**
	AVE					____	**0.75****	**0.50****
Protein								
ING	D						___	0.58**
	N						___	0.76**
LEN	D						___	0.45**
	N						___	0.63**
	AVE						____	**0.59****
Oil								
ING	D		D = Dense Pub.					___
	N		N= Normal Pub.					___
LEN	D		ING = Ingham					___
	N		LEN = Lenawee					___
	AVE		*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.					____

Table 33. Estimates of correlation coefficients and their respective significance among variables by Year x Location x Pubescence Density.

Variable		Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield								
'89I	D	____	-0.47**	-0.30*	-0.00	0.65**	0.56**	-0.30**
	N	____	-0.29*	0.26*	0.16	0.32**	0.45**	-0.30*
'89L	D	____	-0.26*	0.27*	0.08	0.37**	0.37**	-0.40**
	N	____	-0.08	0.73**	0.29*	0.29*	0.23*	-0.23*
'90I	D	____	-0.02	0.08	0.18	0.31*	-0.21	0.04
'90L	D	____	0.07	-0.05	-0.00	0.25*	0.27*	-0.18
	N	____	0.29*	-0.02	0.24	0.22	0.36**	-0.40**
	AVE	**____**	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity								
'89I	D		____	0.73**	0.00	-0.77**	-0.64**	0.21
	N		____	0.67**	0.19	-0.41**	-0.40**	-0.17
'89L	D		____	0.42**	0.63**	-0.10	-0.59**	0.42**
	N		____	0.14	0.34**	0.17	-0.27*	0.40**
'90I	D		____	0.68**	0.61**	0.08	-0.17	-0.36**
	N		____	0.65**	0.53**	0.14	-0.28*	-0.04
'90L	D		____	0.69**	0.75**	-0.41**	-0.31**	-0.28*
	N		____	0.44**	0.63**	0.07	0.02	-0.32**
	AVE		**____**	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height								
'89I	D			____	0.20	-0.66**	-0.47**	0.04
	N			____	0.35**	-0.24*	-0.10	-0.34**
'89L	D			____	0.74**	0.15	-0.11	0.08
	N			____	0.62**	0.54**	0.15	-0.02
'90I	D			____	0.69**	0.07	-0.16	-0.22
	N			____	0.44**	0.01	-0.18	-0.05
'90L	D			____	0.67**	-0.50**	-0.27*	-0.21
	N			____	0.51**	-0.24	-0.13	-0.08
	AVE			**____**	**0.55****	**-0.11**	**-0.09**	**-0.14****

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

Table 33. Cont'd.....

Variable		Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Lodging								
'89I	D				___	-0.12	0.12	-0.18
	N				___	0.16	0.04	0.00
'89L	D				___	-0.01	-0.23	0.20
	N				___	0.22	-0.15	0.32*
'90I	D				___	0.40**	0.06	-0.20
	N				___	0.40**	0.01	-0.03
'90L	D				___	-0.41**	-0.22	-0.21
	N				___	0.00	-0.14	-0.16
	AVE				____	**0.26****	**0.28****	**0.17****
Seed size								
'89I	D					____	0.55**	-0.16
	N					____	0.36**	-0.15
'89L	D					____	0.20	-0.16
	N					____	-0.03	0.08
'90I	D					____	0.22	0.13
	N					____	0.30*	-0.01
'90L	D					____	0.37**	0.08
	N					____	0.29*	-0.17
	AVE					____	**0.75****	**0.50****
Protein								
'89I	D						____	-0.65**
	N						____	-0.48**
'89L	D						____	-0.72**
	N						____	-0.87**
'90I	D						____	-0.47**
	N						____	-0.61**
'90L	D						____	-0.63**
	N						____	-0.73**
	AVE						____	**0.59****
Oil								
'89I	D							____
	N							____
'89L	D							____
	N							____
'90I	D							____
	N							____
'90L	D							____
	N							____
	AVE							____

I= Ingham
L= Lenawee
D= Dense Pubescence
N= normal Pubescence

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.

that the r-coefficients were negative between maturity and protein when computed by location within year, and were opposite to the overall (AVE) estimates. Further, the association between height and lodging were all significantly positive, while with protein and oil were almost always negative, and with seed size it was variable. The association of lodging with seed size , protein and oil were variable, and those of seed size and protein significant positive except for '89-LEN. The estimates of seed size with oil were all weakly negative and non-significant as opposed to the AVE (0.49**). Here again, the association of protein and oil by year and location were highly significant and negative, while the AVE were highly significant positive.

4.6 Estimates of Regression Coefficients and Equations

SAS (1985) General and Stepwise Regression procedures were used to estimate the regression coefficients for the independent variables. In this case, yield, protein and oil were taken as the dependent variables, and for each the remaining six were considered independent. The general regression model produced the coefficients for the independent variables, and an estimate for the intercept. Further, in the stepwise regression model, less important variables were dropped, and estimates of remaining variables and the intercept were readjusted. The values of the stepwise procedure were used to develop the prediction equation for the three dependent variables.

The estimates of regression coefficients (b) with their T-test or F-test and respective probability for the general and stepwise regression for yield, protein and oil are presented in Tables 34-36. In case of yield, the regression coefficients for height and protein were not significant in the general model (Table 34). The coefficients were positive for seed size and maturity, and negative for others. In the stepwise regression, height and protein were dropped from the model, and estimates of intercept also decreased slightly. Using the coefficients of stepwise regression, the prediction equation for yield was developed as follows:

Table 34. Estimates of Regression coefficients by General and Stepwise Regression Analysis for Yield.

# Variable	General			Stepwise		
	b	ITI	P>ITI	b	IFI	P>IFI
1. Intercept	4.9435	5.14	0.0001	4.7727		
2. Maturity	0.0278	4.65	0.0001	0.0268	21.58	0.0001
3. Height	-0.0012	-0.48	0.6285	--------	-------	--------
4. Lodging	-0.1169	-2.86	0.0044	-0.1289	14.21	0.0002
5. Seed size	0.1468	7.22	0.0001	0.1424	79.24	0.0001
6. Protein	-0.0076	-0.53	0.5968	--------	-------	--------
7. Oil	-0.2377	-4.50	0.0001	-0.2434	25.17	0.0001

Table 35. Estimates of Regression coefficients by General and Stepwise Regression Analysis for Protein.

# Variable	General			Stepwise		
	b	ITI	P>ITI	b	IFI	P>IFI
1. Intercept	-1.2864	-0.42	0.6720	-4.9338		
2. Yield	-0.0772	-0.52	0.5968	------	------	------
3. Maturity	0.0665	3.46	0.0006	0.0665	15.20	0.0001
4. Height	-0.0186	-2.37	0.0179	-------	------	------
5. Lodging	0.3262	2.51	0.0125	-------	------	------
6. Seed size	0.8237	14.59	0.0001	0.8501	623.32	0.0001
7. Oil	1.2485	7.75	0.0001	1.3365	81.89	0.0001

b = Regression coefficient. P = Probability level.
ITI = Estimates of 'T'. IFI = Estimates of 'F'.

Yield = 4.7727 + 0.0268 Maturity - 0.1289 Lodging
+ 0.1424 Seed size - 0.2343 Oil

Similarly, the estimates of regression coefficients for protein for the general and stepwise regression models are presented in Table 35. The estimates of coefficients were high and positive in the general model for oil, seed size and lodging, low for maturity and negative for yield and height. However, when stepwise procedure was applied, the estimate for intercept increased considerably (negative), and only maturity, seed size and oil were finally included in the model. Based on these, the prediction equation for protein was developed as follows:

Protein = - 4.9338 + 0.0665 Maturity + 0.8501 Seed size
+ 1.3365 Oil

The estimates for oil under the two models are presented in Table 36. In the general model, the estimate of intercept was high, and those for maturity, lodging, seed size and protein were low and positive. When stepwise procedure was applied, lodging variable was deleted from the model, and the estimates for others were slightly readjusted. The coefficients for yield was high and negative , and those for maturity, seed size and protein were low and positive. Based on these, the prediction equation for oil was developed as follows:

Oil = 15.4194 - 0.1756 Yield + 0.0147 Maturity - 0.0057 Height
+ 0.0517 Seed size + 0.0907 Protein

Table 36. Estimates of Regression coefficients by General and Stepwise Regression Analysis for Oil.

# Variable	General			Stepwise		
	b	ITI	P>ITI	b	IFI	P>IFI
1. Intercept	15.4975	38.87	0.0001	15.4194		
2. Yield	-0.1730	-4.50	0.0001	-0.1756	9.94	0.0017
3. Maturity	0.0141	2.73	0.0065	0.0147	8.54	0.0038
4. Height	-0.0063	-3.02	0.0026	-0.0057	5.32	0.0215
5. Lodging	0.0175	0.49	0.6190	------	-------	-------
6. Size	0.0506	2.79	0.0054	0.0517	11.55	0.0007
7. Protein	0.0902	7.75	0.0001	0.0909	261.10	0.0001

b = Regression coefficient.
ITI = Estimates of 'T'.
IFI = Estimates of 'F'.
P = Probability level.

5 DISCUSSION

5.1 Means, Simple Statistics and their Comparison

It is evident from the study of means and other simple statistics that overall statistics are greatly influenced by the nature of characters, population studied, and the environmental factors operating. The range, variance as percent of mean and C.V. were higher for yield, maturity, height and lodging, while lower for seed size, protein and oil. This may be due to the fact that the two parents used in crossing and developing these populations differed comparatively more for those traits , and less for seed size, protein and oil. This observation also reflects the number of genes involved in the control of these quantitative traits. The greater the number of genes involved, the greater would be the variance in the population, and also, the environmental variance will be large, resulting in an increased C.V. in the population. From the current study, it is evident that for the traits like yield, maturity, height and lodging, there may be larger number of genes involved compared to seed size, protein and oil. This would indicate a comparative ease or difficulty in handling these traits through breeding. Based on these current observations , it appears that it would be easier to manipulate traits like seed size, protein and oil through breeding. However, in the current population, the genotypic variance is quite low for these traits, hence response to selection will be low. The more variability in a population, the greater would be chance of improvement through selection. Therefore, a population with high mean and high variance would be better for manipulation by breeder than one with high mean and low variance.

The trend of range, variance and C.V. for these traits were identical in both the parents and the progeny. This clearly indicates a strong environmental influence on these quantitative traits. Therefore, it would be essential to evaluate the materials over years and locations across the environments before drawing conclusions about them. Predictions based on one year or one location data may not be very reliable. When the ranges and

variances of the progeny were compared with the parents, they were considerably higher in the progeny for all the characters, even beyond the parental limits. This may result from transgressive segregation. This clearly shows one avenue for breeder to exploit and select for superior types even if such genetic combination is not present in the parental population. The opportunity of exploiting transgressive segregation will be higher for quantitative traits where large number of genes are involved. It is evident from Table 6, that the range for yield is the highest among all the traits including height and maturity. This also reflects that yield has greater number of genes than any of these traits. The number of genes and the type of gene action in the control of a trait will determine the breeding procedure to be used for improvement of that trait.

The computations of these statistics by year, location, pubescence density, and their interactions also produced the identical trends. A higher range, variance and C.V. for yield, maturity, height and lodging, and comparatively lower for seed size, protein and oil supported the overall (AVE) results. A significant TTEST for all the characters except height indicated that the means were different due to year. The means were higher in 1990 indicating that the growing season was favorable. During 1989, there was a heavy rainfall resulting in water logging for a period in late May and early June, which may have caused the variable results in 1989. However, a non-significant difference in height may have resulted from genetic factor confounded with other factors like location, density, environment and their interactions. The year effects were more pronounced for protein, oil and seed size, and less for other traits, indicating that different quantitative traits respond differently to the year factor. Therefore, for such traits testing over years is necessary for making valid inferences about them.

Likewise, a differential response of traits to location indicated a similar finding. All treatment means except protein and oil differed significantly across locations. This may be due to the fact that the two locations inter-reacted identically towards these traits, or the parents did not vary much for these traits. On the other hand, this could also result as

the confounding effects of year, pubescence density and other environmental interactions with location, finally neutralizing the difference. Similarly, the effects of pubescence density on seed size and protein showed a non- significant difference. This may be possible that these characters are not influenced by pubescence density, or their effects are not very great. On the other hand, there may be effects of other factors like year, location and their interactions, finally neutralizing the effect of pubescence density. However, a significant effect of pubescence density on yield, maturity, height, lodging and oil with a differential response indicated that the genes for density have a negative pleiotropic effect on these traits.

The study of interaction effects of year, location and pubescence density on the means and other statistics revealed an interesting information. Some characters showed interaction effects , while others did not. For example, there was no effect of location on mean oil both in 1989 and 1990. This indicated that there is little need of location testing for oil. On the other hand, a significant difference in means for height and lodging both in 1989 and 1990 due to location revealed that location testing for these traits is essential. Likewise, a significant difference over years within a location would indicate a need of more testing over years to have reliable conclusions.

The effects of pubescence density within year and location exhibited interesting results. The means did not differ due to pubescence density for seed size and protein at any location or year. Therefore, for studying the effects of density on these traits, no intensive evaluation over years and location would be necessary. However, height and lodging showed almost a significant difference in means due to pubescence density within location and year. This would suggest that an intensive testing of materials over years and locations would be essential to draw inferences about the effects of pubescence density on these characters. Comparing the density types, effects of year and location on the means of characters were quite interesting. For example, year effects were non-significant for height in both dense and normal types, while significant for rest of the traits. Therefore, for

height, not much testing over years will be required, while for others, testing over years will be essential. Likewise, a non-significant effect of location for protein and oil in both the density types, would indicate that location testing will not be essential for these traits in either pubescence density type. However, effect of location for lodging was not significant in the dense type, and significant in the normal type. This differential response would indicate that location testing for lodging though not essential for dense type, will be important for the normal type in order to make valid conclusions.

5.2 Analysis of Variance

The analysis of variance in the General model ANOVA showed in general a significant F-test for all the characters due to genotypic effects. This indicates that there is considerable genotypic differences in the population, and selection for those traits would be effective. Other main and interaction effects were different for the different characters. For example, yield and maturity showed a significant effect of Y x L x G indicating that the performance of the genotypes differed with year and location. Therefore, superior lines need to be selected separately at each site, and be evaluated over years to find a stable one. Likewise, a significant Y x G effect for height indicated a more testing over years than on location for this character. Lodging showed a significant effect due to year, location and interaction of L x G and Y x L x G. This would indicate that this trait is highly influenced by year and location. The interaction effects would also indicate that the response of genotypes to lodging is highly variable over environments. Therefore, location specific selection is important, and also be based on testing over years within the location. Seed size, protein and oil, all showed the effects of Y x L x G interaction indicating that selection for these traits be done on location wise, and be based on several years of testing.

The Nested- Design ANOVA was designed to study the effects of pubescence density (D) on the quantitative traits and their components of variance. The total variance was partitioned into 25 components as shown in the model. The responses were different

for the different traits. The main effects of pubescence density, year, and location were not significant for yield. This observation supports the findings of Hartwig and Edwards (1970), Singh et al.(1971), and Hartung et al. (1980), where they did not find any yield difference between dense and normal pubescence types. Also, Powell et al.(1985) while studying the effects of two major genes, denso and daylength on quantitative traits in barley reported that effects of these genes decreased in the advanced generations. Therefore, this demonstrated that the association between major genes and quantitative characters was due to linkage disequilibria. Similar conditions may be operating for pubescence type in soybean. However, it may be also be possible that the difference in pubescence density between the two normal and dense types was not adequate to bring about the difference in the quantitative traits studied. Other environmental factors like drought and insect incidence were not adequate to bring about a major effect in the present study. Previous workers have reported the positive response of pubescence density on yield in the determinate varieties of soybean.

In the present study, the effects of pubescence density with some interactions, however, were quite pronounced. For example, effects of Y x L x D, Y x F_2, Y x F_3 (F_2) x D, and Y x L x F_3 (F_2) were significant for yield which indicated that density affected yield in a particular year and location only, and not on overall basis. Likewise, pubescence density showed a significant response in a particular year and F_3 (F_2) line which suggested that in the locations or genotypes where pubescence density shows a positive response to yield, density may be used as an important trait in breeding. In the area or population where there is no response of pubescence density, it may not be an important trait. However, several workers (Wolfenbarger and Sleesman, 1963; Hartwig and Edwards, 1970; Singh et al., 1971; and Broersma et al., 1972) reported a positive association of pubescence density with the resistance to potato leaf-hopper. Therefore, in the situation, where insects are the major problems, pubescence density may play an important role indirectly affecting the quantitative traits. Since no deleterious effects of density gene *(Pd)*

has so far been reported, it would be useful to include this trait in breeding as it provides resistance to drought and leafhopper.

A significant F_2, F_3 (F_2), F_3 (F_2) x D, Y x L x F_3 (F_2), and Y x L effects on maturity indicated that maturity differed with the genotypes and also due to interaction of genotypes with year, location and pubescence density. A significant F_3 (F_2) x D revealed that density affect maturity in certain F_3 (F_2), and not in others. A differential response of density with genotypes has also been reported by Singh et al.(1971). They found no significant difference in maturity due to pubescence types in Clark isogenic lines, but significant in Harosoy. Hartung et al. (1980) also found that dense pubescence *(Pd)* allele resulted in more vigorous plants with increased height, lodging, and maturity in Harosoy. Most of these results are however, based on the study of a few genotypes. Therefore, it seems important to study the effects of pubescence density over a range of diverse genotypes in order to make valid conclusions.

Similarly, significant effects of F_2, F_3 (F_2), F_3 (F_2) x D, and Y x L x D on plant height clearly reflect the importance of density. Plant height is influenced by genotype and its interactions with pubescence density. Also, a significant interaction of year and location with pubescence density reveal that the response of density will vary with year and location for height. Therefore, it is important to identify the location where density has response, and test over years at that location to make reliable conclusions. There was no main or interaction effects of pubescence density on lodging in this study. This finding is in agreement with Singh et al.(1971) and Hartung et al (1980) where they did not report any significant difference in lodging between dense and normal types. However, the dense types had increased height and lodging compared to normal types. Hence, it is evident that pubescence density may not be important or an essential trait in breeding for lodging resistance. However, a significant year and location effects indicate that the genotype will show a differential response to lodging over years and locations. Therefore, an extensive

evaluation over years and locations is essential to draw a valid conclusion about the genotypes to lodging.

The ANOVA for seed size showed a significant F-test due to F_3 (F_2), F_3 (F_2) x D and some higher order interactions (Table 17). A non-significant F-test of F_2 indicates that the F_2-derived lines did not differ for seed size , however, the F_3 (F_2)-derived lines differed significantly. Hence, selection in F_3 (F_2) derived families would be effective. Also, a significant F_3 (F_2) x D revealed that pubescence density affected seed size in certain genotypes , and not in all. This result supports the findings of Singh et al.(1971) and Hartung et al. (1980). They also reported an increase in seed weight with pubescence density. Therefore, it would be essential to identify genotypes which show response to density for seed size, and use them in breeding or selection for increased seed size. A higher order interaction of F_2, F_3 (F_2) with Year and location revealed that the genotypes differed in their response to seed size over years and locations. Also, an interaction Y x L x F_2 x D revealed that there was differential effects of pubescence density over years, locations and F_2's. Therefore, it would be important to evaluate F_2's-derived lines over years and locations to detect the effects pubescence density on seed size.

The F-test for protein showed a significant effect due to year, Y x L, and F_2 indicating that the variation in performance of genotypes was great, and needed a testing of materials over years to draw a valid conclusion. There was no direct effect of pubescence density on protein. However, significant higher order interaction of Y x L, F_2, F_3 (F_2), and density revealed that there were differential response of density on genotypes, year and location. Therefore, it is important to identify a genotype that respond to pubescence density for protein. Such genotypes should be evaluated over years and locations to finally identify a superior genotype with a stable response of density to protein. Singh et al.(1971) also observed an effect of pubescence density on protein in Harosoy, being non-significant among dense, normal, sparse and curly, and significantly higher in the glabrous. These findings suggest that pubescence density does not show a positive and

strong effect on protein. The comparison of density means (Table 9) also did not show any significant difference for protein. This may be possible that the genes for density do not affect significantly the path way of protein synthesis, and indirect selection for protein through pubescence density will not be effective.

The analysis of variance for oil showed a significant effect due to year indicating that genotypes must be evaluated over years to make a reliable interpretation. There were no main effects of F_2, F_3 (F_2), or density in this case. This indicated that there were no genotypic variation for oil, which may be possible if the two parents used were identical for oil content, and there were no transgressive segregation for this trait in the progenies to make a significant difference. Also, there may be very high environmental influence in the expression of this trait, and the real genotypic difference being very low. Therefore, selection for high oil will not be effective in this case. A significant Y x D effect revealed that pubescence density affect oil in some years, and not in others. In such situation, materials should be evaluated over years to make any valid conclusions. A significant Y x L x F_3 (F_2) x D effect indicate that density affect oil in certain genotype, location and year only. Selection for high oil should be done in location and year where the effect is significant. In general, there is no significant effect of pubescence density on oil. Singh et al.(1971) also could not find any significant difference of five pubescence types (normal, dense, sparse, curly, and glabrous) on oil percent in Harosoy isolines. However, a more detailed study of the effects of pubescence density on oil on a wide range of germplasm is necessary to draw a vital inference. When the effects of density were separated by year and location(Table 12), the effect of density on oil were non-significant in 1989, but significant in 1990 at both locations. This clearly reflects a greater environmental influence in the expression of the oil percentage than the density factor alone. Therefore, selection should be based on the average performance of lines over years and locations.

5.3 Estimation of Components of Variances

5.3.1 General Model ANOVA

The general ANOVA model provided the estimates of σ^2G (Genotypic) and interaction of variance σ^2G with year (Y) and location (L). Also, the estimates of σ^2e (Error) was obtained. The estimates of σ^2G were higher than σ^2e for all the characters which provided the evidence that σ^2G was the major component of variance for the total variance. The lower estimates of σ^2Y and σ^2L in most cases indicated that these effects were comparatively much lower than the genotypic effects. As clear from the Table 18, the genotypic variance for yield and oil were much lower which indicated that selection for these traits will not be very effective in this population. A comparatively much higher variance for maturity, height, lodging and seed size would indicate a better response to selection for these traits in this population. However, this model did not provide information on the effects of pubescence density on the quantitative traits. This was a good model to estimate the genotypic effects and its interactions with year and location, and to estimate broad sense heritability.

5.3.2 Nested Model ANOVA

The estimates of variance components in the Nested Design ANOVA provided variable estimates under the three different models: Additive(Model-1), Additive & Additive x Additive(Model-2), Additive & Dominance(Model-3). Also, the estimates differed slightly when selected variables based on Principal Component Analysis(PCA) were used in the selected model.

5.3.2.1 Additive Model

In this model the total variance was partitioned into 17 components , which did not include additive x additive (AA) and dominance (D) components of variance. A considerable variation in the estimates of components among seven characters indicated that

the effect of each component was different for different traits. For example, estimates of σ^2e were much larger for height and maturity, and lower for protein and oil. This indicates that height and maturity are under control of comparatively greater number of genes than protein and oil. This could also arise if errors in measurement of height and maturity were more than protein and oil. In general, as the number of genes increase, the genotypic, phenotypic and error variances increase. Hence, these variations in the population or among traits, may dictate the breeding procedure. If the number of genes involved are just a few(eg. kernel color in wheat), breeding and selection would be much easier than breeding for yield where a much larger and complex genetic control is involved. In such case, a much larger population, and intensive evaluation over years, locations and environments would be necessary. Further, a much higher estimate of σ^2A (Additive) than σ^2y (Year) , σ^2l (Location), σ^2d (Pub.density) and their interactions indicated that additive variance for these traits was large and selection would be effective and fixable. Since this model did not provide estimates of dominance or any other interaction components, therefore, the conclusions based on this may not be very sound. However, in the self-pollinated crops like soybean, one would anticipate higher additive type of variance in the advanced generations (F_6 or F_7). This result supports the findings of Brim and Cockerham (1961) and Brim (1973), where they reported presence of high additive variance for these traits in soybean.

5.3.2.2 Additive & Additive x Additive Model

In this model the total variance was partitioned into 25 components without involving dominance component. The estimates of variances both under full and selected model provided nearly identical estimates. The estimates of σ^2e were the same in both, which indicated effectiveness of the selected model. The estimates of F- values in the selected model for all the traits indicated that the selected models were adequate to explain most of the variability in the population. Since the number and type of variance

components included in the selected models varied with the characters, this would indicate that the effects of different variance components differed between traits.The estimates of components were also slightly readjusted in the selected models.

The estimates of σ^2AA were higher than σ^2A in both models for all the characters except protein. This indicates that AxA type of variances are higher than the additive (A) type alone for the quantitative traits studied. This finding is in agreement with Hanson et al.(1967), who reported presence of considerable AxA epistasis in soybean for yield, maturity, and percent seed coat mottling accounting for more than 50% of the total genotypic variance. Since quantitative traits are controlled by a large number of genes, and soybean being a fully self-fertilizing crop, these genes should be nearly in a fixed stage. This indicates that the genes controlling these quantitative traits are mostly in AxA epistasis or higher order additive types of interactions. These results are in agreement to the expectations for a self- pollinated crop. There should be more σ^2AA or higher order AxA.interactions , and a very low or no σ^2A. However, these are contradictory to the findings of Brim and Cockerham (1961), where they reported a high additive variance. It may be possible that their model was not adequate to separate the effect of AxA from Additive variance(as we also had similar results in model-1). These information provide a vital guideline to the breeders of self-pollinated crops. In order for selection to be effective, there must be adequate AxA or higher order AxA epistatic types of variance in the population. This will be possible only in the advanced generations. Therefore, selection for these traits should be delayed until F_5 - F_6 generation for a greater response. Early generation selection will not be effective as many of these genes will still be in the heterozygous condition involving dominance, and will segregate on selfing in the later generations.

5.3.2.3 Additive and Dominance Model

In this model, estimates of σ^2A and σ^2D, and their interactions with other factors were computed both in full and selected models. Here too, the estimates of σ^2e were the

same in both the cases. However, the estimates of σ^2D were much greater than previously reported in soybean, while σ^2A estimates were also much lower. The interaction variances of dominance(D) with year, location and pubescence density (d) were very high. Such high estimates of σ^2D might occur if all the AxD, AxAxD,.or higher order AxD variances were merged into σ^2D component in this model. Existence of higher order AxD or very low σ^2D has been reported by Gates et al.(1960), Cockerham (1961), Croissant and Torrie (1971), and Brim (1973). Brim (1973) reported evidence of heterosis for yield in soybean. However, it is not yet clear how much is due to σ^2D, and how much is due to AxD and its higher type of interactions. If the dominance effects are real and great, and techniques to produce hybrids are cheap, one might attempt hybrid breeding for heterosis. However, since the present model does not separate the AxA or AxD effects, the information may not be very valid.

As is clear now, none of these models included additive, dominance, AxA, AxD or higher order interactions together. Therefore, none of these models is perfect in itself. The more factors we include in the model, the more complicated would be the population structure to develop, and more would be the interaction effects which might jeopardize the important effects. However, in the present study, the Additive & Additive x Additive(model-2) appears to be most suitable for soybean to estimate the components of variance in F_6- F_7 generations.

5.4 Estimation of Heritability and Gain from Selection

The estimates of heritability, gain from selection (Gs) and gain from selection as percent of mean (Gs%) both in Additive, and Additive & Add x Add models appear to be identical (Tables 24 & 25). However, the estimates were a little higher in Additive model. The estimates of height, maturity, lodging, seed size and protein were comparatively higher than those for yield and oil. The heritability of oil was very low which indicated that selection for this trait will require intensive evaluation over years, locations , and

environments. Moreover, a low estimate in this case might have resulted due to little difference for oil between the parents leading to a lower genotypic variance. Therefore, in order to breed for high oil, selection of parents with high oil is important to have high genotypic variance in the population for selection for oil to be effective. However, a trait with high heritability would indicate low environmental influence, phenotype highly reflect genotype, and a visual selection would be effective. The Gs % also indicated that response to selection would be high for height, maturity, lodging and seed size, low for yield, and poor for protein and oil.

However, in the Additive & Dominance model, because of the low estimates of σ^2A, only broad-sense heritability were computed which also indicated a similar trend. The Gs % was very high (>100%) for lodging, height and yield. The heritability(H) for protein and oil were lower than other characters , and the Gs% were also low. The heritability (H) calculated from the General model also showed a similar trend: height had a heritability of 0.99 and those for yield , maturity, lodging, protein and seed size were around 0.70-0.80, and for oil was 0.46. The heritabilities estimated using parent-offspring regression (Table 28) were not in agreement with the previous results, but height again showed the highest value. Yield and lodging had very poor estimates.

It is clear from the results in the present study that the estimates of heritability vary greatly with the method of estimation. The estimates obtained by Additive or Additive & Add x Add models are narrow sense, and are more reliable for a self pollinated crop like soybean. Since these estimates were done in the advanced generations (F_6- F_7), and are based on years and locations evaluation, they should be more precise and reliable. Usually, the estimates of heritability are higher in the early generation, and decrease in the later due to decrease of non-additive genetic variance in the later generations (Kelly and Bliss, 1975). Present findings were in close agreement with Brim (1973), Johnson and Bernard(1963), and Shannon et al. (1972). Openshaw and Hadley (1984) reported the heritability of two populations as 0.90 and 0.75 for protein, 0.93 and 0.73 for oil, and

0.78 and 0.68 for yield respectively. Their estimates for protein and oil were much higher than the present findings. This may be due to fact that estimation in earlier generation using a diverse parental population, or using a different method for estimation might have resulted in such high estimates of heritability. Parent-offspring regression method of estimating heritability is effective in absence of dominance and epistasis(Smith and Kinnman, 1965). Since there is adequate evidence of the presence of epistasis (AxAx...) for the quantitative traits in soybean, estimates of heritability by parent- offspring regression in the present study may not be very reliable. The estimates obtained from other methods were similar. The heritabilities were computed in much later generations based on year and location testing, they must be very stable and precise as other variance components like effects of year, location and density, and their interactions have been separated precisely from the genotypic and phenotypic variances. A moderate to high estimates of h^2 for maturity, height, lodging and seed size would reveal that phenotypic selection for these traits will be effective. Selection for these traits would not require an intensive testing of materials over years and locations. However, a moderate estimates for yield and protein would indicate the influence of higher environmental effects, and the phenotype would not give a true representation of the genotype, and the visual selection will not be very effective. Therefore, moderate testing over years and locations would be necessary for making valid decision. The estimate for yield and oil were usually very low among all the traits in different models. This may be due to lack of variability for yield and oil in parents. Alternatively, this may be due to higher environmental influence on them and phenotypes do not truly represent the genotypes. Hence, for such traits, more testing over environments would be essential for drawing conclusions. A high environmental variance may indirectly indicate a comparatively larger number of genes or gene-complex involved in the inheritance of this trait. Further, more the number of genes involved, more difficult would be to make progress through the conventional breeding, and a non-conventional approach (mutation breeding and /or genetic engineering) might be necessary.

5.5 Estimation of Correlation Coefficients

The estimation of Pearson's correlation coefficients (Genotypic) and the effects of year, location, pubescence density, and their interactions on the r-coefficients in the present study provide an unique and interesting way of understanding the significance of this estimate in breeding. When the correlations were estimated with the overall or average (AVE) genotypic means, yield showed a significant positive association with maturity, seed size and protein. Maturity had a significant positive correlation with all other traits. However, height exhibited a positive association with maturity and lodging, and significant negative association with seed size, protein and oil. This indicated that an increase in height will decrease these traits. Also, lodging had a positive correlation with seed size, protein and oil, and those with seed size, protein and oil were all positive. These observations partially support the findings of Johnson and Bernard (1963) where they found a correlation of 0.4 between yield and maturity, and a very low correlation for yield and oil. Anand and Torrie (1963) and Kwon and Torrie (1964) also reported a positive correlation of yield with height, maturity and lodging. However, Byth et al.(1969) found a negative correlation of yield with height and lodging, which very well supports the current findings. They also found a higher correlation of yield with protein than with oil. Hartwig and Edwards (1970) also found a negative association of yield and height. Johnson et al.(1955) reported a very strong and positive correlation between yield and seed size which fully supports our findings. However, a high positive association for protein and oil on the AVE contradicted the earlier findings (Shorter et al.,1976; Brim and Burton, 1979; Burton and Brim,1983). This might have arisen due to the balancing of positive and negative effects when averaged over years, locations and density.

In this study, the correlation coefficients were further computed across year, location, pubescence density and their interactions. In many cases, the correlations showed a stable response, while in others the estimates and even the direction of effect (plus or minus) changed drastically. For example, when year effects were compared, the

association between yield and maturity was negative in 1989, and positive in 1990. Likewise, when the correlations were computed by location or pubescence density, they were in agreement of the ovrall (AVE) estimates. Again, when these estimates were further computed by location within the year, they were stable for some and quite variable for others. The association of yield with maturity and oil were almost negative. The estimates for seed size with protein and oil were also negative contradictory to the overall (AVE) estimates. Further, the effects of density within the year produced the identical results. However, when the correlations were computed by locations within the year, the estimates greatly supported the overall estimates. Therefore, a more detailed computation of correlation was done by pubescence density within location and year (Table 33) as compared with the overall (AVE) estimates. It is evident from the table that there is a tendency of negative association of yield with maturity, height and oil, while seed size and protein showed a significant positive association with yield. However, there was no association of yield with lodging. It may be possible that lodging occured at late maturity without affecting the yield. There was a strong positive correlation of maturity with height and lodging, while it approached negative with seed size, protein and oil. Height and lodging had a strong positive association. The associations between lodging and seed size were positive for some and negative for others. It was interesting to see that correlation of protein and oil were very high and negative in all cases, while strongly positive on overall (AVE) basis. This negative association of protein and oil supported the findings of earlier workers.

The information on correlation coefficients elucidate the situation on how they are influenced by factors like year, location, pubescence density and their interactions, and methods of estimation. It is evident that some of these estimates are highly stable across the factors effects, while others change considerably, and may produce misleading results. Therefore, those which are quite stable, eg. positive association of yield with seed size and protein, of maturity with height and lodging, of height with lodging, are well established,

and should be used in breeding. The information on correlation can facilitate breeders in utilizing indirect selection for quantitative traits with low heritability, or for traits which measurements are difficult and expensive. However, for others the estimates are influenced by other environmental factors like year, location, pubescence density and their interactions. In such cases, it would be necessary to evaluate the materials over more years and locations, and over a range of environments in order to make any reliable inferences. Based on our detailed study, we can clearly show that there is a strong negative correlation between protein and oil. The estimates of correlation coefficients are important to breeders in deciding breeding procedures and selection programs. A high positive or negative correlation of the secondary trait(s) with the primary trait could be used for indirect selection of the primary trait. Selection for high yield will increase seed size and protein, but decrease oil content. A strong negative correlation between protein and oil will indicate that selection for one will decrease the other. In situations where we need to increase both protein and oil, first we should screen more germplasm to find parents with high protein and oil, or use a different breeding technique like recurrent selection, mutation breeding and/ or genetic engineering to generate more variability.

5.6 Estimation of Regression Coefficients

The estimation of regression coefficients and developing the prediction equations are still another way of looking at the dependence of primary traits on the secondary or independent traits. In the stepwise regression, unimportant variables were dropped. For example, for predicting yield, the model included maturity, lodging , seed size and oil. Similarly, for protein the model included maturity, seed size and oil, while for oil, variables yield, maturity, height, seed size and protein were included. The estimates and direction of regression coefficients will indicate the relationship of independent variables with the dependent variable. The computation of the prediction equation or response curve will indicate the degree of change in the dependent variable with a change in one or more

independent variables. This information is crucial in breeding programs for predicting response to selection. Such estimates are of greater significance particularly when the measurements of dependent variable is difficult, time taking, or need special equipment and facility. For example, these prediction equations could be used to predict gain in yield protein or oil without their immediate analysis. This will help breeders to cut time and resources, and increase efficiency.

6 SUMMARY AND CONCLUSIONS

Most of the cultivated varieties of soybean have a dense covering of erect pubescence (hairs) on stem, leaf, calyx and pod. Considerable genetic variation in pubescence size, form, density, durability and color has been found in the germplasm collection. Pubescence density is a simple inherited trait controlled by a single dominant or recessive gene. The trait has been found to affect plant vigor, and resistance to insects and drought. Pubescence density has been found to increase height and lodging , and reduce yield in the indeterminate cultivars. These information, however, are based on a few genotypes. There is inadequate information on how dense pubescence affect the quantitative traits of economic importance, like yield, maturity, height, lodging, seed size, protein and oil, and their genetic components of variance, heritability and correlations. A clear understanding of these underlying genetic principles is crucial to effective breeding program.

The present research was designed i) to study the effect of dense pubescence on these quantitative traits, ii) to estimate genetic components of variance, iii) to estimate g x e interactions, iv) to determine heritability and gain from selection, v) to compute correlations and regression coefficients among these traits, and vi) to discuss the implications of findings to soybean breeding.

The test lines were developed from the cross of Wells II (++) with normal pubescence and Harosoy *(PdPd)* with dense pubescence. Dense and normal lines were developed in a nested design from F_2 and F_3 (F_2) derived progenies. Sixty progeny lines with the two parents were evaluated in F_6 and F_7 generations for two years at two locations in Michigan.

The comparison of means and simple statistics for different traits revealed that they were highly influenced by year, location, pubescence density, and their interactions. Pubescence density increased maturity, height, lodging and oil, and reduced yield. It

exhibited no significant effect on seed size and protein. However, when the effects of pubescence density were studied within year and location, only height had a stable response, while lodging and oil exhibited response in only one year. Therefore, it is important to evaluate materials over years and locations for making reliable conclusions about the effects of pubescence density on quantitative traits.

The analysis of variance indicated a significant effect of genotypes on all the traits. Therefore, it may be possible to select lines of interest in the population. Pubescence density (D) did not show any main effect on any trait, however, the interactions were present, and varied with the traits. Therefore, it is important to determine the genotypes, locations and environments (drought), where response is evident, and use dense pubescence as an important trait in breeding. Since breeding of quantitative traits is complex and time taking due to polygenic inheritance, a strong linkage of these traits with pubescence density (simple inheritance) may be employed for indirect selection.

The genetic components of variance differed with the models used. In general, Additive and Additive x Additive model appeared most suitable in this study. The estimates of variance Add x Add were in general higher than Additive variance for most traits. The variance due to pubescence density (d) and its interactions with other factors were much lower than the genetic components for all the traits except height. This indicates that pubescence density does not have a major effect on the genetic components of variance of these quantitative traits, and so as on the estimates of heritability. Year and location effects were also evident and varied with the traits. The heritability estimates computed under Additive, and Add & AddxAdd models were nearly similar. The estimates were high for height, maturity and lodging (>0.50) , moderate for seed size and yield (0.35-0.49) and low for protein and oil (0.25-0.34). However, in the General model ANOVA the estimates of heritability (H) as they were broad-sense, were generally high. The traits with high heritability indicate that the phenotype highly reflect the genotype, and visual selection may be effective. For the traits with low heritability evaluation over years and locations

may be necessary for making conclusions. Pubescence density did not show much influence on heritability of any trait except height. Alternatively, isozyme and RFLP techniques may be helpful for indirect selection, provided they are shown to be associated with useful agronomic traits.

The correlation coefficients were highly influenced by year, location, pubescence density and their interactions. The conclusions on correlations made using overall genotypic means may be misleading in some cases. We computed the correlations using the main and interaction means of year, location and pubescence density. Some of the coefficients, like yield with seed size and protein, maturity with height and lodging, and height with lodging were consistently high and positive, while others differed across these factors. The association between protein and oil was significant and positive when computed using overall means, but exhibited significant negative when computed by above factors. Therefore, it is important to use the traits which show a stable correlation for indirect selection in breeding. The general and stepwise regression coefficients were computed and used to predict response of yield, protein and oil. Based on these, maturity, lodging, seed size and oil were important variables for predicting yield; maturity, seed size and oil for protein; and all except lodging were important for oil. They can be used for predicting responses to selection for these traits in breeding. Such estimates are of greater significance particularly when measurements of dependent variable is difficult, time taking, or needs special equipment and facilities.

BIBLIOGRAPHY

BIBLIOGRAPHY

Anand, S. C., and J. H. Torrie. 1963. Heritability of yield and other traits and inter correlationships among traits in the F_3 and F_4 generations of three soybean crosses. Crop Sci. 3:508-511.

Anderson, W. F., C. C. Holbrook, and J. C. Wynne. 1991. Heritability and early generation selection for resistance to early and late leaf spot in peanut. Crop Sci. 31:588-593.

Baldocchi, D. D., S. B. Verma, N. J. Rosenberg, B. L. Blad, A. Gary, and J. E. Spech. 1983. Leaf pubescence effects on mass and energy exchange between soybean canopies and the atmosphere. Agron. J. 75:537-542.

Bernard, R. L. 1975. The inheritance of near-gray pubescence color. Soybean Genet. Newsl. 2:31-33.

Bernard, R. L., and B. B. Singh. 1969. Inheritance of pubescence type in soybeans: glabrous, curly, dense, sparse, and puberulent. Crop Sci. 9:192-197.

Bernard, R. L., and M. G. Weiss. 1973. Qualitative genetics. p.117-146. *In* B. E. Caldwell (ed.) Soybeans. American Society of Agronomy, Inc. Pub. Maidison, WI,U.S.A. p-681.

Brim, C. A. 1973. Quantitative genetics and breeding. p. 155-183. *In* B. E. Caldwell (ed.) Soybeans. American Society of Agronomy, Inc. Pub. Maidison, WI,U.S.A. p-681.

Brim, C. A., and C. C. Cockerham. 1961. Inheritance of quantitative characters in soybeans. Crop Sci. 1:187-190.

Brim, C. A., and J. W. Burton. 1979. Recurrent selection in soybeans. II. Selection for increased percent protein in seeds. Crop Sci. 19:494-498.

Broersma, D. B., R. L. Bernard, and W. H. Luckmann. 1972. Some effects of soybean pubescence on population of potato leafhopper. J.Econ. Ent. 65:78-82.

Burton, J. W. 1987. Quantitative genetics: Results relevant to soybean breeding. p.211-247. *In* J. R. Wilcox (ed.) Soybeans: Improvement, production, and uses. Agronomy, Inc. Pub. Madison, WI, U.S.A.

Burton, J. W., A. E. Purcell, and W. M. Walter, Jr. 1982. Methionine concentration in soybean protein from populations selected for increased percent protein. Crop Sci. 22:430-432.

Burton, J. W., and C. A. Brim. 1981. Recurrent selection in soybeans. III. Selection for increased percent oil in seeds. Crop Sci. 21:31-34.

Burton, J. W., R. F. Wilcox, and C. A. Brim. 1983. Recurrent selection in soybeans. IV. Selection for increased oleic acid percentage in seed oil. Crop Sci. 23:744-747.

Buttery, B. R., and R. I. Buzzell. 1973. Varietal differences in leaf flavonoids of soybeans. Crop Sci. 13:103-106.

Buttery, B. R., R. I. Buzzell, and W. I. Findlay. 1981. Relationships among photosynthetic rate, bean yield and other characters in field grown cultivars of soybean. Can. J. Plant Sci. 61:191-198.

Buzzell, R. I., and B. R. Buttery. 1977. Soybean harvest index in hill-plots.Crop Sci. 17:968-970.

Byth, D. E., and B. E. Caldwell. 1969. Correlated truncation selection for yield in soybeans. Crop Sci. 9:699-702.

Byth, D. E., B. E. Caldwell, and C. R. Weber. 1969. Specific and non-specific index selection in soybeans, *Glycine max* L.(Merrill). Crop Sci. 9:702-705.

Caldwell, B. E. 1973. (ed.) Soybeans. p.ix-x. American Society of Agronomy, Inc. Pub. Madison, WI, USA. p. 681.

Carlson, J. B. 1973. Morphology. p.17-66. *In* B. E. Caldwell (ed.) Soybeans. American Society of Agronomy, Inc. Madison, WI, U.S.A.

Cockerham,C. C. 1963. Estimation of genetic variances. p.53-94. *In* W. D. Hanson and H. F. Robinson (ed.) Statistical genetics and plant breeding. National Academy of Sciences- National Research Council, Washington, D.C.

Cockerham, C. C. 1983. Covariances of relatives from self-fertilization. Crop Sci. 23:1177-1180.

Cooper, R. L., and A. Waranyuwat. 1985. Effects of three genes (Pd, Rps, and ln) on plant height, lodging, and seed yield in indeterminate and determinate near isogenic lines of soybeans. Crop Sci. 25:90-92.

Croissant, C. L., and J. H. Torrie. 1971. Evidence of non-additive effects and linkages in two hybrid populations of soybeans. Crop Sci. 11:675-677.

Dzikowski, B. 1937. Studia nad soja *Glycine hispida* M. Maxim. C_2. Anatomia. Pametnik Panstwowego Instytutu Naukowego Gospodarstwa Wiejskiego w Pulawach. Tom XVI. Rosprawa Nr. 258:229-265.

Ecochard, R. and Y. Ravelomanantsoa. 1982. Genetic correlations derived from full-sib relationships in soybean (Glycine max L. Merr.) Theor. Appl. Genet. 63:9-15.

Ehleringer, J. R., and H. A. Mooney. 1978. Leaf hairs: Effects on physiological activity and adaptive value to a desert shrub. Oecologia 37:183-200.

Falconer, D. S. 1980. Introduction to quantitative genetics. The Ronald Press Co., NY.

FAO. 1989. Soybean. p.155-156. *In* FAO Production year book. FAO, Rome.

Fehr, W. R. 1987. Heritability. *In* Priciples of cultivar development: Theory and techniques. Vol. 1:95-96. McGraw-Hill, Inc. NY.

Ford, D. M., R. Shibles, and D. E. Green. 1983. Growth and yield of soybean lines selected for divergent leaf photosynthetic ability. Crop Sci. 23:517-520.

Franceschi, V. R., and R. T. Giaquinta. 1983. Glandular trichomes of soybean leaves: Cytological differentiation from initiation through senescence. Bot. Gaz. 144:175-184.

Gates, C. E., C. R. Weber, and T. W. Horner. 1960. A linkage study of quantitative characters in asoybean cross. Agron J. 52:45-49.

Gausman, H. W., and R. Cardenas. 1973. Light reflectance by leaflets of pubescent, normal and glabrous lines of soybeans. Agron. J. 65:837-838.

Ghorashy, S. R., J. W. Pendelton, R. L. Bernard, and M. E. Bauer. 1971. Effects of leaf pubescence on transpiration, photosynthetic rate and seed yield of three near-isogenic lines of soybeans. Crop Sci. 11:426-427.

Hanson, W. D., A. H. Probst, and B. E. Caldwell. 1967. Evaluation of a population of soybean genotypes with implication for improving self-pollinated crops. Crop Sci. 7:99-103.

Hanson, W. D., R. C. Leffel, and R. W. Howell. 1961. Genetic analysis of energy production in the soybean. Crop Sci. 1:121-126.

Hartung, R. C., J. E. Spech, and J. W. Williams. 1980. Agronomic performance of selected soybean morphological variants in irrigation culture with two row spacings. Crop Sci. 20:604-609.

Hartwig, E. E., and C. J. Edwards,Jr. 1970. Effects of morphological characteristics upon seed yield in soybeans. Agron. J. 62: 64-65.

Hillsman, K. J., and H. W. Carter. 1981. Performance of F_1 hybrid soybeans in replicated row trials. p.63. Agron. Abstr., American Society of Agronomy, Madison,WI, U.S.A.

Johnson, H. W., and E. A. Hollowell. 1935. Pubescent and glabrous characters of soybeans as related to resistance to injury by the potato leafhopper. J. Agri. Res. 51:371-381.

Johnson, H. W., H. F. Robinson, and R. E. Comstock. 1955. Genotypic and phenotypic correlations in soybeans and their implications in selection. Agron. J. 47:477-483.

Johnson, H. W., and R. L. Bernard. 1963. Soybean genetics and breeding. p.1-73. In A.G. Norman(ed.) The soybean.
Academic Press, NY.

Kawahara, E. 1963. Studies on the gene analysis of soybeans (English summary). Tohoku Agric. Exp. Sta. Acad. Rep. 26:79-147.

Kelly, J. D., and F. A. Bliss. 1975. Heritability estimates of percentage seed protein and available methionine and correlations with yield in drybeans. Crop Sci. 15:753-757.

Kwon, S. H., and J. H. Torrie. 1964. Heritability of and interrelationships among traits of two soybean populations. Crop Sci. 4:196-198.

Lush, J. L. 1940. Intrasire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Proc. Am. Soc. An. Prod. :293-301.

Morse, W. J., and J. L. Carter. 1937. Improvement in soybeans. p.1154-1189 Year book Agr.(USDA), US Govt. printing office, Washington.

Nagai, I., and S. Saito. 1923. Linked factors in soybeans. Jap. J. Bot. 1:121-136.

Nelson, R. L., and R. L. Bernard. 1984. Production and performance of hybrid soybeans. Crop Sci. 24:549-553.

NGLIP. 1988. Annual Report. National Grain Legume Improvement Program(NGLIP), Rampur, Nepal.

Openshaw, S. J., and H. H. Hadley. 1981. Selection to modify sugar content of soybean seeds. Crop Sci. 21:805-808.

Openshaw, S. J., and H. H. Hadley. 1984. Selection indexes to modify protein concentration of soybean seeds. Crop Sci. 24:1-4.

Owen, F. V. 1927. Inheritance studies in soybeans. II. Glabrousness, color of pubescence, time to maturity, and linkage relations. Genetics 12:519-529.

Palmer, R. G., and T. C. Kilen. 1987. Qualitative genetics and cytogenetics. p.135-209. *In* J.R. Wilcox(ed.) Soybeans: Improvement, production, and uses. Agronomy, Inc. Pub. Madison, WI, U.S.A.

Pandy, J. P., and J. H. Torrie. 1973. Path coefficient analysis of seed yield components in soybeans (*Glycine max* (L.) Merr.). Crop Sci. 13:505-507.

Piper, C. V., and W. J. Morse. 1923. The soybeans. McGraw Hill Book Co.,NY. p.329.

Poos, F. W. 1929. Leafhopper injury to legumes. J. Econ. Ent. 22:146-153.

Poos, F. W., and F. F. Smith. 1931. A comparison of oviposition and nymphal development of *Empoasca fabae* (Harris) on different host plants. J. Econ. Ent. 24:361-371.

Powell, W., P. D. S. Caligari, W. T. B. Thomas, and J. L. Jinks. 1985. The effects of major genes on quantitatively varying characters in barley: 2. The denso and daylength response loci. Heredity 54:349-352.

Powers, L. 1955. Components of variance method and partitioning method of genetic analysis applied to weight per unit of tomato hybrid and parental populations. USDA Tech. Bull. 1131. U.S. Govt. Printing Office, Washington, D.C.

Probst, A. H., and R. W. Judd. 1973. Origin, U.S. history and development, and world distribution. p.1-12. In B.E. Caldwell (ed.) Soybeans: American Society of Agronomy, Inc. Pub. Madison, WI, U.S.A.

Rasmusson, D. C. and R. L. Glass. 1967. Estimates of genetic and envionmental variability in barley. Crop Sci. 7:185-188.

SAS. 1985. SAS User's Guide: Statistics. Version 5 ed. SAS Ins. Inc. Cary, NC.

Shannon, J. G., J. R. Wilcox, and A. H. Probst. 1972. Estimated gains from selection from protein and yield in the F_4 generation of six soybean populations. Crop Sci. 12:824-826.

Shorter, R., D. E. Byth, and V. E. Mungomery. 1976. Estimates of selection parameters associated with protein and oil content of soybean seeds (*Glycine max* (L.) Merr.). Aust. J. Agric. Res. 28:211-222.

Simpson, A. M. Jr., and J. R. Wilcox. 1983. Genetic and phenotypic associations of agronomic characteristics in four high protein soybean populations. Crop Sci. 23:1077-1081.

Singh, B. B., H. H. Hadley, and R. L. Bernard. 1971. Morphology of pubescence in soybeans and its relationship to plant vigor. Crop Sci. 11:13-16.

Smith, J. D., and M. L. Kinman. 1965. The use of parent offspring regression as an estimator of heritability. Crop Sci. 5:595-596.

Specht, J. E., J. H. Williams, and D. R. Pearson. 1985. Near-isogenic analysis of soybean pubescence genes. Crop Sci. 25:92-96.

Sprague, G. F., and W. T. Federer. 1951. A comparison of variance components in corn yield trials. Agron. J. 43:535-541.

Takahashi, Y., and J. Fukuyama. 1919. Morphological and genetic studies on the soybean (In Japanese). Hokkaido Agr.Exp. Sta. Rep. 10.

USDA. 1990. Agricultural Statistics, 1989.

Van de Logt, M. B., M. A. Brinkman, and R. A. Forsberg. 1984. Variance components and linkage effects for qualitatively inherited traits in two barley crosses. Crop Sci. 24:323-327.

Waggoner, P. E. 1966. Decreasing transpiration and the effect upon growth. p.49-68.*In* Plant environment and efficient water use (Monograph). American Society of Agronomy, Madison, WI, U.S.A.

Weber, C. R., L. T. Empig, and J. C. Thorne. 1970. Heterotic performance and combining ability of two-way F_1 soybean hybrids. Crop Sci. 10:159-160.

Williams, L. E. 1950. Structure and genetic characteristics of the soybeans. p.111-134. *In* K. S. Markley (ed.) Soybean and soybean products. Vol. I. Interscience Pub. NY.

Wolfenbarger, D. A., and J. P. Sleesman. 1963. Variation in susceptibility of soybean pubescent types, broad bean, and runner bean varieties and plant introductions to the potato leafhopper. J. Econ. Ent. 56:895-897.

Woodworth, C. M. 1921. Inheritance of cotyledon, seed coat, hilum, and pubescence color in soybeans. Genetics 6:487-553.

Woodworth, C. M., and C. Veatch. 1929. Inheritance of pubescence in soybeans and its relation to pod color. Genetics 14:512-518.

Woolley, J. T. 1964. Water relations of soybean leaf hairs. Agron. J. 56:569-571.

Yiran, Y., T. Byrne, and J. Harding. 1990. Quantitative genetic analysis of flowering time in the Davis population of gerbera. I. Components of genetic variance and heritability. Crop Sci. 30:19-23.

APPENDICES

Appendix A.1. Overall Means of the Genotypes across years and locations.

Entry	#Acc.#	Source	Pub	Yield	Mat	HGT	LDG	Size	Protein	oil
1.	E82026	Wells II	N	3.74	27.3	88.1	1.0	17.5	38.9	19.5
2.	I83170	HSY-PD	D	3.11	28.1	103.1	2.1	20.4	39.4	19.3
3.	E89001	01-1 +	N	3.00	36.7	114.4	3.0	18.7	38.2	19.1
4.	E89002	01-1 PD	D	2.95	37.8	132.7	3.6	19.2	38.1	18.6
5.	E89003	01-2 +	N	3.47	37.0	108.8	2.8	19.0	37.7	19.5
6.	E89004	01-2 PD	D	2.97	37.0	125.5	3.5	18.6	38.4	19.1
7.	E89005	02-1 +	N	4.06	30.1	100.1	2.0	18.8	38.9	19.5
8.	E89006	02-1 PD	D	3.64	29.8	102.7	2.5	20.1	39.6	19.1
9.	E89007	02-2 +	N	3.61	28.8	102.0	2.8	18.4	39.2	19.3
10.	E89008	02-2 PD	D	3.52	30.7	113.8	3.0	19.1	39.5	19.1
11.	E89009	04-1 +	N	3.91	30.1	90.5	1.8	19.4	39.4	18.9
12.	E89010	04-1 PD	D	3.39	31.0	109.0	2.2	20.0	39.6	19.3
13.	E89011	04-2 +	N	3.61	29.1	94.0	2.3	19.8	39.3	19.4
14.	E89012	04-2 PD	D	3.30	30.0	106.1	2.6	20.2	39.6	19.4
15.	E89013	05-1 +	N	3.74	31.1	103.2	2.3	21.7	39.1	19.5
16.	E89014	05-1 PD	D	3.68	30.1	101.3	2.0	21.5	39.0	19.2
17.	E89015	05-2 +	N	3.11	29.0	89.2	2.3	19.9	38.8	19.4
18.	E89016	05-2 PD	D	3.01	28.7	102.0	2.5	20.7	39.5	18.8
19.	E89017	06-1 +	N	3.49	27.7	89.7	2.0	21.1	39.4	19.2
20.	E89018	06-1 PD	D	3.07	39.2	118.0	3.0	17.7	38.3	19.4
21.	E89019	06-2 +	N	3.40	28.1	92.6	1.7	20.3	39.7	19.1
22.	E89020	06-2 PD	D	3.52	28.2	96.0	2.5	21.2	39.2	19.1
23.	E89021	07-1 +	N	3.62	27.6	98.1	1.7	19.3	39.8	19.1
24.	E89022	07-1 PD	D	3.37	28.6	102.1	2.0	20.4	39.7	19.1
25.	E89023	07-2 +	N	3.87	29.5	105.1	2.2	18.2	38.9	19.3
26.	E89024	07-2 PD	D	3.59	30.6	120.6	2.5	18.6	39.8	18.8
27.	E89025	08-1 +	N	3.55	28.8	102.5	2.0	18.2	39.7	19.2
28.	E89026	08-1 PD	D	3.29	30.7	112.0	2.3	18.8	40.0	18.9
29.	E89027	08-2 +	N	3.96	28.6	101.3	1.3	17.4	39.7	18.9
30.	E89028	08-2 PD	D	3.34	30.1	116.8	2.2	18.4	39.7	18.8
31.	E89029	09-1 +	N	2.73	27.0	87.3	1.3	21.9	39.4	19.1
32.	E89030	09-1 PD	D	2.79	38.2	136.2	3.5	17.4	38.3	19.1
33.	E89031	09-2 +	N	2.99	38.5	115.6	2.8	17.7	38.7	19.1

Appendix A.1. Continued....

Entry	#Acc.#	Source	Pub	Yield	Mat	HGT	LDG	Size	Protein	oil
34.	E89032	09-2 PD	D	2.84	38.8	118.8	3.0	17.4	38.3	18.8
35.	E89033	10-1 +	N	3.59	27.8	97.8	1.1	18.1	39.2	19.0
36.	E89034	10-1 PD	D	3.44	28.8	106.5	1.8	18.7	39.4	18.9
37.	E89035	10-2 +	N	3.46	27.8	82.7	1.1	18.4	39.1	19.1
38.	E89036	10-2 PD	D	3.25	28.2	91.7	1.1	19.3	39.4	18.7
39.	E89037	11-1 +	N	3.67	28.2	94.1	1.5	19.3	39.4	19.1
40.	E89038	11-1 PD	D	3.69	28.3	101.5	2.2	19.3	39.7	19.2
41.	E89039	11-2 +	N	3.68	24.8	91.6	1.0	18.2	39.0	19.7
42.	E89040	11-2 PD	D	3.36	26.6	97.6	1.3	20.1	39.1	19.5
43.	E89041	14-1 +	N	3.64	28.3	92.3	2.3	18.5	39.0	19.2
44.	E89042	14-1 PD	D	3.64	28.6	105.8	2.3	18.8	39.5	18.9
45.	E89043	14-2 +	N	3.34	26.5	87.7	1.6	19.1	38.5	19.9
46.	E89044	14-2 PD	D	2.91	28.3	103.8	2.2	20.5	38.5	19.9
47.	E89045	15-1 +	N	3.85	30.0	101.8	2.5	20.3	40.6	18.7
48.	E89046	15-1 PD	D	3.27	30.3	109.3	2.7	19.6	40.5	18.6
49.	E89047	15-2 +	N	3.53	28.8	101.7	2.5	19.6	40.0	18.8
50.	E89048	15-2 PD	D	3.31	28.7	109.3	2.6	19.6	39.8	18.9
51.	E89049	17-1 +	N	2.59	27.5	99.7	1.5	18.5	37.6	19.7
52.	E89050	17-1 PD	D	2.89	30.2	108.0	1.8	18.8	38.3	19.7
53.	E89051	17-2 +	N	3.36	34.6	114.7	2.7	18.7	38.4	19.9
54.	E89052	17-2 PD	D	3.21	35.3	115.5	3.0	18.7	38.8	19.2
55.	E89053	18-1 +	N	3.04	26.8	86.0	1.5	18.4	39.2	19.4
56.	E89054	18-1 PD	D	2.89	36.1	121.3	3.3	17.7	38.0	20.1
57.	E89055	18-2 +	N	2.97	28.1	78.0	1.4	19.3	38.6	19.8
58.	E89056	18-2 PD	D	3.31	29.0	92.0	1.5	20.1	39.0	19.3
59.	E89057	19-1 +	N	3.48	28.5	96.0	2.5	19.1	39.5	19.0
60.	E89058	19-1 PD	D	3.23	30.1	104.6	2.7	19.5	39.7	18.9
61.	E89059	19-2 +	N	2.98	25.7	85.3	1.5	17.8	39.0	19.4
62.	E89060	19-2 PD	D	2.98	26.8	97.0	1.7	19.0	38.4	19.6

Where, Pub. = Pubescence type, Yield = Grain yield (t/ha), Mat = Maturity in days (after 8/31), HGT = Plant height (cm), LDG = Lodging in 1-4(1 resistant, 4 susceptible) Size = Seed size (g/100 seeds), Protein = % protein in seed, Oil = % oil in seed, D = Dense pubescence, and N = Normal pubescence.

Appendix B.1. Analysis of variance table of the General model for Yield.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	6.03	6.03	3.81	1	1.59	ns
2.	Location(L)	1	82.02	82.02	3.75	1	21.84	ns
3.	Y x L	1	3.72	3.72	0.32	61	11.50	**
4.	Rep(Y x L)	4	10.83	2.71	0.20	244	13.55	**
5.	Genotype(G)	61	54.65	0.89	0.43	49	2.07	**
6.	Y x G	61	24.63	0.40	0.32	61	1.25	ns
7.	L x G	61	21.53	0.35	0.32	61	1.09	ns
8.	Y x L x G	61	19.77	0.32	0.20	244	1.62	**
9.	Error	244	48.80	0.20				

C.V. = 13.31% Mean = 3.35 t/ha
LSD(0.05) = 0.87t/ha LSD(0.01) = 1.15t/ha
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.2. Analysis of variance table of the General model for Maturity.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	4931.6	4931.6	2774.6	1	1.77	ns
2.	Location(L)	1	2620.2	2620.2	2769.1	1	0.95	ns
3.	Y x L	1	2729.3	2729.3	9.6	61	288.47	**
4.	Rep(YL)	4	114.8	28.7	3.1	244	9.31	**
5.	Genotype(G)	61	6165.5	101.1	14.7	33	6.87	**
6.	Y x G	61	912.1	15.0	9.6	61	1.55	*
7	L x G	61	570.9	9.4	9.6	61	0.97	ns
8.	Y x L x G	61	585.8	9.6	3.1	244	3.11	**
9.	Error	244	752.2	3.1				

C.V. = 5.81% Mean= 30.2 days after 8/31
LSD(0.05) =3.44 days LSD(0.01) =4.52 days
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.3. Analysis of variance table of the General model for Height.

#	Source	df	SS	MS	MSe	dfe	F	Sig
1.	Year(Y)	1	285.0	285.0	1197.6	1	0.23	ns
2.	Location(L)	1	8210.3	8210.3	1124.9	1	7.29	ns
3.	Y x L	1	1128.0	1128.0	68.0	61	16.58	**
4.	Rep(YL)	4	10017.2	2504.3	69.5	244	36.03	**
5.	Genotype(G)	61	69385.5	1137.4	134.4	40	8.46	**
6.	Y x G	61	8392.1	137.6	68.0	61	2.02	**
7	L x G	61	3957.7	64.9	68.0	61	0.95	ns
8.	Y x L x G	61	4148.6	68.0	69.5	244	0.98	ns
9.	Error	244	16960.8	69.5				

C.V.=8.10% Mean = 102.8 cm
LSD(0.05) =16.34 cm LSD(0.01) = 21.45 cm
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.4. Analysis of variance table of the General model for Lodging.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	44.8	44.8	0.04	1	1278.00	*
2.	Location(L)	1	8.0	8.0	0.29	8	27.68	**
3.	Y x L	1	0.0	0.0	0.42	61	0.01	ns
4.	Rep(YL)	4	31.8	9.7	0.34	244	28.47	**
5.	Genotype(G)	61	212.8	3.5	0.74	38	4.74	**
6.	Y x G	61	27.4	0.5	0.42	61	1.07	ns
7	L x G	61	42.9	0.7	0.42	61	1.68	*
8.	Y x L x G	61	25.4	0.4	0.34	244	1.22	*
9.	Error	244	83.3	0.3				

C.V. = 26.51% Mean = 2.2
LSD(0.05) = 1.14 LSD(0.01) = 1.50
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.5. Analysis of variance table of the General model for Seed size.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	1379.1	1379.1	68.2	1	20.20	ns
2.	Location(L)	1	73.4	73.4	68.6	1	1.07	ns
3.	Y x L	1	69.8	69.8	2.6	61	27.10	**
4.	Rep(YL)	4	91.4	22.8	0.6	244	36.90	**
5.	Genotype(G)	61	586.6	9.6	2.6	61	3.74	**
6.	Y x G	61	58.9	1.0	2.6	61	0.37	ns
7	L x G	61	83.8	1.4	2.6	61	0.53	ns
8.	Y x L x G	61	157.3	2.6	0.6	244	4.17	**
9.	Error	244	150.9	0.6				

C.V. = 4.08% Mean = 19.23 gm
LSD(0.05) = 1.54gm LSD(0.01) = 2.02gm
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.6. Analysis of variance table of the General model for Protein.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	5628.1	5628.10	8.75	1	643.20	*
2.	Location(L)	1	21.9	21.97	8.96	1	2.45	ns
3.	Y x L	1	8.5	8.57	0.53	61	16.10	**
4.	Rep(YL)	4	0.4	0.11	0.006	244	1.87	ns
5.	Genotype(G)	61	195.3	3.20	1.10	45	2.91	**
6.	Y x G	61	43.4	0.71	0.53	61	1.38	*
7	L x G	61	56.5	0.92	0.53	61	1.74	*
8.	Y x L x G	61	32.5	0.53	0.006	244	88.30	**
9.	Error	244	1.4	0.006				

C. V. = 0.19 % Mean = 39.16 %
LSD(0.05) = 0.15 % LSD(0.01) = 0.19 %
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix B.7. Analysis of variance table of the General model for Oil.

#	Source	df	SS	MS	MSe	dfe	F	Sig.
1.	Year(Y)	1	130.2	130.20	0.68	3	191.40	**
2.	Location(L)	1	0.3	0.26	0.45	1	0.59	ns
3.	Y x L	1	0.4	0.41	0.24	61	1.72	ns
4.	Rep(YL)	4	0.01	0.003	0.006	244	0.42	ns
5.	Genotype(G)	61	57.3	0.94	0.54	46	1.72	*
6.	Y x G	61	30.9	0.51	0.24	61	2.13	**
7	L x G	61	16.7	0.27	0.24	61	1.14	ns
8.	Y x L x G	61	14.6	0.24	0.006	244	40.00	**
9.	Error	244	1.5	0.006				

C.V. = 0.40 % Mean = 19.24 %
LSD(0.05) = 0.15 % LSD(0.01) = 0.20 %
*, **= Significant at p>0.05 and p>0.01, respectively.
ns = non-significant.

Appendix C.1. Analysis of variance table of the Nested model for Yield.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	6.323	6.323	3.746	1	1.68
2.	Location(L)	1	76.501	76.501	3.478	1	21.99
3.	Y xL	1	3.413	3.413	2.882	5	1.18
4.	Rep(Y,L)	4	10.173	2.543	0.205	236	12.36**
5.	F_2	14	28.292	2.021	1.475	11	1.37
6.	$F_3(F_2)$	15	12.883	0.858	0.326	3	2.63
7.	Pub.Density(D)	1	4.193	4.193	1.246	0	3.36
8.	F_2 x D	14	3.576	0.255	0.064	0	3.99
9.	$F_3(F_2)$ x D	15	3.988	0.265	0.316	15	0.84
10.	L x F_2	14	8.537	0.609	0.552	6	1.11
11.	L x $F_3(F_2)$	15	6.704	0.447	0.440	15	1.01
12.	L x D	1	0.834	0.834	0.943	0	0.88
13.	Y x F_2	14	12.29	0.878	0.319	15	2.74*
14.	Y x $F_3(F_2)$	15	4.794	0.319	0.545	14	0.58
15.	Y x D	1	0.961	0.961	0.991	0	0.97
16.	Y x F_2 x D	14	2.436	0.174	0.341	16	0.51
17.	Y x $F_3(F_2)$ x D	15	3.768	0.251	0.095	15	2.64*
18.	Y x L X F_2	14	7.629	0.544	0.440	15	1.23
19	Y x L x $F_3(F_2)$	15	6.602	0.440	0.205	236	2.14**
20.	Y x L x D	1	1.003	1.003	0.185	14	5.41*
21.	L x F_2 x D	14	1.757	0.125	0.250	13	0.50
22.	L x $F_3(F_2)$xD	15	2.396	0.159	0.095	15	1.68
23.	Y x L x F_2 x D	14	2.598	0.185	0.095	15	1.95
24.	YxLx$F_3(F_2)$xD	15	1.424	0.095	0.205	236	0.46
25.	Error	236	48.549	0.205			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 13.5%
Mean = 3.35

Appendix C.2. Analysis of variance table of the Nested model for Maturity.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	4838.7	4838.7	2667.9	1	1.18
2.	Location(L)	1	2511.6	2511.6	2657.5	0	0.94
3.	Y xL	1	2660.2	2660.2	45.8	10	58.06**
4.	Rep(Y,L)	4	104.1	26.0	3.1	236	8.52**
5.	F_2	14	3395.7	242.5	90.0	15	2.69*
6.	$F_3(F_2)$	15	1115.9	74.4	12.2	5	6.07*
7.	Pub.Density(D)	1	409.6	409.6	117.0	0	3.50
8.	F_2 x D	14	460.2	32.8	44.8	13	0.73
9.	$F_3(F_2)$ x D	15	681.0	45.4	5.9	9	7.73**
10.	L x F_2	14	282.3	20.2	21.4	8	0.94
11.	L x $F_3(F_2)$	15	145.1	9.6	11.1	15	0.87
12.	L x D	1	0.0	0.0	4.5	1	0.00
13.	Y x F_2	14	427.5	30.5	13.6	15	2.24
14.	Y x $F_3(F_2)$	15	204.3	13.6	22.8	14	0.59
15.	Y x D	1	121.7	121.7	4.4	1	27.41
16.	Y x F_2 x D	14	58.3	4.1	4.4	6	0.94
17.	Y x $F_3(F_2)$ x D	15	72.7	4.8	3.5	15	1.38
18.	Y x L X F_2	14	319.6	22.8	11.1	15	2.06
19	Y x L x $F_3(F_2)$	15	165.8	11.1	3.1	236	3.61**
20.	Y x L x D	1	3.4	3.4	3.1	14	1.08
21.	L x F_2 x D	14	59.9	4.3	4.1	5	1.03
22.	L x $F_3(F_2)$xD	15	67.7	4.5	3.5	15	1.29
23.	Y x L x F_2 x D	14	43.3	3.1	3.5	15	0.88
24.	YxLx$F_3(F_2)$xD	15	52.4	3.5	3.1	236	1.14
25.	Error	236	720.8	3.1			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 5.8 %
Mean = 30.3

Appendix C.3. Analysis of variance table of the Nested model for Height.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	238.0	238.0	1418.6	1	0.16
2.	Location(L)	1	8151.0	8151.0	1298.7	1	6.27
3.	Y xL	1	1267.5	1267.5	2391.6	3	0.53
4.	Rep(Y,L)	4	9642.1	2410.5	68.6	236	35.09**
5.	F_2	14	26663.9	1904.5	743.1	15	2.56*
6.	$F_3(F_2)$	15	9937.1	662.4	151.6	7	4.37*
7.	Pub.Density(D)	1	18924.2	18924.2	277.1	0	68.27
8.	F_2 x D	14	4737.2	338.3	514.6	14	0.65
9.	$F_3(F_2)$ x D	15	7367.3	491.1	96.8	9	5.07**
10.	L x F_2	14	1134.9	81.1	25.1	0	3.23
11.	L x $F_3(F_2)$	15	1061.5	70.7	95.4	15	0.74
12.	L x D	1	168.6	168.6	474.9	1	0.35
13.	Y x F_2	14	2814.0	201.0	176.3	15	1.14
14.	Y x $F_3(F_2)$	15	2645.5	176.3	49.8	14	3.53
15.	Y x D	1	18.0	18.0	520.3	1	0.03
16.	Y x F_2 x D	14	1380.8	98.6	79.5	7	1.23
17.	Y x $F_3(F_2)$ x D	15	1454.4	96.6	49.0	15	1.97
18.	Y x L X F_2	14	698.1	49.8	95.5	15	0.52
19	Y x L x $F_3(F_2)$	15	1433.1	95.5	68.6	236	1.39
20.	Y x L x D	1	453.3	453.3	31.6	14	14.32**
21.	L x F_2 x D	14	746.2	53.3	31.5	2	1.69
22.	L x $F_3(F_2)$xD	15	733.4	48.8	49.0	15	0.99
23.	Y x L x F_2 x D	14	443.0	31.6	49.0	15	0.64
24.	YxLx$F_3(F_2)$xD	15	735.3	49.0	68.6	236	0.71
25.	Error	236	16211.1	68.6			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 8.1%
Mean = 103.1

Appendix C.4. Analysis of variance table of the Nested model for Lodging.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	48.13	48.13	0.017	0	2720.4*
2.	Location(L)	1	9.08	9.08	0.725	3	12.50*
3.	Y xL	1	0.00	0.00	8.021	4	0.00
4.	Rep(Y,L)	4	31.05	7.76	0.328	236	23.60**
5.	F_2	14	99.46	7.10	3.884	17	1.82
6.	$F_3(F_2)$	15	46.58	3.11	0.551	5	5.63*
7.	Pub.Density(D)	1	28.78	28.78	1.851	1	15.54
8.	F_2 x D	14	13.37	0.95	1.196	10	0.79
9.	$F_3(F_2)$ x D	15	16.35	1.09	0.351	3	3.11
10.	L x F_2	14	18.39	1.31	0.554	5	2.37
11.	L x $F_3(F_2)$	15	7.48	0.50	0.532	15	0.937
12.	L x D	1	0.79	0.79	0.181	2	4.40
13.	Y x F_2	14	8.48	0.61	0.585	15	1.03
14.	Y x $F_3(F_2)$	15	8.78	0.59	0.587	14	0.99
15.	Y x D	1	1.45	1.45	0.072	0	19.96
16.	Y x F_2 x D	14	3.85	0.27	0.006	0	40.59
17.	Y x $F_3(F_2)$ x D	15	2.87	0.19	0.386	15	0.49
18.	Y x L X F_2	14	8.23	0.59	0.532	15	1.10
19	Y x L x $F_3(F_2)$	15	7.98	0.53	0.328	236	1.61*
20.	Y x L x D	1	0.00	0.00	0.201	14	0.00
21.	L x F_2 x D	14	5.36	0.38	0.361	3	1.06
22.	L x $F_3(F_2)$xD	15	8.18	0.55	0.386	15	1.41
23.	Y x L x F_2 x D	14	2.83	0.20	0.386	15	0.523
24.	YxLx$F_3(F_2)$xD	15	5.79	0.37	0.328	236	1.17
25.	Error	236	77.62	0.33			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 26.2%
Mean = 2.22

Appendix C.5. Analysis of variance table of the Nested model for Seed size.

	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	1327.5	1327.5	58.92	0	22.53
2.	Location(L)	1	70.3	70.3	59.23	0	1.18
3.	Y xL	1	63.8	63.8	26.78	6	2.38
4.	Rep(Y,L)	4	84.2	21.1	0.60	236	34.93**
5.	F_2	14	221.7	15.8	5.63	3	2.81
6.	$F_3(F_2)$	15	131.8	8.7	0.02	0	413.04*
7.	Pub.Density(D)	1	4.2	4.2	9.94	1	0.42
8.	F_2 x D	14	100.2	7.1	4.71	7	1.52
9.	$F_3(F_2)$ x D	15	93.5	6.2	1.48	11	4.20*
10.	L x F_2	14	24.5	1.7	5.51	9	0.38
11.	L x $F_3(F_2)$	15	19.6	1.3	2.12	15	0.61
12.	L x D	1	5.2	6.9	1.3	4	5.02
13.	Y x F_2	14	20.1	1.4	0.82	15	1.73
14.	Y x $F_3(F_2)$	15	12.4	0.8	6.32	14	0.13
15.	Y x D	1	0.6	2.2	1.16	3	1.92
16.	Y x F_2 x D	14	10.3	0.7	1.88	12	0.39
17.	Y x $F_3(F_2)$ x D	15	12.1	0.8	0.66	15	1.21
18.	Y x L X F_2	14	88.5	6.3	2.12	15	2.98*
19	Y x L x $F_3(F_2)$	15	31.8	2.1	0.60	236	3.51**
20.	Y x L x D	1	0.42	0.42	1.73	14	0.24
21.	L x F_2 x D	14	13.4	0.95	2.41	15	0.39
22.	L x $F_3(F_2)$xD	15	20.1	1.33	0.66	15	2.02
23.	Y x L x F_2 x D	14	24.3	1.73	0.66	15	2.62*
24.	YxLx$F_3(F_2)$xD	15	9.92	0.66	0.60	236	1.09
25.	Error	236	142.2	0.6			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 4.1%
Mean = 19.24

Appendix C.6. Analysis of variance table of the Nested model for Protein.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	5447.26	5447.26	6.58	0	827.85*
2.	Location(L)	1	19.76	19.76	7.57	1	2.61
3.	Y xL	1	6.96	6.96	1.12	14	6.18*
4.	Rep(Y,L)	4	0.05	0.012	0.006	236	2.00**
5.	F_2	14	132.90	9.49	1.52	3	6.24*
6.	$F_3(F_2)$	15	27.07	1.80	1.63	29	1.10
7.	Pub.Density(D)	1	3.48	3.48	2.15	1	1.61
8.	F_2 x D	14	20.53	1.47	0.35	0	4.20
9.	$F_3(F_2)$ x D	15	13.63	0.91	1.13	20	0.80
10.	L x F_2	14	24.22	1.73	1.99	27	0.86
11.	L x $F_3(F_2)$	15	13.34	0.89	0.02	15	44.50*
12.	L x D	1	0.00	0	1.86	0	0.00
13.	Y x F_2	14	10.36	0.74	0.76	15	0.97
14.	Y x $F_3(F_2)$	15	11.47	0.76	1.12	14	0.67
15.	Y x D	1	0.00	0.00	2.09	1	0.00
16.	Y x F_2 x D	14	10.41	0.74	1.09	19	0.67
17.	Y x $F_3(F_2)$ x D	15	9.37	0.62	0.21	15	2.95*
18.	Y x L X F_2	14	15.68	1.12	0.02	15	56.00**
19	Y x L x $F_3(F_2)$	15	0.34	0.02	0.006	236	3.33**
20.	Y x L x D	1	2.03	2.03	0.68	14	2.98
21.	L x F_2 x D	14	7.16	0.51	1.19	20	0.42
22.	L x $F_3(F_2)$xD	15	10.73	0.72	0.21	15	3.42*
23.	Y x L x F_2 x D	14	9.51	0.68	0.21	15	3.23*
24.	YxLx$F_3(F_2)$xD	15	3.12	0.21	0.006	236	35.00**
25.	Error	236	1.41	0.006			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 0.2 %
Mean = 39.2

Appendix C.7. Analysis of variance table of the Nested model for Oil.

#	Source	df	SS	MS	MSe	dfe	F
1.	Year(Y)	1	126.58	126.58	1.04	5	121.71*
2.	Location(L)	1	0.33	0.33	0.54	1	0.61
3.	Y xL	1	0.35	0.35	0.35	13	0.98
4.	Rep(Y,L)	4	0.011	0.003	0.006	236	0.50
5.	F_2	14	30.19	2.15	1.74	16	1.23
6.	$F_3(F_2)$	15	13.88	0.93	0.43	10	2.16
7.	Pub.Density(D)	1	2.72	2.72	3.83	0	0.71
8.	F_2 x D	14	4.04	0.29	0.31	3	0.93
9.	$F_3(F_2)$ x D	15	5.72	0.38	0.21	6	1.81
10.	L x F_2	14	7.74	0.55	0.36	8	1.52
11.	L x $F_3(F_2)$	15	2.93	0.20	0.20	15	1.00
12.	L x D	1	0.153	0.40	0.23	6	1.73
13.	Y x F_2	14	14.72	1.05	0.43	15	2.44
14.	Y x $F_3(F_2)$	15	6.38	0.43	0.36	14	1.19
15.	Y x D	1	3.62	3.88	0.22	6	17.63**
16.	Y x F_2 x D	14	2.66	0.19	0.26	7	0.73
17.	Y x $F_3(F_2)$ x D	15	2.74	0.18	0.17	15	1.06
18.	Y x L X F_2	14	4.97	0.36	0.20	15	1.80
19	Y x L x $F_3(F_2)$	15	2.96	0.20	0.006	236	33.33**
20.	Y x L x D	1	0.03	0.03	0.25	14	0.12
21.	L x F_2 x D	14	2.68	0.20	0.28	8	0.71
22.	L x $F_3(F_2)$xD	15	2.91	0.20	0.17	15	1.17
23.	Y x L x F_2 x D	14	3.55	0.25	0.17	15	1.47
24.	YxLx$F_3(F_2)$xD	15	2.607	0.17	0.006	236	28.33**
25.	Error	236	1.474	0.006			

*,** Significant at p>0.05 and P>0.01, repectively.
C.V. = 0.4 %
Mean = 19.2

Appendix D.1. Estimates of correlation coefficients and their respective significance among variables by Year.

Variable	Yield	maturity	Height	Lodging	Seed size	Protein	Oil
Yield							
'89	___	-0.26**	0.04	-0.02	0.37**	0.48**	-0.27**
'90	___	0.51**	-0.17**	-0.08	0.43**	0.21**	0.03
AVE	**___**	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity							
'89		___	0.45**	0.36**	-0.30**	-0.47**	0.24**
'90		___	0.36**	0.37**	0.30**	-0.04	-0.16**
AVE		**___**	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height							
'89			____	0.61**	-0.02	-0.23**	-0.02
'90			____	0.59**	-0.20**	-0.17**	-0.26**
AVE			**____**	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging							
'89				____	0.05	-0.12	0.11
'90				____	0.03	-0.09	-0.19**
AVE				**____**	**0.26****	**0.28****	**0.17****
Seed size							
'89					____	0.29**	-0.09
'90					____	0.31**	-0.02
AVE					**____**	**0.75****	**0.50****
Protein							
'89						____	-0.63**
'90						____	-0.60**
AVE						**____**	**0.59****
Oil							
'89							____
'90							____
AVE							**____**

*,** Significant at $p<0.05$ and $p<0.01$, respectively.

Appendix D.2. Estimates of correlation coefficients and their respective significance among variables by Location.

Variable	Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield							
ING	____	-0.15*	-0.12	-0.03	0.31**	0.12	-0.02
LEN	____	0.24**	0.26**	0.20**	0.38**	0.36**	0.03
AVE	**____**	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity							
ING		____	0.62**	0.48**	0.01	0.11	-0.02
LEN		____	0.30**	0.60**	0.64**	0.76**	0.53**
AVE		**____**	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height							
ING			____	0.39**	-0.27**	-0.20**	-0.28**
LEN			____	0.66**	0.07	0.03	-0.03
AVE			**____**	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging							
ING				____	0.35**	0.32**	0.16*
LEN				____	0.24**	0.27**	0.19**
AVE				**____**	**0.26****	**0.28****	**0.17****
Seed size							
ING					____	0.71**	0.44**
LEN					____	0.81**	0.54**
AVE					**____**	**0.75****	**0.50****
Protein							
ING						____	0.67**
LEN						____	0.54**
AVE						**____**	**0.59****
Oil							
ING		ING= Ingham					____
LEN		LEN= Lenawee					____
AVE		*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively.					**____**

Appendix D.3. Estimates of correlation coefficients and their respective significance among variables by Year x Location.

Variable		Yield	Maturity	Height	Lodging	Seed size	Protein	Oil
Yield								
'89	ING	____	-0.39**	-0.15	-0.05	0.49**	0.50**	-0.29**
	LEN	____	-0.17*	0.45**	0.13	0.30**	0.27**	-0.29**
'90	ING	____	-0.02	-0.06	-0.64	0.09	-0.09	0 .11
	LEN	____	0.16	-0.07	0.09	0.22**	0.32**	-0.65**
	AVE	**____**	**0.27****	**-0.06**	**0.01**	**0.38****	**0.24****	**0.03**
Maturity								
'89	ING		____	0.69**	0.13	-0.61**	-0.53**	0.02
	LEN		____	0.33**	0.54**	0.04	-0.46**	0.41**
'90	ING		____	0.69**	0.57**	0.12	-0.17*	-0.31**
	LEN		____	0.59**	0.70**	-0.14	-0.15	-0.33**
	AVE		**____**	**0.28****	**0.45****	**0.44****	**0.45****	**0.32****
Height								
'89	ING			____	0.37**	-0.47**	-0.31**	-0.13
	LEN			____	0.73**	0.38**	0.03	0.05
'90	ING			____	0.55**	0.07	-0.07	-0.31**
	LEN			____	0.63**	-0.31**	-0.22**	-0.22
AVE				**____**	**0.55****	**-0.11***	**-0.09***	**-0.14****
Lodging								
'89	ING				____	-0.02	0.05	-0.08
	LEN				____	0.13	-0.17	0.24**
'90	ING				____	0.41**	0.05	-0.15
	LEN				____	-0.19*	-0.19*	-0.23**
	AVE				**____**	**0.26****	**0.28****	**0.17****
Seed size								
'89	ING					____	0.47**	-0.15
	LEN					____	0.09	-0.03
'90	ING					____	0.27**	-0.09
	LEN					____	0.3227**	-0.05
	AVE					**____**	**0.75****	**0.50****
Protein								
'89	ING						____	-0.57**
	LEN						____	-0.78**
'90	ING						____	-0.55**
	LEN						____	-0.65**
	AVE						**____**	**0.59****
Oil								
'89	ING		ING= Ingham					____
	LEN		LEN= Lenawee					____
'90	ING							____
	LEN							____
	AVE							**____**

*, ** Significant at $p < 0.05$ and $p < 0.01$, respectively

MICHIGAN STATE UNIV. LIBRARIES
31293010550220