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(*Triticum aestivum* L.)

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THE UNIVERSITY OF ALBERTA

A BIOMETRICAL-GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS

IN A FIVE-PARENT DIALLEL CROSS OF COMMON WHEAT

(*TRITICUM AESTIVUM* L.)

by



BARKAT ALI SOOMRO

A THESIS

SUBMITTED TO THE FACULTY OF GRADUATE STUDIES AND RESEARCH

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DEPARTMENT OF GENETICS

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The undersigned certify that they have read, and recommend to the Faculty of Graduate Studies and Research for acceptance, a thesis entitled A Biometrical-Genetic Analysis of Some Quantitative Characters in a Five-Parent Diallel Cross of Common Wheat (*Triticum aestivum* L.) submitted by Barkat Ali Soomro in partial fulfilment of the requirements for the degree of Doctor of Philosophy.

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ABSTRACT

Common wheat (*Triticum aestivum* L.) cultivars Marquis, Chinook, Khush-hal, Ciano-67 and Inia-66 were used as parents of a five-parent diallel cross. The F_1 , F_2 , backcross and selfed backcross generations of this diallel cross were used as materials in this study. The experimental data were investigated by means of principal factor analysis, general and specific combining ability analysis, diallel cross analysis for genetic components of variation and genotype-environment interaction analysis. The data on ten characters were recorded from materials grown at Ellerslie and Parkland. The characters considered were: onset-of-heading, final heading, heading-span, plant height, number of tillers per plant, number of spikelets per spike, number of seeds per spike, weight of seeds per spike, 1000-kernel weight and yield per plant.

In the factor analyses, correlation matrices indicated that early maturing varieties were high yielding. Yield per plant was positively correlated with its subcharacters or components. There was no correlation between yield and plant height. Varimax rotated factor matrices for each generation of the diallel cross constituted five principal factors which were named according to the magnitude of the factor loading on the characters. The results of the factor analyses confirmed the conclusions drawn from correlation analyses. The scores of factor loadings on various characters were different for two locations but the generations appeared not to affect them significantly.

The general and specific combining ability analyses indicated that parental lines possessing high GCA's usually produced hybrids with low SCA's and therefore general combining ability of the parents does not necessarily constitute a criterion for evolving hybrids with high specific combining ability. The variances for GCA's were usually greater than those for SCA's for all the characters, and in those cases where SCA-variances were larger, the importance of non-additive gene effects for the characters concerned has been emphasized. SCA-variances significantly higher than GCA variances indicated instabilities of the cultivar for the character concerned and therefore these differences may be used as criteria for the selection in pedigree-record breeding. Mean squares for GCA's were in general all significant. Analysis also showed that GCA's were not significantly affected either by generations of the diallel set or by locations. The stability of the response of each cultivar with respect to its GCA was consistent over two locations.

The mean degree of dominance with respect to different characters ranged from partial to over-dominance. The proportions of alleles with positive and negative effects were not the same for all the characters: complete symmetry was observed for some and asymmetry for others. For some characters dominant and recessive genes in the parents were in equal proportions and for others either there was a preponderance of dominants or of recessives. Character differences were found to be controlled by at least one to three groups of genes. The analyses for the characters considered have shown that

the genetic components of variation were relatively stable over the generations. They were more consistent when estimated from the variances and covariances of adjusted treatment means (from ANOVA of partially balanced lattice design) than when estimated from unadjusted means (experiments treated as randomized blocks).

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INTRODUCTION

The degree to which a quantitative or metrical trait is phenotypically expressed in individuals depends on their genotype and the environmental conditions under which they are grown. It is assumed, and the experimental data seems to confirm it in most of the cases, that the genotype considered with respect to a metrical character is a set of genes referred to by Mather individually as polygenes and collectively as a polygenic system (Mather, 1949). These genes are often interdependent both in their action and transmission. In a polygenic system underlying a quantitative character, the allelic and non-allelic interactions are the most usual forms of manifestation of gene effects and inheritance pattern. The interaction of alleles at a given locus is known as dominance, while non-allelic interaction, viz., interaction between the genes at different loci, may take the form of complementary-gene, duplicate-gene or other classical relationships. All these effects are referred to generally as 'epistasis' in biometrical genetics.

Different genotypes defined with reference to a metrical character do not react alike to a given change in environment. This means that genotype and environment are not independent in their action in producing the phenotype. Consequently the variation in the degree of expression of the character is assumed to consist of genotypic, environmental and genotype-environment interaction components which may respectively be partitioned in a biometrically defined experimental design. The measurement of genotype-environment interaction in the diallel cross

is quite efficient and informative, since a number of parental strains can be assessed together with their hybrid generations.

The diallel cross technique is one of the conventional approaches used in biometrical genetics to obtain adequate information regarding the inheritance of a quantitative character. The procedure, first introduced by Schmidt (1919) involves crossing a set of parental lines in all possible combinations, including their reciprocals, in order to obtain an estimation of the magnitude of genetic variability ascribable to the differences among the parental lines. The quantitative genetic analysis of a diallel cross based on a set of postulated assumptions is presented and discussed in detail by Jinks and Hayman (1953), Hayman (1954a, 1954b, 1958 and 1960), Jinks (1954 and 1956) and Kempthorne (1956). means of pertinent parameters obtainable from the analysis of the diallel cross, the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance the proportion of dominant to recessive genes in the parents, and the correlation between the parental order of dominance and parental measurements can be determined. In addition, the graphical analysis of the regression of array covariances (W_p) on array variances (V_p) permits the separation of true dominance from the spurious one caused by non-allelic interaction and categorizes the parents according to their degree of dominance.

The analysis of genotype-environment interaction by means of a diallel cross replicated in time, in space or in both time and space, provides information on the pattern of reaction of homozygous parents and their hybrids to environmental variation. The value of such an analysis

is that the significant inter-environmental differences characteristic of different genotypes are reflected in the array variances and covariances by their effects on the relative magnitude of components of these statistics. The project reported in this thesis deals with this type of analysis of genotype-environment interaction in a five-parent diallel cross in common wheat (*Triticum aestivum* L.). The purpose of the investigation was to obtain information regarding the extent to which the genetic components of variation and the combining abilities of the parental lines are affected by environmental changes.

REVIEW OF LITERATURE

General background

A diallel cross involves the mating of n genotypes, individual clones or homozygous lines in all possible combinations to give $[n(n-1)]$ crosses, including reciprocals. The total number of such combinations comes to n^2 if the parents are also included as selfs. The n^2 combinations may be arranged in the form of a square matrix, the rows and columns of which correspond to the offspring of each parent, the n parents themselves occupying the main diagonal. Such an arrangement of arrays, known as a diallel table, may be complete or incomplete. Complete tables consist of all n^2 entries, while in incomplete ones the parental or reciprocal entries may be absent. Griffing (1956) has developed four possible methods of constructing a diallel table, together with the corresponding forms of analysis. These are: (1) the parents, all the F_1 's and their reciprocals are included (n^2 combinations); (2) the parents and one set of F_1 's are included but not the reciprocals [$\frac{1}{2}n(n+1)$ combinations]; (3) one set of F_1 's and reciprocals are included but parents are not [$n(n-1)$ combinations]; and (4) one set of F_1 's is included but the reciprocal crosses and the parents are not [$\frac{1}{2}n(n-1)$ combinations]. For each of these combinations, Griffing has developed two kinds of statistical analyses, arising from different assumptions regarding the sampling nature of the experimental material; either it is assumed to be a random sample from the population or it is assumed to be deliberately chosen, and therefore not a random sample.

The biometrical-genetic analysis of a diallel cross as formulated by Hayman (1954b) is based on the following set of assumptions:

1. Homozygous parents
2. Normal diploid segregation
3. No differences between reciprocal crosses
4. Independent action of non-allelic genes
5. No multiple allelism
6. Genes independently distributed between the parents.

The genetic analysis, discussed by different authors (Hull 1945; Hayman 1954a, 1954b, 1958, 1960; Jinks 1954, 1956 and Jinks and Hayman 1953) implies the estimation of genetic components of variation from the following second degree statistics:

V_{OLO} = Variance of the parents

W_r = Covariance between the parents and their offspring in one array (r th array)

W_{OLO1} = Mean covariance between the parents and their offspring over the arrays

V_r = Variance of the r th array

V_{1L1} = Mean variance of the arrays

$(M_{L1} - M_{LO})$ = Difference between the mean of the parents and the mean of their r^2 progeny

The description of the genetic components of variation is given below:

D = Component of variation due to additive gene effects

H_1 = Component of variation due to dominance effects of the genes

H_2 = Component of variation due to dominance effects, corrected for gene distribution

F = Covariation between additive and dominance effects over all the arrays. Thus F could be used to determine the relative proportion of dominant to recessive alleles in the parents involved.

The expected values of these genetic components of variation in terms of variances and covariances have been described by Mather (1949), Hayman (1954b, 1958), Jinks (1954, 1956) and Mather and Jinks (1971).

The relationship between the array variances and covariances, expressed graphically, shows the overall genetic situation with respect to the inheritance-pattern of a particular character. When the set of assumptions described earlier are valid, the $W_r - V_r$ differences are constant over the arrays, the regression of covariance on the array variance is a straight line of unit slope and all the points of W_r, V_r intercepts lie on this line. The upper and the lower limits where the W_r, V_r intercepts can lie are the points where the regression line intersects the limiting parabola. These points correspond respectively to the completely recessive and completely dominant parents, and thus show the possible limits of selection.

A deviation from the expected regression line of unit slope indicates the presence of non-allelic interaction. Any type of non-allelic interaction affecting the crosses in an array will inflate the variance of that array and reduce the parent-offspring covariance. Such an increase in variance relative to covariance will move the W_r, V_r graph towards the right, giving an apparent increase in dominance, and will cause the slope of the regression line to be less than unity. Thus, with $H_1 = D$ (complete dominance), $V_{1L1} + W_{0L01} = 1$ and the line of unit

slope will pass through the origin; with $H_1 > D$ (over-dominance), $V_{1L1} \div W_{OLO1} > 1$ and the line will cross the ordinate below the origin; and with $H_1 < D$ (partial dominance), $V_{1L1} \div W_{OLO1} < 1$ and the regression line will pass above the origin. If, of course, $H_1 = 0$ there is no regression. The mean degree of dominance is measured by $(H_1 \div D)^{1/2}$. The ratio $(H_2 \div 4H_1)$ provides an estimate of the proportion of genes with positive and negative effects in the parents. The proportion of dominant to recessive genes in the parents is given by $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F]$ and the number of groups of genes controlling the character and showing dominance can be determined by the formula $[c^2/\bar{E}_L]$.

The failure of any one of the six postulated assumptions invalidates the analysis to a certain extent. The effects of the failure of these assumptions are discussed by Hayman (1954b). The methods of analysis of complete diallel tables as developed by Yates (1947), Hayman (1954a), Durrant (1965) and Jinks *et al.* (1972) allow, among others, for the detection and testing of 'reciprocal differences'. Significance of the c pertaining to reciprocal differences in Hayman's analysis implies the expectation of two values for each of the genetic components of variation, D , H_1 , H_2 and F from the diallel table; one from the use of column arrays and the other from the use of row arrays. This ambiguity may be removed by replacing the off-diagonal cells of the diallel table by the common mean for the cross and its reciprocal. However, with significant c , the errors of the parameters will be inflated. Departure from independent action of non-allelic genes may be checked by examining

the $W_r - V_r$ values for homogeneity. Heterogeneity of $W_r - V_r$ differences indicates failure of the assumptions postulated. If this is the case, the inspection of the V_r, W_r graph would show which of the arrays contribute mostly to this failure. The disparate arrays may be eliminated, leaving a sub-diallel table for analysis that satisfies the null hypothesis. The results of the analysis would be valid, of course, for the remaining arrays.

Manifestations of 'non-allelic interaction', 'multiple allelism' and 'correlated gene distribution' introduce serious complications into the diallel analysis. They disturb the direction and mean degree of dominance, inflate the estimated proportion of dominant to recessive genes in the parents and reduce the estimate of the number of genes controlling a particular character. A test of homogeneity of variances of $W_r - V_r$ values has been advocated as an appropriate method for their detection.

Application of diallel cross analysis

The literature pertinent to diallel cross analysis as applied to plant breeding programmes is fairly impressive. In non-cereal crop plants, the technique has been widely used in the study of various quantitative characters. Thus this technique has been applied to brome grass (Knowles 1950; Greesom and Kalton 1956; Neilson and Kalton 1959; Dunn and Wright 1970), alfalfa (Kehr 1961; Theurer and Elling 1963a, b; Wilcox and Wilsie 1964), flax (Carnahan 1947; Durrant and Tyson 1964; Murty *et al* 1967; Anand and Murty 1968, 1969), cotton (Turner 1953; Marani 1963;

White and Richmond 1963; Marani 1964; Miller and Marani 1963; White and Kohel 1964), tobacco (Jinks 1954, 1956; Matzinger *et al* 1962; Marani and Sachs 1966; Povilaitis 1966; Legg *et al* 1970; Povilaitis 1970), strawberry (Morrow *et al* 1958; Aalders and Craig 1968; Watkins and Spangello 1968; Spangello *et al* 1971) and *brassica* (Johnston 1968a, b; Chiang 1969).

In cereals, a considerable number of studies using diallel analysis have been made with rice (Mohammad and Hanna 1965; Athwal and Singh 1966a, b; Wu 1968a, b; Cheng and Chang 1970), maize (Kinman and Sprague 1945; Sprague and Federer 1951; Bauman 1959; Matzinger *et al* 1959; Sprague 1964; Troyer and Hallauer 1968; Eberhart and Russell 1969; Poneilet and Bauman 1970), barley (Johnson and Aksel 1959; Aksel and Johnson 1961; Eunis *et al* 1962; Fasoulas and Allard 1962; Aksel and Johnson 1963; Johnson and Aksel 1964; Norington 1967, 1968; Persson 1969; Yap and Harvey 1971; Riggs and Hayter 1972, 1973) and *sorghum* (Chiang and Smith 1967a, b; Liang 1967; Liang *et al* 1968).

In wheat, the first report on the use of diallel analysis is that of Whitehouse and co-workers (1958). Of the five characters studied by them in a 4×4 diallel cross, viz., single kernel weight, grains per spikelet, spikelets per spike, ears per plant and yield per plant, all except yield per plant were found to be under additive genic control. For total yield, a generalized type of gene action was found in the F_1 but the F_2 generation exhibited a localized multiplicative type of gene action.

Lupton (1961) performed a diallel analysis of the yield of winter wheats. Though there was no non-allelic interaction (as revealed

by W_r , V_r graphs) in either the drilled or space-planted experiments, the position of the parents with respect to dominance was significantly changed in the two environments. The highest yielding parent, Capelle, exhibited dominance in the space-seeded trial and was reported to be the most recessive in the drilled trial. This change in yield inheritance was attributed to environmental differences of the inter-plant competition type which appeared to affect drill plantings more than space-seedings. In a later study (Lupton 1965), an incomplete diallel system, where reciprocals were excluded, was used to study the yield of spring wheat varieties replicated both in space and time, for F_1 , F_2 and F_3 generations. In all cases, interaction of over-dominance with site was highly significant, establishing consistency in the performance of the parents and their hybrid combinations.

Crumpacker and Allard (1962) analysed heading date in ten spring wheat varieties in a complete diallel test, replicated over three years. The results indicated substantial differences among the parents, generally categorized as highly dominant, moderately dominant, moderately recessive and highly recessive. The genetic system governing the maturation time of the parents, F_1 's and F_2 -generation hybrids consisted of a very few major genes showing dominance and was reported to be operating consistently in different years.

Fonseca (1965) studied the inheritance of yield and yield-components in a seven-parent diallel cross of wheat. The author reported significant differences among the parental lines used. The

graphical analysis revealed partial dominance to slight over-dominance for all the characters studied. Since all the F_1 's yielded higher than either of their respective parents, the author proposed a new term, heterobeltiosis, to describe the better performance of the F_1 over the better parent in the cross.

Bagnara (1967) performed a diallel analysis on normal and radiation-induced mutant lines of durum wheat. The results revealed significant differences between the lines and the mutants derived from them with regard to the expression of the degree of dominance. All the characters under study except spikelets per spike exhibited partial dominance.

Fonseca and Patterson (1968) studied hybrid vigour in a seven-parent wheat diallel to determine the diversity of germ-plasms in hill-planting experiments. The authors reported significant heterobeltiosis for yield and kernel-weight in half of the F_1 hybrids. The yield and kernel-weight estimates, were respectively 100% and 101 to 115% greater than either parent in hilled as against experimental nursery plots.

Walton (1969) studied the association of several morphological characters with yield in a seven-parent spring wheat diallel. He reported that the distance of the spike above the leaf-sheath at maturity and flag-leaf area were directly proportional to yield, and that yield, flag-leaf area and spike length were partially dominant.

Paroda and Joshi (1970) performed a genetic analysis of a complete 6 x 6 wheat diallel test for yield and its principal components: 1000-kernel weight, kernels per spike and tillers per plant. Yield and

1000-kernel weight exhibited non-allelic interaction of the duplicate-gene and complementary-gene type, respectively. For both characters, the variances for additive gene effects were significant.

Hsu and Walton (1970) studied gene action for yield and its components (spikes per plant, spikelets per spike, kernels per spike and 1000-kernel weight) in a 5 x 5 wheat diallel. For all the characters studied, the genetic variation was reported to be due to additive and dominance gene effects. Yield per plant exhibited complete, and its components partial, dominance.

Bitzer *et al* (1971) reported gene action and hybrid vigour in a six-parent wheat diallel. The results of two years of study revealed that the yield of the F_1 hybrids was not significantly higher than that of the parental strains. However, according to the graphical analysis of regression of W_p on V_p , plant height, kernel weight and spikelets per spike exhibited partial dominance while yield per plant showed over-dominance.

Kaltsikes and Lee (1971) estimated the genetic parameters for degree of dominance, ratio of total number of dominant to recessive parental genes and heritability for yield and its components in a 6 x 6 diallel of durum wheat. The average degree of dominance ranged from incomplete dominance to over-dominance and an excess of dominant over recessive alleles in the parents was found for all the characters studied. Since the heritability estimates for yield were as high as 61%, the authors suggested a pedigree selection procedure in breeding for yield characters in durum wheat.

General and specific combining ability

In quantitative genetics two types of combining ability, viz., general combining ability and specific combining ability are considered. General combining ability (GCA) refers to the average performance of a parental line as reflected in its hybrid combinations, while specific combining ability (SCA) refers to the performance of a particular cross. According to Sprague and Tatum (1942), GCA is due to genes which are largely additive, and SCA to genes showing non-additive effects. Nakamura (1956) considers GCA as 'an index of the number of effective genes' and SCA as 'an index of the number of common genes and the interaction between their alleles'. According to Fryxel *et al* (1958), GCA is the ability of a parental strain to produce promising or non-promising genotypes in its hybrids, regardless of the other parent involved, while SCA refers to this ability in hybrid combinations with certain other parental strains.

In a detailed examination of combining ability in the diallel cross, by Griffing (1956), eight procedures of statistical analysis have been proposed. These have been developed for four different diallel crossing schemes and for two alternative assumptions regarding sampling nature.

Kronstad and Foote (1964) using Griffing's diallel analysis for estimating GCA and SCA effects in ten winter wheat varieties found that a large portion of the total genetic variation for yield and yield components was associated with significant GCA effects. SCA effects were significant for yield per plant and plant height but not for yield components.

Fonseca (1965) studied the performance of F_1 hybrids for yield and yield components in a 7 x 7 diallel cross using Griffing's method 4 (one set of F_1 's is included in the diallel table but the reciprocal crosses and the parents are not) with fixed model. The results revealed that all the mean squares for GCA and some of the mean squares for SCA were significant.

Brown *et al* (1966) found that most of the variation in yield and other characters among F_1 wheat hybrids was associated with high GCA rather than with SCA variances.

Singh *et al* (1969) in an analysis of a 7 x 7 wheat diallel for combining ability and genetic parameters for yield and its components, reported importance of additive gene effects for general over the non-additive ones of specific combining ability for yield components. The variances for GCA and SCA in the case of yield were of the same order of magnitude, implying additive as well as non-additive effects.

Bhatt (1971) reported combining ability estimates for earliness, plant height and four yield components in a 5 x 5 wheat diallel. The analysis of GCA indicated that the larger portion of the genetic variation, for six out of seven characters considered, was associated with additive gene effects. The estimates of SCA's were highly significant but lower than GCA's for five characters.

Bitzer *et al* (1971) performed a combining ability analysis in a 6 x 6 diallel and found that GCA mean squares were significant for earliness, plant height and kernels per spike whereas SCA mean squares

were not. The average yield of the F_1 's was 28.1% higher than that of the highest yielding parent.

Paroda and Joshi (1970a) compared the combining ability variances of F_1 and F_2 generations for yield and other characters in a 6 x 6 wheat diallel. The GCA effects were high in the F_1 's and F_2 's but SCA effects were high only in F_1 's. Similar results were also reported by Niehaus and Pickett (1966) in a *sorghum* diallel.

In some of the papers it has been reported that the parents with high GCA values do not necessarily produce hybrids with high SCA values (Larson, 1941 in tomatoes; Crumpacker and Urquhart, 1962 in wheat; Walker 1963, Chang 1967, Soomro 1967, Baluch and Soomro 1969 and Soomro and Baluch 1969 in cotton). It follows, therefore, that the general combining ability should not be taken as a criterion for predicting high specific combining ability.

Genotype-environment interaction

Finlay and Wilkinson's (1963) regression analysis technique permitted for the first time a satisfactory assessment of the performance stability of a strain or cultivar over the range of environments in which it is grown. According to these authors, a regression of varietal-mean-yield on location-mean-yield with a regression coefficient of less than unity indicates that the variety has an above-average stability in its response to environmental influences. Regression coefficients equal to and greater than unity indicate average and less-than-average stability respectively. Eberhart and Russell (1966) interpreted stability in a

different manner, stating that the Finlay-Wilkinson model implies that a stable variety is one which performs relatively well in a poor environment and relatively poor in a favourable one. They proposed that the criteria for stability should be a regression coefficient of unity and minimum deviation from the unit slope. According to them a variety with high mean yield and fulfilling these two criteria would perform well in all the environments.

Another method of genotype-environment interaction analysis, in terms of biometrical genetics, has been developed by Bucio Alanis (1966) and applied to data for two inbred lines of *Nicotiana rustica* grown over a period of sixteen years at two locations. The analysis has shown that the effects of the genotype-environment interaction are linearly related to a particular environmental effect of the genotype. The model, which is essentially an extension of Mather's model (Mather, 1949), was later extended by Bucio Alanis (1966a) to apply to F_1 's with identical and consistent results for this generation also.

For the analysis of genotype-environment interaction by means of the diallel cross, three papers have appeared, one theoretical (Perkins, 1970) and two experimental (Allard, 1956; Crumpacker and Allard, 1962) and are concerned with assessing the stability of genetic components of variation under different environments.

Crumpacker and Allard (1962) studied genotype-environment interaction for heading date in a 10 x 10 wheat diallel over three years. The analysis of variance of heading time for parental genotypes indicated different additive and/or epistatic effects in different years. Because

of the homozygosity of the parents, the epistatic effects attributable to parents were defined by the authors as the result of interaction between homozygous loci, that is, additive x additive type of interaction. Stability of average degree of dominance was tested by the variance ratio for the dominance x year interaction. This was highly significant and showed that the mean degree of dominance for heading date varied from partial to complete dominance in consecutive years.

Porceddu (1968) in a yield test of three wheat varieties over twenty consecutive years at one location showed significant differences between varieties in different years. The results established that the performance of an individual genotype is a linear function of the environment, and that the major portion of the genotype-environment interaction could be accounted for by deviations from the linear response as estimated by the regression analysis.

Baker (1969), analysing the yield of six wheat varieties grown at nine locations over five years, subdivided the sum of squares for genotype-environment interaction into genotype x place, genotype x year and genotype x place x year interactions for each variety. Except for genotype x year, all interactions were highly significant, leading to the conclusion that the stability of performance of a particular cultivar over a range of environments is inversely proportional to the sum of squares for genotype-environment interaction for that particular variety.

Kaltsikes and Larter (1970) analysed genotype-environment interaction for height, maturity and yield in durum wheat. Five varieties

grown over four to five years at five loctions, differed with different environments in all the characters studied. In their analysis, the major portion of the genotype-environment interaction effects was reported to be linearly correlated with the environment.

A considerable amount of work has been reported on genotype-environment interaction analysis with respect to a variety of quantitative characters in different crops (Allard 1961, Parson and Allard 1960, Allard and Workman 1963, in lima-beans; Eagles 1967, Knight 1965, 1970 and Breese 1969, in grasses; Westerman 1970, 1971a, b, in *Arabidopsis*; Hill and Perkins 1969, Perkins and Jinks 1970, 1971a, b, in tobacco; Kaltsikes 1970, in winter rye; Liang and Walter 1966, in *sorghum* and Qualset 1968, and Paroda and Hayes 1957, in barley). In each of these papers, the behaviour of a particular genotype when grown in a particular environment, and when grown with other genotypes over a wide range of environments, is studied using linear regression analysis to measure the environmental effect. The implication of these studies is that the linear regressions of individual genotypic values on the mean values of all genotypes for each of the environments provide measures of the response that are useful in predicting the relative performance of the genotype in question over the range of environmental conditions. The conclusion of these reports focuses on one point: that the performance of an individual genotype in a particular environment is a linear function of the over-all environmental mean in regression analysis, where the slope of regression measures the sensitivity of the genotype to the totality of the environmental factors.

MATERIAL AND METHODS

Five cultivars of common wheat (*Triticum aestivum* L.) described in Appedix I, were used in the diallel study. These varieties were selected on the basis of their diversity of origin, different spike and seed characteristics and their yield performances. The parental material was sown in September 1969 in the green-house to check its trueness to type. Fifteen to twenty phenotypically identical healthy heads were selected from each variety and their seed formed the basis of the present investigations. The parent lines were sown in the green house in January 1970. Crosses were made in all possible combinations, including reciprocals. During summer 1970, the parent material was again seeded at Parkland farm to obtain more F_1 seed. Following the winter, some of the F_1 seeds together with their parents were sown in growth chambers to make backcrosses, reciprocal backcrosses, further F_1 combinations and to provide F_2 seed. During 1971's spring the same procedure was repeated to have sufficient number of seeds for every combination. In the fall of 1971, the backcrosses and their reciprocals were seeded in the growth chambers to obtain seed for their first selfed generation.

By spring 1972, the experimental material consisted of five parents, 20 F_1 's, 20 F_2 's, 80 backcrosses and the selfed generation of these backcrosses, amounting to 205 different entries. A 15 x 15 partially balanced lattice design was chosen for seeding the material in a replicated trial. To meet the requirements of the design, 20 more entries were needed and since the F_2 is the maximum segregation generation,

each F_2 combination was represented twice in each replication to complete the required 225 entries. The names and numerical designations of the entries are given in Appendix II. On 9th and 11th May, 1972, the whole of the experimental material was space-seeded in three replications at two locations, viz., Department of Genetics Ellerslie Field Lab. and Department of Plant Science Parkland Farm, respectively. Each of the fifteen (15' x 15') blocks in a replication consisted of 15 rows of 30 seeds each, with a spacing of 30.48 cm between rows and 15.24 cm between seeds within a row. The following observations were recorded at each of the locations:

- (1) Onset-of-heading: expressed as the number of days between seeding date and the date of appearance of the first head in the row (entry).
- (2) Final heading: recorded in number of days from the date of seeding to the day when 75% of the plants in a row have headed.
- (3) Heading-span: measured by the difference between (1) and (2).
- (4) Plant height: measured in centimeters from the surface of the soil to the tip of the spike on the highest tiller (excluding awns). Ten consecutive plants per row were recorded for height irrespective of their growth performance, leaving the first plant because of susceptibility to border effects, except in those rows where the number of surviving plants was reduced to ten or less. At maturity only those

plants that had been recorded for height were harvested. The following observations for yield and yield components were recorded on the harvested material.

- (5) Number of productive tillers per plant.
- (6) Number of spikelets per spike: Three spikes were taken at random from each plant and their spikelets counted.
- (7) Number of seeds per spike.
- (8) Weight of seeds per spike (in grams): spikes randomly sampled for spikelet-counts were threshed separately and their seeds counted and weighed.
- (9) 1000-kernel weight (in grams): computed from observations (7) and (8).
- (10) Yield per plant (in grams): expressed as total seed weight of all the spikes including those used for (6), (7), and (8).

Statistical analysis

The means were calculated for all the characters except onset-of-heading, final heading and heading-span. For observations (6), (7) and (8) means of three readings were calculated first and treated as individual variables for the calculation of entry means. Missing entries were calculated according to Cochran and Cox's (1957) formula for the randomized block design, except for (1) to (4) at Parkland. Here, since the number of missing entries was less than three, the procedure for the partially balanced lattice design was used. The complete set of data was subjected to analysis of variance for a partially balanced lattice design. This provided a single set of adjusted treatment means at each location. However, unadjusted treatment means (original entry

means as treated in randomized block design) were used for most of the analyses. These were categorized into four diallel sets, viz., F_1 's, F_2 's, backcrosses and selfed backcrosses. The following analyses were performed on each of the sets for all the characters under study.

1. Correlation and factor analyses. Simple correlation coefficients were computed for each of the characters and arranged in the form of a matrix to permit the simultaneous comparison of one character with the other. Factor analysis was performed according to Hotelling's (1933) principal factor method as explained by Harman (1960) and Lawley and Maxwell (1963). The factor analysis approach aims at resolving the covariation into simpler relations in the form of a few factors which explain the larger portion of the variation in the original data.

Statistically speaking, it reduces a large number of correlated variables to a small number of uncorrelated variables called factors, each of which proportionally accounts for the variability in the original observations.

The procedure for the principal factor method used in the present study was based on the following linear model (Harman, 1960):

$$z_j = a_{j1}F_1 + a_{j2}F_2 + \dots + a_{jm}F_m + d_{jj}u_j \quad (j = 1, 2, \dots, n)$$

where z_j represents a character variable in terms of several underlying factors and each of the 'n' observed variables is described linearly in terms of 'm' common factors and the residual error ($d_{jj}u_j$). The coefficients of these factors are referred to as factor loadings. A symmetrical correlation matrix produced from all possible $[1/2n(n - 1)]$ combinations is resolved into an 'nk' factor matrix, where the number of factors 'k' is usually smaller than 'n', the number of variables.

In the correlation matrix, the leading diagonal elements have values of unity and since they are meaningless (the correlation of each variable with itself means nothing) they are replaced by 'communalities' (the approximate values in terms of amount of variance accounted for by the common factors). In the present case the highest correlation value in each column of the correlation matrix was substituted for unity in the diagonal cells because the variance-covariance ratio of the column for that character is expected to be nearer to unity. With these communalities as the approximate values, the correlation matrix was factored by iteration to give a new resultant set of approximations to communalities that are more convergent. The factor matrix was then rotated (in this case by the varimax method) with every new set of communalities produced, till off-the-diagonal elements of the residual matrix were not significantly different from zero.

2. Combining ability analysis. General and specific combining ability analyses were performed following Griffing's (1956) method 1 (where all the n^2 entries of the diallel table are included), model 1 (where the experimental material is not regarded as a random sample from the population). Model 1 was chosen against model 2 (where the experimental material is regarded as a random sample from the population) because the parental lines, producing all the entries in the form of various combinations, were deliberately chosen on the basis of their diversity of origin and yielding capacities.

3. Diallel cross analysis. Diallel analysis was performed in two steps,

viz., diallel analysis for genetic components of variation and graphical analysis of regression of W_r (parent-offspring covariance of the r th. array) on V_r (variance of the r th. array) to complement the former via graphical representation. In the diallel analysis for genetic components of variation, each diallel table was subjected to tests of validity of the following assumptions (Hayman, 1954b):

- (1) Homozygous parents
- (2) Normal diploid segregation
- (3) No differences between the reciprocal crosses
- (4) No multiple allelism
- (5) Independent action of non-allelic genes
- (6) Uncorrelated gene distribution.

The condition of 'homozygous parents' in the present studies could be satisfied, as the parent material was sown preceding crossing and found to be true to type. 'Normal diploid segregation' may be assured from the pedigree-record of the organism used as experimental material.

Wheat, though an amphi-diploid derivative of *Triticum monococcum* for the 'A' genome (Melburne and Thompson, 1927; Zohary and Feldman, 1962), *Aegilops speltoides* for the 'B' genome (Sarkar and Stebbins, 1956; Riley *et al.*, 1958; Sears and Okamoto, 1958) and *Aegilops squarrosa* for the 'D' genome (Kihara, 1944; McFadden and Sears, 1944, 1946; Kihara and Lilienfeld, 1949) behaves cytogenetically as a normal diploid (Sears, 1948; Riley *et al.*, 1961). It follows therefore, that, the assumption of normal diploid segregation could be considered valid.

'No reciprocal differences' were checked after Hayman's (1954a) procedure

of analysis of variance for diallel tables, where significance of the 'c' component indicates failure of this hypothesis. The remaining three conditions, 'no multiple allelism', 'independent action of non-allelic genes' and 'uncorrelated gene distribution' were checked through the analysis of variance of $W_r - V_r$ values for the arrays of each diallel table. Heterogeneity of $W_r - V_r$ variances will reveal non-validity of these assumptions.

After the validity checks for the above-mentioned conditions, the diallel analysis for genetic components of variation (Hayman 1954b, 1958 and Jinks 1954, 1956) was performed, on each of the diallel tables for all the characters under study, by replacing the off-diagonal cells of the diallel table with the common mean of the relevant cross and its reciprocal irrespective of the significance of Hayman's (1954a) 'c' component. In the F_2 -generation diallel, the estimates of genetic components of variation from the second degree statistics were computed after Johnson and Aksel's (1959) notation describing the average effect of Aa in different filial generations. According to their formula:

$$\text{effect of } Aa = [(1/2)^{fn-1} h]$$

where $fn = nth$ filial generation

$$\text{thus in } F_2, \text{ effect of } Aa = [(1/2)^{2-1} h]$$

and in F_3 , the effect of $Aa = [(1/2)^{3-1} h]$ and so on.

From the genetic components of variation, various parameters such as the mean degree of dominance, the proportion of positive to negative alleles at loci exhibiting dominance, the ratio of dominant to recessive genes in the parents

and the number of groups of genes controlling the particular character were estimated. The heritability estimates were calculated after Crumpacker and Allard (1962) using the formula $[D \div (D + H_1 - F + 4E)]$.

The graphical analysis of regression of W_r on V_r was performed after Hayman (1954b) by plotting the regression line and the limiting parabola constructed by calculating its points ($W_r^2 = V_r \times V_{OLO}$) and plotting the V_r , $(W_r \times V_{OLO})^{1/2}$ points. The W_r , V_r graphs were supplemented with Johnson and Aksel's (1959) standardized deviation graphs of parental measurements (Y_r) and parental order of dominance ($W_r + V_r$) where the deviations of the Y_r 's and $W_r + V_r$'s from their respective means were standardized by dividing them by their respective standard deviations. An abscissa (Y_r) and an ordinate ($W_r + V_r$) intersecting each other produce four quadrants of the graph, classified as (+,+), (-,+), (-,-) and (+,-). The plus and minus signs for ($W_r + V_r$) denote 'recessive' and 'dominant' and for Y_r , they refer to 'high' and 'low' performances respectively.

4. Analysis of genotype-environment interaction. The constancy of principal factors with respect to loadings in four generations of diallel cross was studied by means of *factorial ANOVA* where locations, principal factors and generations were treated as main source of variation. The *ANOVA* was based on fixed-effect-model as described by Scheffe (1959) because the set of parents in all the diallel tables could not be regarded as random sample and the two locations at which the materials were grown could not be considered as representing

random sample of the environments. Their choice was dictated by the limitations imposed both by time and facilities available.

The differences between the two locations with respect to general combining ability were also studied by *factorial ANOVA*. Stability of each cultivar was determined by regressing its GCA at Parkland upon that at Ellerslie. The regression analysis used was as given by Mather (1951).

The genotype-environment interaction with respect to D , H_1 and F considered as variables was investigated by using factorial analysis of variance. The concordance of the components in the two locations was studied by regressing the values of D , H_1 and F estimated from Parkland data upon those of Ellerslie and partitioning the total sum of squares into sum of squares due to regression and due to deviation from regression (error). Diallel analysis for genetic components of variation from adjusted treatment means (balanced lattice design) was compared with that of unadjusted treatment means (experiment treated as a randomized block design). The differences between the parameter estimates would reflect the effect of the adjustment factor characteristic of partially balanced lattice design. The regression analysis (Mather, 1951) applied to D , H_1 and F obtained from both the adjusted and unadjusted treatment means, will reveal the degree of concordance between the parameters characteristic of each treatment.

EXPERIMENTAL RESULTS

The experimental data for the two locations; (1) Ellerslie and (2) Parkland, are given in Appendices III to XXII inclusive. Table 1 shows the results of the analysis of variance of the partially balanced lattice design and its efficiency as compared to the analysis as a randomized block. The mean squares of the adjusted treatments except for number of tillers per plant and yield per plant, both at Parkland, all showed significant differences among the entries. The relative efficiency of the balanced lattice design at Parkland over the randomized block design was greater than that at Ellerslie.

ANALYSIS OF F_1 DATA

Simple correlations were computed for all the characters under study and are given in Table 2. As shown in the table:

Onset-of-heading was positively correlated with plant height and number of spikelets per spike, and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. At Ellerslie, it was positively correlated with final heading and negatively with yield per plant, while at Parkland, it showed positive correlation with number of tillers per plant and number of seeds per spike. The negative correlation of onset-of-heading with yield, weight of seeds per spike and 1000-kernel weight indicates that the longer the period between seeding and the appearance of the first head for a particular entry, the lower will be its yield and 1000-kernel weight. Correlations of final heading and heading-span with other characters may be interpreted in the same fashion.

TABLE 1

Mean-square values from the analysis of variance of partially balanced triple lattice design with respect to ten characters at two locations

Character	Replication	Blocks within replications	Treatments (adjusted)	Error	Total sum of squares	Efficiency over randomized block
TD.F.	2	42	224	406	674	
Onset-of-heading	5.7305 19.8980	4.9140** 18.1369**	10.3581** 18.2897**	1.0209 2.5313	2948.5180 5921.1450	119.205 127.013
Final heading	14.4640 204.9375	8.0242** 14.7080**	17.3218** 19.2502**	1.4999 3.1787	4849.0160 6601.6170	118.699 108.332
Heading-span	24.0635 137.0770	2.8539* 6.6719**	3.1996* 4.6495**	1.6111 2.6398	1532.3940 2662.3760	95.829 107.162
Plant height	273.8125 1017.5480	566.9384** 524.6927**	543.1358** 738.0608**	41.0030 129.1721	162503.6250 241583.5620	121.334 99.301
Number of tillers per plant	0.9950 133.0380	4.8374 10.5493**	4.6147 6.0799**	5.6567 3.0278	3495.9080 3288.2760	87.318 109.575
Number of spikelets per spike	10.8070 19.9485	2.5932** 4.1922**	1.8178* 2.2189**	1.3783 1.0273	1087.8420 1125.9980	85.553 109.766
Number of seeds per spike	10.0065 180.0355	50.2140** 36.4799**	39.1424** 25.7529**	18.5529 11.9034	18299.5550 12446.094	91.021 100.465
Weight of seeds per spike	0.0060 0.0940	0.0995** 0.0942**	0.0843* 0.0586*	0.0455 0.0321	41.2460 30.2060	90.426 104.704
1000-kernel weight	12.2045 35.3210	21.8132** 25.9427**	18.7903** 17.5137**	8.4791 7.8801	8616.7660 8251.1520	90.954 104.127
Yield per plant	16.1310 153.8140	20.8652* 18.2453**	10.3075 8.3171*	15.8876 6.2202	9556.6840 5431.8160	86.462 104.334

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

† Corresponding to the missing values in the different characters, the number of degrees of freedom have been subtracted from error D.F. in calculating mean squares.

Plant height was positively correlated with number of spikelets per spike and negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. It was positively correlated with number of tillers per plant at Ellerslie while at Parkland the correlation coefficient was not significant.

Number of tillers per plant was positively correlated with yield per plant at both locations and with number of spikelets per spike at Ellerslie. Correlation of number of tillers per plant with number of seeds per spike, weight of seeds per spike and 1000-kernel weight was not significant at either location. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight could be explained in the same manner.

As far as yield is concerned, it was highly and positively correlated with 1000-kernel weight, weight of seeds per spike and number of tillers per plant at both locations, but negatively correlated with onset-of-heading and final heading at Ellerslie.

Factor analysis

In the factor analysis, the symmetrical correlation matrix produced for all the characters under study was resolved into a varimax-rotated factor matrix. As suggested by Cattell (1965), if the number of factors is kept equal to that of the variables, 100% of the covariation in the data could be accounted for by these factors. In the present case the data was computerized for five factors which explained 92% of the

TABLE 2

Simple correlation coefficients between ten characters from F₁ diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.916** 0.082	0.196 0.028	0.723** 0.821**	0.145 0.291**	0.313** 0.545**	0.191 0.246**	-0.324** -0.304**	-0.615** -0.612**	-0.281** -0.150
2. Final heading	-	0.548** 0.618**	0.744** 0.790**	0.196 0.358**	0.257** 0.588**	0.150 0.267*	-0.331** -0.240*	-0.574** -0.547**	-0.278** -0.058
3. Heading-span	-	-	0.316** 0.241*	0.166 0.219	-0.022 0.270*	-0.012 0.122	-0.135 -0.006	-0.146 -0.114	-0.147 0.105
4. Plant height	-	-	-	0.365** 0.239	0.416** 0.601**	0.149 0.106	-0.250* -0.402**	-0.474** -0.612**	-0.026 -0.162
5. Number of tillers per plant	-	-	0.272* 0.194	-	-	-0.014 0.085	0.059 -0.039	0.117 -0.121	0.574** 0.320**
6. Number of spikelets per spike	-	-	-	-	-	0.582** 0.556**	0.280* 0.206	-0.225 -0.207	0.154 0.184
7. Number of seeds per spike	-	-	-	-	-	-	0.663** 0.659**	-0.165 -0.014	0.144 0.211
8. Weight of seeds per spike	-	-	-	-	-	-	-	0.624** 0.740**	0.502** 0.506**
9. 1000-kernel weight	-	-	-	-	-	-	-	-	0.512** 0.500**
10. Yield per plant	-	-	-	-	-	-	-	-	-

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

total variability with respect to all the characters at respective locations. The values of the rotated factor matrix in terms of the factor loadings together with the communalities for ten characters are given in Table 3.

The first factor was termed *lateness* because it carried the highest loadings for onset-of-heading and final heading at both locations and explained 28% and 32% of the variation in the data at Ellerslie and Parkland. Yield per plant was negatively affected by this factor showing thus that higher the number of days taken by a particular entry to head the larger will be its contribution to *lateness* and lower will be its yield and 1000-kernel weight. Plant height was one of the major contributors to *lateness* as it carried high loadings at both locations. This corresponds proportionally to the positive association between days to head and height of the plant. Number of tillers per plant, number of spikelets per spike and number of seeds per spike contributed very little to this factor.

The second principal factor was termed *yielding ability* as it carried generally higher loadings for yield and yield components: spikelets per spike, number of seeds per spike and, (except at Ellerslie) 1000-kernel weight at both locations. This factor accounted for about 19% of the variation. The loadings on yield and its components for this factor, as against those of the first factor (*lateness*), support a negative relationship between *lateness* and *yielding ability*. There is very little contribution of plant height and number of tillers per plant for this factor at either location.

TABLE 3

Varimax rotated factor matrix for ten characters
from F₁ diallel set at two locations

Character	Communalities	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.964 0.908	0.950 0.892	0.107 -0.242	-0.060 0.062	-0.167 -0.093	-0.010 0.205
Final heading	0.972 0.945	0.901 0.773	0.070 -0.173	-0.022 0.073	-0.153 0.516	0.363 0.212
Heading-span	0.994 1.000	0.215 0.123	-0.040 0.032	0.033 0.039	-0.032 0.987	0.972 0.086
Plant height	0.806 0.906	0.708 0.917	0.175 -0.174	0.294 -0.113	-0.224 0.132	0.139 0.066
Number of tillers per plant	0.886 0.961	0.182 0.177	0.038 0.126	0.915 0.807	-0.010 0.113	0.121 0.949
Number of spikelets per spike	0.867 0.824	0.188 0.756	0.847 0.199	0.282 0.431	-0.182 0.160	-0.047 -0.039
Number of seeds per spike	0.923 0.971	0.160 0.218	0.882 0.626	-0.133 0.957	0.321 0.050	0.005 0.061
Weight of seeds per spike	0.990 0.963	-0.249 -0.258	0.523 0.567	0.086 0.754	0.804 -0.012	-0.034 -0.088
1000-kernel weight	0.884 0.878	-0.486 -0.518	-0.227 0.747	0.268 0.143	0.724 -0.060	-0.030 -0.169
Yield per plant	0.851 0.863	-0.170 0.011	0.109 0.876	0.762 0.114	0.456 0.043	-0.145 0.282
Percent of total variability explained	91.396 92.187	28.203 32.355	18.808 18.226	16.589 17.273	16.165 13.131	11.361 11.202

First reading under each column refers to Ellerslie and the second to Parkland.

The term *tillering-capacity* was chosen for the third principal factor, as the number of tillers per plant contributed highest at both locations. The factor explains approximately 17% of the total variation and is supported by number of spikelets per spike, number of seeds per spike (at Parkland), weight of seeds per spike, 1000-kernel weight and yield per plant. Since this component is closely associated with the *yielding-ability*, the *lateness* factor shows negative effects for onset-of-heading and final heading. This kind of response seems to be logical since high tillering capacity results in higher yield per plant and is associated with earliness.

The fourth principal component, named *heading-period* at Parkland and *seed weight* at Ellerslie, accounted for 13% and 16% of the variation respectively. Different names were chosen for different locations because of the inconsistency between locations of factor loadings on various characters. At Ellerslie, the *seed-weight* component was affected by number of seeds per spike, 1000-kernel weight and yield per plant. The contribution of onset-of-heading, final heading, heading-span, plant height and number of tillers per plant towards this component was negative. At Parkland, *heading-period* was positively affected by final heading, plant height, number of tillers per plant and number of spikelets per spike.

The terms *heading-period* and *tillering-capacity* were also used for fifth principal component at Ellerslie and Parkland, respectively, because of their high contribution towards the loadings of this factor. Only 11% of the total variability was accounted for by this factor at both

TABLE 4

Estimates of general combining ability of five parental lines used in F1 diallel set for ten characters at two locations

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.933 1.9867	1.4667 2.3533	-0.4666 -0.8800	-1.7334 -2.2466	-1.2000 -1.2133
Final heading	2.1600 2.4800	1.7934 2.9466	-0.3733 -1.0867	-2.1066 -2.4867	-1.4733 -1.8533
Heading-span	0.2600 0.4800	0.3933 0.5800	0.1267 -0.2200	-0.4400 -0.2200	-0.3400 -0.6200
Plant height	13.7470 12.3968	12.1740 13.4648	-8.1473 -8.7599	7.8220 7.9252	-9.9516 -9.1766
Number of tiller per plant	-0.0409 0.3351	0.8629 0.3316	0.6390 0.5466	-0.3116 -0.1349	-1.1495 -1.0784
Number of spikelets per spike	0.5123 0.6729	0.3536 0.4595	-0.5752 -0.5058	-0.3151 -0.3616	0.0245 -0.2650
Number of seeds per spike	2.8305 2.0515	-1.5451 -0.9495	-1.1460 0.3450	-1.9094 -2.4385	1.7700 0.9916
Weight of seeds per spike	-0.0103 -0.0326	-0.1285 -0.0958	-0.0092 0.0848	0.0008 -0.0501	0.1472 0.0938
1000-kernel weight	-2.4230 -2.3256	-1.5338 -1.3217	0.7291 1.6523	1.7007 0.8898	1.5269 1.1052
Yield per plant	-0.1646 -0.4672	-1.2333 -0.5154	-0.0382 0.3461	0.1903 0.2629	1.2458 0.3736

First reading under each column refers to Eilerslie and the second to Parkland.

locations. The factor is negatively affected by number of spikelets per spike, weight of seeds per spike and 1000-kernel weight.

Combining ability analysis

Estimates of general and specific combining ability for the F_1 diallel were obtained by Griffing's (1956) procedure following method 1, model 1. General combining ability (GCA) values for all the characters at both locations are given in Table 4. Marquis appeared to be the best combiner for onset-of-heading, final heading, plant height, number of spikelets per spike and number of seeds per spike at both locations. For tillering capacity Chinook exhibited the highest combining ability at Ellerslie while Khush-hal excelled Chinook at Parkland. Inia showed the highest general combining ability for yield per plant, 1000-kernel weight and weight of seeds per spike at both locations. It is interesting to note that Inia excelled Marquis and Chinook (both Canadian standard varieties) in general combining ability for yield in a foreign environment. This might be attributed to a better adaptability of Inia as compared to the other two introductions, viz., Khush-hal and Ciano, of Pakistan and Mexican origin. Generally it could be said that Canadian environments are less suitable for introductions like Khush-hal and Ciano as far as yield per plant is concerned.

The values of specific combining ability (SCA), reciprocal effects and variances for general and specific combining abilities for F_1 hybrids are given in Tables 5 to 15.

Cross (CxI) had the highest SCA for onset-of-heading (Table 5),

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₁ diallel set at two locations.

TABLE 5. Onset-of-heading

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.8667	-0.5333	-1.1000	-1.2999	1.9333	3.6535	-0.2104
		0.6801	-0.0866	-0.8866	-1.2533	1.9867	3.7430	-0.5095
Chinook	-0.3333	-	-0.9000	-0.4667	-0.5000	1.4667	2.0669	0.0400
	0.1667		0.3800	0.2467	-1.1200	2.3533	5.3343	-0.3554
Khush-hal	0.0	-0.5000	-	0.1333	0.4333	-0.4666	0.1336	0.1544
	-0.1667	0.0		-0.6867	-0.8867	-0.8800	0.5705	-0.4589
Ciano	-0.5000	0.0	0.6667	-	1.0334	-1.7334	2.9204	0.2715
	-2.0000**	-0.1667	0.0		0.9800	-2.2466	4.8435	-0.0701
Inia	0.5000	0.5000	0.8333*	-0.1667	-	-1.2000	1.3558	0.8548
	1.0000	0.1667	-0.5000	1.0000		-1.2133	1.2683	1.0144

TABLE 6. Final heading

Marquis	-	1.0733	-0.9267	-1.3600	-1.6000	2.1600	4.5722	-0.2335
		2.9200	-1.7133	-1.4799	-1.4467	2.4800	5.8974	-0.6322
Chinook	0.0	-	-0.8934	-0.3267	-0.2933	1.7934	3.1227	0.1505
	0.0		-1.6799	-1.2800	-2.0800	2.9466	8.4298	2.2100
Khush-hal	-0.5000	-0.5000	-	-0.4933	-0.1266	-0.3733	0.0459	0.3187
	0.3333	-0.1667		0.2534	0.6200	-1.0867	0.9280	1.2870
Ciano	-0.3333	0.0	0.0	-	0.9400	-2.1066	4.3445	0.4979
	-1.1667	-1.1667	0.0		1.1867	-2.4867	5.9306	0.6653
Inia	0.8333	0.0	0.0	0.0	-	-1.4733	2.0773	0.5436
	-0.1667	0.0	0.0	-0.1667		-1.8533	3.1819	2.1050

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

at both locations followed by hybrid (MxCH). This shows that hybrid (CxI) was latest in heading and implicitly in maturity. Cross (MxI) exhibited lowest SCA and hence could be regarded as the earliest of all the F_1 's. It is interesting to note that for both locations, the best hybrid, with the highest SCA, had parents showing the lowest GCA's, while the poorest hybrid, with the lowest SCA, had the female parent with the highest GCA and the male parent with the lowest GCA. Thus it appears unlikely that the best performing parents (those with high GCA's) necessarily produce hybrids showing high SCA's. None of the hybrids showed significant reciprocal effects except (IxK) at Ellerslie and (CxM) at Parkland, and the parental variances for GCA were in general higher than for SCA.

With respect to final heading (Table 6) and heading-span (Table 7), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

With respect to highest SCA for plant height (Table 8) at both locations, the best hybrid was (MxCH) and the poorest (MxI). The parents of cross (MxCH) had the highest GCA at both locations while the poorest hybrid had Marquis as one parent, with the highest GCA and Inia as the other, with the lowest GCA. The parental GCA-variances were larger than their SCA-variances at both locations, suggesting a greater importance of additive gene effects for the parental lines than of non-additive ones for the hybrids, with respect to plant height. The reciprocal effects were significant for (CxM) at both locations and for (IxM) and (IxCH) at Ellerslie. In the case of (IxM), the reciprocal effects could be attributed

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₁ diallel set at two locations.

TABLE 7. Heading-span

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	2.2533	-1.6133	-0.6133	-0.2133	0.4800	-0.0163	-0.2096
		0.0400	-0.0267	-0.2933	0.1067	0.2600	-0.1184	-0.8721
Chinook	-0.1667	-	2.0467	-1.5467	-0.9800	0.5800	0.0709	-0.2091
	0.3333		-0.1600	0.0733	0.1400	0.3933	-0.0124	0.8204
Khush-hal	0.5000	-0.1667	-	0.9200	1.4867	-0.2200	-0.0678	-0.2009
	0.0	0.0		-0.6600	-0.5933	0.1267	-0.3004	1.3018
Ciano	0.8333*	0.0	0.0	-	0.3200	-0.2200	0.1097	-0.0340
	0.1667	0.0	-0.6667		-0.0267	-0.4400	-0.3004	-0.3328
Inia	-0.8333*	-0.1667	0.5000	-1.3333**	-	-0.6200	0.0317	-0.0817
	0.3333	-0.5000	-0.8333	0.1667		-0.3400	0.0356	0.2341

TABLE 8. Plant height

Marquis	-	3.4117	2.0390	-2.3879	-4.1867	13.7470	187.1822	-4.4931
		3.6766	2.7912	-1.9234	-4.4220	12.3968	151.7148	-4.9129
Chinook	0.2933	-	2.4237	1.3784	2.6996	12.1740	146.4086	-0.5994
	-0.1134		1.5132	3.0219	-3.3567	13.4648	179.3356	-0.4071
Khush-hal	-0.4766	0.8250	-	-1.9553	-0.0704	-8.1473	64.5814	-1.1491
	1.2467	1.8566		-0.1367	-0.0287	-8.7599	74.7702	-1.5526
Ciano	-3.7717*	-1.3083	0.9233	-	1.3890	-7.8220	59.3868	-0.6846
	-4.3133	-0.7933	1.3100		2.0900	-7.9252	60.8436	-0.6295
Inia	5.1567**	-4.5567*	1.0980	-2.0700	-	-9.9516	97.2374	4.4238
	3.3467	-1.4767	2.1400	-0.5600		-9.1766	82.2441	6.8172

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

**Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from P₁ diallel set at two locations.

TABLE 9. Number of tillers per plant

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	-0.0903	-0.7628	0.5342	-0.1946	-0.0409	-0.3273	-0.8224
		-0.8068	-1.2051	-0.3143	-1.1968	0.3351	-0.1992	-0.7787
Chinook	1.1667	-	1.8354	-0.1520	-0.4903	0.1629	0.4155	-0.8197
	0.8667	-	0.5318	-0.5535	-0.3603	0.3316	-0.2015	-0.5617
Khush-hal	-0.4297	0.1055	-	-0.3790	-0.4183	0.6390	0.0794	0.4944
	1.0167	-0.6833	0.5982	0.5982	-0.0249	0.5466	-0.0127	-0.2004
Ciano	0.4833	-0.5000	0.7833	-	0.5094	-0.3116	-0.2319	-0.6716
	0.1593	-1.1167	0.6167	0.3500	1.0399	-0.1349	-0.2933	-0.5244
Inia	-0.4500	-1.2500	0.8227	0.3500	-	-1.1495	0.9923	-0.6077
	0.6000	0.4083	0.4167	-0.7333	-	-1.0784	0.8513	0.1064

TABLE 10. Number of spikelets per spike

Marquis	-	-0.2740	0.1741	-0.0388	-0.4728	0.5123	0.1150	-0.3687
		1.1008	-0.2395	-0.1238	-0.1136	0.6729	0.3652	-0.2192
Chinook	-0.3333	-	0.2618	0.3642	-0.0032	0.3536	-0.0224	-0.3436
	0.2668	-	0.1404	-0.1925	-0.5073	0.4595	0.1235	0.1847
Khush-hal	1.0593	-0.2623	-	-0.3403	-0.1155	-0.5752	0.1834	-0.3357
	-0.3278	-0.3167	0.4888	0.1615	-0.3017	-0.5058	0.1682	-0.1935
Ciano	-0.0778	-0.1002	0.4888	-	0.2157	-0.3151	-0.0482	-0.2854
	-0.4012	-0.0277	0.2057	-	0.5208	-0.3616	0.0431	-0.1931
Inia	-0.4388	0.1947	0.4692	0.0222	-	0.0245	-0.1469	-0.2742
	-0.2390	0.3458	0.1447	-0.2168	-	-0.2650	-0.0175	-0.0073

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₁ diallel set at two locations.

TABLE 11. Number of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	-1.9659	2.2792	0.9872	-3.1363	2.8305	6.6103	-3.5029
		1.2486	0.1486	-1.2352	1.7185	2.0515	3.1165	-2.7300
Chinook	-0.6665	-	0.0151	0.9075	2.0447	-1.5451	0.9862	-2.2146
	0.1168		0.1107	-0.3172	0.1696	-0.9495	-0.1904	-2.2104
Khush-hal	3.1140	-1.3513	-	-2.5752	-0.3525	-1.1460	-0.0878	-1.7712
	1.5667	-0.7168		-0.1725	-2.4527	0.3450	-0.9730	-2.2186
Ciano	4.5557**	1.7223	-0.6055	-	2.9756	-1.9094	2.2443	-0.6930
	0.4772	0.5945	1.0333	-	1.9031	-2.4385	4.8542	-2.1780
Inia	-1.5222	0.0723	-0.7965	-2.2833	-	1.7700	1.7317	4.1624
	-1.1278	1.5223	-0.8035	-1.1335		0.9916	-0.1088	1.4764

Reciprocal effects

TABLE 12. Weight of seeds per spike

Marquis	-	-0.0905	0.0739	0.1517	-0.1100	-0.0103	-0.0032	-0.0083
		0.0512	-0.0038	0.0746	0.0983	-0.0326	-0.0027	-0.0095
Chinook	-0.0175	-	0.0364	0.0412	0.0439	-0.1285	0.0132	-0.0056
	-0.0320		0.0194	-0.0762	0.0399	-0.0958	0.0054	-0.0087
Khush-hal	0.1782*	-0.0768	-	-0.1029	0.0727	-0.0092	-0.0033	-0.0061
	-0.0287	-0.0527		0.0249	-0.0356	0.0846	0.0034	-0.0094
Ciano	0.2843**	0.0267	-0.0705	-	0.0391	0.0008	-0.0033	0.0036
	0.0622	0.0268	0.1142		0.0487	-0.0501	-0.0013	-0.0055
Inia	-0.0590	-0.1433	0.0425	-0.0505	-	0.1472	0.0183	-0.0014
	-0.0805	-0.0038	0.0427	-0.0460		0.0938	0.0050	-0.0046

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₁ diallel set at two locations

TABLE 13. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA	
	Marquis	Chinook	Khush-hal	Ciano				Inia
Marquis	-	-0.1201	-0.5650	2.0236	0.1734	-2.4230	-1.0311	-2.6455
		0.0835	-0.2523	2.6151	0.8063	-2.3256	-0.2340	-1.2556
Chinook	0.2312	-	0.7965	0.0375	-0.7600	-1.5338	0.4528	-2.5316
	-0.7130		0.3194	-1.5360	0.9759	-1.3217	-0.2366	-1.2425
Khush-hal	1.1725	-0.6182	-	0.0280	1.8405	0.7291	-1.0567	-1.1211
	-1.7405	-0.4882		0.7257	1.4420	1.6523	-0.3825	-1.2450
Ciano	2.1175	-0.9577	-1.2283	-	-1.5895	1.7007	-1.0220	-0.6646
	1.0338	0.1613	1.7450		-0.4875	0.8898	-0.4331	-0.9974
Inia	-0.0403	-3.1903*	1.4478	0.8910	-	1.5269	0.4939	-1.2788
	-1.0033	-1.3335	1.8997	0.0420		1.1052	-0.3636	-0.9555

TABLE 14. Yield per plant

Marquis	-	-0.5845	-0.9024	2.4220	-0.3343	-0.1646	-1.0311	-2.6455
		-0.1980	0.1755	0.8520	0.0911	-0.4672	-0.2840	-1.2556
Chinook	1.1575	-	1.9387	0.0545	-0.7460	-1.2330	0.4628	-2.5316
	-0.6980		0.0337	-0.2106	-0.6938	-0.5154	-0.2366	-1.2425
Khush-hal	0.3260	-0.7188	-	-0.2716	1.6500	-0.0382	-1.0567	-1.1211
	-0.1923	-0.5447		-0.0804	0.2976	0.3461	-0.3825	-1.2450
Ciano	2.5833	-0.5388	0.8368	-	-0.9329	0.1903	-1.0220	-0.6646
	-2.0633*	-0.3382	1.6012		0.5674	0.2629	-0.4331	-0.9974
Inia	-0.2452	-3.2108*	0.5890	0.5675	-	1.2458	0.4939	-1.2788
	-1.0785	-0.0700	2.5692*	-0.4895		0.3736	-0.3626	-0.9555

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

to the female parent (Inia) while for (CxM) and (IxCH), the male parents Marquis and Chinook are responsible, because of the negative sign associated with the effects.

For number of tillers per plant (Table 9), the hybrids (CHxK) and (CxI) had the highest SCA's at Ellerslie and Parkland respectively. The parental GCA for (CHxK) at Ellerslie was highest whereas that for (CxI) at Parkland was the lowest. The poorest hybrid was (MxK) at both locations, having the lowest SCA value, although one of its parents (Khush-hal) showed high GCA. The variances for GCA were generally higher than those for SCA.

Hybrid (CHxC) at Ellerslie and (MxCH) at Parkland, respectively ranked highest for number of spikelets per spike with respect to their SCA's, whereas cross (MxI) at Ellerslie and (CxI) at Parkland ranked lowest. It could be argued that the hybrid (MxI) had one parent (Marquis) ranking highest in GCA and hybrid (CHxC) had one parent (Ciano) with a very low GCA which shows that high parental GCA's might not result in higher SCA's for the hybrids. In general, the variances for GCA, were higher than those for SCA. The reciprocal effects were non-significant for all crosses.

The interpretation of the results for general and specific combining ability and the reciprocal effects for number of seeds per spike (Table 11), weight of seeds per spike (Table 12), 1000-kernel weight (Table 13) and yield per plant (Table 14) follow the same pattern. Differences may be found with respect to relative positions of the parents and hybrids concerned but the general conclusions are the same.

TABLE 15

Analysis of variance of general and specific combining ability for ten characters from F₁ diallel set at two locations.

Character	M.S. for GCA		M.S. for SCA		M.S. for reciprocal effects		Error M.S.
	4	4	10	10	10	48	
Onset-of-heading	26.3438**	41.9375**	1.9125**	2.2312**	0.4556	1.2722	0.3155 0.7640
Final heading	36.5000**	64.0469**	2.8562**	7.1312**	0.2611	0.3167	0.3504 0.9482
Heading-span	1.3688**	2.6199	0.4951	4.5816**	0.3333	0.7500	0.3144 1.3089
Plant height	1409.4062**	1396.7344**	22.8000**	22.6250**	14.1257*	8.6772	6.7393 7.3723
Number of tillers per plant	6.4326**	4.2588*	1.2214	2.6332*	1.0437	0.8791	1.2336 1.1674
Number of spikelets per spike	2.0459*	2.8027**	0.2086	0.5035	0.4016	0.1455	0.5531 0.3284
Number of seeds per spike	46.2188**	30.4062**	9.3219	4.4004	8.8449	2.0571	5.2554 4.0978
Weight of seeds per spike	0.0959**	0.0719**	0.0169	0.0137	0.0306*	0.0065	0.0124 0.0142
1000-kernel weight	34.9531**	29.7500**	3.0262	5.2500	4.3586	2.8623	3.2919 2.7816
Yield per plant	7.8486	2.0332	3.8074	0.6977	4.1329	3.1529	3.9663 1.8834

First reading under each column refers to Ellerslie and the second to Parkland.
 * Significant at 5% level
 ** Significant at 1% level

A general review of the results of the combining ability analyses with respect to all the characters under study suggests that:

- (i) The high GCA of the parents can not be taken as a criterion for the evolution of hybrids with high SCA's since the hybrids with high SCA's were associated with respective parents of low GCA's and *vice versa*.
- (ii) Since the variances for GCA were usually larger than those for SCA, and since GCA is the result of additive, and SCA non-additive gene effects (Sprague and Tatum, 1942; Fryxel *et al* 1958 and Griffing 1956), the selection of the parental lines on the basis of their GCA's should be given priority over selection on the basis of their SCA's. This conclusion may also be supported from the analysis of variance for general and specific combining ability (Table 15). The results of Table 15 reveal that the variances for GCA were significant except for heading-span at Parkland and for yield per plant at both locations. The variances for SCA were significant only for onset-of-heading, final-heading and plant height (at both locations) and for heading-span and number of tillers per plant (at Parkland). Significance of variances for GCA thus suggests the importance of additive gene effects and emphasizes that substantial differences exist among the parental lines used in the study.
- (iii) The significant variances for SCA imply that non-additive gene effects for the particular characters are relatively more important and that the hybrids with highest SCA's may be selected for further breeding adaptability tests.

TABLE 16

Mean squares from the analysis of variance of the 5 x 5 F₁ diallel table for ten characters at two locations.

Source of variation	D.F.	Number-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seedin per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	79.1719**	109.6075**	4.1074	4224.0000**	19.3008*	6.1320*	130.7031*	0.2477*	104.227*	23.5332
		125.8750**	192.2500**	7.8604	4191.0000**	12.7686	8.4102**	91.2108	0.2156*	89.2031**	6.0947
b	10	5.7750	8.5250**	1.4852	68.4654	3.6668	0.6289	28.0187	0.0507	9.0875	11.4297
		6.7125*	21.3812**	13.7445*	67.7000	7.9043	1.5145	13.2562	0.0413	15.7437	2.1000
b ₁	1	16.3333	38.1633	5.8800	67.5947	0.7123	0.1574	4.1706	0.0726	10.4398*	15.1135
		20.8033	66.2700	12.4033	31.1918	15.8674	0.5796	3.7705	0.1749	66.0398	2.0817
b ₂	4	2.4219	4.4375*	1.8822	112.5625	2.4049	0.7930	14.0703	0.0092	5.3457	5.1953
		4.7959	1.0469	5.1289	93.1719*	13.1410*	1.1104	14.2686	0.0390	8.9922	3.6924
b ₃	5	6.3625**	5.8500**	0.2113	33.0125	5.2719	0.5953	43.9750	0.0796	11.8000	15.6836
		5.4500*	28.6750**	20.1060*	54.8625**	2.1195	2.0281	14.3625*	0.0166	11.1000	0.8312
c	4	2.1333	0.6167	1.4333	11.1538	3.8020	0.0725	37.5303	0.0977	11.6772	18.0605
		4.1833	0.5833	2.4667	6.6066	1.9934	0.4659	4.6971	0.0398	14.9461	12.4107
d	6	0.8556	0.8944	0.7111	63.1929*	2.6837	1.9599	19.2044	0.0880*	14.0084	8.6244
		3.5722*	1.1944	2.1056	38.9815**	3.0668	0.4170	7.0210	0.0061	4.3472	7.4908
Blocks x a	8	1.0312	0.6328	2.2113	17.7266	4.7915	1.7173	25.6719	0.0542	20.7422	7.8745
		3.5937	4.6406	5.6348	35.4094	4.7622	0.8608	24.4531	0.0572	7.6406	5.7969
Blocks x b	20	1.1312	0.6406	0.7294	27.3656	4.9238	2.1734	19.0937	0.0398	8.8656	15.2057
		2.5469	3.6719	5.1647	24.7844	4.9705	0.9705	6.5250	0.0412	10.3906	5.3535
Blocks x b ₁	2	9.2467	2.4866	1.5800	77.0164	13.4714	2.2294	42.1510	0.0717	0.4583	47.2437
		8.8466	15.8650	6.2067	270.1160	38.0653	0.0713	6.3986	0.1328	33.9540	1.2941
Blocks x b ₂	8	1.0688	0.9307	1.0355	31.9712	4.3863	1.3899	16.3372	0.0487	8.8271	8.9218
		4.0024	1.3726	6.2955	20.4922	7.9459	1.5215	10.4583	0.0377	8.2334	3.0371
Blocks x b ₃	10	0.4750	0.3000	0.4725	21.6625	4.9898	3.0066	20.9125	0.0335	10.6437	18.5426
		0.9937	4.6562	4.6720	6.1167	2.8008	0.7113	4.0633	0.0390	10.8035	8.1539
Blocks x c	8	0.8333	1.4667	1.0583	16.0278	3.1607	1.2033	12.4407	0.0273	6.5340	8.6371
		2.1833	0.3083	2.1417	24.9243	3.1579	1.3036	17.3466	0.0666	7.7739	8.0467
Blocks x d	12	0.6385	1.7444	0.3778	13.0140	1.3007	1.0707	5.8792	0.0293	6.5789	11.2731
		1.0722	1.8944	1.9056	6.9826	1.9370	0.8900	10.4261	0.0204	5.8304	4.4533
Error	48	0.9418	1.0529	0.9433	20.2814	3.7021	1.6601	15.7776	0.0375	9.8848	11.9059
		2.2921	2.8450	3.9244	22.1612	3.5057	0.9876	12.2919	0.0429	8.354	5.6517

* Significant at 5% level

** Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a-b) and. Each component has been tested against its own block interaction.

Diallel cross analysis

F_1 entries from Appendices III to XXII were sorted out and complete diallel tables were constructed for each replication with respect to all the characters at both locations. All the entries were subjected to Hayman's (1954a) analysis of variance. The results of this analysis are presented in Table 16. In this table component a tests the significance of additive effects and b the dominance effects of genes, while b_1 tests the mean deviations of F_1 's from their mid-parent values. The dominance-deviations, if predominantly in one direction, may result in significance of b_1 in an analysis of variance. The component b_2 indicates the extent to which the mean dominance deviations within a given array of the diallel table differ from those of the other arrays. A significant b_2 thus implies that some of the parents contain an excess of dominant alleles. The b_3 component tests the portion of the dominance deviations attributable to individual F_1 's. The difference between the reciprocal crosses is assessed by the significance of the c component and maternal effects not ascribable to c are reflected by d . In Table 16 each of the components has been tested for significance against its own block-interaction mean-square. The c was not significantly different from zero at either location for any of the characters studied. Substantial differences among the parents are suggested by the significance of the a component (additive gene effects) for onset-of-heading, final heading, plant height, number of spikelets per spike and 1000-kernel weight at both locations and number of tillers per plant and number of seeds per spike at Ellerslie. Item b was significant for final heading at both locations and for onset-of-heading and heading-span at Parkland.

TABLE 17

Analysis of variance of $W_p - V_p$ differences
for ten characters from F_1 diallel set at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.	F for Entries
Onset-of-heading	9.2560 18.9050	0.5815 0.0396	0.1617 0.2974	3.4689 0.1332
Final heading	5.1354 73.2777	1.4540 11.9745	0.4502 4.6422	3.2297 2.5795
Heading-span	0.9138 31.5321	0.1887 18.5786	0.1845 11.9478	1.0227 1.5550
Plant height	17021.1562 4453.5938	344.3201 180.5625	200.6953 58.2656	1.7157 3.0990
Number of tillers per plant	37.6399 9.8207	6.5010 0.7379	3.5646 2.0809	1.8238 0.3546
Number of spikelets per spike	4.3689 0.5617	0.7859 0.1118	0.2638 0.1100	2.9796 0.9640
Number of seeds per spike	989.3882 24.4063	83.1030 23.2917	64.5087 12.2852	1.2882 1.9959
Weight of seeds per spike	0.0021 0.0041	0.0002 0.0002	0.0003 0.0002	0.5844 1.1813
1000-kernel weight	128.4015 134.1506	7.3713 21.2359	6.6094 7.2551	1.1153 2.9270
Yield per plant	102.4395 28.0996	19.8542 5.8340	11.9046 5.6502	1.1638 1.0325

First reading under each column refers to Ellerslie and the second to Parkland.

Directional dominance (significance of b_1) was exhibited by 1000-kernel weight at Ellerslie. Significance of b_2 for final heading at Ellerslie and for plant height and number of tillers per plant at Markland indicates that some parents probably possess more dominant alleles than others for these characters.

The assumptions of no non-allelic interaction, no multiple allelism and uncorrelated parental gene distribution, were checked by analysis of the variance of $W_p - V_p$. The test of homogeneity of $W_p - V_p$ is given in Table 17. None of the characters showed heterogeneity at either location and the conditions underlying the diallel cross analysis could therefore be accepted as valid. For analysis of the genetic components of variation, the offdiagonal values of the diallel table were replaced with the common mean of the corresponding cross and its reciprocal. The array variances (V_p) and parent-offspring covariances (W_p) over five arrays provided the basis for calculating other second degree statistics which are presented in Table 18. The estimates of genetic components of variation obtained from second degree statistics (Hayman 1954b) are presented in Table 19. Table 18 supplied 35 statistics [(15 V_p 's of five arrays and three replications, 15 W_p 's, V_{OLO} , $OL01$, V_{OL1} , V_{1L1} and $(M_{L1} - M_{LO})^2$] and 10 constants were fitted to them (5 values, D , H_1 , H_2 , h and E ; F was not considered, as it is the mean of five F_p 's), leaving 25 degrees of freedom for error to test the significance of genetic components of variation. The proportional estimates of the genetic parameters from Table 19 for all the characters are given in Table 20. The results shown in Table 19 and 20 supported by the

TABLE 18

Estimates of second degree statistics parameters
 for ten characters from F_1 diallel set at two locations.

Character	V_{OLO}	W_{OLO1}	V_{OL1}	V_{LL1}	$(M_{L1} - M_{LO})^2$
Onset-of-heading	15.0000 15.7002	6.2693 7.8816	2.6367 4.1963	3.6055 5.3152	0.8710 1.1096
Final heading	16.9668 27.1514	7.6781 13.1479	3.6621 6.4092	5.0816 9.9770	2.0354 3.5344
Heading-span	0.5889 3.6111	0.1901 0.8584	0.1370 0.2621	0.3845 2.5528	0.3136 0.6614
Plant height	486.7744 518.4434	257.0203 264.6565	140.9746 139.7002	152.3508 150.9949	3.6043 1.6638
Number of tillers per plant	1.4343 5.4749	0.8816 1.1369	0.6432 0.4255	1.2544 1.7429	0.0379 0.8462
Number of spikelets per spike	1.2283 0.5749	0.4720 0.3638	0.2047 0.2805	0.3093 0.5328	0.0083 0.0309
Number of seeds per spike	28.9980 12.2275	11.1666 5.3820	4.6221 3.0371	9.2889 5.2459	0.2224 0.2010
Weight of seeds per spike	0.0384 0.0360	0.0187 0.0142	0.0096 0.0072	0.0180 0.0141	0.0038 0.0093
1000-kernel weight	16.7744 13.1670	7.4203 5.8156	3.4941 2.9736	5.0057 5.5967	0.5568 3.5220
Yield per plant	5.4558 0.8875	1.8886 0.2405	0.7846 0.2034	2.6896 0.5532	0.8060 0.1110

First reading under each column refers to Ellerslie and the second to Parkland.

TABLE 19

Estimates of components of variation
for ten characters from F₁ diallel set at two locations.

Character	D	F	H ₁	H ₂	h ²
Onset-of-heading	14.6845 ± 0.3196**	4.5440 ± 0.7983**	3.5241 ± 0.8630**	3.2439 ± 0.7828**	3.2826 ± 0.5285**
	14.9359 ± 0.4053**	-1.0433 ± 1.0125	3.4473 ± 1.0946**	2.9471 ± 0.9924**	3.9492 ± 0.6703**
Final heading	16.6165 ± 0.5209**	2.8008 ± 1.3011*	5.6702 ± 1.4066**	4.9776 ± 1.2758**	7.9178 ± 0.8614**
	26.2030 ± 1.0947**	0.5733 ± 2.7346	12.0021 ± 2.9564**	12.3744 ± 2.6815**	13.5304 ± 1.8104**
Heading-span	0.2745 ± 0.1321*	0.0402 ± 0.3300	0.5491 ± 0.3568	0.3612 ± 0.3236	1.0532 ± 0.2185**
	2.3939 ± 1.1997*	2.2189 ± 2.7495	6.9876 ± 2.9726**	6.5466 ± 2.6962**	1.8008 ± 1.8203
Plant height	480.0347 ± 4.6656**	-62.6197 ± 11.6546**	50.5735 ± 12.5999**	32.0255 ± 11.4283**	10.1059 ± 7.7158
	511.0740 ± 6.7485**	-30.5825 ± 16.0827	44.6366 ± 18.2521*	30.4400 ± 16.5549	1.9389 ± 11.1770
Number of tillers per plant	0.92006 ± 0.5712	-2.1343 ± 1.4269	-0.2819 ± 1.5427	-0.0226 ± 1.3992	-0.6376 ± 0.9447
	4.3068 ± 0.3162**	5.005 ± 0.9648**	4.8621 ± 1.0430**	2.9335 ± 0.9460**	2.6375 ± 0.6387**
Number of spikelets per spike	0.6753 ± 0.0312**	-0.0351 ± 0.0780	-0.8882 ± 0.0844**	-0.6873 ± 0.0765**	-0.3203 ± 0.0517**
	0.2460 ± 0.2050	-0.7193 ± 0.5121	0.3765 ± 0.5536	0.3513 ± 0.5021	-0.0868 ± 0.3399
Number of seeds per spike	23.7437 ± 2.5748**	7.0245 ± 6.4318	7.6258 ± 6.9535	8.1585 ± 6.3069	-2.4732 ± 4.2581
	8.1325 ± 1.5171**	-1.9871 ± 3.7897	1.0359 ± 4.0970	0.6450 ± 3.7161	-1.8166 ± 2.5089
Weight of seeds per spike	0.0259 ± 0.0038**	-0.0132 ± 0.0096	0.0031 ± 0.0103	0.0088 ± 0.0096	0.0075 ± 0.0063
	0.0217 ± 0.0035**	-0.0021 ± 0.0086	-0.0018 ± 0.0093	-0.0011 ± 0.0085	0.0282 ± 0.0057**
1000-kernel weight	13.4832 ± 0.7218**	-0.0819 ± 1.8030	-1.4414 ± 1.9492	-0.5364 ± 1.7680	0.1206 ± 1.1936
	10.3857 ± 1.0709**	-0.2660 ± 2.6750	5.0600 ± 2.8920	4.9297 ± 2.6231	12.3080 ± 1.7710**
Yield per plant	1.4876 ± 0.2376**	-1.4048 ± 0.5936*	-1.6575 ± 0.6418*	-0.3163 ± 0.5821	0.6845 ± 0.3930
	-0.9960 ± 0.2306**	-1.4472 ± 0.5761*	-2.7585 ± 0.6229**	-2.3675 ± 0.5649**	-0.7613 ± 0.3814

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

graphical analysis of regression of W_p upon V_p lead to the following conclusions:

At both locations, onset-of-heading as inherited as a partially dominant trait, as shown by the mean degree of dominance $[(H_1 + D)^{1/2} = 0.48]$ and regression line (b_{W_p/V_p}) which passes above the origin (Figure 1). The proportion of genes with positive and negative effects in the parents $[H_2 + 4H_1]$ is 0.23 at Ellerslie and 0.21 at Parkland, suggesting a slight asymmetry of alleles at the loci exhibiting dominance. The proportion of dominant to recessive genes in the parents $[(4DH_1)^{1/2} + F] + [(4DH_1)^{1/2} - F]$ is 1.92 at Ellerslie and 0.86 at Parkland, suggesting a preponderance of dominant genes in the parents at Ellerslie and equal proportions of dominant and recessive genes at Parkland. The coefficient of correlation between the parental order of dominance, i.e. $(W_p + V_p)$ and the parental measurements $[(Y_p)]$; the corresponding values of the main diagonal of the diallel table] are 0.97 and 0.66 at Ellerslie and Parkland respectively. High positive correlation at both locations suggests an association between recessive genes with late heading and dominant genes contributing towards early heading. This situation is reflected in the standardized deviation graph (Figure 2) where all the $Y_p, (W_p + V_p)$ parental intercepts occupy (+,+) and (-,-) quadrants, except Khush-hal at Parkland. Figure 1 classifies Marquis as the highly recessive and Inia as the highly dominant parents at both locations, since they lie, respectively, farthest and nearest to the point of intersect of regression line and limiting parabola. Figure 2 supplements this conclusion by revealing

TABLE 20

Proportional values of the estimates of genetic parameters for ten characters from F₁ diallel set at two locations.

Character	$(H_1 + D)^{1/2}$	$(H_2 + 4H_1)$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	$-h^2/H_2$	$r^2_{Y_r, H_r + V_r}$	Heritability
Onset-of-heading	0.4899*	0.2301*	1.9232*	1.0119*	0.9742	0.9837
	0.4804*	0.2137*	0.8645*	1.3400*	0.6627	0.6642
Final heading	0.5042*	0.2195*	1.5372*	1.5907*	0.9712	0.7955
	0.6768*	0.2578*	1.0329*	1.0934*	0.9661	0.6325
Heading-span	1.4144	0.1644	1.1093	2.9160	0.1322	0.1344
	1.7419*	0.2342*	1.7646 †	0.2763	0.7382	0.1875
Plant height	0.3246*	-0.1583*	0.6654*	0.3156	0.1720	0.7740
	0.2955*	0.1705*	0.8161†	0.0637	0.0770	0.8299
Number of tillers per plant	1.1855	0.0200	-0.6361	28.1984	0.8341	0.0281
	1.0625*	0.1508*	3.4090*	0.8991*	0.8924	0.4885
Number of spikelets per spike	1.1286*	0.1997*	0.8826†	0.4661*	-0.2485	0.3182
	1.2370	0.2333	-0.0833	-0.2472	0.7543	0.0925
Number of seeds per spike	0.5741*	0.2606	1.6942	-0.3031	-0.3653	0.5211
	0.3569	0.1557	0.4900	-2.8162	-0.0519	0.2953
Weight of seeds per spike	0.3434	0.7000	0.1561	0.8524	-1.1500	0.2809
	0.2912	0.1445	0.7188	-26.4099	-0.8890	0.2739
1000-kernel weight	0.3270	0.0930	0.9816	-0.2248	-0.7287	0.5331
	0.6980	0.2436	0.9640	2.4967	-0.9252	0.3869
Yield per plant	1.0556	0.0477	0.3819	-2.1646	-0.0082	0.0869
	1.6642	0.2146	0.3922	0.3216	-0.8646	-0.1905

First reading under each column refers to Ellerslie and second to Parkland.

*Genetic component of variation for characters significantly different from zero at $P < 0.05$.

†Components D and H₁ significant, F non-significant ($P > 0.05$).

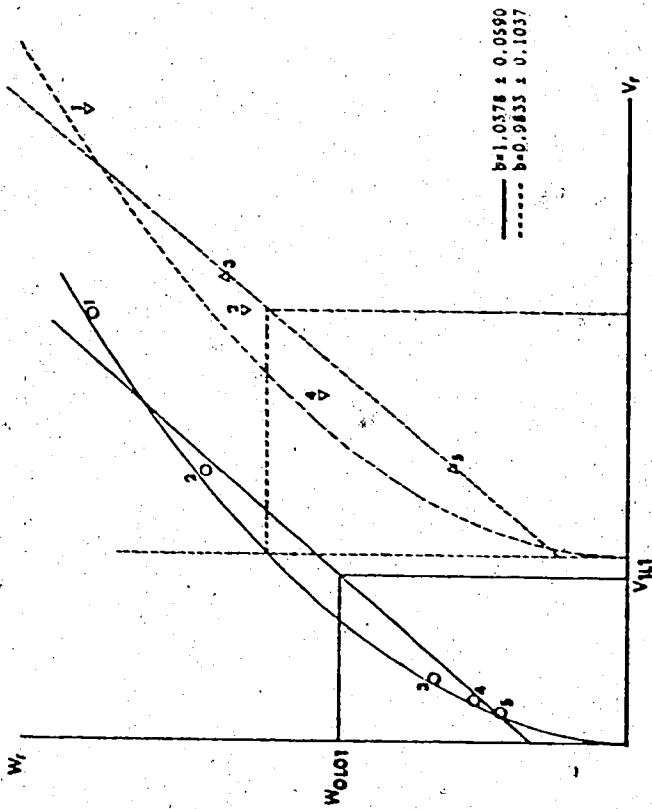


Figure 1. W_p , V_r graph for onset-of-heading from F_1 diallel set.
 — $o = W_p$, V_r intercepts at Ellerslie
 --- $\Delta = W_p$, V_r intercepts at Parkland

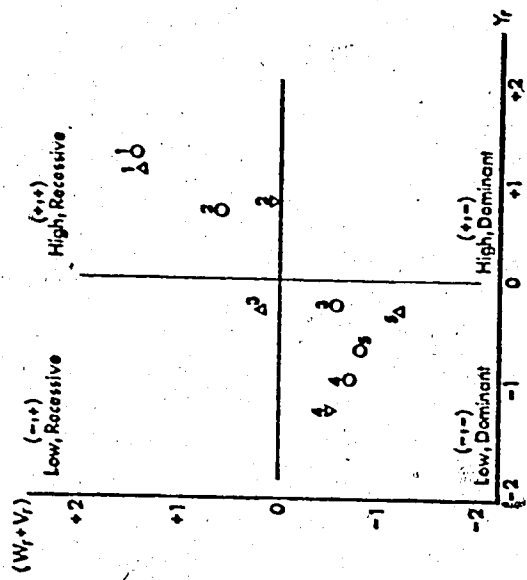


Figure 2. Standardized deviation graph of $[Y_p]$ and $[W_p + V_r]$ for onset-of-heading from F_1 diallel set.

$o = Y_p$, $[W_p + V_r]$ intercepts at Ellerslie
 $\Delta = Y_p$, $[W_p + V_r]$ intercepts at Parkland

that at both locations the highly recessive parent contributes towards late heading (+,+ quadrant) and the highly dominant one towards early heading (-,- quadrant). As far as other parents are concerned, Chinook and Ciano, lying in (+,+) and (-,-) quadrants, may be classified as recessive late headers and dominant early headers. Khush-hal's order of dominance seems to be affected by the environmental influence, being a dominant early header at Ellerslie (-,- quadrant) and a recessive medium-early header (medium-early heading quadrant) at Parkland. The number of groups of genes (n) at both locations, suggests that at least one group of genes control onset-of-heading and exhibit dominance. The heritability estimates of 98.37% at Ellerslie and 66.42% at Parkland show that the character is highly heritable.

The results from Table 19 and 20 for Final heading (Figures 3, 4) and heading-span (Figures 5,6) are subject to the same kind of interpretation as for onset-of-heading except for changes in the relative positions of the parents with respect to their ranking order for dominance, and therefore they are not discussed separately.

For plant height, the mean degree of dominance of 0.3 at both locations shows that height is inherited as a partially dominant character. The W_p/V_p graph (Figure 7) with a regression line intersecting the limiting parabola above its origin supports the above conclusion. The proportion of genes with positive and negative effects in the parents is approximately the same for both locations (0.158 at Ellerslie and 0.170 at Parkland), indicating asymmetry in the distribution of alleles at loci exhibiting dominance. The ratio of dominant to recessive

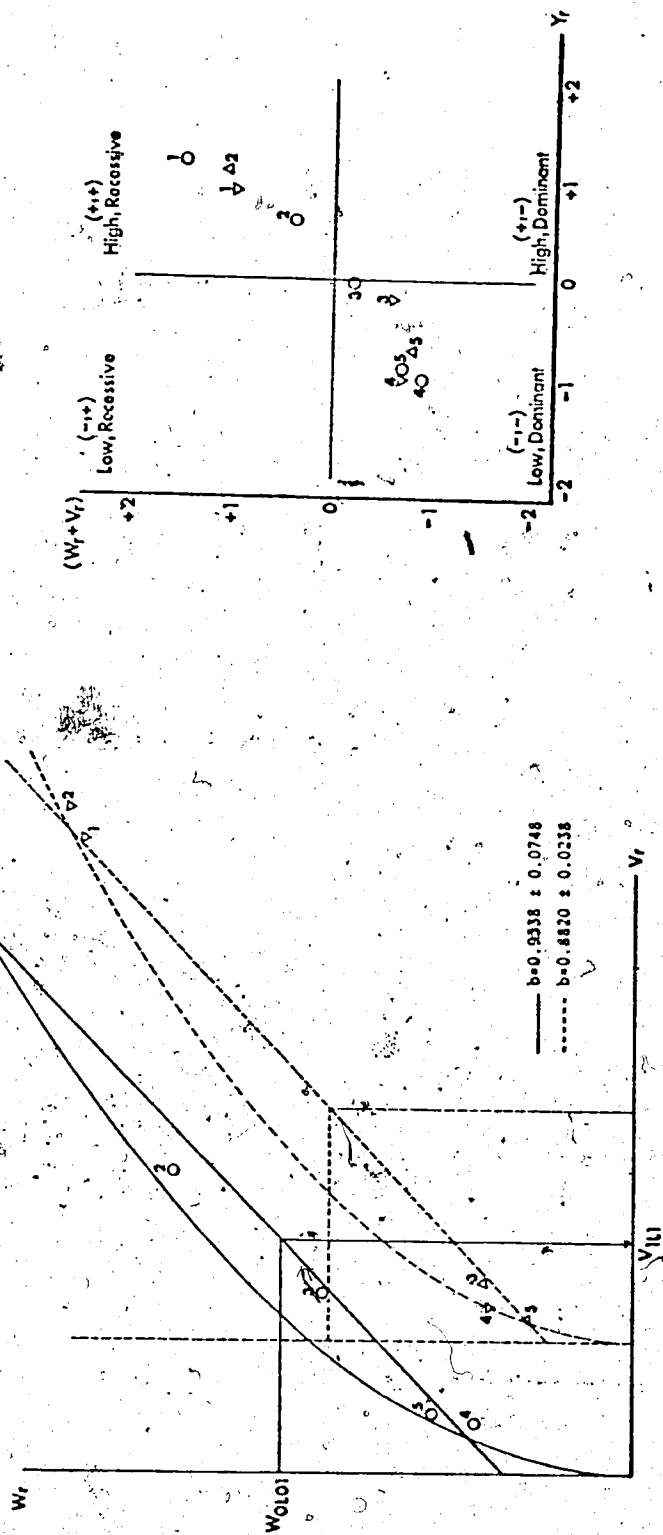


Figure 3. W_p, V_p graph for final heading from F₁ diallel set.
 — $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

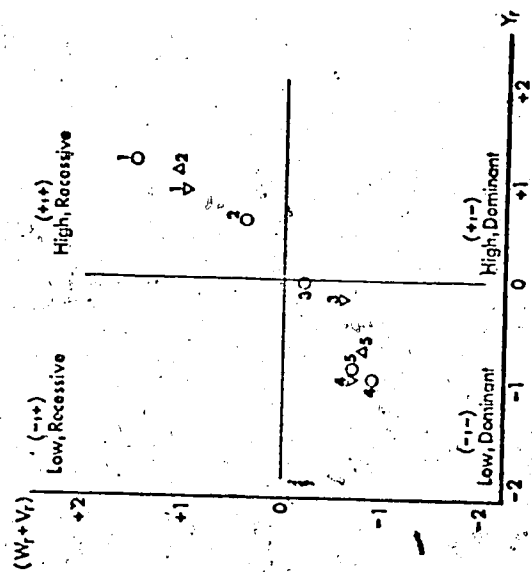


Figure 4. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for final heading from F₁ diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

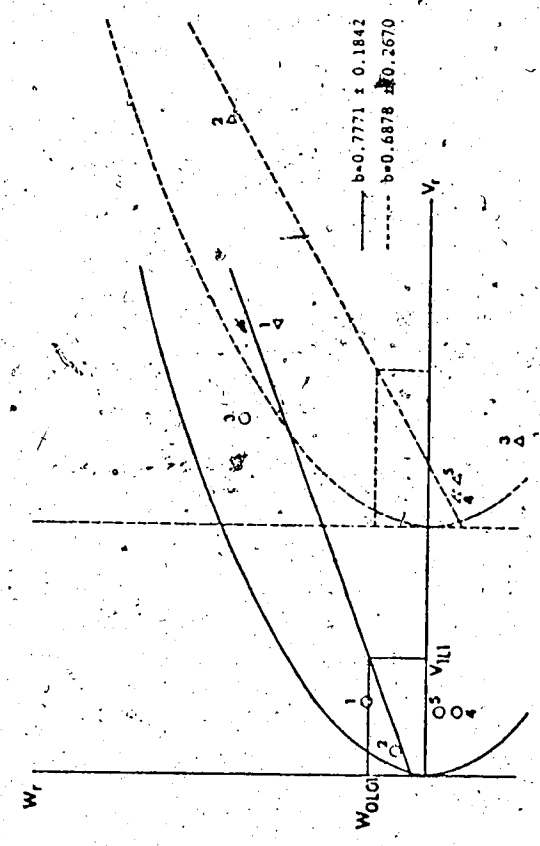


Figure 5. W_r, V_r graph for heading-span from F₁ diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

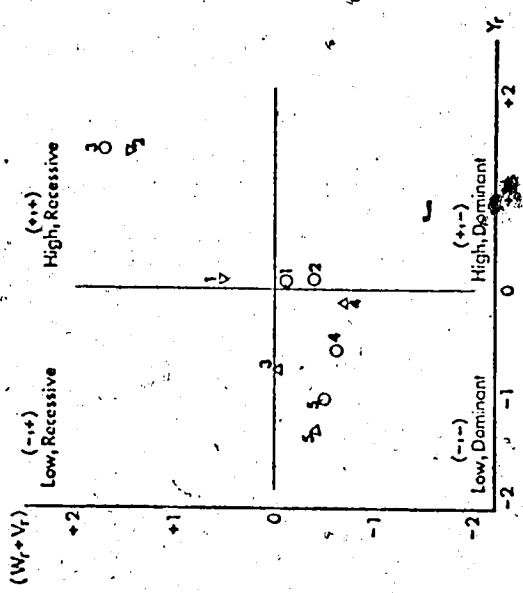


Figure 6. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for heading-span from F₁ diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

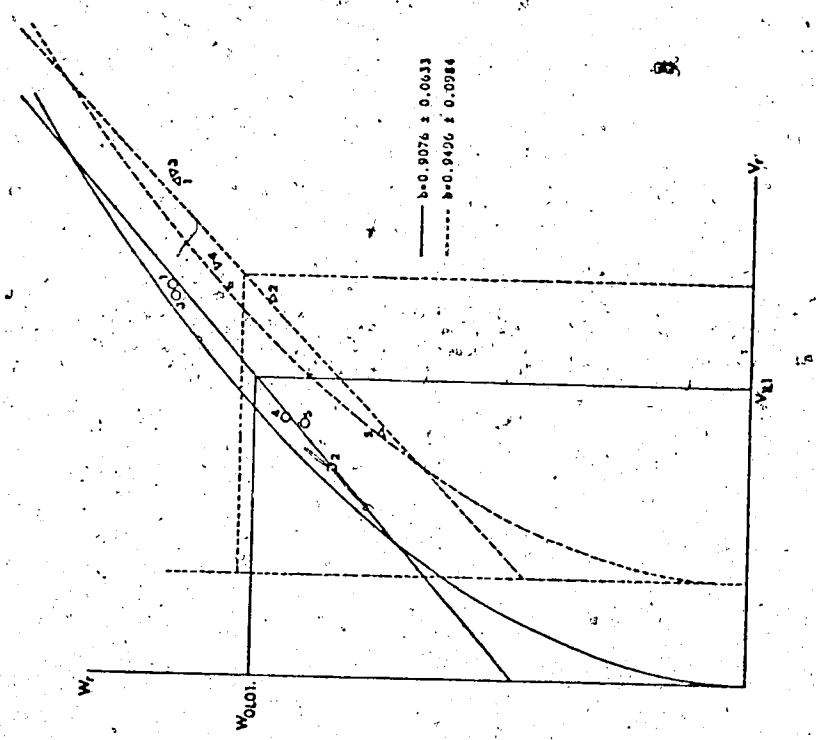


Figure 7. W_p, V_p graph for plant height from F_1 diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

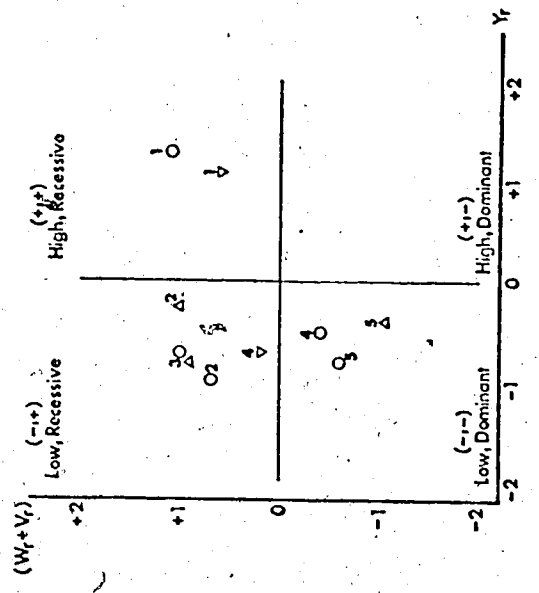


Figure 8. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for plant height from F_1 diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

genes in the parents is approximately equal to one at both locations, suggesting that the parents contain equal numbers of dominant and recessive genes. The coefficient of correlation between the parental order of dominance and parental measurements is 0.17 at Ellerslie and 0.07 at Parkland, indicating weak association between the measurements of the parents and their order of dominance. Figure 7 indicates that Marquis at Ellerslie and Khush-hal at Parkland are the most recessive parents, while Inia at both the locations is the most dominant parent. Figure 8 classifies the parental order of dominance together with their height performance. It places highly recessive parents Marquis (at Ellerslie) and Khush-hal (at Parkland) into (+,+) and (-,+) quadrants, showing that recessiveness of the former is responsible for tallness, while the recessive genes of the latter carry effects decreasing height. The position of Inia in the (-,-) quadrant of the graph (Figure 8) at both locations suggests that it contains a preponderance of dominant genes contributing towards shortness. The ranking order of Ciano appears to be influenced by location effects. At Ellerslie, it is highly dominant, contributing towards reduced height while at Parkland it has an excess of recessive genes, again responsible for shortness. The character seems to be consistently highly heritable over the locations (77.40% heritability at Ellerslie and 82.99% at Parkland).

The genetic components of variation, D , F , H_1 and H_2 are not significant for number of tillers per plant at Ellerslie and therefore estimates of mean degree of dominance, proportion of dominant to

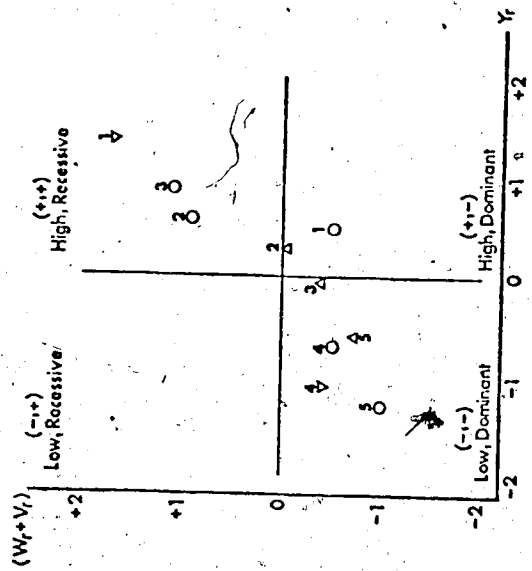


Figure 10. Standardized deviation graph of $[Y_r]$.
 $[W_r + V_r]$ for number of tillers per plant from F_1 diallel set.
 $O = Y_r, [W_r + V_r]$ intercepts at Ellerslie,
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

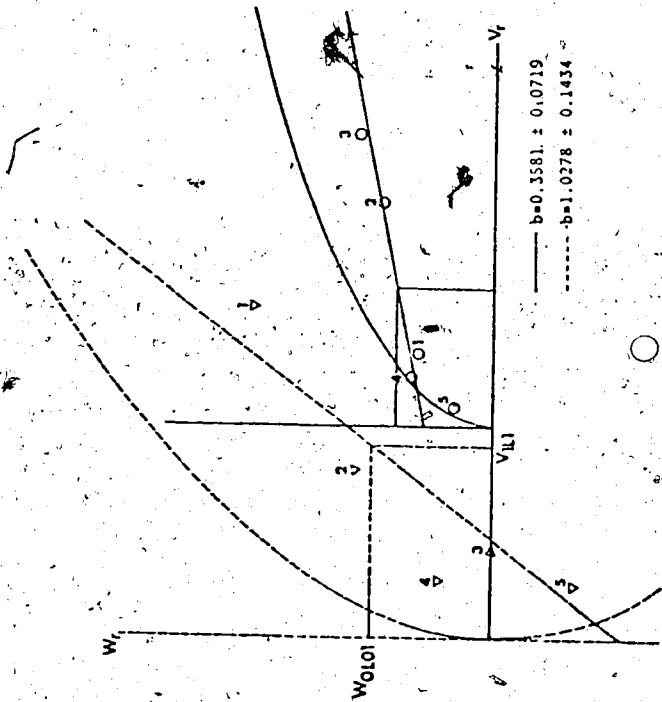


Figure 9. W_r, V_r graph for number of tillers per plant from F_1 diallel set.
 $O = W_r, V_r$ intercepts at Ellerslie
 $\Delta = W_r, V_r$ intercepts at Parkland

recessive genes in the parents etc. should be meaningless (as suggested by Hayman, 1954b). Moreover, the W_p, V_p graph (Figure 9) for Ellerslie is distorted. The mean degree of dominance at Parkland (1.06) indicates over-dominance. This is supported by Figure 9 in which the regression line intersects the limiting parabola above its origin. The proportion of genes with negative and positive alleles at loci exhibiting dominance is 0.15 revealing asymmetry in distribution of alleles. The proportion of dominant to recessive genes in the parents is 3.409 which indicates an excess of dominant genes in the parents. Consequently Khush-hal, Ciano and Inia are categorized as parents with a preponderance of dominant genes, and of these Inia is the most dominant one as it lies closest to the point of intersection of the regression line with the limiting parabola (Figure 9). The significant positive correlation between the parental order of dominance and the parental measurements (0.80) shows that the genes with negative effects for number of tillers per plant are mostly dominant and those with positive effects are mostly recessive. This is shown graphically in Figure 10 where parental $Y_p, (W_p + V_p)$ intercepts occupy only the (+,+) and (-,-) quadrants. Ciano and Inia contain an excess of dominant genes (-,- quadrant) with lower tillering capacity. Chinook appears to be recessive, with a higher number of tillers per plant at Ellerslie, but shows an equal number of recessive and dominant genes at Parkland. Marquis and Khush-hal appear to be inconsistent with respect to order of dominance. At Ellerslie, Marquis has an excess of dominant genes but at Parkland it has become highly recessive. The reverse situation exists with Khush-hal which is placed in the (+,+)

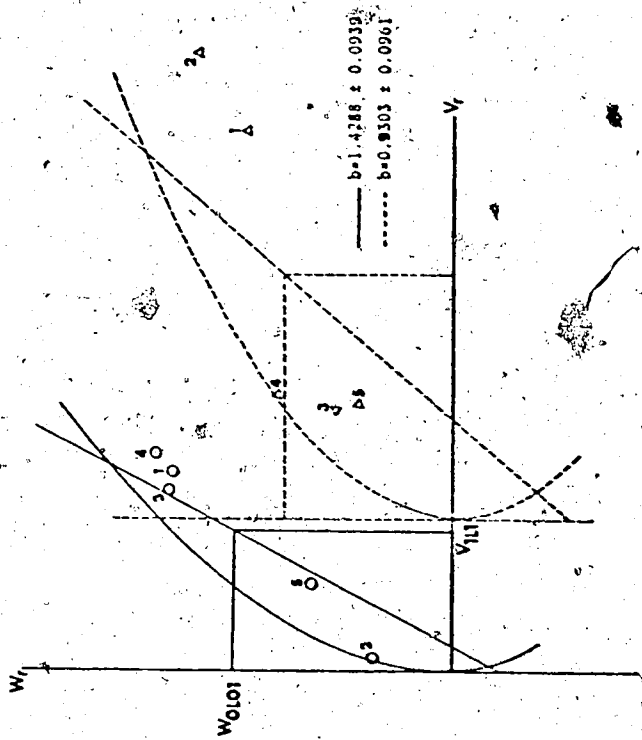


Figure 11. W_p, V_p graph for number of spikelets per spike from F_1 diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

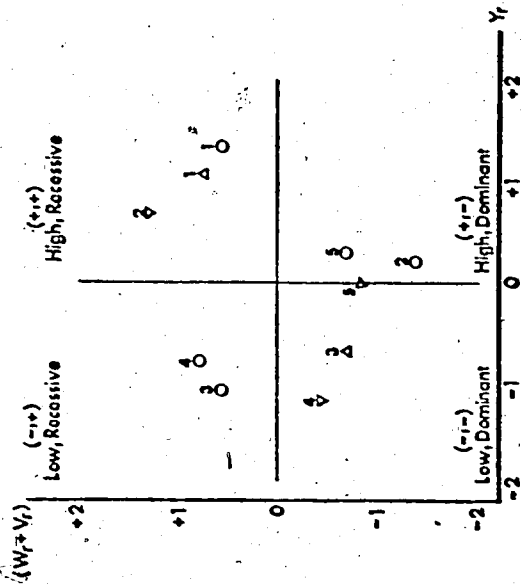


Figure 12. Standardized deviation graphs of $[Y_p]$

and $[W_p + V_p]$ for number of spikelets per spike from F_1 diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

quadrant at Ellerslie and in the (-,-) quadrant at Parkland. The estimate for the number of groups of genes controlling tiller number seems to be questionable for Ellerslie (Table 20) where the relevant components of variation were nonsignificant (Table 19). However it is approximately equal to one at Parkland, showing that at least one group of genes exhibiting dominance controls tillering. The heritability of this character, low at Ellerslie (2.86%) and relatively high at Parkland (48.85%) seems to be affected by environmental differences.

With regard to number of spikelets per spike, there was over-dominance at both locations, since $[H_1/D]^{1/2} > 1$ and the W_r/V_r regression line intersects the limiting parabola below its origin (Figure 11). The genetic components of variation were not significant for Parkland and the proportional estimates of genetic parameters given in Table 20 have therefore to be ignored. For Ellerslie, the proportion of genes with positive and negative alleles at loci exhibiting dominance is approximately 0.2, indicating a slight asymmetry in distribution. The proportion of dominant to recessive genes in the parents is 0.99, suggesting approximately equal proportions of dominant and recessive genes. Figure 11 classifies Marquis, Khush-hal and Ciano as having an excess of recessive genes. The correlation coefficient ($r_{Y_p, W_p + V_p}$) of -0.2 at Ellerslie suggests that parental measurements are not related with their order of dominance, while $r = 0.75$ at Parkland suggests that genes for lower spikelet number per spike are dominant. Order of dominance of the parents (Figure 12) seems to be inconsistent for the two locations except Marquis and Inia. Chinook, the highly recessive parent at Parkland

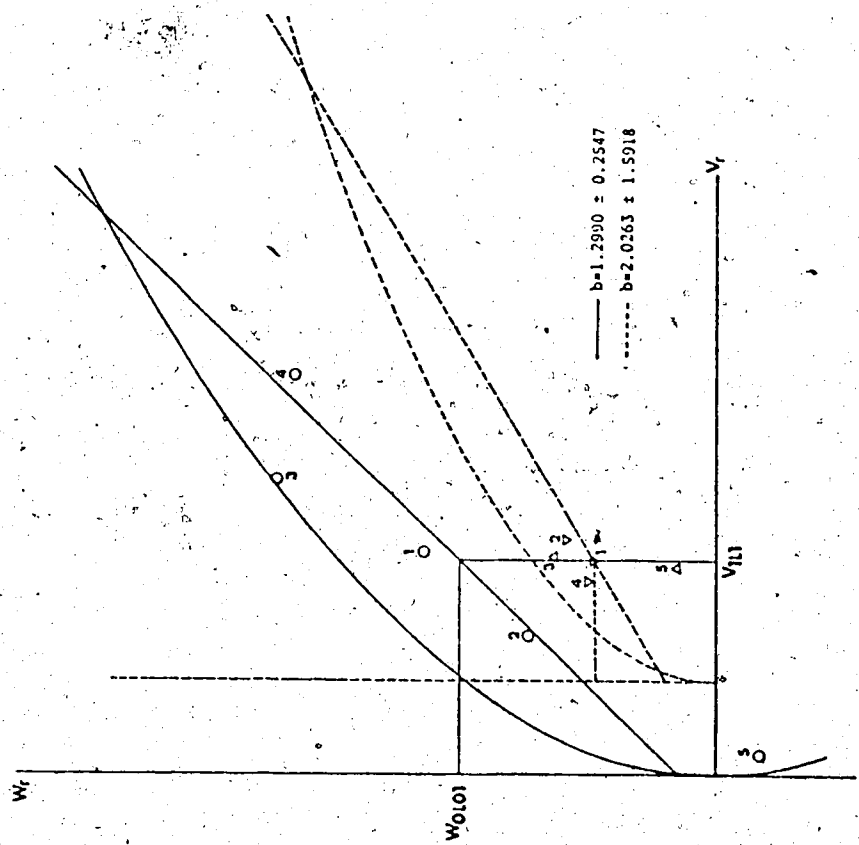


Figure 13. W_p, V_p graph for number of seeds per spike from F_1 diallel-set.
 — $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

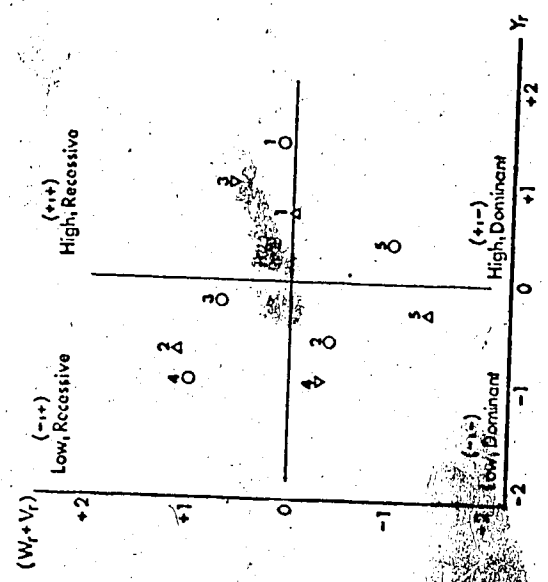


Figure 14. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of seeds per spike from F_1 diallel set.
 $o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

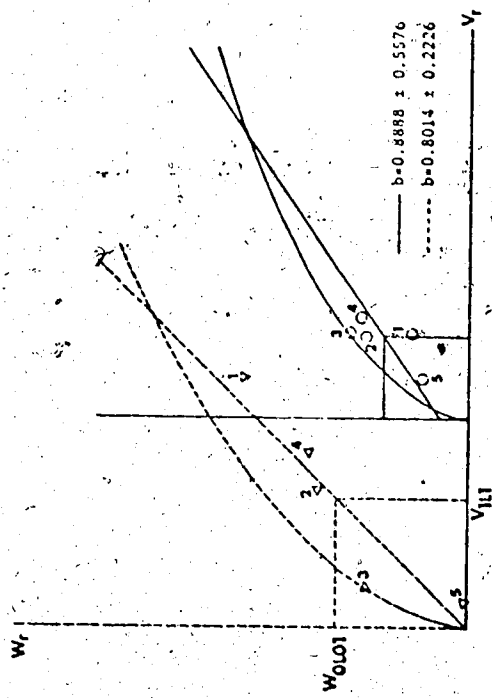


Figure 15. W_p, V_r graph for weight of seeds per spike from F_1 diallel set.
 — $o = W_p, V_r$ intercepts at Ellerslie
 --- $\Delta = W_p, V_r$ intercepts at Parkland

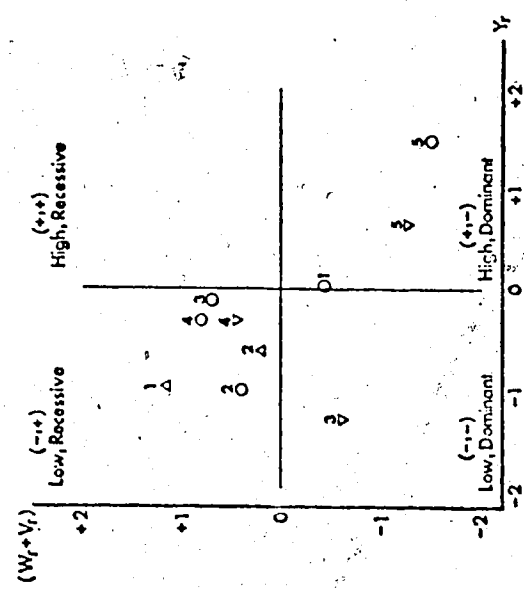


Figure 16. Standardized deviation graph of $[Y_r]$ and $[W_p + V_r]$ for weight of seeds per spike from F_1 diallel set.
 $o = Y_r, [W_p + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_p + V_r]$ intercepts at Parkland

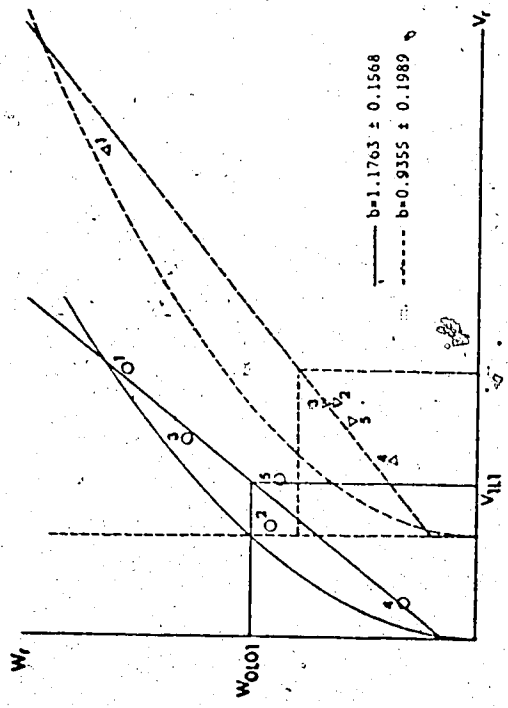


Figure 17. W_r, V_r graph for 1000-kernel weight from F_1 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Ellerslie

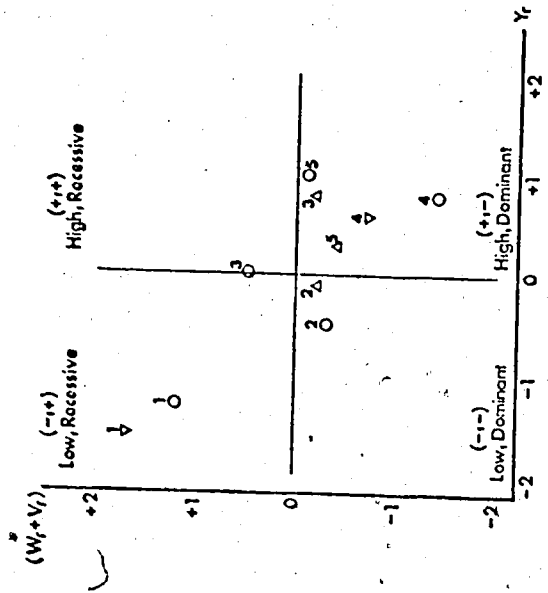


Figure 18. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for 1000-kernel weight from F_1 diallel set.

$o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

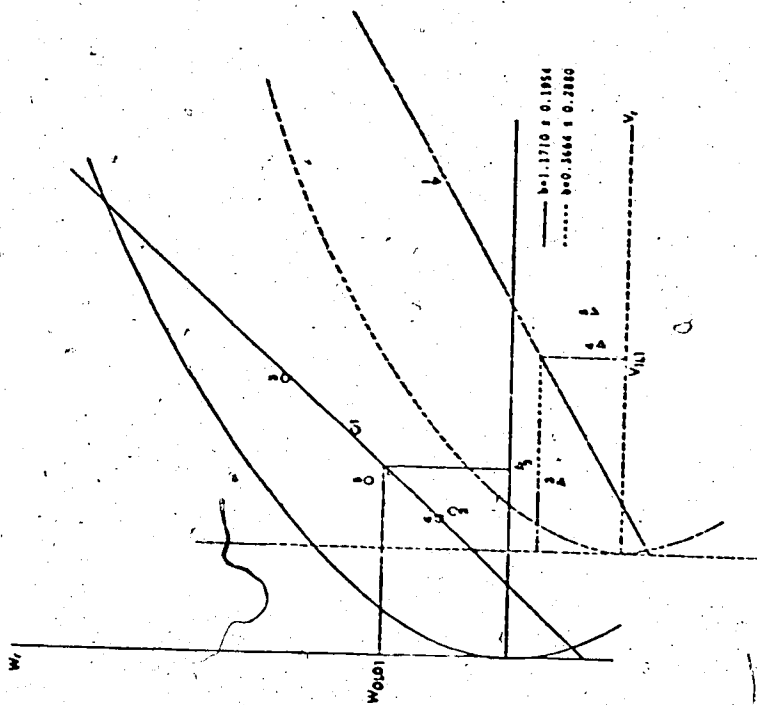


Figure 19. W_p, V_p graph for yield per plant from F_1 diallel set.
 — $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

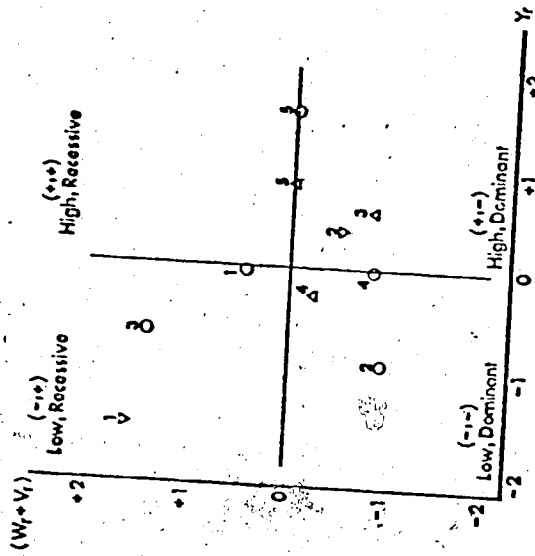


Figure 20. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for yield per plant from F_1 diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

appeared highly dominant at Ellerslie. Khush-hal and Ciano with a preponderance of recessive genes at Ellerslie (-,+ quadrant) contained mostly dominant genes at Parkland (-,+ quadrant). The ratio $h^2/H_2 = 0.46$ suggests that possibly one group of dominant genes is controlling the number of spikelets per spike. Heritability estimates of 31.82% at Ellerslie and 9.25% at Parkland suggest that not only the character is low heritable but inconsistent over the locations also.

As far as the other components of yield i.e. number of seeds per spike (Table 19, 20 and Figure 13, 14), weight of seeds per spike (Table 19, 20 and Figure 15, 16) and 1000-kernel weight (Table 19, 20 and Figure 17, 18) are concerned, the interpretation of the results from relevant tables and figures will be similar. The changes in the relative positions of the parents for their order of dominance may be encountered which may be interpreted accordingly.

The results of diallel cross analysis for yield per plant are meaningless both for Ellerslie and Parkland data. Paradoxically, H_1 for Ellerslie and D , H_1 and H_2 for Parkland have negative values significantly different from zero. Consequently the V_p , W_p graph (Figure 19) for Parkland appears to be severely distorted. The respective graph for Ellerslie does not seem to be distorted and suggests the validity of the hypotheses underlying the diallel analysis. However, a significant negative H_1 invalidates the interpretation of the graph. The same objection applies to standardized deviation graph (Figure 20) also.

ANALYSIS OF F_2 DATA

It will not be out of place to mention again that the F_2 generation hybrids were duplicated in each replication at both locations,

TABLE 21

Simple correlation coefficients between ten characters from F₂ diallel set at two locations.

Character	1	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	-	0.382** 0.831**	0.115 -0.040	0.763** 0.798**	0.196 0.522**	0.433** -0.536**	0.275* 0.306**	-0.274* -0.490**	-0.610** -0.686**	-0.249* -0.126
2. Final heading			0.025 0.522**	0.253* 0.750**	0.176 0.556**	0.142 0.516**	0.087 0.234*	-0.114 -0.398**	-0.229* -0.638**	-0.021 -0.089
3. Heading-span				0.302** 0.122	0.166 0.205	0.027 0.102	-0.074 -0.049	-0.299** -0.102	-0.322** -0.095	-0.201 -0.037
4. Plant height					0.394** 0.506**	0.575** 0.652**	0.263* 0.246*	-0.287* -0.412**	-0.633** -0.687**	0.009 -0.034
5. Number of tillers per plant						0.204 0.353**	0.081 0.060	-0.032 -0.278*	-0.113 -0.505**	0.565** 0.238*
6. Number of spikelets per spike							0.625** 0.444**	0.218, 0.192	-0.346** -0.349**	0.267* 0.329**
7. Number of seeds per spike								0.657** 0.160	-0.130 -0.141	0.259* 0.065
8. Weight of seeds per spike									0.650** 0.701**	0.392** 0.473**
9. 1000-kernel weight										0.252* 0.265*
10. Yield per plant										

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

partly to meet the entry requirements of the partially balanced lattice design, and partly to reduce the genetic sampling error inherent in the segregating generation. Though the heading data and yield observations were recorded separately for the two repetitions, the analysis of the data is based on their average.

Simple correlation coefficients for all the characters are shown in Table 21. The results reveal that:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike, and negatively correlated with weight of seeds per spike, 1000-kernel weight and yield per plant at both locations. Correlation with number of tillers per plant was only exhibited at Parkland. The negative association of onset-of-heading with yield and its two components, weight of seeds per spike and 1000-kernel weight, suggests that early maturing varieties are higher yielders and consequently their seed weighs more than the late maturing ones. This kind of relationship was also noticed for F_1 hybrids. Correlation of final heading and heading-span with other characters has the same kind of interpretation.

Plant height exhibited significant positive correlation with number of tillers per plant, number of spikelets per spike, number of seeds per spike and 1000-kernel weight at both locations. Correlation with yield per plant was not significant.

Number of tillers per plant exhibited positive correlation with yield per plant at both locations and with number of spikelets per spike at Parkland but was negatively associated with weight of seeds per

TABLE 22

Varimax rotated factor matrix for ten characters from F₂ diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.977 0.886	0.958 0.896	0.149 0.023	-0.047 0.253	-0.178 -0.116	-0.055 -0.075
Final heading	0.981 0.940	0.695 0.794	0.129 0.001	-0.029 0.252	-0.208 -0.090	0.346 0.488
Heading-span	0.996 0.993	0.152 0.050	-0.051 -0.036	0.009 0.071	-0.140 0.019	0.975 0.992
Plant height	0.851 0.889	0.746 0.922	0.267 0.012	0.250 0.194	-0.372 -0.004	0.148 0.049
Number of tillers per plant	0.912 0.917	0.277 0.351	-0.039 0.013	0.903 0.848	-0.006 0.235	0.133 0.142
Number of spikelets per spike	0.834 0.883	0.288 0.688	0.811 0.590	0.162 0.046	-0.257 0.233	-0.022 0.071
Number of seeds per spike	0.903 0.981	0.186 0.156	0.904 0.967	0.039 0.098	0.221 0.049	-0.014 -0.050
Weight of seeds per spike	0.994 0.943	-0.234 -0.381	0.581 0.725	0.082 -0.346	0.760 0.391	-0.129 -0.024
1000-kernel weight	0.913 0.880	-0.462 -0.625	-0.155 0.059	0.072 -0.546	0.802 0.411	-0.162 -0.005
Yield per plant	0.898 0.929	-0.285 -0.045	0.278 0.252	0.839 0.129	0.105 0.920	-0.156 0.008
% of total variability explained	92.590 92.399	28.424 34.420	20.287 18.768	16.261 13.540	15.814 13.089	11.805 12.581

First reading under each column refers to Ellerslie and second to Parkland

spike and 1000-kernel weight at Parkland. Negative correlations with weight of seeds per spike and 1000-kernel weight establish an inverse relationship indicating that more the tillers per plant, the higher is the yield and the lower the weight of seeds per spike and 1000-kernel weight. The correlation coefficients of other components of yield, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be explained in the same manner.

Yield per plant was positively correlated with its components, viz., number of tillers per plant, number of spikelets per spike, weight of seeds per spike and 1000-kernel weight. It was negatively associated with onset-of-heading at Ellerslie, while its correlation at Parkland was not significant. Negative correlation of yield with onset-of-heading indicates that high yielding varieties are usually early maturing.

Factor analysis was performed on the complete F_2 diallel data. Four principal factors, derived by factorizing correlation matrix into a varimax rotated factor matrix, accounted for 81.7% of the variability present in the data. Since it was thought that 82% of the variation (as explained by these four factors) was not sufficient, the number of factors was raised to five and the procedure was repeated through computerization. The five factors were found to explain 92% of the variation in the data. A further six factor matrix explained 96% of the variability, it was not significantly different from the five factor-matrix which was therefore considered and the results are given in Table 22.

Since the first factor showed the highest loadings for

onset-of-heading and final heading at both locations and accounted for 28%^{of} variability at Ellerslie and 34% at Parkland, it was named *lateness*. It was positively affected by plant height and negatively by weight of seed per spike, 1000-kernel weight and yield per plant at both locations. This implies that a longer heading period causes the plants to grow taller but yield less, with lower seed weight per spike and consequently lower 1000-kernel weight. Number of tillers per plant, number of spikelets per spike and number of seeds per spike at both locations contributed very little to this factor.

The second principal component was termed *yield-components*. Although earlier the term *yielding-capacity* was applied in the F₁ factor analysis, the above term is considered more suitable because of the consistently higher loadings for yield components. Thus this component shows maximum loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike at both locations. Negative contributions towards this factor due to heading-span at both locations and number of tillers per plant and 1000-kernel weight at Ellerslie reveal that varieties with longer maturing times yield less, produce fewer tillers per plant and show lower 1000-kernel weight.

The third principal component was named *tillering-capacity* as it provided the maximum contribution to number of tillers per plant at both locations. The factor accounted for 16% and 13.5% of the total variability in the data at Ellerslie and Parkland respectively. Yield was significantly affected at Ellerslie, but at Parkland, the contribution towards yield was comparatively low. Number of spikelets per spike,

TABLE 23

Estimates of general combining ability of five parental lines used in F_2 diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8000	1.3167	-0.3667	-1.6833	-1.0667
	2.2267	2.0267	-1.0900	-2.0066	-1.1566
Final heading	1.9767	1.5767	-0.0733	-1.9733	-1.5066
	2.0334	2.5667	-0.9167	-2.0333	-1.6570
Heading-span	0.1500	0.3667	0.2667	-0.3167	-0.4667
	-0.2033	0.5467	0.1800	-0.0367	-0.4867
Plant height	13.3708	10.0921	-6.7329	-7.3467	-9.3831
	12.9692	12.0445	-7.7827	-9.2980	-8.9530
Number of tillers per plant	-0.0055	0.4139	0.4435	-0.2707	-0.8512
	0.8860	0.6827	0.5310	-0.9973	-1.1023
Number of spikelets per spike	0.7264	0.2257	-0.6355	-0.4576	0.1412
	0.6867	0.4672	-0.3060	-0.7084	-0.1394
Number of seeds per spike	3.1883	-1.5763	-1.7061	-2.1989	2.2930
	2.2384	-1.1155	0.2738	-2.4032	1.0865
Weight of seeds per spike	0.0283	-0.1592	-0.0475	-0.0079	0.1863
	-0.6274	-0.1023	+0.0665	-0.0431	0.1063
1000-kernel weight	-2.0321	-2.2150	0.4223	1.7856	2.0392
	-2.2536	-1.3656	1.2445	1.2144	1.1603
Yield per plant	0.0508	-1.4712	-0.7275	0.6961	1.4518
	-0.5307	0.1256	0.6319	-0.5374	0.3109

First reading under each column refers to Ellerslie and second to Parkland.

number of seeds per spike and heading-span at both locations, weight of seeds per spike and 1000-kernel weight at Ellerslie contributed positively to this factor.

The fourth principal factor, accounting for 15% and 13% variability at Ellerslie and Parkland and carrying the highest loadings for 1000-kernel weight at both locations, was called *kernel-weight*. The factor was contributed to by weight of seeds per spike and yield per plant at both locations, although the effect of number of seeds per spike appears to be slight. Other characters such as plant height, final heading and onset-of-heading at both locations were negatively affected.

The fifth principal factor, since it was termed *heading period*, was strongly affected by heading-span. It explained 12% of the total variation at both locations, and was adversely affected by yield and its components. Final heading, plant height and number of tillers per plant at both locations scored positively for this factor but their contribution was relatively low.

Combining ability analysis

Estimates of general combining ability for the five parental lines are presented in Table 23. Marquis scored highest for onset-of-heading and Ciano lowest at both locations. The same was true for final heading. For heading-span, Chinook ranked first and Ciano last. In plant height, Marquis excelled at both locations while Inia at Ellerslie and Ciano at Parkland were lowest. For number of tillers per plant, Khush-hal ranked first at Ellerslie and Chinook ranked first at Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₂ diallel set at two locations.

TABLE 24 Onset-of-heading

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	-0.0500	-1.1166	-0.7166	-0.9166	1.8000	3.1762	-0.1594
		1.2066	-0.2600	-1.5100	-1.1100	2.2267	4.8224	-0.3394
Chinook	-0.3333	-	-0.4667	-0.7333	-0.5167	1.3167	1.6699	-0.1586
	0.1667		-0.6434	0.1900	-1.8267	2.0267	3.9718	0.1459
Khush-hal	-0.4167	-0.4167	-	0.1167	0.3334	-0.3667	0.0707	0.3288
	0.4167	0.1667		-0.3600	-1.0434	-1.0900	1.0522	-1.1789
Ciano	0.0	0.8333*	0.3333	-	0.5667	-1.6833	2.7697	0.1956
	-0.4167	0.2500	-0.2500		1.2066	-2.0066	3.8908	0.4759
Inia	0.0833	0.6667	0.3333	0.4167	-	-1.0067	1.0740	0.3537
	-0.6667	-0.0833	-0.2500	-0.4167		-1.1556	1.2020	2.0317

TABLE 25 Final heading

Marquis	-	0.2233	-1.1267	-0.6434	-1.0267	1.9767	3.8498	-0.1441
		1.0167	-1.3833	-1.4333	-1.2333	2.0334	3.9308	-0.5093
Chinook	-0.0833	-	0.3566	-1.0767	-0.2100	1.5767	2.4284	-0.1275
	0.5833		-1.8333	-0.8000	-1.6833	2.5667	6.3842	-0.0158
Khush-hal	-0.0833	-0.6667	-	-0.3434	-0.5600	-0.0733	-0.0523	0.3214
	0.3333	0.2500		0.5167	0.3000	-0.9167	0.6366	1.2490
Ciano	-0.6667	0.6667	0.4167	-	1.2567	-1.9733	3.8362	0.4396
	0.1667	-0.3333	-0.6667		-1.0833	-2.0333	3.9306	0.4779
Inia	0.7500*	0.6667	0.3333	0.4167	-	-1.5066	2.2123	0.8529
	-0.0833	0.3333	0.3333	-0.6667		-1.6500	2.8188	1.3635

First reading under each column refers to Ellerslie and the second to Parkland.

*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₂ diallel set at two locations.

TABLE 26. Heading-span

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.1667	0.0167	0.1000	-0.0833	0.1500	-0.0443	-0.1671
		0.0200	-1.1133	0.0200	-0.1133	-0.2033	-0.2013	-0.6067
Chinook	0.2500	-	0.7167	-0.4500	0.2000	0.3667	0.0676	-0.1578
	0.4167		-1.1967	-0.9800	0.1367	0.5467	0.0562	-0.6065
Khush-hal	0.3333	-0.2500	-	-0.4333	-0.8667	0.2667	0.0043	0.0042
	0.7500	0.0333		0.8867	1.3367	0.1800	-0.2103	0.2838
Ciano	-0.6667	-0.1667	0.0833	-	0.7167	-0.3167	0.0334	-0.0337
	0.3333	-0.5833	-0.4167		-0.1133	-0.0367	-0.2413	-0.0243
Inia	0.6667	0.0	0.0	0.0	-	-0.4667	0.1509	0.2701
	0.5833	0.2500	0.5833	-0.2500		-0.4867	-0.0058	-0.0037

TABLE 27. Plant height

Marquis	-	2.8015	0.0336	-1.9122	-5.2829	13.3708	177.5788	-2.9988
		1.8702	5.4357	-1.9114	-6.1106	12.9892	166.6538	-5.1606
Chinook	-1.1342	-	1.3486	-3.5393	2.7586	10.0921	100.6507	-0.9129
	2.0642		1.2654	-1.3834	0.2390	13.0445	168.0942	-3.9947
Khush-hal	3.3558*	1.7808	-	1.3133	-0.2195	-6.7329	44.1325	-2.3549
	0.8525	3.4392		0.1846	-2.8154	-7.7827	58.5057	5.2222
Ciano	-0.8783	3.8492*	0.0467	-	1.0260	-7.3467	52.7748	2.9703
	0.0633	5.0650*	0.0592		1.3933	-9.2980	84.3886	-3.2934
Inia	12.9255**	5.8667**	-0.2958	1.5775	-	-9.3831	86.8439	9.5876
	8.2025**	5.3258*	-0.4642	-0.7742		-8.9530	78.0926	10.5941

First reading under each column refers to Ellerslie and the second to Parkland.
 * Significant at 1% level
 ** Significant at 5% level

For number of spikelets per spike, Marquis was highest at both locations while Khush-hal at Ellerslie and Ciano at Parkland ranked lowest. For number of seeds per spike, Marquis ranked highest at both locations and Ciano was the lowest. For weight of seeds per spike and 1000-kernel weight, Inia ranked first at both locations, while Chinook ranked last for weight of seeds per spike; and for 1000-kernel weight, Marquis at Parkland and Chinook at Ellerslie ranked last. For yield, Inia at Ellerslie and Khush-hal at Parkland scored highest GCA and Khush-hal at Ellerslie and Ciano at Parkland ranked lowest.

Specific combining abilities of the F_2 hybrids, the reciprocal effects and the variances for general and specific combining abilities are given in Tables 24 to 33. These are discussed under individual characters.

Cross (CxI) had the highest SCA for onset-of-heading (Table 24) at both locations and (MxK) at Ellerslie and (MxI) at Parkland were the lowest. Hybrid (CxI) with the highest SCA had parents with the lowest GCA's at both locations. Similarly the lowest ranking hybrids (MxK) and (MxI) had one parent (Marquis) with the highest GCA at both locations. These kinds of results support those of the F_1 combining ability analyses. Thus it is seen that parental lines with high GCA's do not necessarily produce hybrids with high SCA's. The variances for GCA were usually larger than those for SCA except for Khush-hal at Ellerslie and Inia at Parkland. Relatively high SCA variances for Inia and Khush-hal imply an inconsistency in their SCA performance of their hybrids at both locations. Reciprocal effects were generally non-significant except for (CxCH) at Ellerslie which may be ascribed to the female parent of the hybrid.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₂ diallel set at two locations.

TABLE 28. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.0155	-0.5057	0.05200	0.0377	-0.0055	-0.4646
		-0.7810	-0.5043	-0.6510	-0.3043	0.8860	-0.5129
Chinook	0.0833	-	0.4832	-0.9860	0.7246	0.7246	-0.4646
	-0.3583		0.9407	-0.2310	-0.2427	0.6827	-0.3096
Khush-hal	0.7260	0.5167	-	0.8520	-0.7987	0.4435	-0.3012
	-1.0667	1.750		-0.2043	0.1827	0.5310	-0.1332
Ciano	-0.4185	0.3667	0.5158	-	0.7167	-0.2707	0.1023
	0.6250	0.8583	-0.0167		0.3123	-0.9973	-0.3400
Inia	0.8230	0.7500	0.2437	0.4908	-	-0.5812	0.0947
	0.6667	0.1250	0.0333	-0.0500		-1.1023	-0.4188

TABLE 29. Number of spikelets per spike

Marquis	-	-0.0184	0.3592	-0.2315	-0.0934	0.7264	0.4810	-0.1169
		0.5606	0.1479	0.1164	-0.1162	0.6867	0.4044	-0.1677
Chinook	0.8083*	-	-0.0646	-0.1672	0.5422	0.2257	0.0042	-0.1168
	0.0222		0.4920	-0.3278	-0.1107	0.4672	0.1512	-0.0629
Khush-hal	-0.2523	-0.0500	-	0.3346	-0.5709	-0.6356	0.3537	-0.0725
	-0.0472	0.3832		-0.3072	-0.1203	-0.3060	0.0266	-0.0796
Ciano	-0.0117	0.1972	0.2123	-	0.1788	-0.4576	0.1626	-0.0524
	-0.0870	-0.2613	0.2750		0.2484	-0.7084	0.4348	-0.0959
Inia	0.2678	0.1057	-0.3203	-0.1243	-	0.1412	-0.0268	0.1033
	0.3723	0.6473	0.1305	0.0418		-0.1394	-0.0476	-0.1337

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₂ diallel set at two locations.

TABLE 30. Number of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Claro	Inia			
Marquis	-	1.1545	-0.7005	0.1160	0.5999	3.1893	9.3728	-1.9670
	0.1278	0.2870	-0.0244	1.3941	0.6768	2.2384	4.0955	-2.2876
Chinook	-0.7028	-	0.0982	-0.0284	2.0048	-1.5763	1.6979	-1.5227
	0.1278	-	0.0492	-0.1192	0.7419	-1.1155	0.3293	-2.2601
Khush-hal	0.1287	-1.4832	-	0.2428	-1.4129	-1.7061	2.1238	-1.8002
	-1.2997	0.0360	-	-1.8748	-0.5793	0.2738	-0.8401	-2.2866
Ciano	0.7217	0.0697	-0.1442	-	1.3696	-2.1989	4.0483	-1.9426
	-0.7168	-1.2167	0.3277	-	0.7678	-2.4832	5.2511	-0.4635
Inia	1.7125	-0.0612	1.0087	0.5783	-	2.2930	14.4710	0.7809
	0.9752	0.4083	-0.7652	1.0390	-	1.0865	0.2653	-1.6431

TABLE 31. Weight of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Claro	Inia			
Marquis	-	-0.0530	0.0072	0.0107	0.1000	0.0283	-0.0017	-0.0064
	0.0172	0.0068	-0.0384	0.0898	0.1372	-0.0274	-0.0018	-0.0063
Chinook	0.0022	-	-0.0560	0.0218	0.0196	-0.1592	0.0228	-0.0054
	0.0172	-	-0.0018	-0.006	-0.0131	-0.1083	0.0079	-0.0063
Khush-hal	0.0283	-0.0740	-	0.0447	-0.0299	-0.0475	-0.0003	-0.0053
	-0.0558	-0.0208	-	-0.0383	0.0114	0.0665	0.0019	-0.0058
Ciano	0.1072	0.0355	-0.0413	-	-0.0030	-0.0079	-0.0025	-0.0055
	0.0700	-0.0573	-0.0225	-	0.0051	-0.0431	-0.0007	-0.0031
Inia	0.0237	0.0072	-0.0377	-0.0052	-	0.1863	0.0322	-0.0026
	0.0885	-0.0143	-0.0503	0.0277	-	0.1063	0.0088	0.0001

First reading under each column refers to Ellorslie and the second to Parkland.

With respect to final heading (Table 25) and heading-span (Table 26), although there are some differences in relative positions of the parents and hybrids concerned, the general conclusions are the same as for onset-of-heading.

Cross (MxCH) at Ellerslie and (MxK) at Parkland ranked highest for plant height while (MxI) at both locations was the lowest (Table 27). Cross (MxCH) had both parents with highest GCA's at both locations while cross (MxK) with highest SCA at Parkland had one parent (Khush-hal) with a comparatively low GCA. Similarly (MxI) with lowest SCA at both locations had Marquis parent with highest GCA at both locations. In all cases the variances for GCA were greater than those for SCA. Crosses (CxCH), (IxM) and (IxCH) at both locations and (KxM) at Ellerslie showed significant reciprocal effects, which may be ascribed to the female parents because of the positive sign appended to each effect.

For number of tillers per plant (Table 28), crosses (KxC) at Ellerslie and (CHxK) at Parkland scored highest in SCA and (CHxC) at Ellerslie and (MxCH) at Parkland scored lowest. It is again noteworthy that one parent of the hybrids with high SCA (Ciano) had the second lowest GCA at both locations, while one parent of those scoring lowest in SCA (Chipook) had the highest GCA at both locations. The variances for GCA were, in general, greater than those for SCA and the reciprocal effects were non-significant.

The general interpretations for the remaining components of yield, viz., number of spikelets per spike (Table 29), number of seeds per spike (Table 30), weight of seeds per spike (Table 31) and 1000-kernel

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from F₂ diallel set at two locations.

TABLE 32. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	-0.0159	0.2364	-0.1336	1.4490	3.4447	-1.7115
Chinook	-0.5203	-	-0.8323	1.4480	2.2354	4.5162	-1.4056
Khush-hal	0.2470	-0.2108	-1.4490	0.4314	-1.1334	4.3318	-1.7114
Ciano	-0.2907	-0.4162	0.1446	-0.2289	-0.7060	1.3026	-1.3909
Inia	1.6177	-0.5518	-	0.9701	0.9718	-0.5063	-0.9926
Reciprocal effects	0.2192	0.0647	-1.0387	0.3904	0.9605	0.9866	-1.1678
	-0.7592	-0.3352	-0.0517	-	0.3992	2.5039	-1.3299
	1.0892	-0.5033	-0.8753	-0.6647	2.0392	0.9125	-0.6385
					1.1603	3.4739	-0.3453
						0.7640	-0.7068

TABLE 33. Yield per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.5420	-0.0646	1.1590	-0.1661	0.0508	-0.9980
Chinook	-0.4107	-0.8039	0.7455	0.0267	0.7448	-0.5307	-1.0655
Khush-hal	0.6045	-	0.1689	-1.0782	0.1929	-1.4712	1.7653
Ciano	2.1502*	0.5530	1.3541	-0.7700	0.3538	0.1255	-0.4104
Inia	-1.5562	-0.0635	-	1.7764	-0.4546	-0.7275	-0.7394
Reciprocal effects	-0.9003	-0.1892	-0.4672	0.0255	-1.2061	0.6319	-0.2690
	1.3395	-0.1583	-0.2452	-	0.0659	0.0854	0.8891
	1.0152	1.1928	0.6962	-0.4528	0.1652	-0.1373	-0.8674
	0.5628	-0.4918	-0.3988	-0.1468	1.4518	1.7084	-0.9061
					0.3109	-0.3296	-0.3448

*First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

weight (Table 32) and the conclusions derived therefrom with respect to SCA's do not differ from number of tillers per plant. Only the relative positions and respective ranking orders of the parents and hybrids are changed.

For yield per plant (Table 33), crosses (KxC) at Ellerslie and (CHxK) at Parkland, respectively scored highest in SCA while (CixC) at Ellerslie and (KxI) at Parkland ranked lowest. One parent of (KxI), Inia, scored highest for GCA at both locations while one parent of (CHxC), Chinook, scored lowest at Ellerslie and other parent, Ciano, scored second highest at Ellerslie. (KxC) had one parent (Khush-hal) with the second lowest GCA at Ellerslie. The variances for GCA were greater than those for SCA except for Marquis and Ciano at both locations, and Chinook, Khush-hal and Inia at Parkland. The reciprocal effects were non-significant except for (KxM) at Ellerslie which may be ascribed to Khush-hal because of the positive sign appended to the effect.

The following conclusions may be drawn from the analysis of general and specific combining ability for all the characters considered: (1) In all cases, since hybrids with high SCA's were associated with the parents with low GCA's, the high GCA's of the parental lines may not be taken as criteria to predict high SCA's of their hybrids. (2) In most cases, the variances for GCA's were greater than those for SCA's. The analysis of variance for general and specific combining ability (Table 34) also supports this conclusion. In all cases, the mean squares for GCA in Table 34 are significant except for heading-span and yield per plant at Parkland. This implies that GCA which is largely due to

TABLE 34

Analysis of variance of general and specific combining ability and reciprocal effects from F₂ diallel set for ten characters at two locations.

Character	M.S.		M.S. for		Error
	for GCA	for SCA	reciprocal effects	M.S.	
D.F.	4	10	10	48	
Onset-of-heading	22.7031** 39.0469**	2.1187** 4.0062**	0.4000 0.2431	0.2390 0.5096	
Final heading	31.3750** 46.0000**	2.3062** 5.6812**	0.5625* 0.3375	0.2126 0.7635	
Heading-span	1.3652* 1.5268	0.5275* 1.9586*	0.2319 0.4347	0.2507 0.9094	
Plant height	1169.9375** 1415.1094**	17.7062** 25.2250**	47.0742** 27.7873	4.4982 39.3587	
Number of tillers per plant	1.9502* 9.3584**	0.8008 1.0986	0.5834 0.4896	0.6970 1.2179	
Number of spikelets per spike	3.0322** 3.2627**	0.2066 0.2785	0.2304 0.0921	0.1753 0.9593	
Number of seeds per spike	64.1406* 34.2031*	3.4828 2.9781	1.6961 1.3182	2.9497 10.7170	
Weight of seeds per spike	0.1579** 0.0720*	0.0063 0.0126	0.0046 0.0048	0.0096 0.0163	
1000-kernel weight	41.4063** 28.2812**	2.6574 3.3535	1.5148 0.4488	2.5674 6.8000	
Yield per plant	13.2227** 2.7109	1.8699 1.3242	1.8725 1.0820	1.4968 2.2172	

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

TABLE 35

Mean squares from the analysis of variance of 5 x 5 F₂ diallel net for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading, span	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
<i>a</i>	4	68.0938** 117.0937**	73.1250 138.1719**	4.0957 4.5820	3510.5000** 4245.5000**	5.8467 26.0713**	9.0909** 0.7852*	192.3750** 190.9219*	0.4730** 0.2159**	124.1875** 84.8135**	39.6543** 8.1191
<i>b</i>	10	6.3812** 12.0687**	61.2437 17.0125**	1.5824 5.8754	53.0000** 75.7000*	2.6473 3.2988	0.6227 0.8395	10.5312 68.5313	0.0188 0.0377	7.9812 10.0750	5.6172 3.9770
<i>b</i> ₁	1	36.7496 51.6675	79.5675 82.6875	0.0208 3.7408	6.4420 10.0833	1.0440 10.2491	0.2168 1.0195	3.8450 40.0176	0.0116 0.0698	0.0029 23.5447	5.3993 1.2118
<i>b</i> ₂	4	4.1406 4.2607*	44.9219 5.1094	0.9528 7.6094	59.7031 93.1250*	1.0060 3.9525	0.0506 0.9189	17.0752 75.6230	0.0249 0.0582	9.5039 9.9443	4.0752 1.6973
<i>b</i> ₃	5	2.1000** 10.3750**	70.6500* 13.4250**	2.3992 4.9156	56.9000** 74.6125*	4.2852* 1.3898	1.1625 0.7453	6.6250 68.5625	0.0156 0.0149	8.3625 7.5000	6.8937* 6.3586**
<i>c</i>	4	2.2541 1.1625	71.7542 0.5542	0.5375 2.0292	239.1536** 141.6374**	2.8807 1.7982	0.4980 0.1374	8.5938 93.4017	0.0072 0.0091	2.2230 1.3426	6.1870 1.2746
<i>d</i>	6	0.4972 0.4403	56.6431 1.3101	0.8014 0.8208	75.9351** 44.5118*	0.9563 1.2493	0.8108* 0.3691	2.7512 83.4116	0.0180 0.0178	6.0919 1.3408	5.2380 4.5601
Blocks x <i>a</i>	8	0.6094 2.6172	35.5859 2.0547	1.2484 5.3865	22.0469 59.4609	1.7603 3.1372	0.7969 1.4517	8.4609 30.6875	0.0289 0.0298	14.6484 7.3843	3.1318 12.6904
Blocks x <i>b</i>	20	0.8375 1.2875	42.0594 3.4312	0.8220 3.5931*	14.4500 24.2156	2.9328 2.8902	0.6866 0.5960	12.5031 67.5125	0.0395 0.0373	7.5344 9.5207	4.9216 3.4434
Blocks x <i>b</i> ₁	2	4.4151 7.9850	17.8050 19.1850	1.7017 3.0817	30.5184 181.8318	3.0592 30.4552	1.7195 0.1034	63.1927 34.0421	0.0729 0.1419	8.1275 51.5334	5.6767 10.2759
Blocks x <i>b</i> ₂	8	1.2927 1.0347	23.4004 4.0889	1.2711 5.8376	22.0747 18.0625	5.5184 2.8100	0.8450 0.9053	15.7554 53.9883	0.0651 0.0589	11.1401 10.5664	9.3918 6.4728
Blocks x <i>b</i> ₃	10	0.1875 0.9437	63.5938 1.6625	0.4566 2.2668	8.3312 10.0437	1.1445 0.4828	0.5141 0.4555	6.0937 88.4437	0.0196 0.0133	5.3578 5.4691	1.8984 0.6773
Blocks x <i>c</i>	8	0.9041 0.7812	71.3666 0.8979	0.4500 1.4104	9.2411 3.1023	1.2472 1.5910	0.2572 0.4212	4.8894 60.4627	0.0130 0.0084	3.9115 1.1626	3.0324 2.6685
Blocks x <i>d</i>	12	0.4597 1.0944	57.7347 1.5056	0.5056 0.4000	9.1118 11.1003	1.4759 1.2712	0.2664 0.7791	5.7155 94.8401	0.0207 0.0262	5.9257 3.7547	5.5405 3.2056
Error	48	0.7161 1.5265	49.7818 2.2982	0.7520 2.7299	13.5133 23.3919	2.0922 2.3101	0.5275 0.7561	8.8636 67.0319	0.0286 0.0285	7.7141 6.3335	4.4923 4.7959

*Significant at 5% level
**Significant at 1% level

First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a+b+c+d). Each component has been tested against its own block interaction.

TABLE 36

Analysis of variance of $\bar{y}_i - \bar{y}$
from F_2 diallel set for ten characters at two locations.

Character	Block M.S.	Inty M.S.	Error M.S.
Onset-of-heading	7.3143	0.7075	0.4378
	8.3204	2.4403	0.9515
Final heading	2.3424	0.7644	0.2210
	35.5027	5.2120	3.7671
Heading-span	0.0046	0.1472	0.2028
	8.1741	4.4720	2.0416
Plant height	10493.0312	150.1719	157.5547
	4912.7612	427.7612**	38.5703
Number of tillers per plant	1.2452	2.4152*	0.5635
	0.8319	0.5920	2.3435
Number of spikelets per spike	0.9566	0.0984	0.0807
	0.0373	0.1622	0.3598
Number of seeds per spike	636.7512	26.2899	19.7265
	189.8423	15.5951	6.5623
Weight of seeds per spike	0.0069	0.0022	0.0031
	0.0025	0.0004	0.0003
1000-kernel weight	313.4819	7.3413	1.9450
	2.6203	11.5522	18.5355
Yield per plant	61.0167	9.5905	3.0673
	12.4054	2.6444	2.7121

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level.

** Significant at 1% level.

TABLE 37

Estimates of second degree statistics parameters
for ten characters from F_2 diallel set at two locations.

Character	V_{GJJ}	V_{GJJ}	V_{GJJ}	V_{GJJ}	$(M_{L1} - M_{L2})^2$
Onset-of-heading	15.0600	5.8158	2.2734	3.3381	1.9600
	15.7002	7.6168	30.9072	5.9146	2.7759
Final heading	16.9668	7.2016	3.1475	4.3006	1.5891
	27.1514	11.1402	4.6084	7.4500	4.4100
Heading-span	0.5099	0.2362	0.1367	0.4033	0.0011
	3.6100	0.6751	0.1528	1.1320	0.1995
Plant height	486.7784	235.7205	117.0059	125.6615	0.3456
	518.4434	226.4807	141.3420	154.1107	0.5377
Number of tillers per plant	1.4343	0.5030	0.1948	0.6359	0.0557
	5.4749	2.1069	0.9158	1.4656	0.5465
Number of spikelets per spike	1.2203	0.6072	0.3030	0.4072	0.0115
	0.5749	0.4241	0.3264	0.4663	0.0543
Number of seeds per spike	28.9930	12.8064	6.4111	8.1627	0.2050
	12.2275	5.6326	3.4180	4.9113	0.2781
Weight of seeds per spike	0.0384	0.0241	0.0158	0.0189	0.0006
	0.0360	0.0133	0.0072	0.0135	0.0037
1000-kernel weight	16.7744	7.8586	4.1396	5.4666	0.6001
	13.1670	5.6221	2.8271	4.5039	1.2557
Yield per plant	5.4558	2.4023	1.3221	2.2580	0.4412
	0.6875	0.4078	0.2711	0.9338	0.0646

First reading under each column refers to Ellerslie and the second to Parkland.

additive gene effects, is relatively more important than SCA, which is due to non-additive gene effects, as far as selection on the basis of these characters is concerned. (3) The significance of SCA variances implies that hybrids yield much less than would be expected on the basis of the GCA's of their parents. This suggests that character instability of a hybrid is largely due to high SCA variances associated with its parents.

Diallel cross analysis

The results of the analysis of variance performed after Hayman (1954a) on the F_2 diallel table are given in Table 35. The presence of additive gene effects is shown by significant a 's for onset-of-heading, plant height, number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight at both locations; also for yield per plant at Ellerslie and final heading and number of tillers per plant at Parkland. Significant additive gene effects for these characters suggest substantial differences among the parental lines used. Significant b 's for onset-of-heading, final heading and plant height shows that dominance is present while significant b_2 's indicate some asymmetry of loci exhibiting dominance for these characters, suggesting that some parents contain more dominant alleles than others. Significant b_3 's for onset-of-heading, final heading, plant height and yield per plant at both locations, and for number of tillers per plant at Ellerslie, imply that specific combining ability for these characters is comparatively more important than general combining ability when a pedigree selection procedure is followed in a breeding programme (Mather and Jinks, 1971).

TABLE 30

Estimates of genetic components of variation and their standard errors from P₂ diallel set for ten characters at two locations.

Character	D	F	H ₁	H ₂	H ₃	H ₄	E
Onset-of-heading	14.6708 ± 0.2067**	6.4457 ± 0.5162**	4.4673 ± 0.5581**	3.7801 ± 0.5062**	7.6875 ± 0.3418**	0.2391 ± 0.0644**	
	15.1911 ± 0.6740**	0.3223 ± 1.6036	7.5679 ± 1.0502**	7.0214 ± 1.0509**	10.6973 ± 1.1146**	0.5091 ± 0.2752	
Final heading	16.7506 ± 0.3746**	4.0680 ± 0.9356**	4.0009 ± 1.0115**	4.1802 ± 0.9173**	6.2127 ± 0.6194**	0.2161 ± 0.1529	
	20.3075 ± 0.5316**	8.8221 ± 1.3243**	10.4043 ± 1.4339**	9.8386 ± 1.3006**	17.1511 ± 0.8781**	0.7639 ± 0.2186**	
Heading-span	0.3381 ± 0.1606*	-0.0677 ± 0.4012	0.5230 ± 0.4337	0.5534 ± 0.3934	-0.1560 ± 0.2656	0.2407 ± 0.0656**	
	2.7012 ± 0.7337**	3.4300 ± 1.8327	3.0730 ± 1.9014	2.6971 ± 1.7971	0.2157 ± 1.2133	0.9100 ± 0.3995**	
Plant height	482.2761 ± 5.3403**	25.2691 ± 13.1401	35.6425 ± 14.4221**	26.4261 ± 13.0810*	-1.4982 ± 8.8316	4.4003 ± 2.1802*	
	510.7024 ± 11.6837**	-38.3252 ± 28.6062	48.9409 ± 31.0130	34.9049 ± 28.1292	-2.6030 ± 18.9913	7.7409 ± 4.6882	
Number of tillers per plant	0.7373 ± 0.1694**	0.0199 ± 0.4212	0.1536 ± 0.4575	0.3705 ± 0.4150	-0.2232 ± 0.2802	0.6970 ± 0.0692**	
	4.7055 ± 0.1993**	1.5989 ± 0.4978**	0.9894 ± 0.5382	0.6605 ± 0.4681	1.6941 ± 0.3286**	0.7694 ± 0.0814**	
Number of spikelets per spike	1.0529 ± 0.0515**	-0.1027 ± 0.1287	-0.0278 ± 0.1391	0.0658 ± 0.1262	-0.0660 ± 0.0852	0.1753 ± 0.0210**	
	0.3233 ± 0.1134**	-0.0849 ± 0.2934**	0.0036 ± 0.3064	0.0562 ± 0.2779	0.0565 ± 0.1876	0.2536 ± 0.0403**	
Number of seeds per spike	20.0475 ± 1.1122**	3.2297 ± 2.7783	2.7517 ± 3.0037	1.1052 ± 2.7444	-1.0691 ± 1.8394	2.9505 ± 0.4541**	
	8.7961 ± 1.0111**	-2.1931 ± 2.5257	0.4207 ± 2.7306	-0.8894 ± 2.4767	-1.0627 ± 1.6721	0.0095 ± 0.0021**	
Weight of seeds per spike	0.0208 ± 0.0019**	-0.0113 ± 0.0047**	-0.0073 ± 0.0050	0.0065 ± 0.0046	-0.0036 ± 0.0031	0.0095 ± 0.0008**	
	0.3266 ± 0.0052**	0.0075 ± 0.0130	0.0121 ± 0.0140	0.0067 ± 0.0127	0.0088 ± 0.0086	0.0095 ± 0.0021**	
1000-kernel weight	14.2071 ± 0.8036**	-0.9663 ± 2.0075	0.5315 ± 2.1703	0.1733 ± 1.9685	1.6424 ± 1.3290	2.5673 ± 0.3281**	
	11.0585 ± 1.3289**	1.3155 ± 3.3195	3.2122 ± 3.5888	2.4900 ± 3.2551	3.6732 ± 2.1976	2.1085 ± 0.5425**	
Yield per plant	3.9500 ± 0.7207**	-0.8142 ± 1.8203*	0.6660 ± 1.9679	0.7492 ± 1.7049	0.1937 ± 1.2051	1.4970 ± 0.2975**	
	-0.7106 ± 0.3310*	-1.7740 ± 0.6287*	-1.1636 ± 0.8960	-0.5453 ± 0.0126	-0.7644 ± 0.5487	1.5982 ± 0.1354**	

First reading under each column refers to Ellerslie and second to Parkland.
 * Significant at 5% level
 ** Significant at 1% level

TABLE 39

Proportional estimates of genetic parameters
for ten characters from F₂ diallel set at two locations.

Character	$(H_1/D)^{1/2}$	$(H_2/4H_1)$	$\frac{[(4DH_1)^{1/2} + F]}{[(4DH_1)^{1/2} - F]}$	$r^2 (Y_r/W_r + V_r)$	$\frac{h^2}{H_2}$	(Heritability)
Onset-of-heading	0.5501*	0.2116*	2.3175*	0.9658	2.0336*	1.0751
	0.7058*	0.2316*	1.0305†	0.8792	1.5257*	0.6206
Final heading	0.5354*	0.2177*	1.7451*	0.9906	1.4862*	0.9545
	0.6279*	0.2364*	1.7279*	0.9550	1.7432*	0.8596
Heading-span	1.3249	0.2330	0.8596	0.9362	-0.2018	0.1689
	1.0666	0.1706	3.9415	0.2426	0.1028	0.4513
Plant height	0.2719*	0.1854*	1.2131†	0.7522	-0.0566	0.9443
	0.3096	0.1783	0.7838	0.0827	-0.0803	0.8120
Number of tillers per plant	0.4565	0.6029	1.0610	-0.1501	-0.6023	0.2015
	0.4585	0.1669	2.1772	0.9489	2.5648	0.6559
Number of spikelets per spike	0.1626	-0.5913	0.3040	0.8604	-1.0027	0.5515
	0.5264	0.1569	-0.4273	-0.1745	1.0043	0.1425
Number of seeds per spike	0.3250	0.1004	1.4714	0.0765	-0.9664	0.6969
	0.2187	-0.5285	0.2739	-0.1187	1.2174	0.7683
Weight of seeds per spike	0.5034	0.2241	-0.0379	-0.2629	0.5555	0.3171
	0.6752	0.1272	1.5290	-0.3126	1.4330	0.3843
1000-kernel weight	0.1934	0.0815	0.7009	-0.5825	-9.4800	0.5469
	0.5390	0.1938	1.2481	-0.8244	1.4752	0.5170
Yield per plant	0.4102	0.2812	0.5991	0.1919	0.2585	0.3464
	1.2795	-0.1172	0.0125	-0.4069	1.4016	-0.1129

First reading under each column refers to Eilerslie and second to Parkland.

*Genetic components of variation for the characters significantly different from zero at $P < 0.05$

†Components D and H₁ significant, F non-significant ($P > 0.05$).

In regard to the testing of the assumptions underlying the analysis, significant c 's for plant height at each of the two locations indicate that there are reciprocal differences for this character. The results of a test of other assumptions, by the analysis of variance of $W_p - V_p$ differences are given in Table 36. Except for plant height at Parkland and number of tillers per plant at Ellerslie, the $W_p - V_p$ differences were homogeneous and therefore these other assumptions were generally not invalidated by the data. Two exceptions (for plant height and number of tillers per plant) will be considered later.

Estimates of second degree statistics and components of genetic variation derived from the analysis of F_2 diallel table after replacement of off-the-diagonal cells with their corresponding common means, are given in Tables 37 and 38. In Table 38, component significances are tested with 25 D.F. (35 statistics provided by Table 37, with 10 constants fitted to them). Proportional values of the genetic parameters calculated from Table 38 are given in Table 39, which shows the over-all genetic situation with regard to the inheritance of each character. The results of Tables 38 and 39 together with W_p, V_p graphs and standardized deviation graphs of Y_p and $(W_p + V_p)$ are discussed under each character.

All components of variation for onset-of-heading (Table 38) except F and E at Parkland were significant. The mean degree of dominance (0.55 at Ellerslie and 0.75 at Parkland) indicates that the character is partially dominant at both locations. This is also shown by the regression line in the W_p, V_p graph (Figure 21) which intersects the limiting parabola

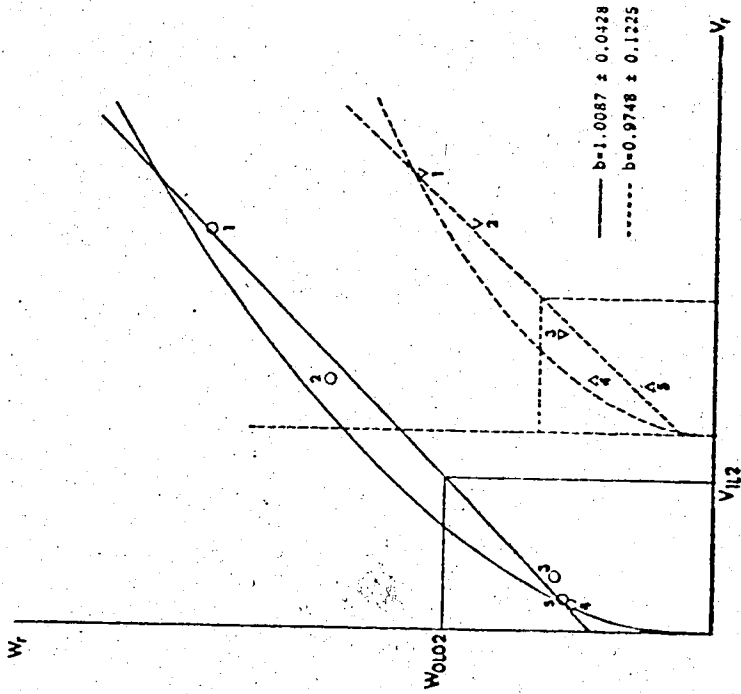


Figure 21. W_p, V_p graph for onset-of-heading

from F_2 diallel set.

— $\circ = W_p, V_p$ intercepts at Ellerslie

--- $\Delta = W_p, V_p$ intercepts at Parkland

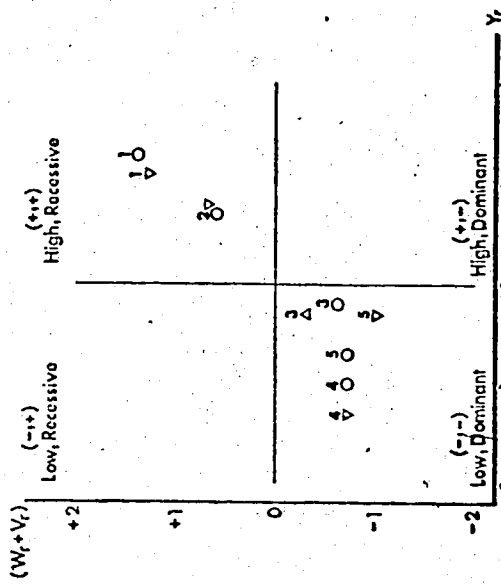


Figure 22. Standardized deviation graph of $[Y_p]$ and

$[W_p + V_p]$ for onset-of-heading from F_2 diallel set.

$\circ = Y_p, [W_p + V_p]$ intercepts at Ellerslie

$\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

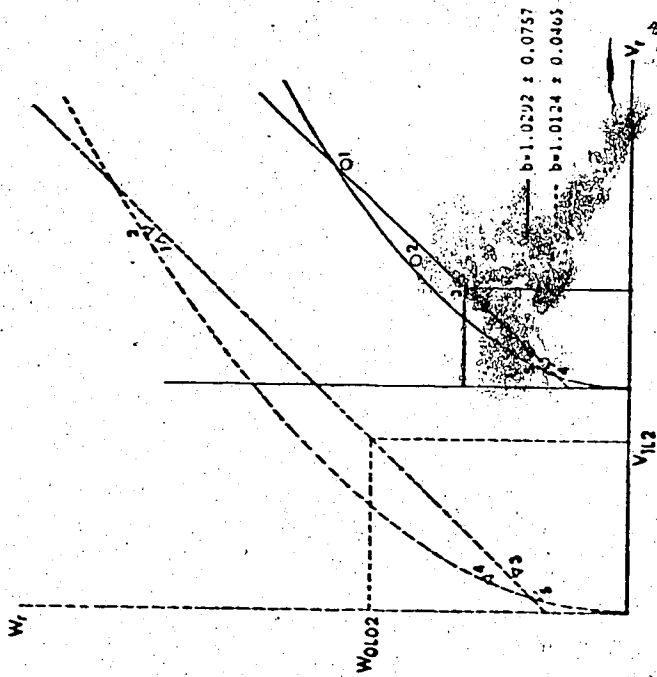


Figure 23. W_r, V_r graph for final heading from F2 diallel set.

— $\circ = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

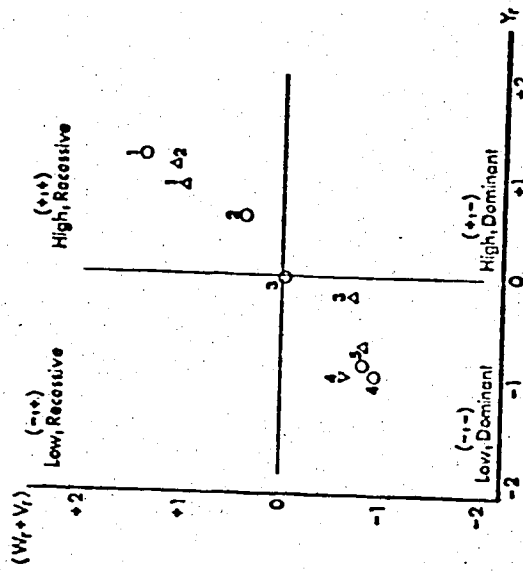


Figure 24. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for final heading from F2 diallel set.

$\circ = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

above the origin. The proportion of positive to negative alleles in the parents at loci exhibiting dominance is approximately 0.25, indicating equal proportions at both locations. The proportion of dominant to recessive genes in the parents is 2.3 and 1.03 for Ellerslie and Parkland, suggesting a preponderance of dominant genes in the parents. Figure 21 shows that Marquis is the highly recessive parent at both locations, as it lies farthest from the point of origin of the regression line. Ciano at Ellerslie and Inia at Parkland rank as the two most dominant parents because of their nearness to the point of origin of the regression line. The coefficient of correlation between parental order of dominance and parental measurements is 0.96 at Ellerslie and 0.87 at Parkland suggesting that most of the negative genes (for early maturing) are dominant. The distribution of parents with respect to order of dominance is shown in standardized deviation graph of Figure 22. Marquis and Chinook at both locations fall into the (+,+) quadrant indicating that they contain mostly recessive genes responsible for lateness while Khush-hal, Ciano and Inia fall into the (-,-) quadrant and are therefore early heading dominant parents. The number of groups of genes controlling onset-of-heading has been estimated as 2.03 for Ellerslie and 1.52 for Parkland indicating that at least two groups of genes exhibiting dominance control the onset-of-heading. The heritability estimates of 107.51% and 62.06% show that the character is highly heritable but with low stability under different environments.

The results of the analysis for final heading (Tables 38, 39; Figures 23, 24) and heading-span (Tables 38, 39; Figures 25, 26) are subject

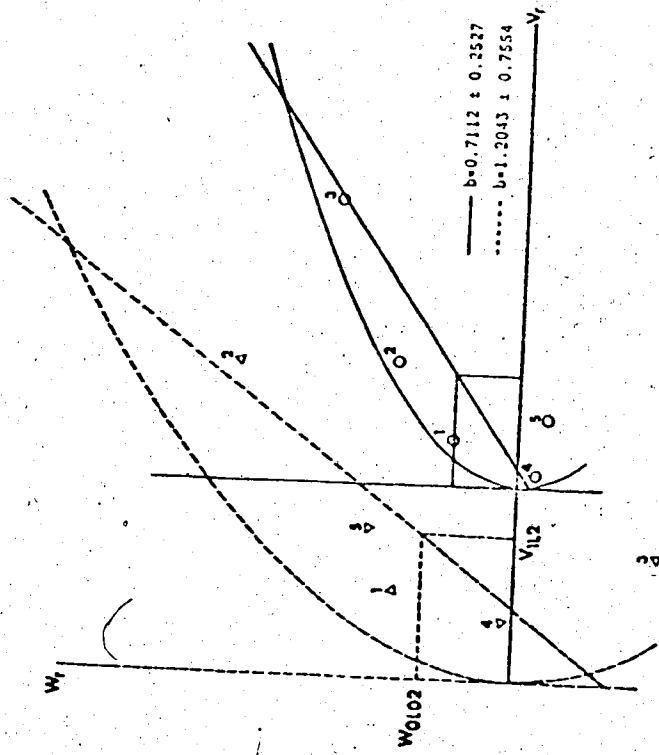


Figure 25. W_p, V_p graph for heading-span from F2 diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

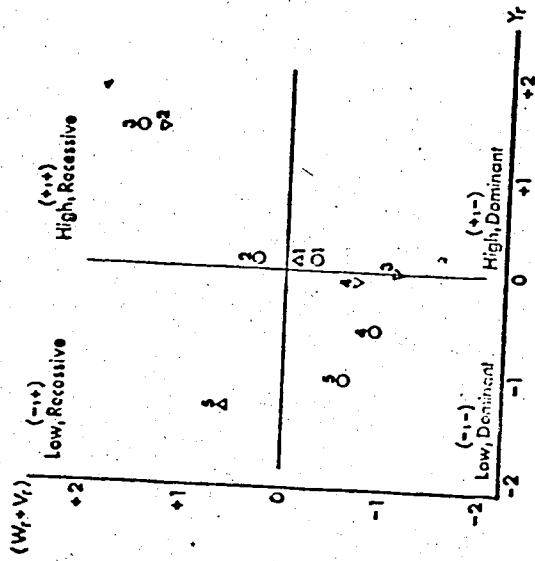


Figure 26. Standardized deviation graph

of $[Y_p]$ and $[W_p + V_p]$ for heading-span from F2 diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie

$\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

to the same kind of interpretations as for onset-of-heading.

For plant height, the components of variation, D , H_1 , H_2 and E were significant for Ellerslie but none except D were significant at Parkland. Heterogeneity of W_p - V_p values (Table 36) implies either non-allelic interaction, multiple allelism or correlated gene distribution. In the case of correlated gene distribution, the W_p , V_p curve is convex upwards and the mean degree of dominance is seriously inflated, giving an impression of apparent over-dominance (Hayman, 1954b) in a situation where, in fact, partial dominance exists. In the case of multiple allelism, the effects are extremely complicated. Models to explain the consequences in terms of W_p , V_p graphs, are pending. It might show spurious dominance (Hayman, 1954b) by scattering the W_p , V_p points and thus causing their mean (V_{1L2} , W_{OL02}) to lie inside, and not on the limiting parabola. Non-allelic interaction of the complementary type distorts the (W_p , V_p) graph, inflates the $(H_1 + D)^{1/2}$ and depresses (h^2/H_2) , but has very little effect on the estimator of gene frequency. A duplicate type of interaction depresses (h^2/H_2) by increasing the proportion of dominants, but does not alter $(H_1 + D)^{1/2}$, $H_2/4H_1$ and the W_p , V_p graph.

Considering the various effects of the three above-mentioned conditions, and examining the W_p , V_p graph for plant height at Parkland (Figure 27) we come to the conclusion that there is actually no non-validity of any of the above-mentioned hypotheses.. This is because the regression of W_p upon V_p is not significantly different from one, the array W_p , V_p intercepts do not show any convexity upwards or downwards

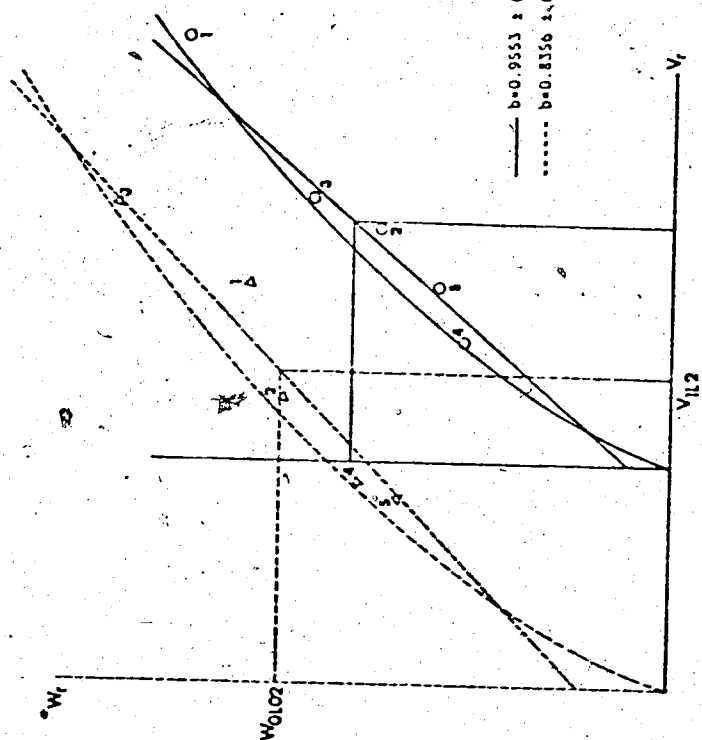


Figure 27. W_{Y_1} , V_{Y_1} graph for plant height from F_2 diallel set.

— $O = W_{Y_1}$, V_{Y_1} intercepts at Ellerslie
 --- $\Delta = W_{Y_1}$, V_{Y_1} intercepts at Parkland

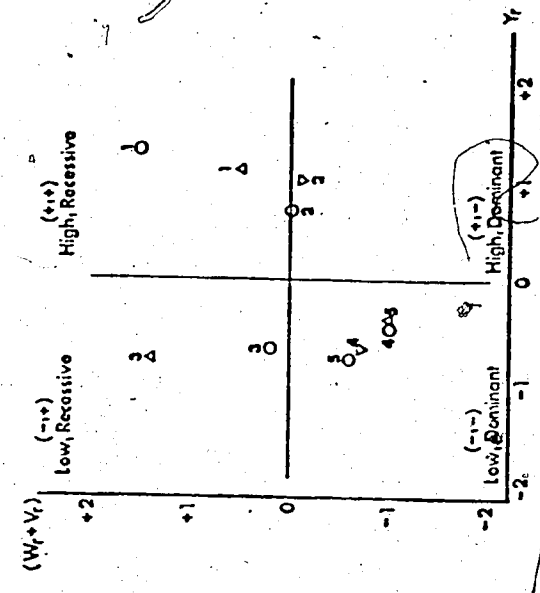


Figure 28. Standardized deviation graph of $[Y_{Y_1}]$ and $[W_{Y_1} + V_{Y_1}]$ for plant height from F_2 diallel set.

$\phi = Y_{Y_1}$, $[W_{Y_1} + V_{Y_1}]$ intercepts at Ellerslie
 $\Delta = Y_{Y_1}$, $[W_{Y_1} + V_{Y_1}]$ intercepts at Parkland

and there are no serious effects on the estimates of genetic parameters (Table 39). Our conclusion is supported by the fact that all the estimates of genetic components of variation at Parkland except D are non-significant (Table 38). The only reason we might give for the heterogeneity of $W_p - V_p$ over the arrays is a strong environmental effect.

At Ellerslie, plant height is inherited as a partially dominant trait since the mean degree of dominance is 0.27 (See also Figure 27). The proportion of positive to negative alleles at loci exhibiting dominance is 0.18 indicating asymmetry, while the proportion of dominant to recessive genes in the parents is 1.2 (close to equality). The coefficient of correlation between the parental order of dominance and parental measurements is 0.75 at Ellerslie and 0.08 at Parkland, indicating that the genes contributing towards shortness are mostly dominant. With respect to parental order of dominance (Figure 27 and 28) Marquis rates as the highly recessive parent for tallness at Ellerslie and Khush-hal likewise at Parkland. Ciano ranks as the most dominant parent for shortness at Ellerslie and similarly Inia at Parkland. Examination of Figure 28 reveals that though Marquis and Khush-hal rank as the highly recessive parents, Khush-hal nevertheless contributes towards reduced expression of the character (-,+ quadrant) as compared to Marquis (+,+ quadrant). Ciano and Inia rank as the most dominant parents for shortness because of their position in the (-,-) quadrant. Chinook, contributing towards tallness, has recessive and dominant genes in equal proportions. The character has high heritability (94.43% at Ellerslie and 81.20% at Parkland) and thus seems to be little affected by environmental conditions.

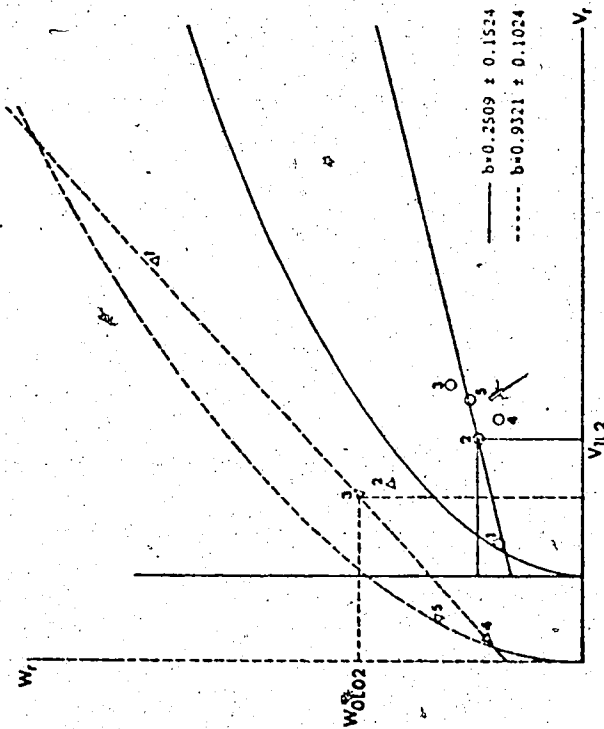


Figure 29. W_1, V_1 graph for number of tillers per plant from F_2 diallel set.

— $o = W_1, V_1$ intercepts at Ellerslie
 --- $\Delta = W_1, V_1$ intercepts at Parkland

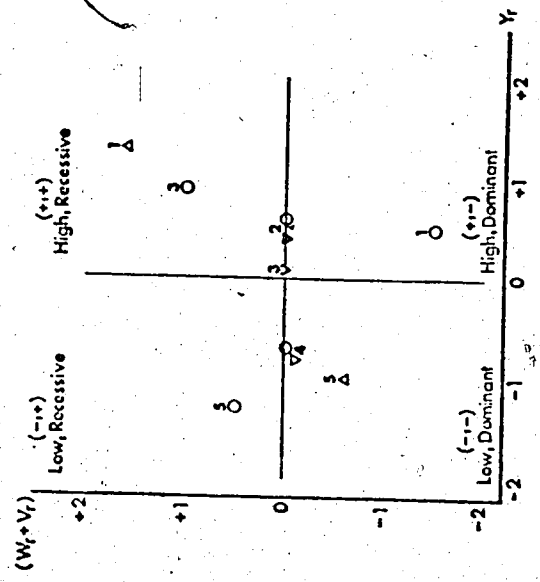


Figure 30. Standard deviation graph

of $[Y_1]$ and $[W_1 + V_1]$ for number of tillers per plant from F_2 diallel set.

$o = Y_1, [W_1 + V_1]$ intercepts at Ellerslie

$\Delta = Y_1, [W_1 + V_1]$ intercepts at Parkland

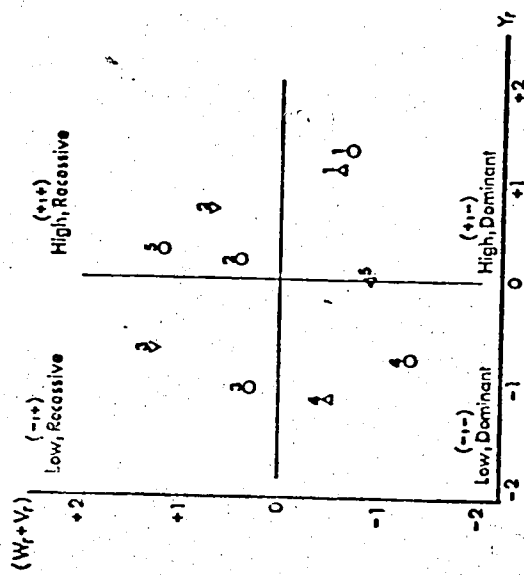


Figure 32. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of spikelets per spike from F_2 diallel set.

o = $Y_p, [W_p + V_p]$ intercepts at Ellerslie
 Δ = $Y_p, [W_p + V_p]$ intercepts at Parkland

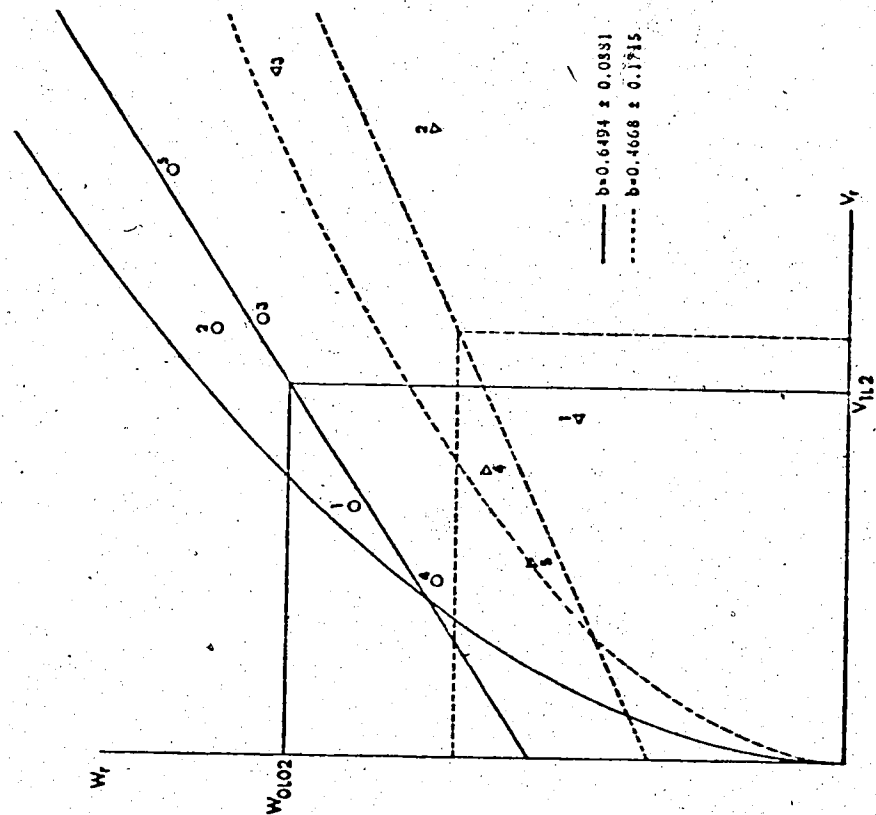


Figure 31. W_p, V_p graph for number of spikelets per spike from F_2 diallel set.
 — o = W_p, V_p intercepts at Ellerslie
 --- Δ = W_p, V_p intercepts at Parkland

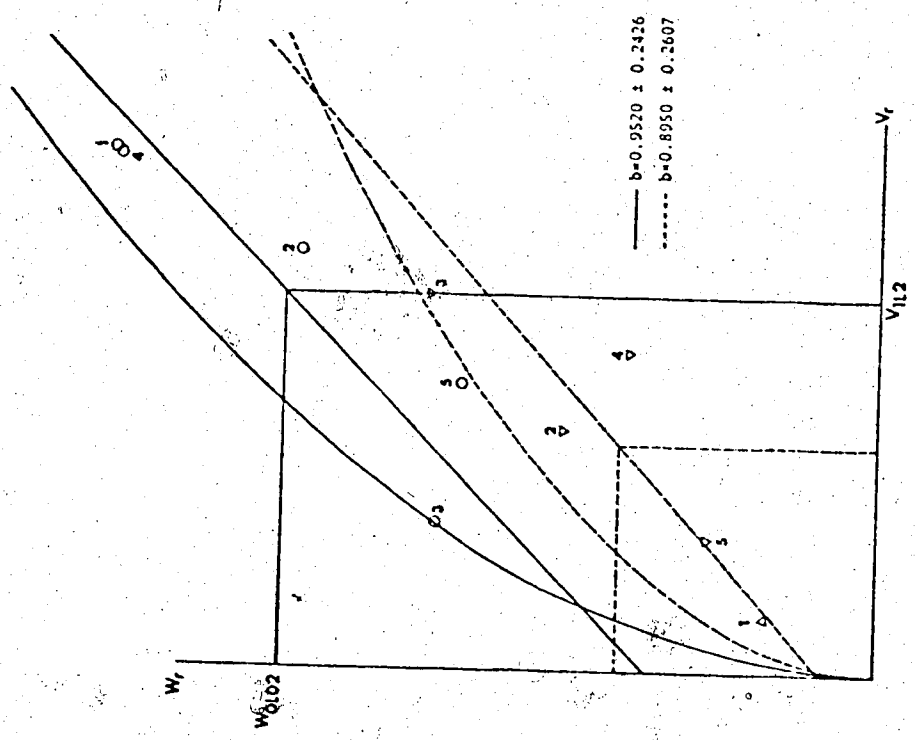


Figure 33. W_p, V_p graph for number of seeds per spike from F_2 diallel set.
 — $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

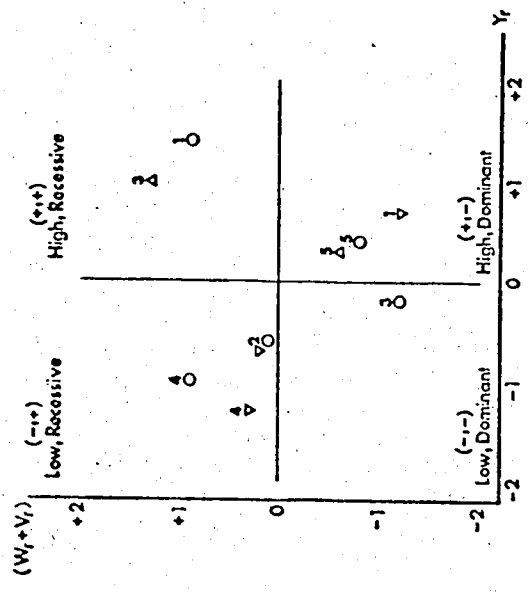


Figure 34. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of seeds per spike from F_2 diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

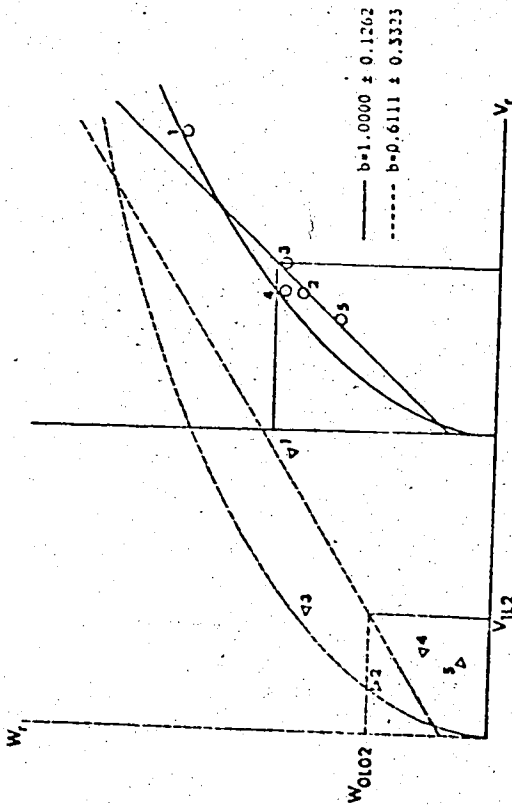


Figure 35. W_r, V_r graph for weight of seeds per spike from F_2 diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie
 --- $\Delta = W_r, V_r$ intercepts at Parkland

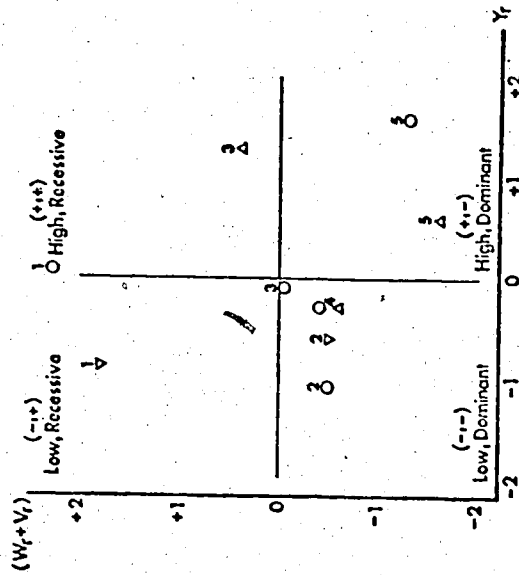


Figure 36. Standardized deviation graph

of $[Y_r]$ and $[W_r + V_r]$ for weight of seeds per spike from F_2 diallel set.
 $o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

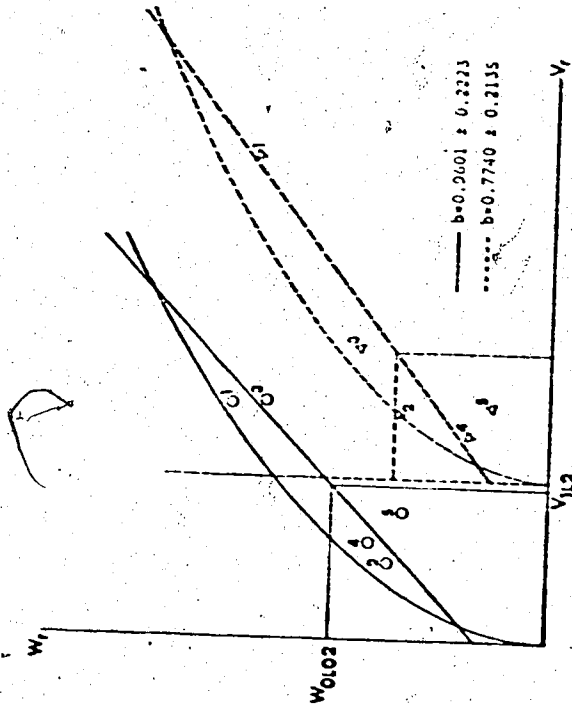


Figure 37. W_p, V_p graph for 1000-kernel weight from F₂ diallel set.

- $o = W_p, V_p$ intercepts at Ellerslie
- $\Delta = W_p, V_p$ intercepts at Parkland

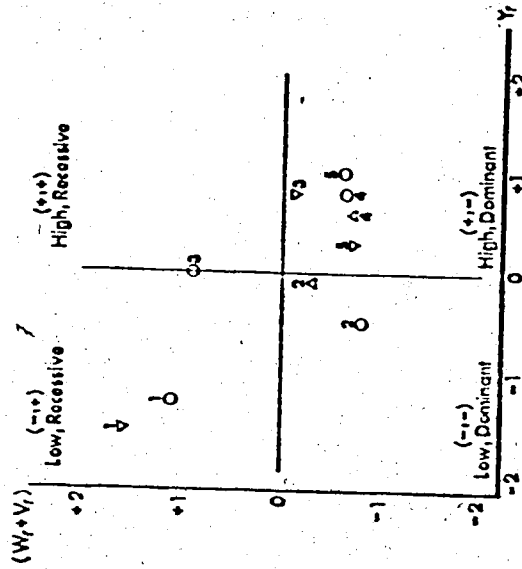


Figure 38. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for 1000-kernel weight from F₂ diallel set.

- $o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
- $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

Number of tillers per plant showed heterogeneity of $W_p - V_p$ values (Table 36). Examination of the W_p, V_p graph (Figure 29) and a review of the effects of non-allelic gene interaction, multiple allelism and correlated gene distribution upon the analysis, reveals that none of these conditions invalidate the corresponding null hypotheses. Moreover, since at Ellerslie the environmental component of variation is highly significant and all other components of genetic variation but D non-significant, the environmental variation is the most probable reason for heterogeneity of $W_p - V_p$ values. Since the ratios (Table 39) expressing the mean degree of dominance, the proportion of alleles with positive and negative effects at loci exhibiting dominance, the proportion of dominant and recessive genes in the parents and the number of groups of genes controlling the character were based on parameters some of which were not significant (Table 38) their interpretation as well as the interpretation of the graphs is of little value.

The general features of the diallel analysis with respect to the interpretation of the results from Tables 38 and 39 for other yield components, viz., number of spikelets per spike (Figures 31, 32), number of seeds per spike (Figures 33, 34), weight of seeds per spike (Figures 35, 36) and 1000-kernel weight (Figures 37, 38) are the same. The conclusions drawn therefrom differ with respect to the relative position of the parents for their ranking order of dominance.

For yield per plant, only D and E components of variation

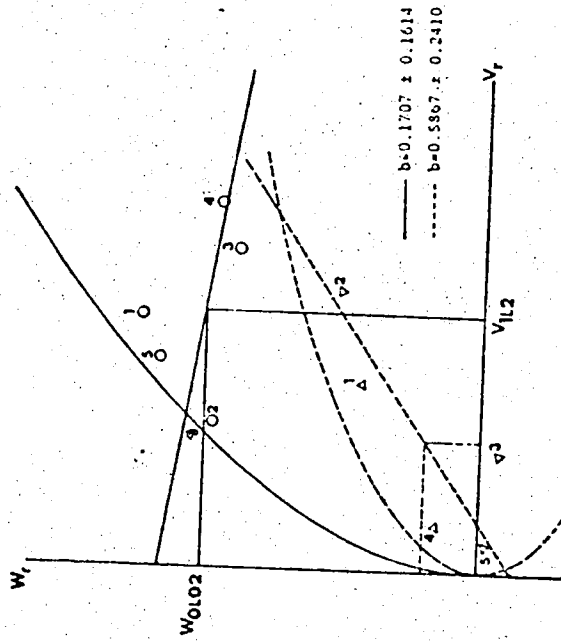


Figure 39. W_r, V_r graph for yield per plant from F_2 diallel set.

- $\circ = W_r, V_r$ intercepts at Ellerslie
- $\Delta = W_r, V_r$ intercepts at Parkland

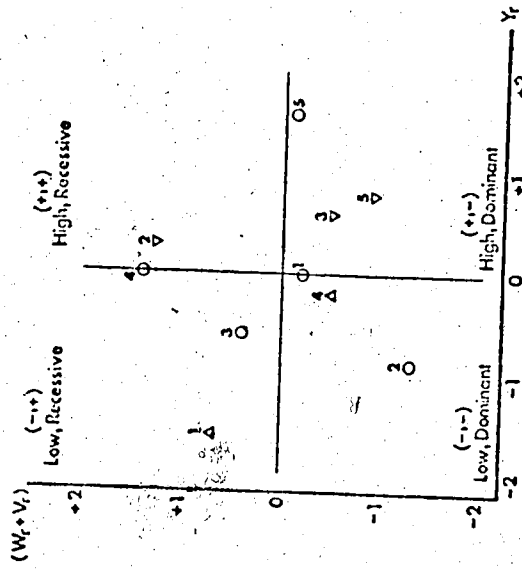


Figure 40. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for yield per plant from F_2 diallel set.

- $\circ = Y_r, [W_r + V_r]$ intercepts at Ellerslie
- $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

were significant at Ellerslie while D , F and E at Parkland. Because of non-significance of other components of variation, the interpretation of estimates of genetic parameters given in Table 39 would be meaningless.

The W_p , V_p and standardized deviation graphs are interesting in their absurdity. The location effect on yield is sufficiently drastic so that the regression line, though cutting the limiting parabola above its origin (apparent partial dominance) shows a negative slope. The latter (at Ellerslie) implies that for every increase in variance of the r th array, there is a proportional decrease in parent-offspring covariance of that array. The regression line, in this case, cuts the limiting parabola in such a way that the recessive and dominant W_p , V_p array intercepts are difficult to define. However Figure 39 suggests that Ciano may be regarded as the highly recessive and Chinook the most dominant parent. At Parkland, the regression of W_p upon V_p reveals over-dominance. Chinook may be classified as the highly recessive and Inia the most dominant parents. The standardized deviation graph of Figure 40 reveals that, except for Inia, the ranking order for dominance of the parents seems to be altered between locations. Marquis, the recessive parent, with low yielding capacity at Parkland ($-$, $+$ quadrant) becomes dominant and comparatively high yielding at Ellerslie ($+$, $-$ quadrant). Chinook, low yielding and dominant ($-$, $-$ quadrant) at Ellerslie, becomes recessive and high yielding ($+$, $+$ quadrant) at Parkland. A similar

situation exists with Ciano. The coefficient of correlation between the parental order of dominance and parental measurements is 0.19 at Ellerslie and -0.40 at Parkland. A positive but weak correlation at Ellerslie suggests however, that genes responsible for low yielding are mostly dominant, while the comparatively high negative correlation at Parkland indicates that the genes contributing toward increased yielding are mostly dominant. The estimates of heritability seem to be questionable because of the non-significance of relative components of genetic variation.

ANALYSIS OF BACKCROSS DATA

The expected mean of a pair of reciprocal backcrosses is the same as that of F_2 generation of the cross between the two parents provided the differential loci are independent in their action (Jinks, 1956). Therefore, assuming no non-allelic interaction, the expected statistics for the analysis of backcross family means in a diallel set are the same as those for F_2 family means.

In Appendix II there are eighty backcrosses including reciprocals. A complete diallel table for these backcrosses therefore requires an amalgamation of four backcrosses to compute the appropriate means for each of the off-diagonal cells in the diallel matrix. Using the same symbols as in Appendix II, and taking any two parents, the appropriate backcross combinations can be shown to be equivalent to the mean of the corresponding F_2 hybrid. Thus the mean of $M(M \times CH)$, $(M \times CH)M$, $CH(M \times CH)$ and $(M \times CH)CH$ means is equivalent to the $(M \times CH)F_2$ mean, while the mean of $M(CH \times M)$, $(CH \times M)M$, $CH(CH \times M)$ and $(CH \times M)CH$ means is equivalent to the mean of its reciprocal, i.e., $(CH \times M)F_2$ hybrid.

Denoting the parents Marquis, Chinook, Khush-hal, Ciano and Inia as 1, 2, 3, 4 and 5 the following two diallel tables (Tables 40, 41) may be constructed, the one by keeping the parents of rows as recurrent parents and the other by keeping the parents of columns as recurrent parents. The numbers in the brackets in Table 40 and Table 41 denote the F_1 hybrids while those outside the brackets denote the recurrent parents. From these two tables a complete diallel table can be constructed which will correspond statistically to the F_2 diallel table.

TABLE 40
Arrangement of backcrosses and reciprocals
in which the parents of rows are kept as recurrent parents.

	1	2	3	4	5
1.	11	11(12) + (12)11	11(13) + (13)11	11(14) + (14)11	11(15) + (15)11
2.	22(21) + (21)22	22	22(23) + (23)22	22(24) + (24)22	22(25) + (25)22
3.	33(31) + (31)33	33(32) + (32)33	33	33(34) + (34)33	33(35) + (35)33
4.	44(41) + (41)44	44(42) + (42)44	44(43) + (43)44	44	44(45) + (45)44
5.	55(51) + (51)55	55(52) + (52)55	55(53) + (53)55	55(54) + (54)55	55

TABLE 41
Arrangement of backcrosses and reciprocals
in which the parents of columns are kept as the recurrent parents.

	1	2	3	4	5
1.	11	22(12) + (12)22	33(13) + (13)33	44(14) + (14)44	55(15) + (15)55
2.	11(21) + (21)11	22	33(23) + (23)33	44(24) + (24)44	55(25) + (25)55
3.	11(31) + (31)11	22(32) + (32)22	33	44(34) + (34)44	55(35) + (35)55
4.	11(41) + (41)11	22(42) + (42)22	33(43) + (43)33	44	55(45) + (45)55
5.	11(51) + (51)11	22(52) + (52)22	33(53) + (53)33	44(54) + (54)44	55

and may therefore be used for the analysis of genetic components of variation as described by Jinks (1956). Thus, for example, if the entry $[11(12) + (12)11]$ above the main diagonal in Table 40 is denoted as x and the corresponding entry $[22(12) + (12)22]$ in Table 41 as y , then the corresponding element of the F_2 diallel table would be $1/2[1/2x + 1/2y] = 1/4(x + y)$. The entries in the remaining cells of the F_2 diallel table are obtained in the same way. Such a table may be called a *synthetic F_2 diallel table*.

Simple coefficients of correlation between the characters on the basis of the *synthetic complete F_2 diallel table* are given in Table 42. Onset-of-heading was positively correlated with final heading plant height, number of tillers per plant, number of spikelets per spike at both locations. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The correlations with heading-span and yield per plant at both locations and with weight of seeds per spike at Ellerslie were not significant. The correlations of final heading and heading- with other characters may be interpreted in the same way.

Plant height was positively correlated with number of tillers per plant, number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. No correlations were observed between plant height and yield per plant at either location or with number of seeds per spike at Parkland.

Number of tillers per plant was positively associated with

TABLE 42

Simple correlation coefficients between ten characters from backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917** 0.830**	0.214 -0.025	0.727** 0.714**	0.552** 0.565**	0.592** 0.498**	0.327** 0.291**	-0.209 -0.289*	-0.607** -0.627**	-0.118 -0.111
2. Final heading	-	0.576** 0.532**	0.818** 0.720**	0.395** 0.671**	0.598** 0.550**	0.292** 0.254*	-0.305** -0.332**	-0.679** -0.631**	-0.179 0.096
3. Heading-span	-	-	0.507** 0.211	0.270* 0.341**	0.218 0.233*	-0.009 0.027	-0.362* -0.162	-0.411** -0.199	-0.233* 0.325**
4. Plant height	-	-	-	0.458** 0.538**	0.710** 0.650**	0.02* 0.169	-0.303** -0.470**	-0.638** -0.708**	0.006 -0.106
5. Number of tillers per plant	-	-	-	-	0.305** 0.411**	-0.041 0.216	-0.132 -0.289*	-0.094 -0.531**	0.491** 0.173
6. Number of spikelets per spike	-	-	-	-	-	0.604** 0.651**	0.115 0.105	-0.405** -0.460**	0.149 0.212
7. Number of seeds per spike	-	-	-	-	-	-	0.621** 0.600**	-0.160 -0.212	0.116 0.236*
8. Weight of seeds per spike	-	-	-	-	-	-	-	0.638** 0.644**	0.365** 0.444**
9. 1000-kernel weight	-	-	-	-	-	-	-	-	0.400** 0.333**
10. Yield per plant	-	-	-	-	-	-	-	-	-

First reading under each column refers to Elloralle and second to Parkland.
 * Significant at 5% level
 ** Significant at 1% level

number of spikelets per spike at both locations and with yield per plant at Ellerslie. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at Parkland. There was no correlation with number of seeds per spike at either location or with weight of seeds per spike and 1000-kernel weight at Ellerslie and yield per plant at Parkland. The correlations of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight respectively with other characters may be interpreted in the same way.

Yield per plant was positively correlated with 1000-kernel weight and weight of seeds per spike at both locations, with number of seeds per spike and heading-span at Parkland and with number of tillers per plant at Ellerslie. It was negatively correlated with heading-span at Ellerslie. Correlations with onset-of-heading, final heading and plant height at both locations were not significant.

The results of the factor analysis as the factor loadings of the varimax-rotated five factor matrix are given in Table 43. Approximately 93% of the total variability at both locations was explained by these factors.

The first principal factor was termed *lateness* because of its highest loadings for onset-of-heading and final heading at both locations. This factor negatively contributed towards weight of seeds per spike, 1000-kernel weight and yield per plant at both locations thus confirming the inverse relationship between time of maturity and yield as observed for F_1 and F_2 diallel data. Plant height at Ellerslie and number of tillers per plant contributed proportionately more towards

TABLE 43

Varimax rotated factor matrix for ten characters
from backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.986 0.913	0.958 0.721	0.154 0.561	0.023 0.061	0.210 -0.118	-0.005 -0.248
Final heading	0.982 0.885	0.869 0.709	0.135 0.532	0.026 0.024	0.252 -0.009	0.380 0.314
Heading-span	0.987 0.965	0.182 0.171	-0.040 0.109	-0.016 -0.038	0.180 0.139	0.959 0.951
Plant height	0.868 0.915	0.621 0.397	0.216 0.847	0.252 -0.086	0.501 -0.163	0.348 0.074
Number of tillers per plant	0.893 0.859	0.380 0.883	-0.139 0.152	0.812 0.054	0.009 0.027	0.243 0.227
Number of spikelets per spike	0.868 0.914	0.415 0.173	0.659 0.768	0.261 0.511	0.426 0.068	0.105 0.169
Number of seeds per spike	0.924 0.981	0.205 0.168	0.937 0.211	-0.048 0.952	-0.024 0.029	-0.004 0.012
Weight of seeds per spike	0.984 0.959	-0.188 -0.274	0.702 -0.266	0.103 0.732	-0.642 0.498	-0.184 -0.169
1000-kernel weight	0.911 0.892	-0.473 -0.489	-0.003 -0.502	0.232 -0.012	-0.768 0.601	-0.208 -0.199
Yield per plant	0.898 0.904	-0.182 0.092	0.193 0.021	0.860 0.167	-0.123 0.899	-0.196 0.244
Percent of total Variability explained	92.910 91.870	29.523 23.700	19.529 23.085	16.343 19.029	15.894 14.832	13.714 12.771

First reading under each column refers to Eilerslie and second to Parkland.

lateness than either the number of spikelets per spike or number of seeds per spike at both locations. *Lateness* explained 29% and 23% of the total variation present in the data for Ellerslie and Parkland respectively.

Number of spikelets per spike, number of seeds per spike and weight of seeds per spike could be grouped into the second factor *yielding ability* at Ellerslie, because of their higher contribution to this factor. At Parkland, this factor was termed *height* since it carried maximum loading for that character. Both the factors explained 19% and 23% variability in the data at respective locations. At Ellerslie, other yield components such as number of tillers per plant and 1000-kernel weight negatively contributed towards *yielding ability* confirming the results of Table 42. At Parkland, onset-of-heading, final heading and number of spikelets per spike had proportionately higher contributions towards *height* while weight of seeds per spike and 1000-kernel weight turned out to be the negative contributors to this factor.

Yield at Ellerslie and *seeds per spike* at Parkland were classified as the third principal factor which explained 16% and 19% of the total variability for respective locations. At Ellerslie, only number of tillers per plant contributed appreciably towards *yield*, otherwise the contributions of number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight were comparatively low. The factor *lateness* also made a very poor contribution towards *yield*. At Parkland, number of spikelets per spike

and weight of seeds per spike were the major contributors towards *seeds per spike*. Plant height and 1000-kernel weight were negatively affected by this factor.

The term *low yield* was selected for the fourth factor at Ellerslie because of the negative loadings for number of seeds per spike, weight of seeds per spike, 1000-kernel weight, yield per plant and the fact that the lowest positive value was found for number of tillers per plant. At Parkland the alternative fourth principal factor was chosen as *high yield* as it carried the highest loading for yield per plant and positive loadings for 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant. Onset-of-heading and final heading contributed positively toward *low yield* and negatively toward *high yield*. Plant height revealed an inverse relationship with respect to its contribution towards the yield factor at both locations.

The fifth principal factor, classified as *heading period*, explained 13% of the total variation at both locations. It carried maximum loadings for heading-span at both locations. The contribution of yield and its components, viz., number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight towards *heading period* was either very low or negative at both locations, indicating an inverse relationship of yield with heading period.

The negative contribution of initial heading towards this factor indicates that earlier heading entries take a longer period to complete

TABLE 44

Estimates of general combining ability of five parental lines used in backcross diallelset for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	1.8350 1.9650	1.1600 1.4316	-0.1316 -0.0350	-1.5753 -2.4650	-1.2899 -0.8766
Final heading	2.3333 1.8967	1.4667 2.1800	-0.0166 -0.3450	-1.8500 -2.2034	-1.9333 -1.5283
Heading-span	0.4667 -0.0417	0.4167 0.7750	0.0917 -0.3500	-0.3083 0.2417	-0.6667 -0.6250
Plant height	14.2345 14.8495	9.8032 10.2860	-7.6700 -8.0976	-6.3678 -7.7471	-10.1798 -9.2909
Number of tillers per plant	0.3025 1.0841	0.6791 0.4932	0.2759 0.0704	-0.2361 -0.5536	-1.0213 -1.0940
Number of spikelets per spike	0.8035 0.6312	0.2629 0.2373	-0.4382 -0.3260	-0.5110 -0.5021	-0.1172 -0.0404
Number of seeds per spike	3.5835 2.0422	-1.8660 -1.2955	-1.1196 0.5107	-2.1986 -2.4295	1.6006 1.1722
Weight of seeds per spike	-0.0059 -0.0342	-0.1185 -0.0813	-0.0222 0.0577	-0.0306 -0.0309	0.1771 0.0888
1000-kernel weight	-2.6314 -2.3445	-1.2960 -0.7879	0.3155 0.9186	1.4580 1.4448	2.1540 0.7690
Yield per plant	0.0570 -0.4631	-0.7077 0.2377	-0.6801 -0.0136	0.3461 -0.0030	0.9848 0.2419

First reading under each column refers to Ellorslie and second to Parkland.

their maturity. This kind of relationship was found to be in contradiction with the results obtained for F_1 and F_2 diallels.

Combining ability analysis

The general combining ability values of the parental lines used in the backcross diallel are given in Table 44. At both locations, Marquis ranked first in GCA for onset-of-heading and Ciano the lowest, and therefore these parents were regarded as being late and early maturing respectively. Similar interpretations may be given for final heading and heading-span. For plant height, Marquis and Inia at both locations ranked highest and lowest respectively, while for tiller number Chinook at Ellerslie and Marquis at Parkland scored highest. At both locations, Marquis and Ciano possessed the highest and the lowest GCA for number of spikelets per spike and number of seeds per spike respectively. Similar interpretations may be given for other yield components. As far as yield is concerned, at both locations Inia may be regarded as the best combiner, while Chinook at Ellerslie and Marquis at Parkland were the poorest.

The values of specific combining ability for heading data are given in Tables 45, 46 and 47. The results of Table 45 show that the cross (CxI) possessed the highest SCA and (MxI) the lowest at both locations. The best hybrid was associated with the parents with the lowest GCA's at both locations and the worst was from parents with the highest GCA's. The variances for GCA's were larger than those for SCA's. The reciprocal effects were not significant in all cases. Similar

Estimation of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 45. Onset-of-heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA	
	Marquis	Chinook	Khush-hal	Ciano				Inia
Marquis	-	0.5067	-0.7017	-0.9267	-1.4183	1.8350	3.3042	-0.1577
		-0.1399	0.0351	-0.5150	-1.3733	1.9650	3.7204	-0.3519
Chinook	-0.2917	-	-0.5267	-0.9600	-0.9100	1.1600	1.2825	-0.0721
	-0.5833		0.1100	-1.1483	-0.8816	1.4316	1.9089	-0.3453
Khush-hal	0.0417	-0.4593	-	0.3733	0.3817	-0.1316	-0.0458	0.0989
	-0.1250	-0.6667		-0.2233	0.0850	-0.0350	-0.1395	-0.3474
Ciano	-0.2917	0.3333	0.0417	-	1.1566	-1.5733	2.4122	0.4822
	-0.7083	-0.2083	0.0		0.1600	-2.4650	6.0344	0.1927
Inia	-0.1667	-0.0833	0.0	0.0	-	-1.2899	1.6009	1.2034
	0.0417	0.0	0.1667	-0.0417		-0.8766	0.6277	0.5468

TABLE 46. Final heading

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA	
	Marquis	Chinook	Khush-hal	Ciano				Inia
Marquis	-	0.8584	-0.5333	-0.2417	-1.7000	2.3333	5.3936	-0.1267
		-0.3133	-0.7883	-0.8883	-0.8967	1.8967	3.4204	-0.4424
Chinook	-0.2093	-	-0.5416	-0.5000	-0.5000	1.4667	2.1004	0.1189
	-1.0000		-0.2383	-1.1716	-0.9330	2.1800	4.5753	-0.4097
Khush-hal	0.2500	-0.6250	-	-0.4333	0.1917	-0.0166	-0.0504	0.0658
	0.1667	-0.1667		0.6451	0.3450	-0.3450	-0.0579	0.2758
Ciano	-0.2083	0.0833	0.1667	-	0.8584	-1.6500	3.3718	0.0307
	-0.1250	-0.3750	0.6667		0.4117	-2.2034	4.6779	0.4169
Inia	0.3333	0.1667	0.0417	0.1250	-	-1.9333	3.6871	1.1777
	0.2083	0.3750	0.2083	-0.1667		-1.5283	2.1588	0.2101

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 47. Heading-span

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.2500	0.2000	0.6833	-0.2500	0.4667	0.1601	-0.1442
	-0.4167	-0.2000	-0.7833	-0.3333	0.4500	0.0417	-0.1984	-0.5003
Chinook	0.0933	-	-0.1250	0.3583	0.3000	0.4167	0.1159	-0.1234
	-0.4167	-	-1.3683	0.0167	-0.0750	0.7750	0.4005	-0.4870
Khush-hal	0.2003	-0.1667	-	-0.7750	-0.1667	0.0917	0.0493	-0.1257
	0.2917	0.5000	0.6417	0.6417	0.3000	-0.3500	-0.0776	0.2748
Ciano	0.0417	-0.2500	0.1250	-	-0.2676	-0.3083	0.0374	0.2544
	0.5833	-0.1667	0.3333	0.2917	0.2917	0.2417	-0.1417	-0.3259
Inia	0.5000	0.2500	0.0417	0.1250	-	-0.6667	0.3867	-0.0604
	0.1667	0.3750	0.0417	-0.1250	-	-0.6250	0.1905	-0.3726

TABLE 48. Plant height

Marquis	-	1.2204	2.4292	0.7733	-5.9562	14.2345	201.2519	-3.4246
	-0.9280	-1.5368	6.4507	3.8329	-4.4574	14.8495	218.5630	-4.8617
Chinook	1.6708	-	0.2537	0.8719	1.8012	9.9832	98.2939	-2.9272
	-0.9280	-	-0.4441	0.9886	-1.2487	10.2860	103.8967	-4.0744
Khush-hal	2.0138	-1.9303	-	-2.2625	1.5805	-7.6700	57.4592	-1.4352
	-1.1430	-2.0403	-	-1.2273	-0.0541	-8.0976	63.6259	9.0746
Ciano	-2.3949	-2.6567	0.6065	-	0.5592	-6.3678	39.1798	-1.2646
	-1.6303	-1.9159	0.3160	-	-0.9246	-7.7471	58.0724	0.8631
Inia	4.3404*	2.5614	0.8408	1.1077	-	-10.1798	102.2588	10.4201
	4.2671*	1.7700	-0.0917	0.1983	-	-9.2909	84.3766	2.5667

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

interpretations for Tables 46 and 47 may be made.

Hybrids (MxK) and (MxI) showed the highest and the lowest SCA for plant height (Table 48) at both locations. The best hybrid at both locations was associated with the parent (Khush-hal) with the second lowest GCA, and the poorest hybrid was associated with one parent (Marquis) having the highest GCA and another (Inia) showing the lowest GCA at both locations. The variances for GCA were greater than those for SCA and the reciprocal effects at both locations were significant only for (IxM). This effect was attributed to the female parent because of the positive sign appended to it.

At both locations, hybrid (CxI) had the highest SCA while (KxI) at Ellerslie and (MxI) at Parkland ranked lowest and produced the lowest number of tillers per plant (Table 49). The best hybrid had a parent with the lowest GCA at both locations, while the poorest ranking hybrids had high GCA parents (Marquis and Khush-hal, respectively). The reciprocal effects were non-significant for all hybrids and GCA variances were usually higher than those for SCA, except for Marquis, Khush-hal and Ciano, all at Ellerslie. The larger SCA variances for the latter parents imply an importance of non-additive gene effects for number of tillers per plant, and reveal instability in the performance of their hybrids.

The results for the other components of yield, such as number of spikelets per spike (Table 50), number of seeds per spike (Table 51) weight of seeds per spike (Table 52) and 1000-kernel weight (Table 53) may be interpreted in a similar way.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 49. Number of tillers per plant

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.0587	0.1659	-0.2478	-0.0077	0.2025	-0.0735	-0.4126
	-0.2190	-0.2333	-0.6416	-0.3376	-0.7573	1.0841	1.0034	-0.4296
Chinook	-0.5267	-	0.2268	0.4683	-0.2315	0.6791	0.2961	-0.4114
	-0.2190	-	-0.3802	-0.2684	0.0716	0.4932	0.0714	-0.4114
Khush-hal	0.4750	0.0875	-	-0.2497	-0.6937	0.2759	-0.0889	-0.3863
	0.3750	0.2375	-	0.2336	-0.2010	0.0704	-0.1669	-0.2422
Ciano	-0.1367	-0.5357	0.1792	-	0.4877	-0.2361	-0.1093	-0.2982
	-0.2033	0.2167	-0.1958	0.6943	0.3607	-0.5536	0.1346	-0.3494
Inia	0.2042	-0.0013	-0.2167	0.6943	-	-1.0213	0.8701	-0.1550
	0.2448	0.0412	-0.0938	0.1668	-	-1.0940	1.0251	-0.1799

TABLE 50. Number of spikelets per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.3019	0.2495	-0.0846	-0.3061	0.6035	0.6124	-0.0831
	-	0.1083	0.4159	0.0875	-0.0067	0.6312	0.3646	-0.0845
Chinook	-0.0593	-	0.1926	-0.0259	-0.1115	0.2629	0.0359	-0.0145
	0.0133	-	-0.3419	0.2164	0.1788	0.2373	0.0215	-0.0805
Khush-hal	0.4042	-0.1623	-	0.1214	-0.0359	-0.4382	0.1588	-0.0500
	0.1975	-0.1708	-	0.0086	0.0971	-0.3260	0.0725	0.0122
Ciano	-0.2898	-0.1656	0.0675	-	0.0676	-0.5110	0.2279	-0.0756
	0.1233	0.2927	0.1573	-	-0.1626	-0.5021	0.2183	-0.0663
Inia	0.0325	0.0280	0.1557	0.1650	-	-0.1172	-0.0195	-0.0457
	0.3435	0.3020	0.0558	-0.0790	-	-0.0404	-0.0322	-0.0618

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross diallel set at two locations.

TABLE 51. Number of seeds per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.1015	0.0655	0.4011	3.5835	12.0552	-1.9664
		0.2519	0.1132	0.8717	2.0422	3.7491	-1.0532
Chinook	0.1910	-	-0.3113	0.0544	-1.8660	2.6953	-1.9630
	-0.6400		-1.5280	0.2122	-1.2955	1.2570	-1.0321
Khush-hal	0.6403	-0.7640	-	-0.9921	-1.1196	0.4670	-1.9327
	0.7335	0.4013		-0.8981	0.5107	-0.1605	-0.2707
Ciano	-1.1300	-1.0005	-0.5227	-	-2.1906	4.0471	-1.5837
	0.7405	0.4957	1.0112	-	-2.4295	5.4813	-0.5161
Inia	-0.4867	0.0320	-0.2068	-1.2177	1.6006	1.7754	-0.2588
	0.3572	0.0558	0.3255	-0.5962	1.1722	0.9527	-0.4097

Reciprocal effects

TABLE 52. Weight of seeds per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-	0.0490	-0.0030	-0.0624	-0.0059	-0.0029	-0.0074
		0.0461	-0.0314	0.0606	-0.0342	-0.0004	-0.0039
Chinook	0.0552	-	-0.0406	-0.0150	-0.1195	0.0111	-0.0066
	0.0045		-0.0746	0.0018	-0.0813	0.0050	-0.0032
Khush-hal	0.0022	-0.0190	-	0.0007	-0.0322	-0.0025	-0.0068
	0.0150	0.0120		-0.0103	0.0577	0.0018	-0.0017
Ciano	-0.0810	-0.0268	-0.0028	-	-0.0306	-0.0020	-0.0068
	0.0340	0.0335	0.0553	-	-0.0309	-0.0036	-0.0027
Inia	0.0638	0.0252	-0.0277	-0.0853	0.1771	0.0284	-0.0056
	-0.0573	-0.0090	0.0240	-0.0190	0.0888	0.0063	-0.0021

Reciprocal effects

First reading under each column refers to Ellerslie and the second to Parkland.

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from backcross dialled set at two locations.

TABLE 53. 1000-kernel weight

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.6721	-0.3252	-0.8322	0.3192	-2.6314	6.4507	-1.1837
		0.8088	-0.7900	0.4879	1.4128	-2.3445	5.0647	-1.0796
Chinook	0.5477	-	-0.5540	-0.4490	-0.4911	-1.2960	1.2062	-1.0332
	0.4982		-0.5859	-0.1117	-0.5019	-0.7879	0.1889	-0.8615
Khush-hal	-0.5490		-	0.5533	0.3476	0.3155	-0.3740	-1.0425
	-0.1602			0.8728	-0.0248	0.9186	0.4120	-0.7540
Ciano	0.5182	0.3412	0.5002	-	-0.5193	1.4580	1.6523	-0.7835
	0.4058	0.3108	-0.0305		-0.1230	1.4448	1.6556	-0.7422
Inia	-0.8022	0.5862	-0.1982	-0.7360	-	2.1540	4.1662	-0.9392
	-1.3710	-0.2028	0.2245	-0.0402		0.7690	0.1496	-0.3250

TABLE 54. Yield per plant

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-	0.5268	0.1073	-0.2337	-0.6415	0.0570	-0.3228	-0.8150
		0.6335	-0.0471	-0.3599	0.0177	-0.4831	0.0377	-0.4891
Chinook	0.7010	-	0.6673	-0.0782	-0.6920	-0.7077	0.1748	-0.7225
	-0.4425		-0.6144	-0.2531	0.0680	0.2577	-0.1292	-0.3553
Khush-hal	0.3332	-0.1002	-	0.2599	-1.2433	-0.6801	0.1365	-0.6627
	0.1092	0.6103		0.5103	-0.7849	-0.0136	-0.1995	-0.3635
Ciano	-0.3713	-0.8415	0.7498	-	0.3511	0.3461	-0.2062	-0.7715
	0.5293	0.0917	0.6003		0.0547	-0.0030	-0.1956	-0.3378
Inia	-0.6825	0.2547	-0.4963	1.1603	-	0.9843	0.6438	0.0374
	-0.8422	0.7200	0.0167	0.1920		0.2419	-0.1371	-0.2811

First reading under each column refers to Ellerslie and the second to Parkland.

TABLE 55

Analysis of variance of general and specific combining ability and reciprocal effects for ten characters from backcross diallel set at two locations.

Character	M.S.		M.S.		Error M.S.
	for GCA	for SCA	for reciprocal effects	for reciprocal effects	
Onset-of-heading	22.1406**	2.5500**	0.1059	0.2363	0.2363
	32.1406**	2.3875**	0.2753	0.5273	0.5273
Final heading	36.8594**	1.7687**	0.1462	0.1901	0.1901
	39.1250**	3.8375**	0.3823	0.6637	0.6637
Heading-span	2.3482**	0.5423*	0.0976	0.2164	0.2164
	2.9344**	1.2388	0.2347	0.7498	0.7498
Plant height	1263.1875**	13.8687**	10.2239	5.1350	5.1350
	1345.4687**	26.5062**	6.8296	7.2887	7.2887
Number of tillers per plant	4.3223**	0.3368	0.2838	0.6138	0.6138
	7.3193**	0.9020	0.0941	0.6445	0.6445
Number of spikelets per spike	2.9551**	0.1430	0.0776	0.1247	0.1247
	2.0391**	0.1289	0.0736	0.1266	0.1266
Number of seeds per spike	62.4219**	1.6523	1.1293	2.9885	2.9885
	33.4844**	2.1719	0.7036	1.5811	1.5811
Weight of seeds per spike	0.1172**	0.0032	0.0047	0.0110	0.0110
	0.0499**	0.0078	0.0020	0.0058	0.0058
1000-kernel weight	38.6975**	0.8004	0.7034	.7762	.7762
	24.1055**	1.5766	0.5068	1.6191	1.6191
Yield per plant	5.1455**	1.2141	0.7258	1.2218	1.2218
	0.9004	0.5074	0.5015	0.7331	0.7331

First reading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

In yield per plant (Table 54), cross (MxCH) had the highest SCA and consequently was the highest yielding at both locations, while cross (KxI) was the lowest yielding as it had the lowest SCA. The highest yielding hybrid had the parents (Marquis at Parkland and Chinook at Ellerslie) with the lowest GCA, while the poor yielding cross (KxI) had one parent (Khush-hal) with the lowest and one (Inia) with the highest GCA at both locations. The GCA variances were higher than those for SCA only for Marquis at Parkland and Chinook, Khush-hal and Inia at Ellerslie. The reciprocal effects were non-significant in all cases.

The analysis of variance for general and specific combining ability together with the reciprocal effects (Table 55) reveals important additive gene effects for all the characters at both locations, with the exception of yield per plant at Parkland. Thus the significance of mean squares for GCA's substantiates the differences among the parental lines. The significant mean squares for SCA's for onset-of-heading, final heading and plant height at both locations and heading-span at Ellerslie suggest a relatively greater importance of SCA over GCA. Thus for earliness and plant height, selection for SCA should be given priority in breeding programmes aimed at evolving desired lines.

Diallel cross analysis

Preceding the analysis, the validity of the assumption of no reciprocal differences was tested by means of Hayman's (1954a) analysis of variance. The results are given in Table 56. Heading-span at Ellerslie and plant height at Parkland showed a significant

TABLE 56

Mean squares from the analysis of variance of 5 x 5 backcross diallel set for ten characters at two locations.

Source of variation	D.F.	Onset-of-heading	Final heading	Heading-span	Plant height	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1000 kernel weight	Yield per plant
a	4	66.5333**	110.6095**	7.0449*	3790.0000**	12.9970*	8.6532**	187.3125**	0.2514*	115.9843**	15.4229**
		96.3306**	117.4511**	8.6067*	4037.0000**	21.9541**	6.1113*	169.3968**	0.1495*	72.2969**	2.6934
b	10	7.6625**	5.3062*	1.6266	41.5000*	1.0152	0.4316	5.0000	0.0018	2.4312	3.6477
		7.1937**	11.5375**	3.7156	79.3000*	2.7094	0.2918	6.5812	0.0234	4.7312	1.5289
b _j	1	27.4519	19.3802*	0.1302	4.8411	0.0016	0.5952	0.0135	0.0091	4.9872	2.8814
		.4352	69.8419	3.3000	5.6988	14.0152	1.0854	0.6248	0.0113	6.2116	1.8030*
b ₂	4	4.5637*	1.3437	2.8215	33.0156	1.2312	0.6533	4.7842	0.0036	1.3271	5.6994
		3.8926*	7.8437	6.3035	120.1719	2.6053	0.2109	12.2314	0.0489	5.3594	1.1279
b ₃	5	6.1100**	5.6250**	0.9711	55.6125	1.0459	0.2281	6.2000	0.0149	2.8600	2.1734
		2.1875	2.8375	3.7891*	61.0000**	0.5344	0.4019*	3.2625	0.0055	3.9750**	1.7084
c	4	0.2365	0.2542	0.4969*	46.9664	0.6718	0.1605	2.9225	0.0112	1.5768	1.0532
		1.1062	0.7573	0.8417	18.1423*	0.4849	0.3921	3.6308	0.0083	1.0007	1.4769
d	6	0.0192	0.5615	0.1566	19.8087	0.9712	0.2808	3.6648	0.0160	2.4660	2.2368
		1.1953	1.4066	0.6125	22.0532	0.1470	0.1070	1.0973	0.0045	1.8668	1.5227
Blocks x a	8	1.5701	0.6404	0.6697	14.9219	2.4395	0.9517	17.9219	0.0558	11.2734	1.6191
		1.9625	2.2578	2.5236	38.5359	2.3799	0.8740	8.5703	0.0308	4.4165	3.7525
Blocks x b	20	0.9625	0.8375	0.6468	19.0409	2.4242	0.2797	8.5250	0.0369	6.3781	5.4461
		1.9500	3.5156	3.5516	28.0469	2.5652	0.4021	5.3062	0.0257	7.2645	2.5219
Blocks x b _j	2	0.3767	0.9554	1.5654	13.4177	3.3930	0.6469	31.2310	0.0079	4.1977	16.2239
		9.2654	25.2762	5.1350	217.9466	25.4726	0.6840	0.5020	0.0585	17.8517	0.1580
Blocks x b ₂	8	0.9014	0.8165	1.0515	26.3394	4.8573	0.2700	9.7495	0.0580	13.1274	7.6665
		1.8023	3.0779	7.5964	33.3281	2.5774	0.6656	11.6685	0.0530	15.1216	4.5069
Blocks x b _j	10	0.5602	0.9125	0.9352	17.3562	0.6220	0.2527	6.0667	0.0167	3.8535	3.1770
		1.4375	1.8112	0.9326	7.5562	0.5107	0.9073	1.2094	0.0032	0.6453	1.4113
Blocks x c	8	0.2918	0.2079	0.1600	13.7962	0.9417	0.1568	5.6410	0.0118	3.5511	3.5762
		1.3125	0.3369	0.6120	4.0368	1.9616	0.2277	3.6050	0.0098	5.2596	1.8341
Blocks x c _j	12	0.2467	0.2771	0.5253	9.4492	1.1389	0.2946	5.9210	0.0276	2.1627	2.1360
		1.1012	0.3283	0.7044	12.6719	0.5089	0.1605	2.0142	0.0053	0.9139	0.8413
Error	48	0.7079	0.5759	0.6491	15.4430	1.8594	0.3752	8.8616	0.0332	5.3357	3.6694
		1.5308	1.9922	2.2514	21.9569	1.9246	0.3817	4.7487	0.0176	4.8681	2.2023

* Significant at 5% level
 ** Significant at 1% level
 First reading under each column refers to Ellerslie and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a-b-c-d). Each component has been tested against its own block interaction.

TABLE 57

Analysis of variance of \bar{y} , \bar{y} for ten characters
from backcross diallel but at two locations.

Character	Block M.S.	Entry M.S.	Error M.S.
Onset-of-heading	4.9120	1.5911*	0.3734
	16.4215	1.6003*	0.8179
Final heading	0.2722	6.7155*	0.1721
	38.3562	2.5496	1.9131
Heading-span	0.5133	0.6653	0.2203
	1.1121	0.7220	1.1663
Plant height	12060.9687	306.5619	229.9219
	9119.5650	303.1556*	77.2656
Number of tillers per plant	6.5341	0.8383	0.7602
	1.0551	6.6511	0.0997
Number of spikelets per spike	0.3622	0.0215	0.0578
	2.0270	0.0133	0.6426
Number of seeds per spike	426.5668	9.7215	13.6523
	54.6648	3.2219	4.9556
Weight of seeds per spike	0.0549	0.0302	0.0662
	0.0221	0.00	0.00
1000-kernel weight	205.2457	2.3595	3.4363
	30.0292	1.3192	4.9232
Yield per plant	6.7647	1.9657	2.6477
	0.2112	0.7162	0.9051

First reading under each column refers to Ellerslie and second to Parkland.
* significant at 5% level

TABLE 58

Estimates of second degree statistics
for ten characters from backcross diallel set at two locations.

Character	\bar{y}_{11}	\bar{y}_{22}	\bar{y}_{12}	\bar{y}_{11}^2	\bar{y}_{22}^2	\bar{y}_{12}^2	$\bar{y}_{11}\bar{y}_{22}$	$\bar{y}_{11}\bar{y}_{12}$	$\bar{y}_{22}\bar{y}_{12}$	$\bar{y}_{11}\bar{y}_{22}\bar{y}_{12}$
Onset-of-heading	15.0000	5.7393	2.2227	2.2227	3.4973	1.4641	2.4233	1.4641	2.4233	1.4641
	15.7602	6.6334	3.2148	3.2148	4.4137	2.4233	3.7249	3.7249	3.7249	3.7249
Final heading	16.9668	7.8656	3.6934	3.6934	4.5766	1.0336	3.7249	1.0336	3.7249	1.0336
	27.1514	10.1422	3.9199	3.9199	5.8430	3.7249	3.7249	3.7249	3.7249	3.7249
Heading-span	0.5869	0.2610	0.2349	0.2349	0.5060	0.0669	0.1600	0.0669	0.1600	0.0669
	3.6111	0.8947	0.2936	0.2936	0.9129	0.1600	0.1600	0.1600	0.1600	0.1600
Plant height	466.7740	246.3824	126.3608	126.3608	133.2646	0.2528	0.3040	0.2528	0.3040	0.2528
	518.4434	250.1760	134.5703	134.5703	147.5088	0.3040	0.3040	0.3040	0.3040	0.3040
Number of tillers per plant	1.4343	0.7289	0.4319	0.4319	0.6010	0.0500	0.0500	0.0500	0.0500	0.0500
	5.4749	1.9703	0.7317	0.7317	1.1034	0.0500	0.0500	0.0500	0.0500	0.0500
Number of spikelets per spike	1.2203	0.5699	0.2957	0.2957	0.3676	0.0317	0.0317	0.0317	0.0317	0.0317
	0.5749	0.3369	0.2039	0.2039	0.2692	0.0317	0.0317	0.0317	0.0317	0.0317
Number of seeds per spike	28.9980	13.2521	6.2422	6.2422	7.0221	0.0037	0.0037	0.0037	0.0037	0.0037
	12.2275	5.7904	3.1457	3.1457	4.4383	0.0037	0.0037	0.0037	0.0037	0.0037
Weight of seeds per spike	0.0384	0.0211	0.0117	0.0117	0.0133	0.0004	0.0004	0.0004	0.0004	0.0004
	0.0360	0.0116	0.0050	0.0050	0.0089	0.0004	0.0004	0.0004	0.0004	0.0004
1000-kernel weight	16.7744	7.9937	3.8662	3.8662	4.2670	0.2660	0.2660	0.2660	0.2660	0.2660
	13.1070	5.4320	2.4092	2.4092	3.1975	0.3312	0.3312	0.3312	0.3312	0.3312
Yield per plant	5.4553	1.5937	0.5142	0.5142	1.1225	0.1538	0.1538	0.1538	0.1538	0.1538
	0.16975	0.2552	0.0899	0.0899	0.3447	0.0961	0.0961	0.0961	0.0961	0.0961

First reading under each column refers to Ellerslie and second to Parkland.

c component, indicating significant reciprocal differences. Significance for a confirms the existence of parental differences for all characters at both locations, with the exception of yield per plant at Parkland. Significance of b shows that dominance is present for onset-of-heading, final heading and plant height at both locations while b_1 shows that dominance is directional for final heading at Ellerslie. Other assumptions underlying the diallel analysis were tested by analysis of variance of $W_p - V_p$ differences. The heterogeneity of $W_p - V_p$ over arrays for onset-of-heading and heading-span at Ellerslie and plant height at Parkland (Table 57) indicates non-validity of at least one of the assumptions: no multiple allelism, uncorrelated gene distribution and no non-allelic gene interaction. This situation is discussed later, during the graphical analysis of these characters.

The estimates of second degree statistics calculated from array variances and parent-offspring covariances are presented in Table 58. The genetic components of variation were computed according to Johnson and Aksel's (1959) procedure, where the effects of heterozygote is halved because the backcross entries were made equal to those of F_2 's (Jinks, 1956). The estimates of genetic components of variation are given in Table 59. Significance was tested in a manner similar to that used for F_2 's. Proportional estimates of genetic parameters, calculated from Table 59 are presented in Table 60. The interpretation of the results in Tables 59 and 60, together with, the graphical analysis of the data for all the characters under study is as follows:

Except E at Ellerslie and F at Parkland, all components

TABLE 59

Estimates of genetic components of variation
from backcross diallel set for ten characters at two locations.

Character	D	F	H ₁	H ₂	h	E
Onset-of-heading	14.7635 ± 0.5151**	6.7573 ± 1.2692**	5.4162 ± 1.3938**	4.6253 ± 1.2642**	5.7051 ± 0.8535**	0.2364 ± 0.2107
	13.9224 ± 0.5422**	1.7335 ± 1.3543	4.1991 ± 1.4642**	3.7397 ± 1.3280**	9.3553 ± 0.8766**	0.5278 ± 0.2213*
Ear-to-heading	16.7767 ± 0.4061**	2.2430 ± 1.2193	3.3163 ± 1.3142**	3.1536 ± 1.1956**	4.0130 ± 0.6322*	0.1901 ± 0.1993
	25.6080 ± 0.1919**	11.5703 ± 0.4993**	7.5494 ± 0.5333**	6.3669 ± 0.4996**	14.4746 ± 0.3305**	0.6636 ± 0.0815**
Heading-span	0.3726 ± 0.2020*	-0.0498 ± 0.5665	1.0865 ± 0.5455*	0.6157 ± 0.4947	-0.1107 ± 0.3340	0.2164 ± 0.0825**
	2.9149 ± 0.4003**	2.6513 ± 1.4247**	1.7867 ± 1.3249	0.9762 ± 1.2009	0.1597 ± 0.8105	0.7505 ± 0.2001**
Plant height	461.6369 ± 6.3139**	-18.1432 ± 15.7872	20.9514 ± 17.0677	17.4245 ± 15.4805	-2.2534 ± 10.4517	5.1354 ± 2.5801**
	511.1536 ± 11.9083**	-4.5684 ± 29.7476	58.0338 ± 32.1602	38.3688 ± 29.1700	-3.4512 ± 19.6940	7.3925 ± 4.8716
Number of tillers per plant	0.8154 ± 0.0969**	-0.7879 ± 0.2422**	-0.0763 ± 0.2619**	-0.5614 ± 0.2375*	-0.3957 ± 0.1603**	0.6189 ± 0.0396**
	4.6395 ± 0.1591**	2.2954 ± 0.3753**	0.6520 ± 0.4854	0.5160 ± 0.3677	2.5775 ± 0.2482	0.6444 ± 0.0613**
Number of spikelets per spike	1.1617 ± 0.0509**	0.8027 ± 0.1472	0.0348 ± 0.1591	0.0382 ± 0.1443	0.6472 ± 0.0978	0.1246 ± 0.0341**
	0.4852 ± 0.0213**	-0.3494 ± 0.0762**	-0.0263 ± 0.0845	0.0090 ± 0.0767	0.1504 ± 0.0518**	0.1267 ± 0.0128**
Number of seeds per spike	26.6481 ± 0.7394**	1.4479 ± 1.6245	-3.3914 ± 1.9724	-2.5798 ± 1.7690	-1.6849 ± 1.2078	2.9497 ± 0.2982**
	10.6477 ± 0.6544**	-0.6035 ± 1.6345	2.7113 ± 1.7672	3.6210 ± 1.6628	-0.8779 ± 1.0622	1.5799 ± 0.2671**
Weight of seeds per spike	0.6278 ± 0.0107**	-0.3719 ± 0.0917**	-0.0215 ± 0.0913**	-0.0356 ± 0.0917**	-0.0051 ± 0.0011**	0.0111 ± 0.0003**
	0.2302 ± 0.0017**	0.0168 ± 0.0034**	0.0101 ± 0.0043**	0.0038 ± 0.0043	-0.0014 ± 0.0029	0.0059 ± 0.0007**
1000-kernel weight	14.9484 ± 0.1177**	-0.5959 ± 0.2949	-2.7422 ± 0.3173**	-1.9401 ± 0.2862**	-0.0724 ± 0.1946	1.7756 ± 0.0489**
	11.5476 ± 0.3052**	2.6495 ± 0.9136**	0.6153 ± 0.6677	-0.0656 ± 0.3958	0.2886 ± 0.6048	1.6194 ± 0.1493**
Yield per plant	4.2333 ± 0.3366**	3.0766 ± 0.9832**	0.3925 ± 1.0630	-0.0118 ± 0.9642	-0.1673 ± 0.6509	1.2225 ± 0.1607**
	0.1536 ± 0.1558	-0.1264 ± 0.3492	-0.6622 ± 0.4236	-0.4461 ± 0.3817	-0.0849 ± 0.2577	0.7336 ± 0.0631**

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level.

** Significant at 1% level.

TABLE 60

Proportional estimates of genetic parameters from the backcross diallel set for ten characters at two locations.

Character	$(H_1/D)^{\frac{1}{2}}$	$(H_2/4H_1)$	$(4DH_1)^{\frac{1}{2}} + F$	$(4DH_1)^{\frac{1}{2}} - F$	h^2/H_2	$r_{y/H_p + V_r}$	Heritability
Onset-of-heading	0.5057*	0.2135*	2.2149*	1.2334	0.9758	1.0275	
	0.5492*	0.2227*	1.2557*	2.5016	0.9398	0.7527	
Final heading	0.4446*	0.2377*	1.3539*	1.2729	0.9466	0.9003	
	0.5409*	0.2105*	2.4173*	2.2741	0.9072	1.0562	
Heading-span	1.7077*	0.1500	0.9305†	-0.1699	0.6344	0.1571	
	0.7829	0.1366	4.3292	0.1636	0.4387	0.6007	
Plant height	0.2086	0.2079	0.8343	-0.1293	0.3243	0.8898	
	0.3369	0.1653	0.9738	-0.0899	-0.6073	0.8477	
Number of tillers per plant	0.9174	0.2045	0.3090	0.7049	0.8415	0.2403	
	0.3674	0.1986	4.6612	4.9754	0.9151	0.8379	
Number of spikelets per spike	0.2931	0.1007	1.0880	1.2373	-0.5694	0.9423	
	0.2375	-0.0787	-0.2433	18.8908	-0.8324	0.3502	
Number of seeds per spike	0.3608	0.1902	1.1669	0.7306	-0.5376	0.7891	
	0.5046	0.1116	0.8938	-0.7552	0.2682	0.5250	
Weight of seeds per spike	0.8864	0.1014	0.3949	0.3291	-0.1965	0.3034	
	0.5775*	0.0946	3.3493*	-0.3582	0.3449	0.6696	
1000-kernel weight	0.4281	0.1772	0.9169	0.0371	0.5993	0.7533	
	0.0364	-1.4023	-1.9226	-3.3718	-0.4941	0.7507	
Yield per plant	0.3045	-0.0075	-11.4843	14.1870	0.9215	0.6567	
	2.0749	0.1692	0.6694	0.1894	-0.4361	0.0602	

First reading under each column refers to Ellerslie and second to Parkland.

*Genetic components of variation for the characters are significantly different from zero ($P \leq 0.05$)

†Components D and H_1 significant, F non-significant ($P > 0.05$)

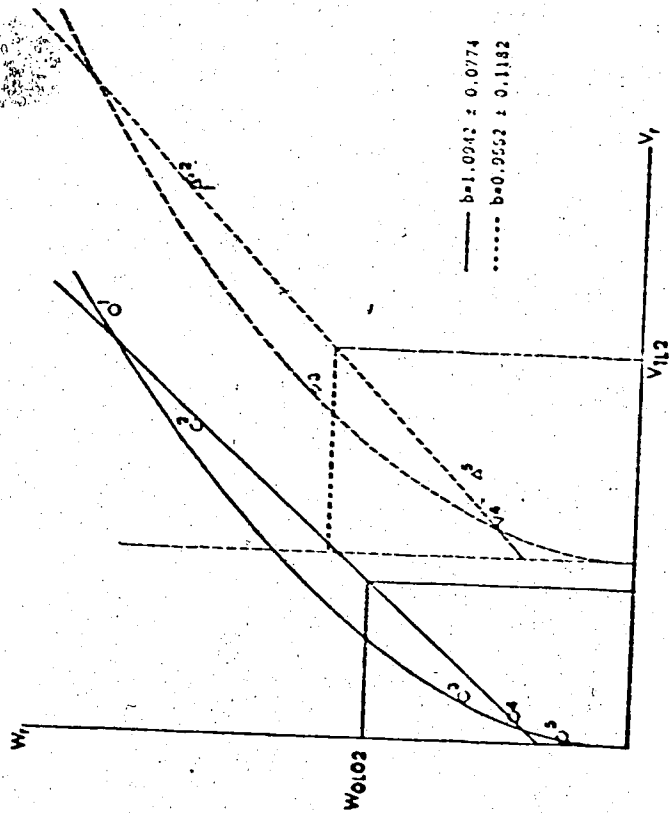


Figure 41. W_p, V_p graph for onset-of-heading from backcross diallel set.

— $\sigma = W_p, V_p$ intercepts at Ellerslie
 - - - $\Delta = W_p, V_p$ intercepts at Parkland

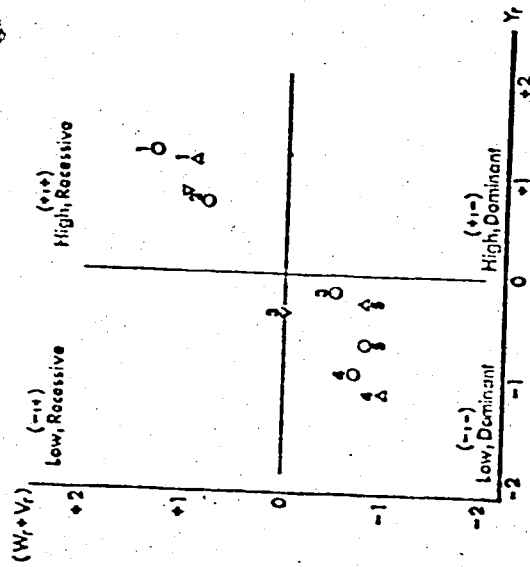


Figure 42. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for onset-of-heading from backcross diallel set.

$\sigma = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

of variation were significant (Table 59) for onset-of-heading. The mean degree of dominance (Table 60) and the regression of W_p upon V_p (Figure 41) at both locations show that onset-of-heading is inherited as a partially dominant trait. The proportion of positive to negative alleles at loci exhibiting dominance in the parents is approximately 0.25 and consequently the parents may be assumed to have equal proportions of genes with positive and negative effects respectively. The estimates of $[(4DH_1)^{1/2} + F] \div [(4DH_1)^{1/2} - F] > 1$ for both locations suggest that dominant genes are in excess in the parents. Moreover, since \bar{n}^2/H_2 is 1.2 for Ellerslie and 2.5 for Parkland, at least one and at least two groups of genes, respectively, are showing dominance in regard to the expression of the character. The correlation coefficient between Y_p and $(W_p + V_p)$ at both locations is 0.9, indicating that the genes for early heading are mostly dominant. The parents Marquis and Inia at Ellerslie and Chinook and Ciano at Parkland are the most highly recessive and highly dominant ones (Figure 41). The standardized deviation graph of Figure 42 categorized the late heading parents as recessives (Marquis and Chinook, in the +,+ quadrant) and the early parents as dominants (Khush-hal, Ciano and Inia, in the -,- quadrant) for both locations. Heritability estimates of 102.75% at Ellerslie and 75.27% at Parkland show that the character is highly heritable and fairly stable over the environmental fluctuations.

Only F and E for final heading were not significant at Ellerslie (Table 59). The character is partially dominant in its inheritance since $(H_1 \div D)^{1/2} < 1$ (see also Figure 43). Table 57 shows $W_p - V_p$

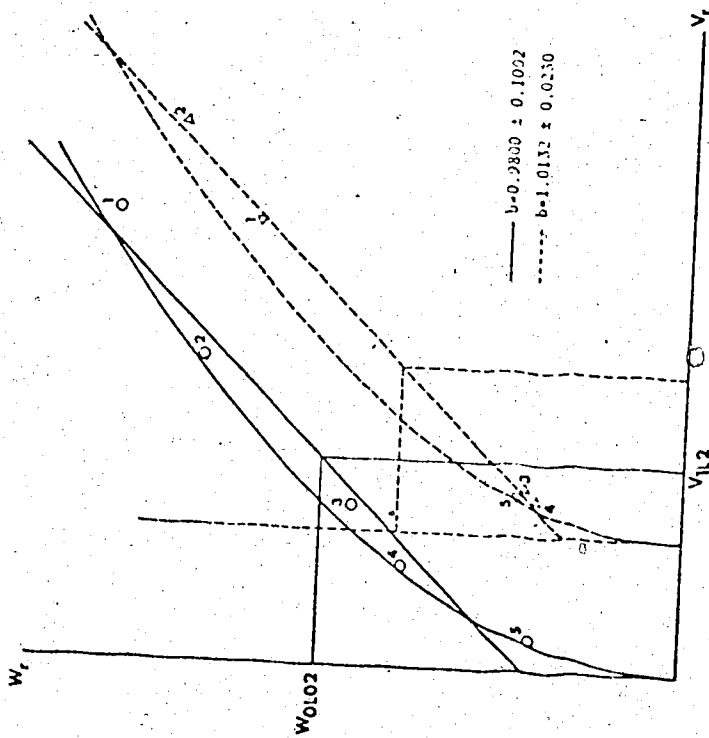


Figure 43. W_p, V_r graph for final heading from backcross diallel set.

— $\circ = W_p, V_r$ intercepts at Ellerslie
 --- $\Delta = W_p, V_r$ intercepts at Parkland

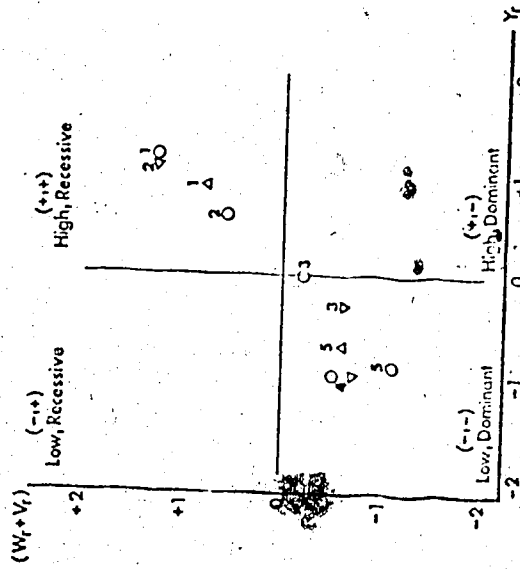


Figure 44. Standardized deviation graph of $[Y_r]$ and $[W_p + V_r]$ for final heading from backcross diallel set.

$\circ = Y_r, [W_p + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_p + V_r]$ intercepts at Parkland

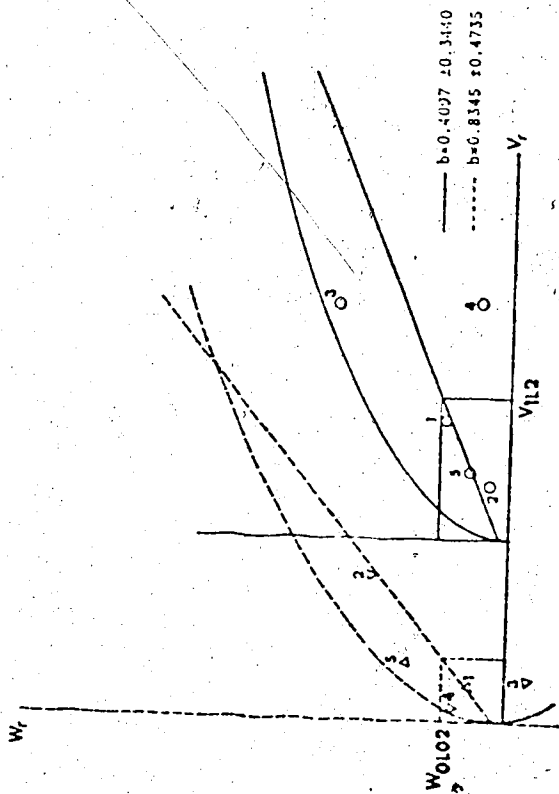


Figure 45. W_p, V_p graph for heading-span from backcross diallel set.

— $\circ = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

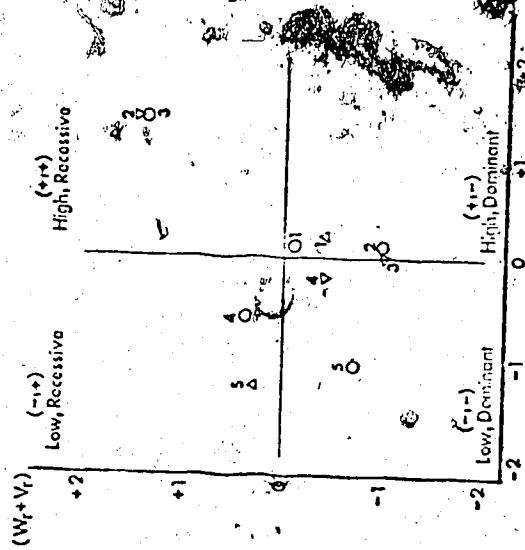


Figure 46. Standardized deviation graph of $[Y_p]$

and $[W_p + V_p]$ for heading-span from backcross diallel set.

$\circ = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

heterogeneity which can be ascribed to either non-allelic interaction, multiple allelism or correlated gene distribution. It could be ascertained from Figure 41 (onset-of-heading) and Figure 43 (final heading) that the regression line does not deviate significantly from the expected unit slope and the W_p, V_p graph does not appear to be distorted. Therefore the question of non-validity of any of the above mentioned conditions has been ignored. The general conclusions of the diallel analysis for final heading (see Tables 59, 60; Figures 43, 44) and heading-span (see Figure 45, 46) are similar to that for onset-of-heading except for changes in the ranking order of parents for their dominance.

For plant height, all components of genetic variation except D were non-significant at both locations. The $W_p - V_p$ heterogeneity at Parkland (Table 57) has been ignored, since the regression of W_p upon V_p is not significantly different from unity (Figure 47) and the W_p, V_p array-intercepts do not show distortion. Because of the non-significance of components of variation, interpretations of proportional estimates and genetic parameters are meaningless. However, the mean degree of dominance may be given as $(H_1 : D)^{1/2} < 1$ indicating partial dominance (see also Figure 47). The correlation between the parental order of dominance and parental measurements is 0.32 at Ellerslie and -0.607 at Parkland. The positive correlation at Ellerslie indicates that genes for shortness are mostly dominant; the negative correlation at Parkland that genes for tallness are mostly dominant. The most highly recessive parent (+,+ quadrant, Figure 48) contributing to tallness at Ellerslie is Marquis, while Khush-hal is the most highly recessive parent at Parkland

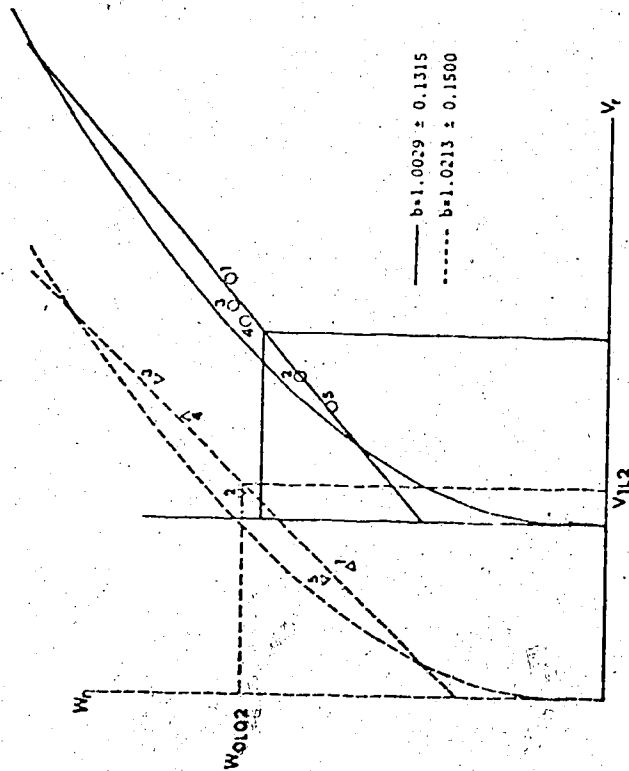


Figure 47. W_r, V_r graph for plant height from backcross diallel set.

- $\circ = W_r, V_r$ intercepts at Ellerslie
- $\Delta = W_r, V_r$ intercepts at Parkland

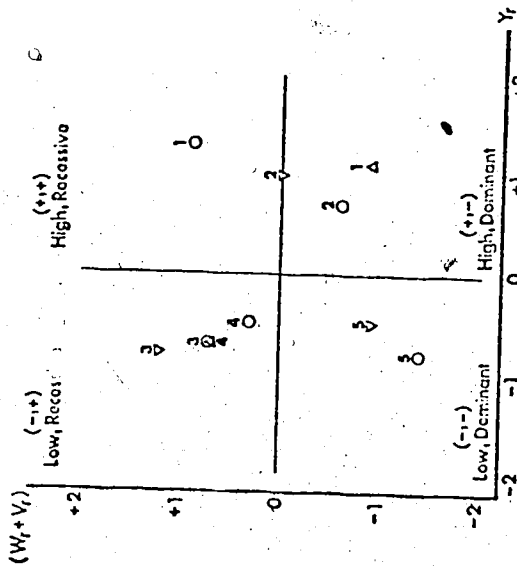


Figure 48. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for plant height from backcross diallel set.

- $\circ = Y_r, [W_r + V_r]$ intercepts at Ellerslie
- $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

(-,+ quadrant) contributing to shortness. The most dominant parent, Inia, at both locations occupies the (-,-) quadrant and thus reflects its shortness. Marquis and Chinook show a discrepancy in dominance ranking order between locations. Chinook, highly dominant at Ellerslie had equal proportion of dominants and recessives at Parkland, while Marquis, highly recessive at Ellerslie is highly dominant at Parkland. The heritability estimates of 88.98% at Ellerslie and 84.77% at Parkland suggests that plant height, being highly heritable is quite stable with respect to environmental changes.

For number of tillers per plant, all components of variation except D and F are non-significant at Parkland. Consequently, proportional values discussed below may have a value only in showing trends and not definite conclusions. The same condition applies to the interpretation of graphs. At Ellerslie, $(H_1 \div D)^{1/2} \approx 1$, showing that dominance is nearly complete (see also Figure 49). The value of $(H_2/4H_1) = 0.204$ indicates a certain degree of asymmetry of positive and negative alleles at loci exhibiting dominance. the proportion of dominant to recessive genes in the parents (0.309), indicates a preponderance of recessive genes. Since $H_2/H_1 = 0.704$, probably at least one group of genes controls tillering capacity. The correlation between parental order of dominance and parental measurements at both locations is 0.9, suggesting that genes with low tillering capacity are mostly dominant. This situation is presented graphically in Figure 50, where almost all the parents at both locations occupy

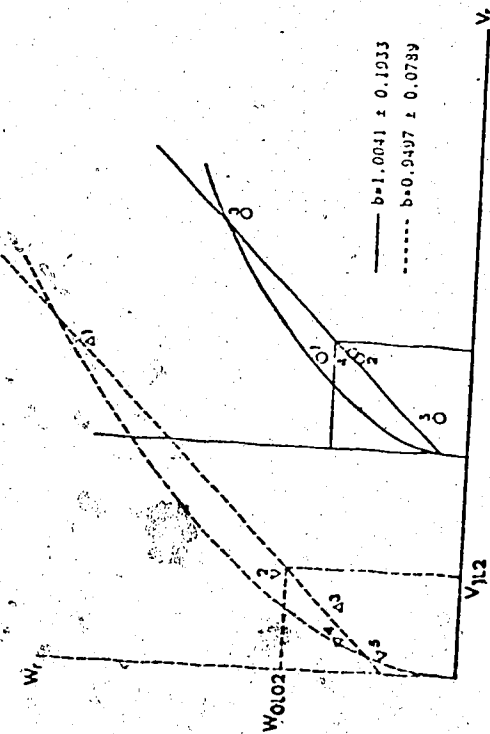


Figure 49. W_r, V_r graph for number of tillers per plant from backcross diallel set.

- $o = W_r, V_r$ intercepts at Ellerslie
- $\Delta = W_r, V_r$ intercepts at Parkland

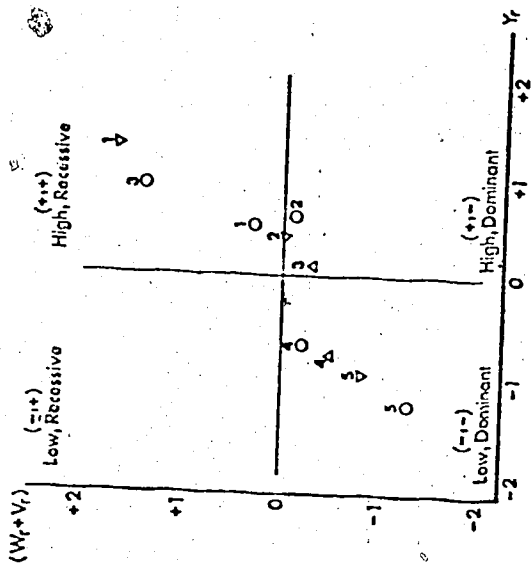


Figure 50. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of tillers per plant from backcross diallel set.

- $o = Y_r, [W_r + V_r]$ intercepts at Ellerslie
- $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

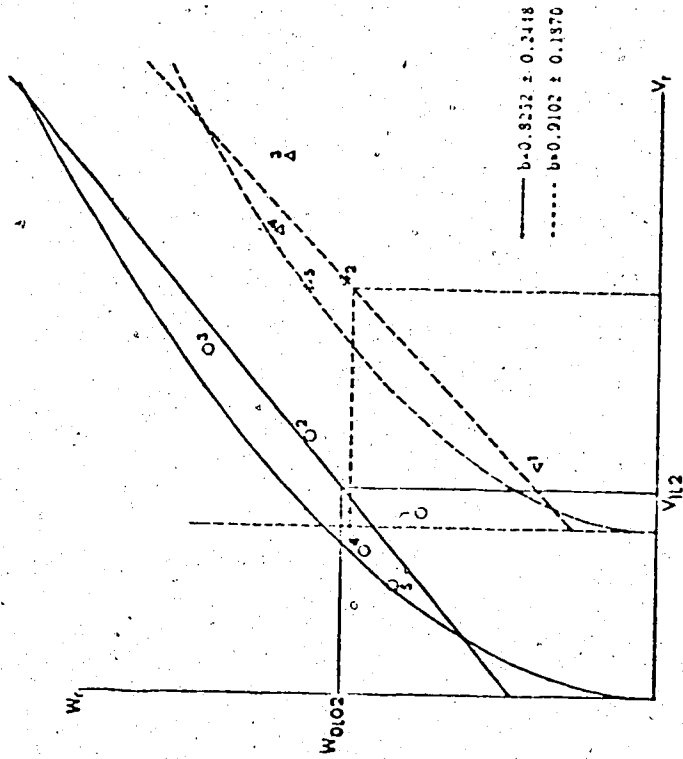


Figure 51. W_r, V_r graph for number of spikelets per spike from backcross diallel set.

— $o = W_r, V_r$ intercepts at Ellerslie

--- $\Delta = W_r, V_r$ intercepts at Parkland

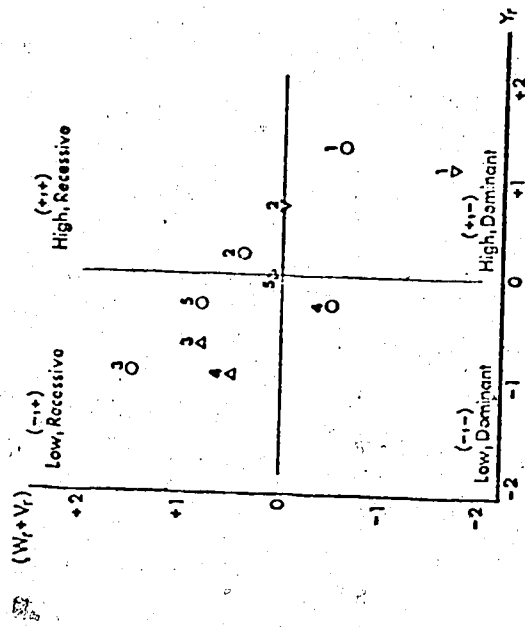


Figure 52. Standardized deviation graph of $[Y_r]$ and $[W_y + V_r]$ for number of spikelets per spike from backcross diallel set.

$o = Y_r, [W_y + V_r]$ intercepts at Ellerslie

$\Delta = Y_r, [W_y + V_r]$ intercepts at Parkland

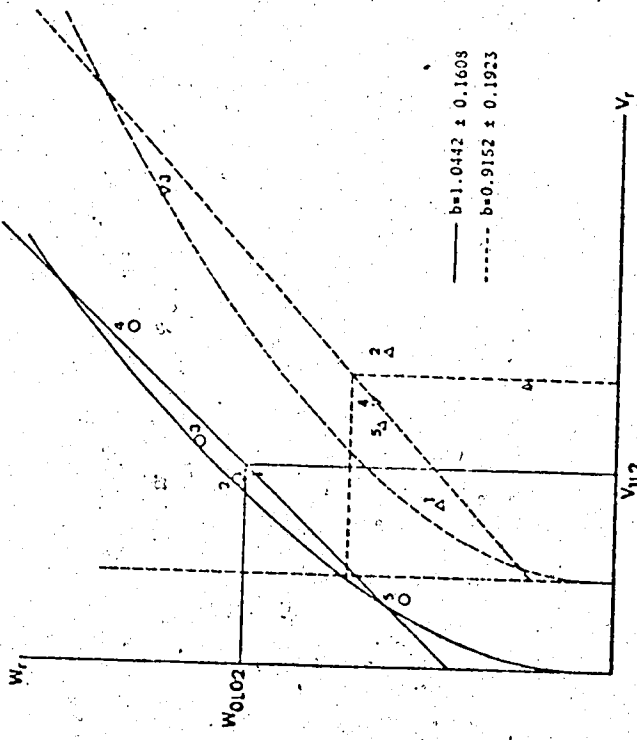


Figure 53. W_p, V_p graph for number of seeds per spike from backcross diallel set.

— $O = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

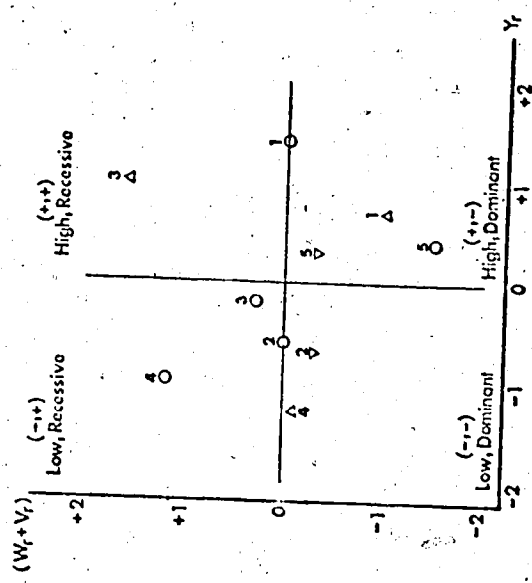


Figure 54. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of seeds per spike from backcross diallel set.

$O = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

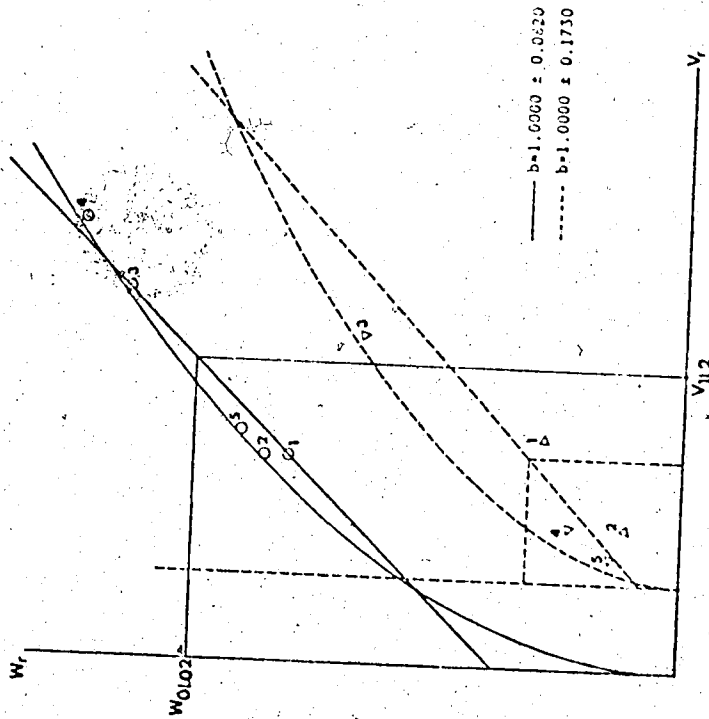


Figure 55. W_p, V_p graph for weight of seeds
Per spike from backcross diallel set.

- $o = W_p, V_p$ intercepts
at Ellerslie
- $\Delta = W_p, V_p$ intercepts
at Parkland

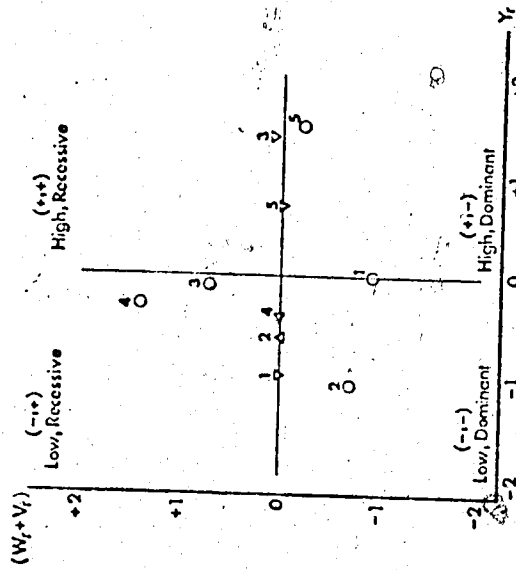


Figure 56. Standardized deviation graph of $[W_p]$
and $[W_p + V_p]$ for weight of seeds,
per spike from backcross diallel set.

$$o = Y_p, [W_p + V_p] \text{ intercepts}$$

at Ellerslie

$$\Delta = Y_p, [W_p + V_p] \text{ intercepts}$$

at Parkland

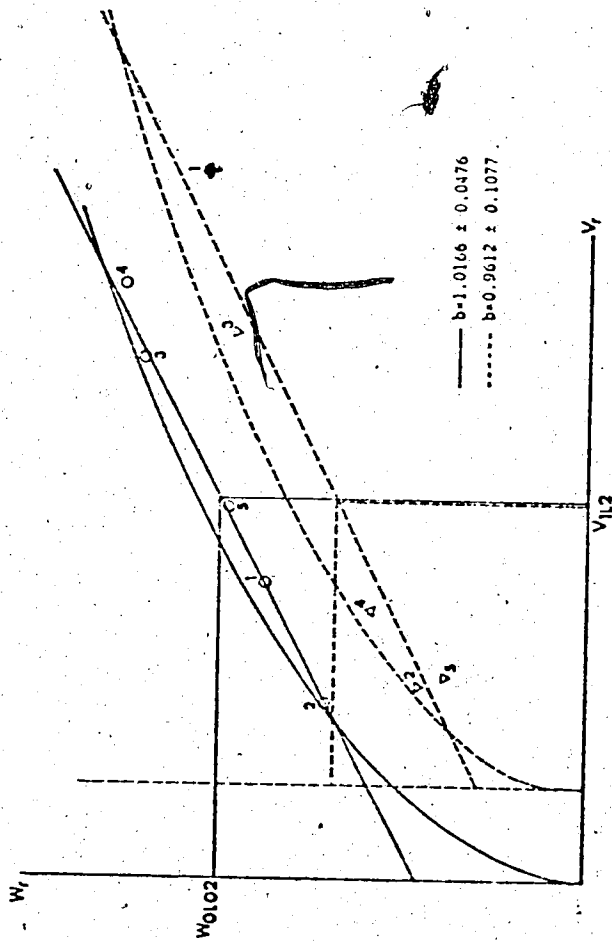


Figure 57. W_p, V_p graph for 1000-kernel weight from backcross diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

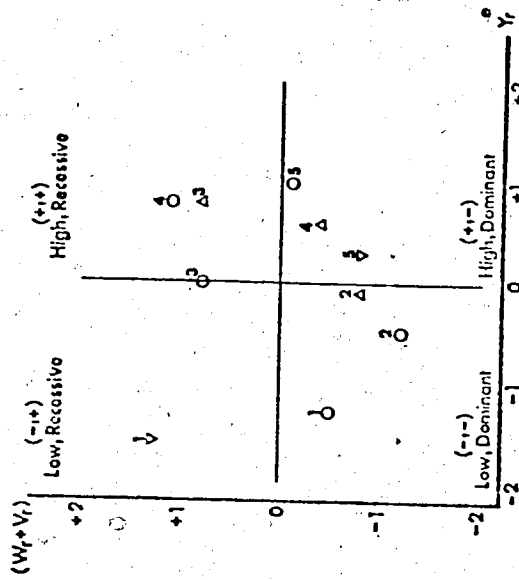


Figure 58. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for 1000-kernel weight from backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

the (-,-) and (+,+) quadrants. Ciano and Inia, in the (-,-) quadrant, may be regarded as highly dominant for low tillering at both locations. Khush-hal at Ellerslie and Marquis at Parkland, in the (+,+) quadrant, may be said to be highly recessive for higher tillering. Chinook, with higher tillering capacity at both locations, shows more dominant than recessive genes at Ellerslie but equal proportions of dominants and recessives at Parkland. Only Khush-hal has changed its order of dominance between the two locations. Highly recessive at Ellerslie, it shows a preponderance of dominant genes at Parkland. Heritability values of 24.03% at Ellerslie and 83.79% at Parkland suggest that the heritability of tillering capacity is strongly influenced by environmental fluctuations.

The graphical interpretations of the results of Tables 59, 60 for other components of yield, are shown in Figures 51 - 58, (i.e. number of spikelets per spike, Figures 51, 52; number of seeds per spike, Figures 53, 54; weight of seeds per spike, Figures 55, 56; and 1000-kernel weight, Figures 57, 58). These may be explained in the same way as for number of tillers per plant.

For yield per plant, the components of variation in Table 59 were mostly non-significant. The overall picture of inheritance of yield seen from the W_p , V_p graph of Figure 59 is one of partial dominance at both locations. The correlations between parental order of dominance and parental measurements are 0.921 at Ellerslie and -0.436 at Parkland. These highly significant correlations indicate

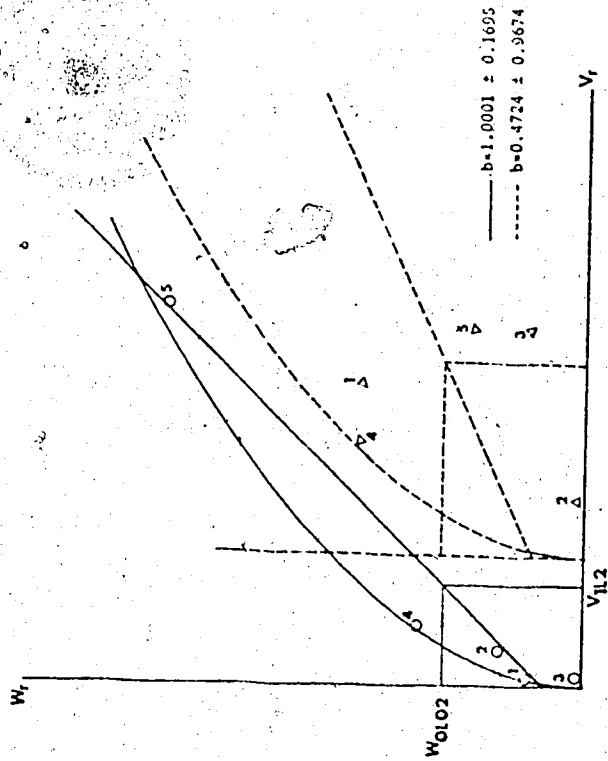


Figure 59. W_p, V_p graph for yield per plant from backcross diallel set.

— $\sigma = W_p, V_p$ intercepts at Ellerslie

--- $\Delta = W_p, V_p$ intercepts at Parkland

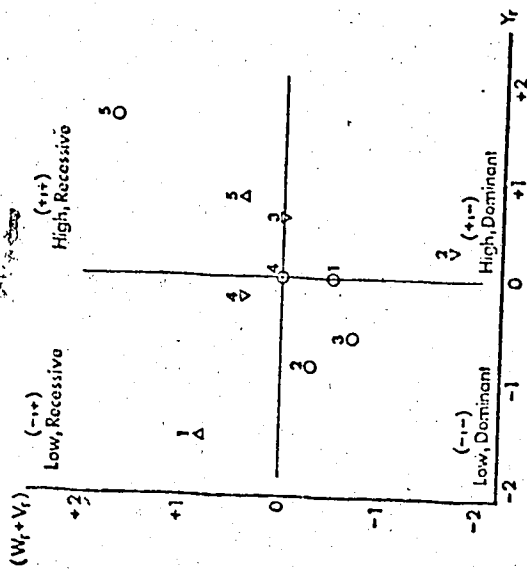


Figure 60. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for yield per plant from backcross diallel set.

$\sigma = Y_p, [W_p + V_p]$ intercepts at Ellerslie

$\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

that the genes for low yield at Ellerslie are mostly dominant while at Parkland high yielding is dominant over low. The dominance ranking order of parents seems to be significantly different for the two locations. Thus, from Figure 59, Inia and Marquis are the most recessive and Khush-hal and Chinook are the most dominant parents at Ellerslie and Parkland, respectively. Marquis, highly recessive at Parkland contains an excess of dominant genes at Ellerslie, while Khush-hal, with equal proportion of dominants and recessives at Parkland shows a preponderance of dominants at Ellerslie. Ciano, with equal proportions of dominant and recessive genes at Ellerslie possesses an excess of recessive genes at Parkland. The heritability values of 65.67% at Ellerslie and 6.02% at Parkland reflect this instability of yield inheritance between the two locations.

ANALYSIS OF SELFED BACKCROSSES.

In the absence of non-allelic interaction the expected statistics for the analysis of family means of the first selfed backcross generation are the same as those of F_3 generation crosses. The diallel table of selfed backcross family means, i.e., 'synthetic F_3 diallel table' was subjected to simple correlation analysis and the results are presented in Table 61. The following conclusions may be made from Table 61:

Onset-of-heading was positively correlated with final heading, plant height, number of spikelets per spike, number of seeds per spike at both locations and with number of tillers per plant at Parkland only. It was negatively correlated with weight of seeds per spike at Parkland and 1000-kernel weight at both locations. The negative correlation with weight of seeds per spike and 1000-kernel weight indicates that early maturing varieties produce higher yields and higher seed weights than the late maturing ones. Similar results were also obtained for F_1 , F_2 and backcross diallel data.

Plant height was positively correlated with number of tillers per plant and number of spikelets per spike at both locations and with number of seeds per spike at Ellerslie only. It was negatively correlated with weight of seeds per spike and 1000-kernel weight at both locations. Correlation with yield at both locations was not significant.

Number of tillers per plant was positively correlated with number of spikelets per spike and yield per plant at both locations

TABLE 61

Simple correlation coefficients between ten characters from a selfed backcross diallel set at two locations.

Character	2	3	4	5	6	7	8	9	10
1. Onset-of-heading	0.917**	0.142	0.777**	0.194	0.534**	0.345**	-0.206	-0.643**	-0.206
	0.642**	0.047	0.818**	0.500**	0.534**	0.301**	-0.288*	-0.636**	-0.162
2. Final heading	-	0.515**	0.779**	0.197	0.445**	0.316**	-0.273*	-0.687**	-0.307**
		0.578**	0.771**	0.617**	0.527**	0.238*	-0.347	-0.655**	-0.009
3. Heading-span		-	0.259*	0.055	-0.081	-0.003	-0.275*	-0.330**	-0.349**
			0.191	0.390**	0.169	-0.011	-0.204	-0.254*	0.231*
4. Plant height			-	0.351**	0.636**	0.278*	-0.244*	-0.606**	0.016
				0.511**	0.588**	0.155	-0.405**	-0.723**	-0.103
5. Number of tillers per plant				-	0.285*	-0.056	-0.034	0.046	0.517**
					0.428**	0.239*	-0.255	-0.536**	0.253*
6. Number of spikelets per spike					-	0.619**	0.212*	-0.412**	0.252*
						0.686**	0.194	-0.345**	0.373**
7. Number of seeds per spike						-	0.695**	-0.302**	0.126
							0.639**	-0.061	0.409**
8. Weight of seeds per spike							-	0.526**	0.442**
								0.724**	0.511**
9. 1000-kernel weight								-	0.418**
									0.309**
10. Yield per plant									-

First reading under each column refers to Ellerslie and second to Parkland.
 *Significant at 5% level
 **Significant at 1% level

and with number of seeds per spike at Parkland. It was negatively correlated with 1000-kernel weight at Parkland. The correlation of tiller number with number of seeds per spike and 1000-kernel weight at Ellerslie and with weight of seeds per spike at both locations was not significant. A positive correlation with number of spikelets per spike, number of seeds per spike and yield per plant indicates a direct proportional relationship between tillering capacity and these characters, while negative correlation with 1000-kernel weight shows that plants with high tillering capacity tend to have a low kernel weight. The correlation coefficients for other components of yield, viz., number of spikelets per spike, number of seeds per spike and 1000-kernel weight among themselves and with heading dates have a similar interpretation.

Yield per plant was positively correlated with its components: 1000-kernel weight, weight of seeds per spike, number of seeds per spike, number of spikelets per spike and number of tillers per plant at both locations. The single exception was number of seeds per plant at Ellerslie. The positive correlation of yield with its components exhibits a direct proportional relationship of the former with the latter. Yield was negatively correlated with final heading and heading-span at both locations, indicating that the late heading entries are low yielding and vice versa. The negative correlation of yield with onset-of-heading was not significant at either location.

The results of the factor analysis are summarized in a varimax-rotated, five factor matrix in Table 62. 93% of the total

TABLE 62

Varimax rotated factor matrix for ten characters
from a selfed backcross diallel set at two locations.

Character	Communality	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Onset-of-heading	0.982 0.899	0.977 -0.905	0.057 0.135	-0.034 0.193	-0.025 -0.005	0.147 -0.159
Final heading	0.985 0.956	0.908 0.766	0.036 0.078	-0.045 0.241	0.364 0.520	0.157 -0.065
Heading-span	0.986 0.991	0.163 0.066	-0.078 -0.057	-0.063 0.159	0.973 0.970	0.054 0.122
Plant height	0.850 0.924	0.787 0.924	0.010 -0.079	0.266 0.348	0.166 0.053	0.383 0.017
Number of tillers per plant	0.877 0.693	0.245 0.344	-0.120 0.079	0.889 0.817	0.100 0.227	0.030 0.234
Number of spikelets per spike	0.872 0.826	0.452 0.634	0.470 0.552	0.310 0.166	-0.158 0.058	0.572 0.296
Number of seeds per spike	0.955 0.978	0.251 0.199	0.695 0.953	-0.060 0.121	0.030 -0.011	0.293 0.122
Weight of seeds per spike	0.995 0.964	-0.206 -0.325	0.899 0.749	0.138 -0.309	-0.146 -0.112	-0.332 0.366
1000-kernel weight	0.939 0.962	-0.534 -0.581	0.126 0.115	0.261 -0.617	-0.204 -0.139	-0.727 0.388
Yield per plant	0.899 0.946	-0.222 -0.066	0.261 0.298	0.817 0.085	-0.261 0.140	-0.018 0.908
Percent of total Variability explained	93.695 92.841	31.330 33.077	19.500 19.144	17.231 14.361	12.604 13.203	12.421 13.115

First reading under each column refers to Ellerslie and second to Parkland.

variability present in the data for all the characters considered was explained by these factors at both locations.

The first factor was termed *lateness*. It carried highest loadings for onset-of-heading and final heading at both locations.

Weight of seeds per spike, 1000-kernel weight and yield per plant were negative contributors to *lateness*. Of the remaining characters, the highest contributor to *lateness* was plant height at both locations. This confirms the results of the earlier F_1 , F_2 and backcross diallel factor analyses. *lateness* explained 31.33% and 33.07% of the total variability at Ellerslie and Parkland respectively.

The second principal factor was termed *yielding-ability* since it carried the highest loadings on number of seeds per spike, weight of seeds per spike and number of spikelets per spike. As expected, yield per plant appreciably contributed to this factor. The contributions of onset-of-heading and final heading, though positive, were the lowest. Heading-span and plant height showed a negative effect on *yielding-ability*. The factor explained 19% of the variability present in the data at both locations.

Tillering-capacity was chosen as the third principal factor as it carried the highest loadings for number of tillers per plant at both locations. Yield per plant showed the highest contribution to *tillering-capacity* at Ellerslie but its effect at Parkland was very low. Other components of yield, viz., number of seeds per spike, weight of seeds per spike and 1000-kernel weight, contributed negatively or very slightly to *tillering-capacity* at both locations. A negative effect

TABLE 63

Estimates of general combining ability for five parental lines used in selfed backcross diallel set for ten characters at two locations.

Character	Marquis	Chinook	Khush-hal	Ciano	Inia
Onset-of-heading	2.0733 2.3117	1.2483 1.5534	-0.5433 -0.6300	-1.6100 -2.3216	-0.0683 -0.9133
Final heading	2.8616 2.1917	1.4983 2.2334	-0.2433 -0.5500	-2.0103 -2.2250	-1.5183 -1.6500
Heading-span	0.1967 -0.1033	0.3717 0.6633	0.2550 0.0967	-0.4533 0.0967	-0.3700 -0.7533
Plant height	14.0397 12.5270	9.8603 12.5012	-6.6035 -8.7700	-6.1142 -7.7140	-9.1824 -8.5442
Number of tillers per plant	0.0554 0.7212	0.5642 0.7512	0.3819 0.3558	-0.0788 -0.7265	-0.9226 -1.1017
Number of spikelets per spike	0.7318 0.5099	0.1207 0.3313	-0.4789 -0.2941	-0.2321 -0.4894	-0.1415 -0.0577
Number of seeds per spike	3.7367 1.8352	-2.1898 -1.0895	-1.2477 0.4308	-1.6029 -1.8508	1.3047 0.6653
Weight of seeds per spike	0.0230 -0.0314	-0.1290 -0.0845	-0.0362 0.0607	-0.0017 -0.0282	0.1439 0.0834
1000-kernel weight	-2.3425 -2.0504	-1.1454 -1.0151	0.2400 0.9964	1.4072 0.9224	1.8379 1.1968
Yield per plant	-0.0471 0.5386	-0.8473 0.0681	-0.7653 0.3231	0.6451 -0.2341	1.0147 0.3815

First reading under each column refers to Ellerslie and second to Parkland.

was observed for onset-of-heading, final heading and heading-span at Ellerslie, but their effect at Parkland, though positive, was very low. *Tillering-capacity* explained 17.23% and 14.30% of the variability in the data at Ellerslie and Parkland.

The fourth principal component was chosen as *heading-span* because heading-span provided the highest contribution to this factor. It explained 12.6% and 13.2% of the variability at Ellerslie and Parkland. Yield per plant and its components had either a negative or a minimal effect on *heading-period*. This kind of response was also observed in the F_1 , F_2 and backcross factor analyses.

The fifth principal factor was named *low seed weight* at Ellerslie and *high yield* at Parkland because of the inconsistency in factor loadings between the two locations; 1000-kernel weight carrying maximum negative loading at Ellerslie and yield per plant maximum positive loading at Parkland. *Low seed weight* explained 12.421% and *high yield* 13.115% of the variability in the data at the respective locations. The contribution of yield and its components towards *low seed weight* at Ellerslie was expectedly low except number of spikelets per spike. On the other hand the contribution of yield components towards *high yield* at Parkland was definitely positive. *Low seed weight* was associated with earliness, as reflected by the factor loadings for heading data at the two locations.

Combining ability analysis

The results of the general combining ability analysis are presented in Table 63. For onset-of-heading Marquis was the highest

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 64. Onset-of-heading

♀ Parent	Specific combining ability					Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.4433	-0.9317	-0.0733	-1.1817	4.2302	-0.1713
		0.3217	-0.6016	0.6616	-0.9200	5.2404	-0.2584
Chinook	-0.4583	-	-0.8566	-0.8733	-0.1066	1.4898	-0.1058
	-0.1667		-0.3617	-0.9617	-0.1617	2.3096	-0.2239
Khush-hal	0.5417	-0.2917	-	0.2933	0.5183	0.2257	0.3626
	0.3333	-0.5417		0.4717	0.0217	0.2935	-0.0689
Ciano	0.3333	0.1250	0.4167	-	0.5433	2.5235	0.1134
	0.5000	0.2500	-0.5000	-	-0.3700	5.2867	0.2494
Inia	0.1667	-0.2500	0.0633	-0.3750	-	1.2965	0.4859
	-0.0417	-0.1250	0.8750	0.2250	-	0.7308	0.0782

TABLE 65. Final heading

♀ Parent	Specific combining ability					Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia		
Marquis	-	0.4517	-0.6616	-0.2460	-0.8233	2.2816	-0.1169
		0.5417	-1.4000	-0.5167	-0.9250	2.1917	-0.4233
Chinook	-1.0417**	-	-0.5817	-0.4983	0.6350	1.4963	-0.0489
	-0.5833		-1.4833	-1.3500	-1.2583	2.2334	-0.1277
Khush-hal	0.5000	-0.3333	-	0.3683	-0.0483	-0.2433	0.3592
	0.1250	-0.0833		1.0167	0.8167	-0.5500	0.9634
Ciano	0.6667*	0.7983*	0.7500**	-	0.1433	-2.0183	0.0303
	0.5000	0.2917	-0.3750	-	0.4500	-2.2250	0.6177
Inia	1.0213**	-0.4583	-0.2500	-0.2500	-	-1.5183	0.3491
	0.2500	0.6417	0.2550	0.0417	-	-1.6500	0.6795

First reading under each column refers to Upperslu and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 66. Heading-span.

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chirook	Khush-hal	Ciano	Inia			
Marquis	-0.0600	0.2867	-0.1300	0.3700	0.1967	0.1967	-0.0175	-0.1405
	0.6200	-0.5893	-1.1467	-0.0050	-0.1033	-0.1033	-0.1874	-0.4982
Chirook	-0.6550	-0.2217	-0.2783	0.8200	0.3717	0.3717	0.0819	-0.1304
	-0.4167	-1.1217	-0.3717	-1.1467	0.6633	0.6633	0.3419	-0.3700
Khush-hal	-0.0417	-	0.0200	-0.5217	0.2550	0.2550	0.0988	-0.0968
	-0.1250	0.4503	0.5283	0.7950	0.0967	0.0967	-0.1087	0.0821
Ciano	0.3333	0.5833	-	-0.3550	-0.4533	-0.4533	0.1493	-0.1089
	0.0	0.0417	0.1250	0.8367	0.0967	0.0967	-0.1687	0.0822
Inia	0.9167**	-0.2083	0.1250	-	-0.3700	-0.3700	0.0807	0.2620
	0.2917	0.2500	-0.0883	-	-0.7533	-0.7533	0.3694	0.3871

TABLE 67. Plant height

Marquis	-0.9476	0.7593	2.0884	-3.1555	14.0397	195.9310	-2.9557
	-0.2017	2.1257	2.3297	-4.4209	12.5270	155.3739	-3.8799
Chirook	-0.8675	-1.0685	0.9945	5.5803	9.8603	96.0433	-2.6564
	1.6562	0.3258	0.1680	2.0956	12.5012	154.7285	3.8664
Khush-hal	2.7257	-	0.4511	0.6493	-8.6035	72.0374	-2.3832
	2.7450	-	2.1056	-0.2384	-9.7700	75.3602	-2.3383
Ciano	5.4176**	0.8667	-	-2.4269	-6.1142	36.2005	-1.1045
	5.5917**	3.7682	0.1045	-1.6792	-7.7160	57.9532	-0.5836
Inia	4.6572**	4.8160**	0.4758	-	-9.1824	83.1345	12.8684
	3.6565*	3.6762*	-0.1612	-	-8.5442	71.4512	5.3504

First heading under each column refers to Ellerslie and the second to Parkland.

* Significant at 5% level

** Significant at 1% level

in GCA and Ciano was the lowest. Marquis at Ellerslie and Chinook at Parkland ranked first for final heading while Ciano at both locations ranked last. For heading-span, Chinook showed the highest GCA and Inia the lowest at both locations. Marquis was the best combiner for plant height at both locations, while Inia at Ellerslie and Khush-hal at Parkland were the poorest. Chinook showed the highest GCA for number of tillers per plant at both locations and Inia was the lowest. Interpretations of GCA's for number of spikelets per spike, number of seeds per spike, weight of seeds per spike and 1000-kernel weight may be made in the same way. For yield per plant, Inia at Ellerslie and Marquis at Parkland had the highest GCA while Chinook at Ellerslie and Ciano at Parkland were the poorest.

The estimates of specific combining abilities, reciprocal effects and variances for general and specific combining abilities for onset-of-heading, final heading and heading-span are presented in Tables 64, 65 and 66. For onset-of-heading, cross (CxI) at Ellerslie and (MxC) at Parkland had the highest SCA while cross (MxI) at Ellerslie and (CHxC) at Parkland scored lowest. The best hybrid (CxI) at Ellerslie had parents with the lowest GCA's at both locations while the worst (MxI) and (CHxC) had one parent Marquis and Chinook which showed the highest GCA's at both locations. The variances for GCA were greater than those for SCA in all cases and the reciprocal effects were not significant. Interpretations for final heading (Table 65) and heading-span (Table 66) may be made in the same way.

For plant height (Table 67), hybrid (CHxI) at both locations

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from slofed-backcross diallel set at two locations.

TABLE 68. Number of tillers per plant

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	-0.2910	-0.7515	0.5171	0.2983	0.0554	-0.4926	-0.4891
	-0.1161	-0.5486	-0.6927	-1.0161	0.7212	0.3487	-0.4286
Chinook	-0.0792	-0.0109	1.0864	-0.1939	0.5642	0.1227	-0.4681
	0.1237	-0.7988	0.2752	0.6594	0.7512	0.3928	-0.4241
Khush-hal	-0.1787	-0.6125	0.1419	0.6200	0.3819	-0.0498	-0.3008
	-0.6792	-0.4780	0.7439	0.4993	0.3598	-0.0448	-0.1156
Ciano	0.5208	-0.4260	0.3893	-0.6341	-0.0788	-0.1894	0.0001
	1.3028	-0.7470	0.2823	-0.3619	-0.7265	0.3563	-0.0590
Inia	-0.1033	0.3393	0.4685	-	-0.9226	0.6556	-0.1848
	-0.0542	0.5090	-0.2125	0.0857	-1.1017	1.0423	0.1873

TABLE 69. Number of spikelets per spike

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis	0.0734	0.6184	0.2291	-0.1514	0.7318	0.5031	-0.0810
	0.5629	0.1757	-0.6347	-0.0683	0.5699	0.2252	-0.0870
Chinook	-0.1043	-0.0157	0.5060	-0.3085	0.1207	-0.0178	-0.0792
	0.2835	-0.0718	-0.0863	0.1980	0.3313	0.0750	0.0186
Khush-hal	0.2930	0.2042	0.1958	0.3165	-0.4789	0.1969	-0.0801
	0.2293	0.6835	0.3633	0.0295	-0.2941	0.0517	-0.0750
Ciano	0.5625	0.0867	-	-0.1921	-0.2321	0.0215	0.0346
	0.4038	0.4050	0.4162	0.1660	-0.4894	0.2047	-0.0402
Inia	-0.1140	0.3238	0.1035	-0.4457	-0.1415	-0.0124	0.0041
	0.1040	0.6657	0.0598	-0.2070	-0.0577	-0.0315	-0.0595

First reading under each column refers to Bjerslie and the second to Parkland.
*Significant at 5% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 70. Number of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	-0.7567	0.5266	0.3948	1.6680	-1.1312	3.7367	13.2888	-1.6858
Chinook	1.1823	0.3948	0.3948	1.0759	-0.8422	1.8352	2.9362	-1.0793
Khush-hal	-0.0193	-1.5155	-0.9569	1.7828	0.5295	-2.1908	4.1253	-1.4949
	0.3758	-0.9569	0.2750	0.2750	1.0215	-1.0805	0.7357	-0.6134
Ciano	2.2258*	0.6565	-0.6815	-0.6317	1.1138	-1.2477	0.8823	-0.8277
	0.4473	1.2037	-0.6815	-0.6317	-0.3786	0.4308	-0.2461	-0.7157
Inia	3.6933**	0.1728	0.1728	-	0.4189	-1.6029	1.8950	-0.4341
	1.9765	2.0132	1.6680	-	1.2470	-1.8508	2.7759	-0.5141
	-0.1647	1.2072	-1.7647	-1.2285	-	1.3047	1.0280	-0.6937
	0.1228	-0.5362	-0.0292	-1.0437	-	0.6653	0.0109	-0.0279

TABLE 71. Weight of seeds per spike

♀ Parent	Specific combining ability					GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano	Inia			
Marquis	0.6128	0.0927	0.0927	0.0572	-0.6088	0.0230	-0.0013	-0.0045
Chinook	0.0847	0.0141	0.0141	0.0760	0.0454	-0.0314	-0.0005	-0.0039
Khush-hal	0.0192	-0.0387	-0.0387	0.0596	-0.0314	-0.1290	0.0148	-0.0044
	0.0398	-0.0251	-0.0251	0.0611	-0.0083	-0.0845	0.0056	-0.0030
Ciano	0.6016	0.0010	-	-0.0354	0.0368	-0.0362	-0.0305	-0.0040
	0.0115	0.0365	-	-0.0536	0.0111	0.0607	0.0021	-0.0037
Inia	0.6635	0.0053	-0.0500	-	-0.0179	-0.0017	-0.0018	-0.0018
	0.0322	0.0066	0.0683	-	0.0659	-0.0252	-0.0008	-0.0013
	-0.0452	0.0062	-0.0368	-0.0763	-	0.1439	0.0189	-0.0036
	-0.0005	-0.0223	-0.0732	-0.0942	-	0.0834	0.0354	-0.0016

First reading under each column refers to Ellerslie and the second to Parkland.
 * Significant at 5% level
 ** Significant at 1% level

Estimates of specific combining ability, reciprocal effects and variances of general and specific combining ability from selfed backcross diallel set at two locations.

TABLE 72. 1000-kernel weight

♀ Parent	Specific combining ability				GCA	Variance of GCA	Variance of SCA
	Marquis	Chinook	Khush-hal	Ciano			
Marquis		0.1205	-0.4528	-0.2336	-2.3425	5.0186	-1.1713
		0.3031	0.0634	0.5471	-2.0504	3.8294	-0.9369
Chinook	0.6497		0.4032	-0.1392	-1.1454	0.8434	-1.1665
	6.4662		0.04	-0.2633	-1.0151	0.6557	-0.9063
Khush-hal	-0.2550	-0.3190		-0.3410	0.2448	-0.4096	-1.0488
	-0.0027	0.5133		0.5745	0.9864	0.6180	-0.9325
Ciano	-0.9073	-0.9833	-1.1687		1.4072	1.5116	-1.1070
	-0.9827	-0.2765	0.1962	-	0.9224	0.4760	-0.7040
Inia	-1.5043	-0.5807	0.6037	-0.5812	1.9379	2.9294	-0.3055
	-1.1452	-0.1232	-1.6265	-1.0067	1.1468	0.9405	0.4212

TABLE 73. Yield per plant

Marquis		-0.7261	-0.3066	-0.7549	0.5342	-0.0471	-0.2104	-0.5317
		0.5455	0.4427	0.1542	0.1742	-0.5386	0.0529	-0.5930
Chinook	-0.7872		0.0690	2.2204	-0.7179	-0.9473	0.5052	-0.3559
	0.9510		-2.0145	0.3140	0.4450	0.0681	-0.2316	-0.4939
Khush-hal	0.4678	-0.4383		0.2590	0.3710	-0.7653	-0.3731	-0.4868
	0.0276	0.3663		0.4008	0.7432	0.3231	-0.1328	-0.1846
Ciano	-0.3572	-0.6105	0.1245		-1.7015	0.6451	0.2034	1.3389
	0.7125	0.7363	1.4293*		-0.5442	-0.2341	-0.1824	-0.4987
Inia	-0.1232	-0.2025	-0.0010	0.0565		1.0147	0.8169	0.7462
	0.2093	0.5000	-0.4568	-0.1675		0.3815	-0.0917	-0.2341

First reading under each column refers to Ellerslie and the second to Parkland.
*Significant at 5% level

ranked highest while (MxI) ranked lowest. One parent of (CHxI), Chinook, showed the second highest GCA and the other, Inia, the lowest GCA at both locations. Similarly one parent of (MxI), Marquis, showed the highest GCA and other parent, Inia, the lowest GCA at both locations. The variances for GCA were greater in all the cases than those for SCA and the reciprocal effects were non-significant, except for (CxI), (IxI) and (KxI) at both locations. These effects may be attributed to the female parents of the respective crosses, because of the positive sign appended to each effect.

For number of tillers per plant, (CHxC) at Ellerslie and (KxC) at Parkland scored highest for SCA while cross (MxK) at Ellerslie and (MxI) at Parkland scored lowest (Table 68). The highest scoring hybrids at both locations had one parent, Ciano, with the second lowest GCA, while the poorest hybrids had one parent, Marquis, scoring second highest for GCA at both locations. The variances for GCA were greater than those for SCA except for Kxsh-hal at both locations and for Marquis and Ciano at Ellerslie. The reciprocal effects were generally non-significant except for (CxI) at Parkland. The results of the specific combining ability analysis for number of spikelets per spike (Table 69), number of seeds per spike (Table 70), weight of seeds per spike (Table 71) and 1000-kernel weight (Table 72) may be interpreted in the same way. Respective changes in the relative positions of the parents and hybrids for their GCA's and SCA's may be pointed out accordingly.

For yield per plant (Table 73), (CHxC) at Ellerslie and (KxI) at Parkland ranked highest for SCA while cross (CxI) at Ellerslie

TABLE 74

Analysis of variance, of general and specific combining ability and reciprocal effects from selfed backcross diallel set at two locations.

Character	M.S. for SCA		M.S. for Reciprocal effects		Error M.S.
	4	10	10	48	
Onset-of-heading	25.2656**	1.5062**	0.2253	0.2568	0.3877
Final heading	35.9375**	1.0437*	0.8927	0.1753	0.6340
Heading-span	34.6875**	0.0500**	0.1934	0.2107	0.7428
Plant height	41.3750**	3.8562**	0.3882	0.7428	
	1.4606**	0.4036	0.1924		
	2.5920**	1.9051			
Number of tillers per plant	1225.0937**	13.5937**	19.2065**	4.4336	5.8198
	1306.5469**	13.6375*	16.0161**		
	3.3135**	0.7664	0.4297	0.7332	0.6427
	7.3857**	1.8497*	0.6839		
Number of spikelets per spike	2.1357**	0.2266	0.1581	0.1166	0.1306
	1.7500**	0.2414	0.1404		
Number of seeds per spike	61.4688**	3.6574	5.4534*	2.5252	1.6190
	21.4844**	2.8805	2.7848		
Weight of seeds per spike	8.0980**	0.0033	0.0059	0.0068	0.0059
	0.0469**	0.0095	0.0066		
1000-kernel weight	30.5469**	1.0941	1.4595	1.7574	1.4052
	21.0039**	2.0250	1.3617		
Yield per plant	6.8789**	2.5621**	0.3304	0.7980	0.8897
	1.4990	0.7430	0.9333		

First reading under each column refers to Ellerslie and second to Parkland.

* Significant at 5% level

** Significant at 1% level

and (CHxK) at Parkland ranked lowest. The best hybrid at Ellerslie had one parent (Chinook) with the lowest GCA for that location while the best hybrid (KxI) at Parkland had one parent (Khush-hal) with the second lowest GCA for that location. On the other hand, the poorest ranking hybrid (CxI) at Ellerslie had one parent, Inia, with the highest GCA for that location while the lowest scoring hybrid at Parkland had one parent (Chinook) with the second highest GCA for that location. Variances for GCA were larger than those for SCA except for Marquis at Ellerslie, Chinook, Khush-hal and Inia at Parkland, and Ciano at both locations. Only cross (IxK) at Parkland showed significant reciprocal effect which may be ascribed to Inia.

Analysis of variance of general and specific combining ability (Table 74) yielded significant mean squares for GCA for all characters except for plant height, number of tillers per plant and yield per plant at Parkland. Significance for SCA mean squares for onset-of-heading, final heading and plant height at both locations and for yield per plant at Ellerslie show a relatively greater importance of SCA over GCA for these characters in the selection procedures of the breeding programmes.

Diallel cross analysis

The assumption of no differences between reciprocal crosses is tested in Table 75. Significance of the σ component for plant height, number of seeds per spike and 1000-kernel weight at both locations and heading-span and weight of seeds per spike at Parkland indicates reciprocal

TABLE 75

Mean squares from the analysis of variance of 5 x 5 selfed bulmoss diallel set for ten characters at two locations.

Source of variation	D.F.	Plant height	Heading span	Number of tillers per plant	Number of spikelets per spike	Number of seeds per spike	Weight of seeds per spike	1200 kernel weight	Yield per plant
a	4	75.7811**	104.2741**	4.3018*	3675.7595**	9.9355	6.4014**	184.4062**	0.2940*
b	10	107.8155**	133.2011**	7.7773	3919.7509**	22.1445**	5.2451*	64.4659**	0.1408*
b ₁	1	4.5912**	3.1675**	1.2113	60.6509*	2.3070	0.0810	11.0250	0.0099
b ₂	1	3.1750	11.5562**	5.7148	60.9920	4.0539	0.7270	8.6667	0.0236
b ₃	1	14.8519	6.5769	0.0513	25.4775	2.0295	1.4763	12.0519	0.0301
b ₄	1	12.1002	41.2552	8.6700	10.2661	5.5126	4.5693*	19.1136	0.0721
b ₅	4	2.5409	2.1135	1.2226	22.5409	1.4173	0.8140	10.5610	0.0395
b ₆	4	14.1405	5.7969	4.6944	61.6034	5.2762	0.0742	11.3848	0.0482
b ₇	5	4.1175**	3.1625**	1.3690**	58.2030*	3.6798*	0.4086	11.1500	0.0124
b ₈	3	3.6070	10.2500**	5.9672**	39.0375*	2.7453**	0.4307	4.4373	0.0344
c	4	6.6923	2.4437	0.6652	134.9273**	1.1618	0.6294	31.6001*	0.0241
d	4	0.4830	0.2065	0.6625*	111.7655**	2.1591	0.9578	18.2904**	0.0421**
e	6	0.7952	2.6344	1.4912	13.1473	1.3726	0.3740	6.8195	0.0134
f	1	1.9217	0.7924	0.5291	5.6034	1.6966	0.6032	2.1623	1.9465
Blocks x c	8	0.6754	2.8987	0.6746	35.1194	4.2524	0.4226	6.0583	3.5156
Blocks x b	20	1.1750	0.6219	0.7927	11.6169	1.7526	0.4217	6.4220	0.0207
Blocks x b ₁	2	1.5245	2.7504	2.6783	27.2594*	2.4264	0.4600	5.3156	0.6241
Blocks x b ₂	2	7.9587	1.1337	1.9829	35.1591	0.6399	0.9345	28.6114	0.6227
Blocks x b ₃	2	4.2094	22.6379	9.6817	243.6152	29.1593	0.6720	1.6645	0.0962
Blocks x b ₄	2	1.4365	0.7193	1.3752	11.5615	3.1234	0.5036	6.4907	0.0112
Blocks x b ₅	2	1.1451	2.1184	4.2745	27.5602	2.6386	0.9176	10.4700	0.6195
Blocks x b ₆	2	0.4207	6.0642	0.0983	10.7312	0.6729	0.3669	4.7377	0.0715
Blocks x b ₇	2	1.6175	1.5125	0.2515	8.1107	0.4510	0.2303	2.0075	0.0565
Blocks x b ₈	2	6.4682	0.7219	0.6130	6.4521	1.6612	0.2022	4.5607	0.0101
Blocks x b ₉	2	0.7101	0.5036	0.1562	5.3491	0.5033	0.1417	1.2152	0.6034
Blocks x b ₁₀	2	5.1179	0.7473	0.1552	6.2776	2.4184	0.2315	2.2112	0.0334
Blocks x b ₁₁	2	0.5923	0.7542	0.5359	3.0176	0.7033	0.1323	2.0715	0.3046
Blocks x b ₁₂	2	0.6279	0.6624	0.6624	11.0620	2.2925	0.3665	7.6619	0.0204
Blocks x b ₁₃	2	1.2605	1.2645	2.2221	17.5610	1.1210	0.1935	4.8671	0.0178
error	48								

* Significant at 5% level
 ** Significant at 1% level
 First reading under each column refers to Kilaru and second to Parkland. Error D.F. comprises of block interaction with D.F. of (a-broad).
 Each component has been tested against its own block interaction.

TABLE 77

Estimates of second degree statistics from selfed backcross diallel set for ten characters at two locations.

Character	1952	1953	1954	1955	1956	1957
Sheath-of-heading	15.660	6.1531	2.9312	3.5941	0.7921	0.7921
	15.7502	7.4624	3.9777	4.1244	0.6434	0.6434
Final heading	16.0006	7.6016	3.4756	4.0042	0.9581	0.9581
	27.1914	10.9432	4.4403	6.1744	0.2201	0.2201
Heading-span	3.5067	0.2219	0.1462	0.1100	0.0346	0.0346
	3.0111	0.5279	0.2793	1.2118	0.4024	0.4024
Plant height	409.7744	241.1279	122.5274	124.1212	0.3583	0.3583
	516.4112	257.2312	135.0756	137.4928	0.2476	0.2476
Number of tillers per plant	1.4143	0.6190	0.3113	0.7159	0.1081	0.1081
	5.4749	1.8428	0.7383	1.4139	0.2944	0.2944
Number of spikelets per spike	1.2283	0.4789	0.2116	0.3275	0.0787	0.0787
	0.5749	0.3149	0.1750	0.2965	0.2436	0.2436
Number of seeds per spike	20.0000	12.0000	6.1455	47.9799	0.6227	0.6227
	12.2475	4.0342	2.1465	3.5206	1.0207	1.0207
Weight of seeds per spike	0.0384	0.0369	0.0398	0.0115	0.0093	0.0093
	0.0360	0.0115	0.0049	0.0097	0.0238	0.0238
1000-kernel weight	16.7448	7.1279	3.0517	3.6014	0.5468	0.5468
	13.1070	4.9053	2.0977	3.1123	0.5517	0.5517
Yield per plant	5.4331	1.7342	0.6600	1.9697	0.0668	0.0668
	0.0079	0.0533	0.1502	0.5220	0.2755	0.2755

First reading under each column refers to Elliptical and second to Parkland.

TABLE 76

Analysis of variance of $\bar{X}_i - \bar{Y}_i$ from selfed backcross diallel set for ten characters at two locations.

Character	D.F.	Mean Square	Error M.S.
Sheath-of-heading	9, 496	0.2775	0.1127
	3, 485	2.5160	0.2300
Final heading	6, 483	0.1561	0.1025
	34, 473	1.1202	1.2708
Heading-span	3, 487	17.12	0.0024
	4, 929	0.4502	1.1094
Plant height	9, 496	106.16	0.0001
	644, 485	100.075	194.000
Number of tillers per plant	3, 484	0.2379	0.1126
	28, 487	0.0073	0.0001
Number of spikelets per spike	3, 485	0.0035	0.0445
	6, 482	0.1384	3.2724
Number of seeds per spike	20, 482	9.104	15.0000
	27, 480	2.000	0.1600
Weight of seeds per spike	9, 490	0.0001	0.00
	6, 484	0.0001	0.0001
1000-kernel weight	16, 484	1.5762	2.7421
	19, 481	5.2293	5.6779
Yield per plant	3, 486	0.2160	4.8807
	6, 483	0.1368	0.0050

First reading under each column refers to Elliptical and second to Parkland.

differences for these characters. Significance of the a for all characters except heading-span at Ellerslie, number of tillers per plant at Parkland and yield per plant at both locations indicates substantial differences among the parents. Significance of b for final heading at both locations and onset-of-heading and plant height at Ellerslie shows that dominance is present while b_1 for number of spikelets per spike at Ellerslie shows that dominance is directional. Analysis of $W_p - V_p$ (Table 76) indicates that other assumptions, viz., no non-allelic interaction, no multiple allelism and uncorrelated gene distribution, are valid for all characters at both locations.

After Hayman's (1954a) procedure of replacement of reciprocal crosses by their common means, diallel analysis for genetic components of variation was carried out. Estimates of second degree statistics are given in Table 77 and the genetic components of variation obtained from them are presented in Table 78. Significance of components of variation was tested as in the previous diallel analyses of F_1 , F_2 and backcross sets. The proportional values of the estimates of genetic parameters from Table 78 are given in Table 79.

The ratio $(H_1/D_1)^{1/2} < 1$ for onset-of-heading at both locations (Table 79) shows that dominance is partial (see also Figure 61). The estimate of $[H_2 \div 4H_1] = 0.21$ at Ellerslie and 0.24 at Parkland implies some asymmetry in numbers of positive and negative alleles at loci exhibiting dominance at Ellerslie and equal proportion of positive and negative effects at Parkland. The proportion of dominant to recessive genes in the parents is > 1 at both locations indicating thus

TABLE 78

Indicates if genetic component of variation from selfed ancestors dialleled out for ten characters at two locations.

Character	D	F ₁	H ₁	H ₂	H ₃	F
Grain-of-head	14.743 ± 0.215**	5.072 ± 0.115**	2.060 (5.595*)	2.577 ± 0.517**	3.042 ± 0.1010**	0.250 ± 0.0871**
	15.112 ± 0.121**	1.007 ± 0.507**	1.335 ± 0.322**	1.319 ± 0.297**	2.336 ± 0.2010**	0.307 ± 0.0190**
Fanal heading	10.794 ± 0.195**	3.149 ± 0.401**	2.132 ± 0.520**	1.705 ± 0.478**	1.704 ± 0.323**	0.175 ± 0.070**
	20.910 ± 0.172**	2.701 ± 1.400**	7.224 ± 1.503**	6.435 ± 1.438**	0.394 ± 0.9711**	0.030 ± 0.3307**
Heading-span	2.370 ± 0.170**	-0.022 ± 0.464	0.552 ± 0.481	0.369 ± 0.430	0.045 ± 0.205*	0.110 ± 0.075**
	2.004 ± 0.306**	2.615 ± 0.734**	2.815 ± 0.976**	2.325 ± 0.839**	1.372 ± 0.590**	0.728 ± 0.1476**
Plant height	42.211 ± 2.71**	-4.101 ± 31.793	23.104 ± 15.924	16.372 ± 14.492	2.591 ± 9.757	4.436 ± 2.410**
	52.111 ± 4.041**	1.752 ± 12.035	24.479 ± 13.073	15.001 ± 11.685	-1.534 ± 8.002	5.819 ± 1.970**
Number of tillers per plant	0.700 ± 0.030**	-0.474 ± 0.404	-0.132 ± 0.526	0.070 ± 0.470**	-0.095 ± 0.321*	0.737 ± 0.070**
	4.611 ± 0.200**	2.002 ± 0.514**	2.063 ± 0.530**	1.415 ± 0.504**	0.701 ± 0.343*	0.643 ± 0.084**
Number of spikelets per spike	1.154 ± 0.031**	0.303 ± 0.133*	0.172 ± 0.163	0.210 ± 0.147	0.212 ± 0.094**	0.121 ± 0.024**
	0.441 ± 0.041**	-0.206 ± 0.111	0.101 ± 0.117	0.228 ± 0.103	0.691 ± 0.071**	0.130 ± 0.017**
Number of seeds per spike	20.600 ± 0.777**	3.414 ± 1.922**	2.828 ± 2.103*	2.202 ± 1.953	0.525 ± 1.310	2.526 ± 0.325**
	10.755 ± 0.703**	3.977 ± 1.972**	3.341 ± 2.001	2.587 ± 1.670	3.045 ± 1.202**	1.019 ± 0.311**
Weight of seeds per spike	0.336 ± 0.057**	-0.017 ± 0.003	-0.002 ± 0.003**	-0.070 ± 0.002**	-0.003 ± 0.0015**	0.006 ± 0.0004**
	2.042 ± 0.025**	0.010 ± 0.006**	0.013 ± 0.006**	0.037 ± 0.006	0.016 ± 0.004**	0.035 ± 0.001**
Yield per plant	15.015 ± 0.305**	2.908 ± 0.938**	-1.03 ± 0.973	-1.323 ± 0.683	1.050 ± 0.596	1.750 ± 0.147**
	11.716 ± 0.703**	5.019 ± 1.877**	2.306 ± 2.002	1.247 ± 1.644	1.307 ± 1.232	1.454 ± 0.306**
	4.001 ± 1.105**	3.010 ± 2.509*	4.125 ± 3.207	3.519 ± 2.919	-0.241 ± 1.901	0.797 ± 0.404**
	-0.074 ± 2.112	-0.706 ± 0.357	-0.703 ± 0.304	-0.513 ± 0.345	0.539 ± 0.233	0.886 ± 0.047**

First rowing under each column refers to Ellerslie and second to parkland.

* Significant at 5% level

** Significant at 1% level

TABLE 79

Proportional values of the estimates of genetic parameters from selfed backcross diallel set for ten characters at two locations.

Character	$(H_1/D)^{1/2}$	$(H_2/3H_1)$	$\left[\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} \right]$	H_2^2/H_1	$r_{Y_r^2}$	$r_{Y_r^2+V_r}$	Heritability
Onset-of-heading	0.4432*	0.2119*	2.2715*	1.1839*	0.9161	1.0850	1.0850
	0.2957*	0.2487*	1.2712*	1.7521*	0.6870	0.6845	0.6845
Final heading	0.3557*	0.2076*	1.7689*	0.7248*	0.7816	1.0301	1.0301
	0.5223*	0.2229*	2.0905*	1.3020*	0.9245	1.0001	1.0001
Heading-span	1.1562	0.1909	0.9939	0.0116	-0.0581	0.2186	0.2186
	0.9908*	0.2064*	2.7079*	0.5912*	0.7279	0.4752	0.4752
Plant height	0.2043	0.2276	0.9584	0.1418	-0.4065	0.9198	0.9198
	0.2185	0.1596	1.0099	-0.0982	-0.6697	0.9165	0.9165
Number of tillers per plant	0.3488	-0.2083	0.0013	-0.5189	-0.7496	0.1735	0.1735
	0.6572*	0.1697*	2.5634*	0.5408	0.6240	0.7228	0.7228
Number of spikelets per spike	0.5209	0.1733	2.0258	1.1137	-0.8852	0.7355	0.7355
	0.6031	0.3477	0.3357	3.9638	-0.0175	0.3166	0.3166
Number of seeds per spike	0.5293	0.1979	1.5011	0.4177	-0.6535	0.7359	0.7359
	0.6020	0.1651	1.9039	1.2000	-0.5900	0.6257	0.6257
Weight of seeds per spike	0.5352	0.1904	0.6546	0.6502	0.9431	0.6159	0.6159
	0.6643*	0.1357	2.8052*	1.6045	-0.2946	0.6270	0.6270
1000-kernel weight	0.3557	0.1741	1.7554	-0.7852	0.3482	0.8722	0.8722
	0.4407	0.1329	2.8281	1.0111	-0.3856	0.8002	0.8002
Yield per plant	0.5035	0.2042	2.0130	-0.3888	0.2	0.5088	0.5088
	18.9020	0.0972	-0.7970	-1.2260	0.5145	-0.0005	-0.0005

First reading under each column refers to Ellerslie and second to Parkland.

*Proportional values involving genetic components of variation significantly different from zero ($P < 0.05$)

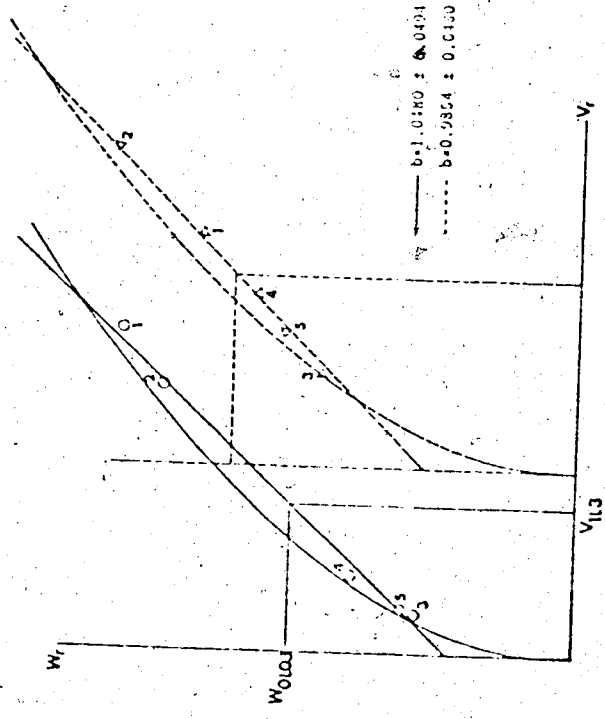


Figure 61. W_p, V_p graph for onset-of-heading

from selfed backcross diallel set.

— $o = W_p, V_p$ intercepts

at Ellerslie

--- $\Delta = W_p, V_p$ intercepts

at Parkland

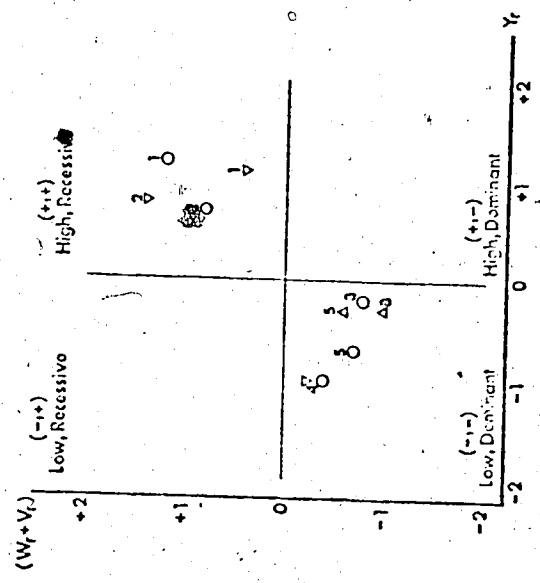


Figure 62. Standardized deviation graph of $[Y_p]$

and $[W_p + V_p]$ for onset-of-heading

from selfed backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts

at Ellerslie

$\Delta = Y_p, [W_p + V_p]$ intercepts

at Parkland

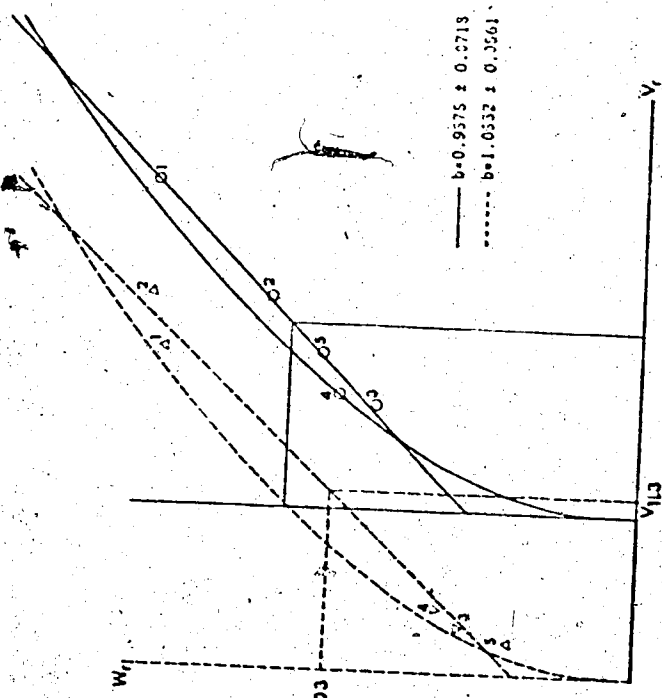


Figure 63. W_Y, V_Y graph for final heading from selfed backcross diallel set.

— $o = W_Y, V_Y$ intercepts at Ellerslie
 --- $\Delta = W_Y, V_Y$ intercepts at Parkland

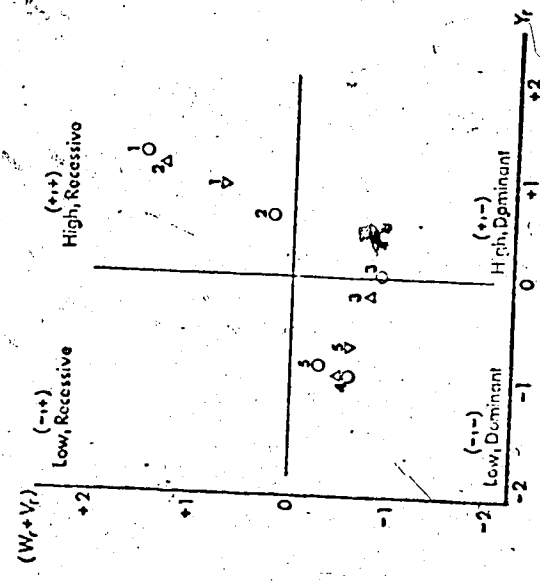


Figure 64. Standardized deviation graph of $[Y_Y]$ and $[W_Y + V_Y]$ for final heading from selfed backcross diallel set.

$o = Y_Y, [W_Y + V_Y]$ intercepts at Ellerslie
 $\Delta = Y_Y, [W_Y + V_Y]$ intercepts at Parkland

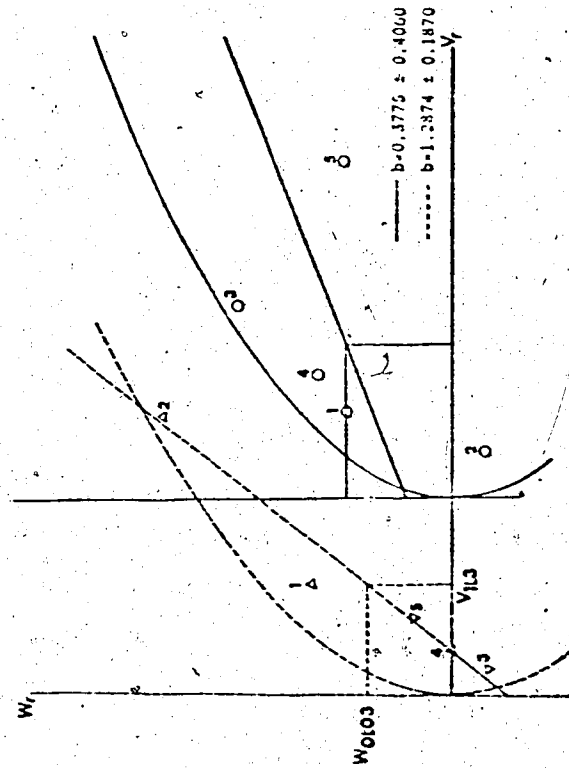


Figure 65. W_p, V_p graph for heading-span from selfed backcross diallel set.

— $\Omega = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

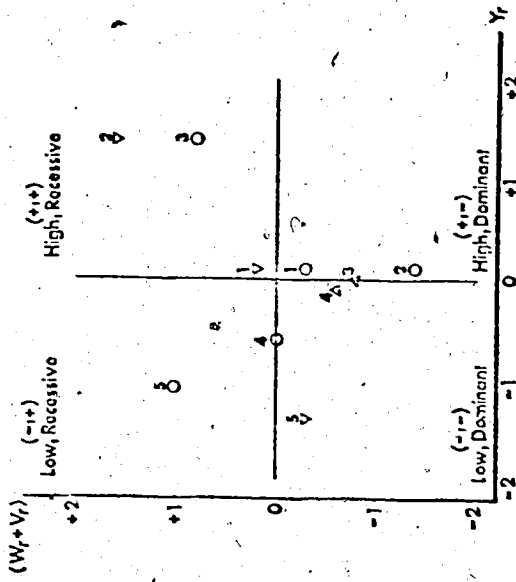


Figure 66. Standardized-deviation graph of $[Y_p]$

and $[W_p + V_p]$ for heading-span from selfed backcross diallel set.
 $\circ = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

a preponderance of dominant genes. $[h^2/H_2] > 1$ at both locations suggests that at least two groups of genes exhibiting dominance contribute to the control of onset-of-heading. The coefficients of correlation between parental order of dominance and parental measurements (0.916 at Ellerslie and 0.687 at Parkland) indicate that earliness is dominant over lateness. Figure 61 shows that Marquis at Ellerslie and Chinook at Parkland are the most recessive parents while Khush-hal at both locations is the most dominant. Figure 62 places Marquis and Chinook in the (+,+) quadrant, indicating that lateness of these parents is associated with recessive genes. Khush-hal, Ciano and Inia occupy the (-,-) quadrant at both locations, suggesting that these parents are early maturing dominants.

The interpretations from Tables 78 and 79 for final heading (Figures 63, 64) and for heading-span (Figures 65, 66) may be made in the similar fashion. The changes in the relative position of the parents with respect to their order of dominance at the two locations could be attributed to environmental effects.

In case of plant height, the ratio of $[H_1/D]^{1/2} < 1$ at both locations indicates that the character is inherited as a partially dominant trait. Since all other components of variation, except D and E are non-significant at both locations (Table 78), the interpretation of proportional values of genetic parameters is meaningless. Figure 67 classifies Ciano at Ellerslie and Khush-hal at Parkland as the most recessive parents and Chinook as the most dominant at both locations. Figure 68 indicates that the most dominant parent (Chinook) at both

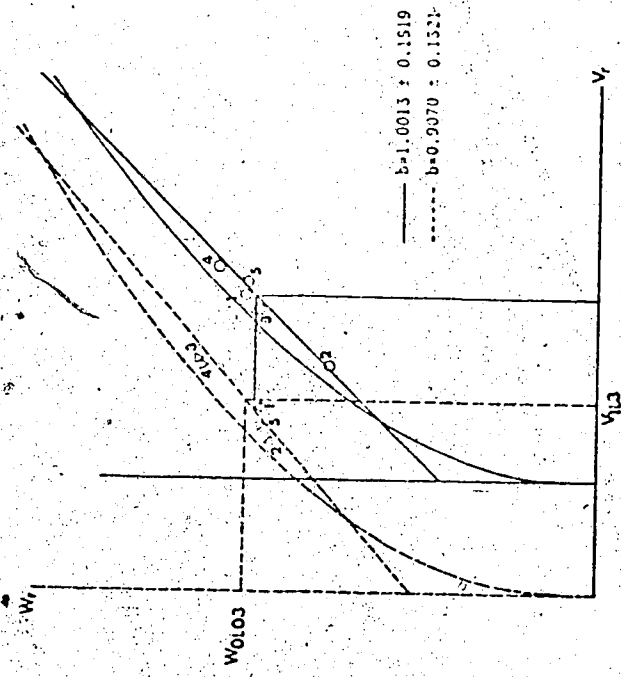


Figure 67. W_p, V_p graph for plant height from selfed backcross diallel set.

— $O = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

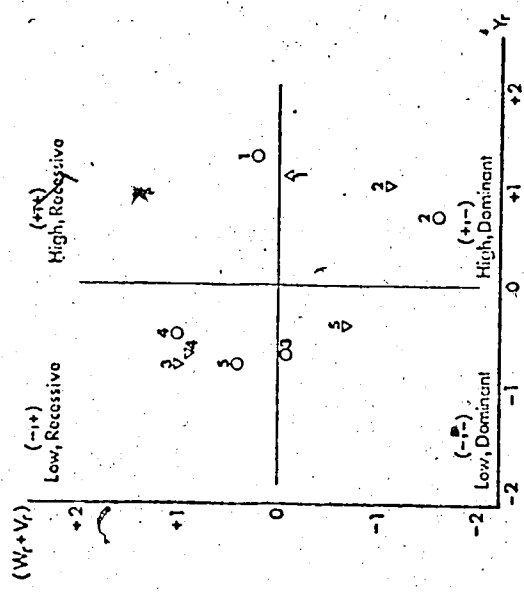


Figure 68. Standardized deviation graph of $[Y_p]$.

and $[W_p + V_p]$ for plant height from selfed backcross diallel set.

$O = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

locations, contributes to tallness, while the most recessives (Ciano and Khush-hal) contribute to shortness; i.e. the order of dominance of the parents is negatively correlated with their measurements. However, as shown in Table 79, the respective coefficients of correlation do not reach the 5% level of significance. The order of dominance of parents seems to differ at the two locations (Figure 58). The most recessive parent at Parkland (Khush-hal; -, + quadrant) possesses an excess of dominant genes (-, - quadrant) at Ellerslie, while Iria with an excess of recessive genes at Ellerslie (-, + quadrant), appears to have a preponderance of dominants at Parkland (-, - quadrant). Marquis, recessive at Ellerslie becomes dominant at Parkland. The ranking order of Ciano and Chinook remained unchanged. The coefficient of heritability was very high (91%) at both locations.

For number of tillers per plant, only the *D* and *E* components of variation were significant at Ellerslie, while all components except h^2 were significant at Parkland. Consequently, the proportional values of the estimates of parameters for Ellerslie data are not discussed. However, the mean degree of dominance may be given, since $(H_1 \div D)^{1/2} < 1$ for both locations indicating that tillering capacity is inherited as partially dominant. The ratio $[H_2 \div 4H_1] = 0.169$ at Parkland suggests asymmetry of positive and negative alleles at loci exhibiting dominance. The proportion of dominant to recessive genes in the parents is 2.58 indicating a preponderance of dominants. Since $[h^2/H_1] = 0.54$, it may be assumed that at least one group of genes exhibit dominance and control the inheritance of tiller number. The correlation coefficient between

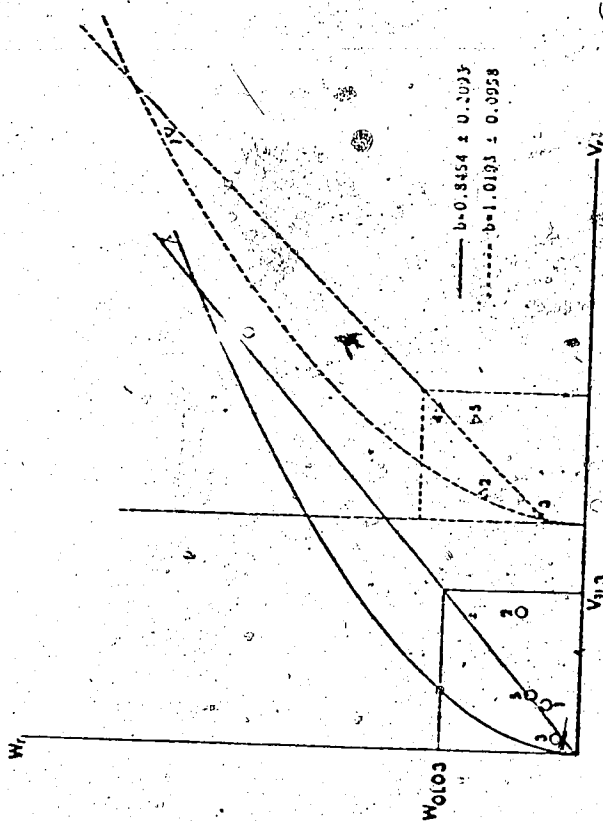


Figure 69. W_p, V_p graph for number of tillers per plant from selfed backcross diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

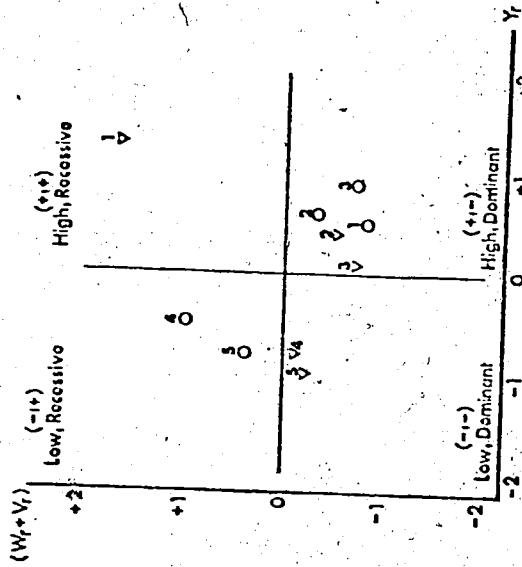


Figure 70. Standardized deviation graph of $[Y_p]$ and $[W_p, V_p]$ for number of tillers per plant from selfed backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

parental order of dominance and parental measurements is -0.748 at Ellerslie and 0.624 at Parkland. The significant negative correlation at Ellerslie indicates that the high tillering capacity is dominant over low tillering capacity while positive correlation at Parkland concludes that lower tiller number is dominant over higher. Figure 69 classifies Ciano and Khush-hal at Ellerslie as the most recessive and the most dominant parents, respectively. At Parkland, Marquis and Khush-hal are the most recessive and the most dominant parents, respectively. Figure 70 shows changes in the dominance ranking order of the parents between the two locations. Marquis, the most recessive parent at Parkland, (+,+ quadrant) appears to contain an excess of dominant genes at Ellerslie (+,+ quadrant) while Ciano and Inia, recessive parents at Ellerslie (+,+ quadrant) appear as dominant at Parkland (-,- quadrant). Ranking order of Khush-hal and Chincok remain unchanged. The heritability estimates of 17.35% at Ellerslie and 72.28% at Parkland show that the character is highly unstable. This instability may be due to non-significance of genetic components of variation at Ellerslie and significance of environmental components of variation at both locations.

The results of diallel cross analysis from Tables 78 and 79 for number of spikelets per spike (Figures 71, 72), number of seeds per spike (Figures 73, 74), weight of seeds per spike (Figures 75, 76) and 1000-kernel weight (Figures 77, 78) may be interpreted in the same way as number of tillers per plant. Respective changes in the ranking order of parents for order of dominance and significance or non-significance

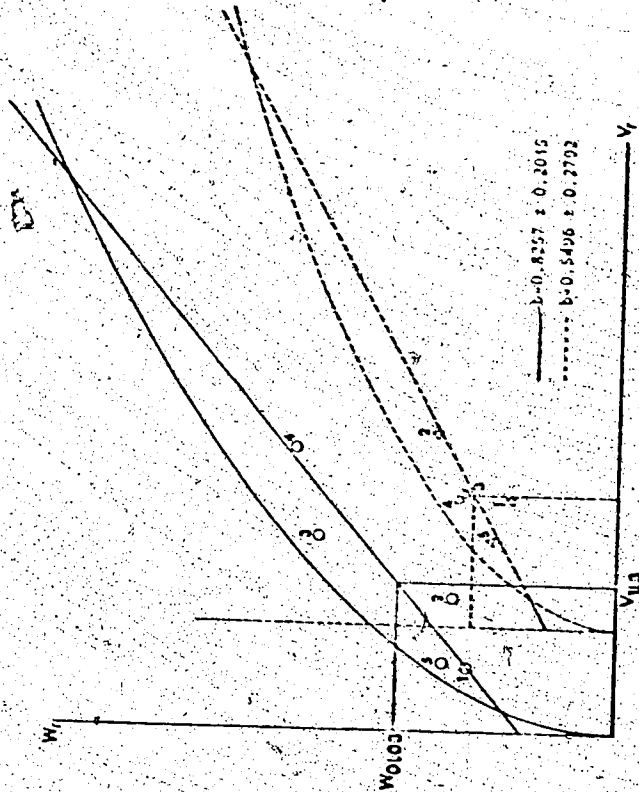


Figure 71. W_1, V_1 graph for number of spikelets per spike from selfed backcross diallel set.

— $\circ = W_1, V_1$ intercepts at Ellerslie
 --- $\Delta = W_1, V_1$ intercepts at Parkland.

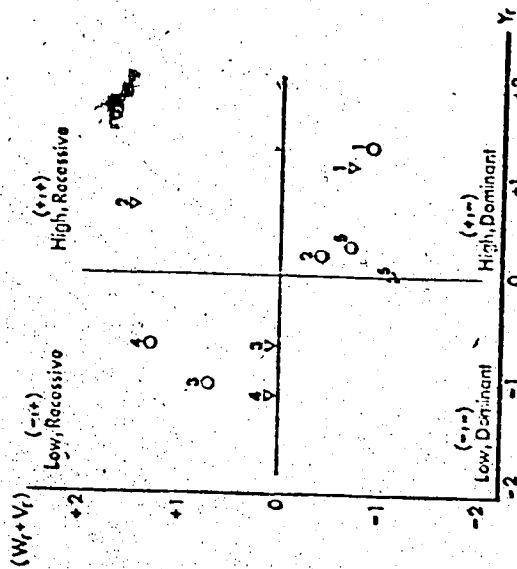


Figure 72. Standardized deviation graph of $[Y_r]$ and $[W_r + V_r]$ for number of spikelets per spike from selfed backcross diallel set.

$\circ = Y_r, [W_r + V_r]$ intercepts at Ellerslie
 $\Delta = Y_r, [W_r + V_r]$ intercepts at Parkland

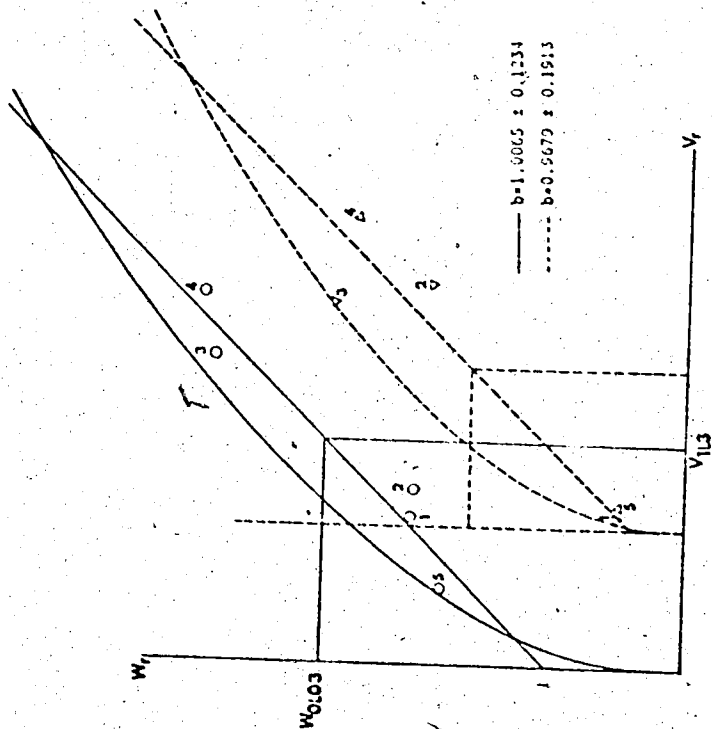


Figure 73. W_p, V_p graph for number of seeds per spike from selfed backcross diallel set.

— $O = W_p, V_p$ intercepts at Ellerslie
 - - - $\Delta = W_p, V_p$ intercepts at Parkland

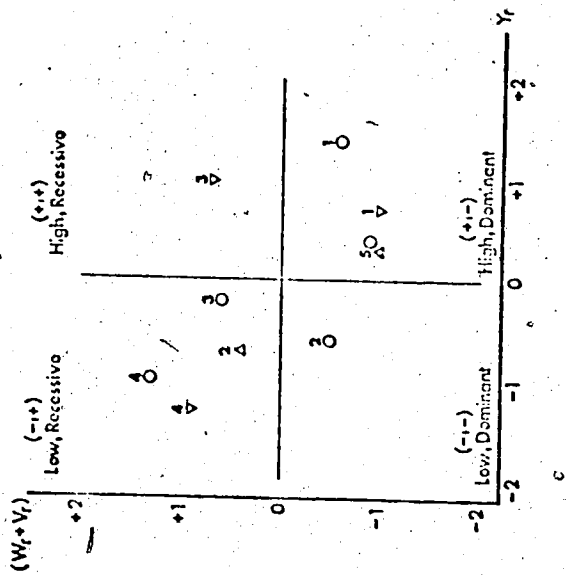


Figure 74. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for number of seeds per spike from selfed backcross diallel set.

$O = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

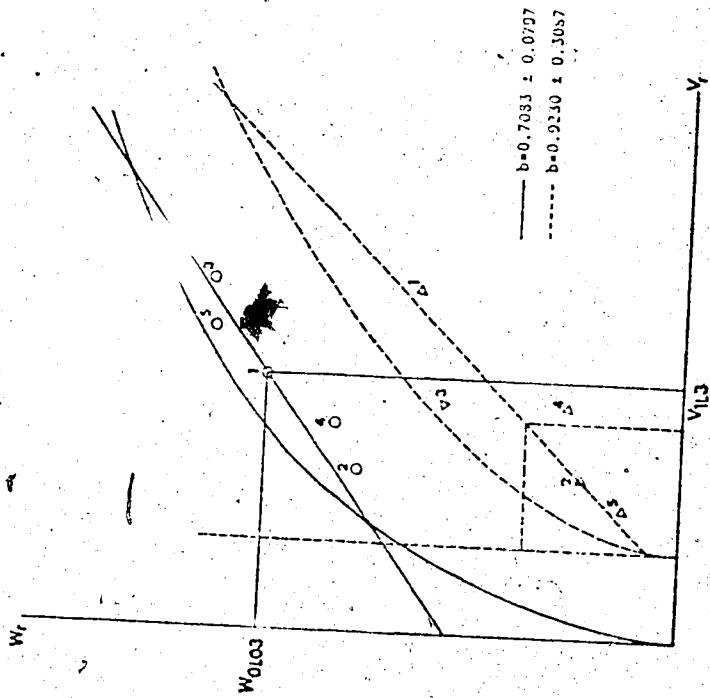


Figure 75. W_p, V_p graph for weight of seeds per spike from selfed backcross diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 --- $\Delta = W_p, V_p$ intercepts at Parkland

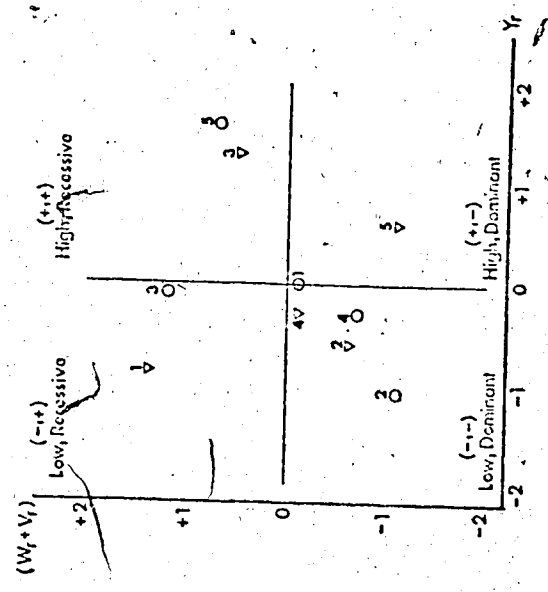


Figure 76. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for weight of seeds per spike from selfed backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

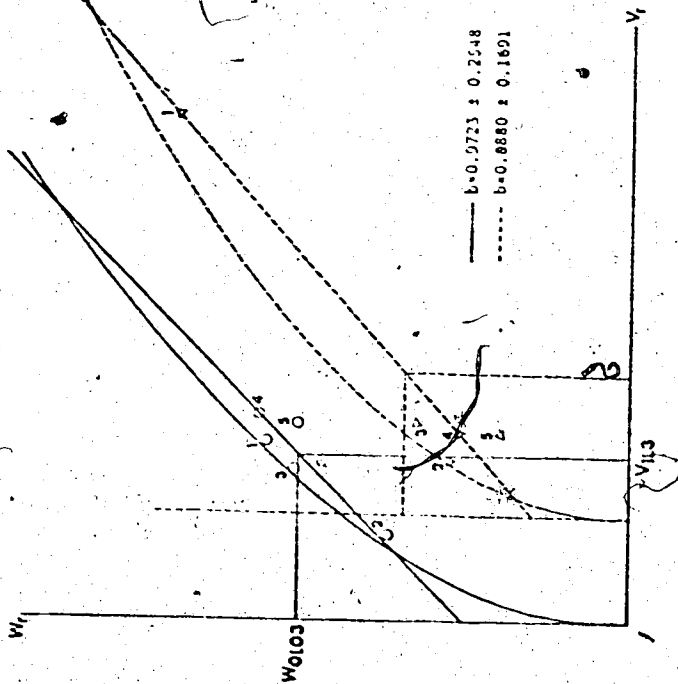


Figure 77. W_p, V_p graph for 1000-kernel weight from selfed backcross diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie
 ---- $l = W_p, V_p$ intercepts at Parkland

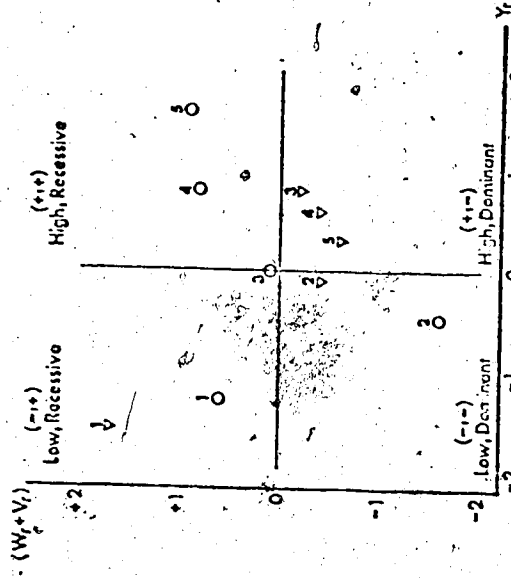


Figure 78. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for 1000-kernel weight from selfed backcross diallel set.

$o = Y_p, [W_p + V_p]$ intercepts at Ellerslie
 $\Delta = Y_p, [W_p + V_p]$ intercepts at Parkland

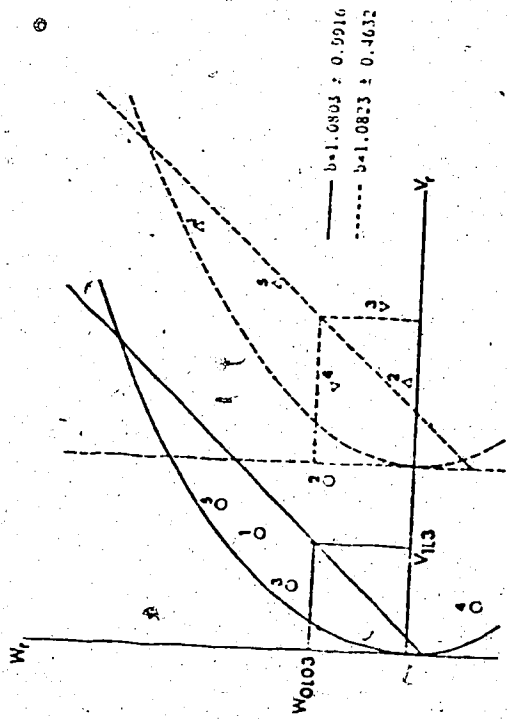


Figure 79. W_p, V_p graph for yield per plant from selfed backcross, diallel set.

— $o = W_p, V_p$ intercepts at Ellerslie

--- $\Delta = W_p, V_p$ intercepts at Parkland

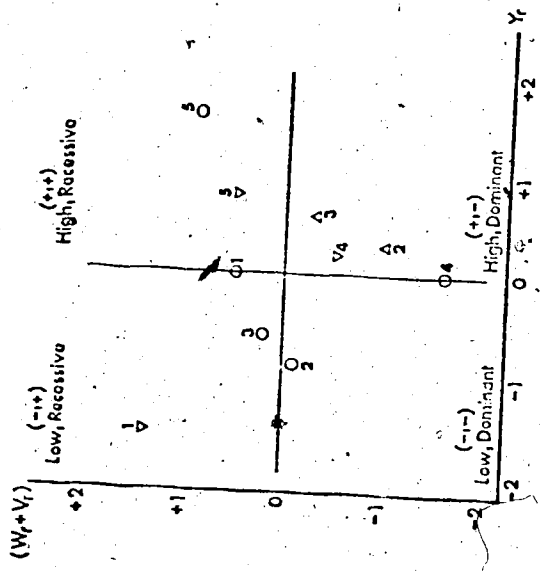


Figure 80. Standardized deviation graph of $[Y_p]$ and $[W_p + V_p]$ for yield per plant from selfed backcross diallel set.

$o = W_p, V_p$ intercepts at Ellerslie

$\Delta = W_p, V_p$ intercepts at Parkland

of genetic components of variation over the two locations may be interpreted accordingly.

In case of yield per plant, all the components of variation except D and E at Ellerslie and E at Parkland were non-significant. The proportional values of the genetic parameters given in Table 79 therefore do not carry valid conclusions. The ratio $[H_1 = D]^{1/2} > 1$ at Parkland and ≈ 1 at Ellerslie suggests over-dominance and nearly complete dominance. The W_p, V_p graph (Figure 79) shows over-dominance at both locations (the regression line intersects the limiting parabola below the origin). The correlation coefficient of 0.127 at Ellerslie and -0.594 at Parkland suggests that low yielding capacity is dominant over high yield at Ellerslie and vice versa at Parkland. Figure 79 categorizes Inia and Ciano as the most recessive and dominant parents, respectively, at Ellerslie, while Marquis and Chinook as the most recessive and dominant parents, respectively, at Parkland. Figure 80 suggests that the highly recessive parent at Ellerslie is high yielding (+, + quadrant), while the highly recessive parent at Parkland is low yielding (-, + quadrant). Figure 80 also reveals changes in the ranking of parents with respect to their order of dominance at both locations. Khush-hal, recessive low-yielding at Ellerslie, appears to be dominant high-yielding at Parkland. Marquis, the most recessive parent at Parkland, appears comparatively less recessive at Ellerslie. Inia, Chinook and Ciano remained unchanged. Heritability of 51% at Ellerslie and $-0.0005 = 0\%$ at Parkland suggests, respectively, high and non-heritable nature of yield. This reflects the inter-location environmental effect on the inheritance of yield.

GENOTYPE-ENVIRONMENT INTERACTION

This section of the experimental results deals with the comparison of the estimates of factor loadings, general combining abilities and genetic components of variation obtained from the analyses of four diallel sets considered over two locations.

In order to assess the stability of five principal factors with respect to their loadings on different characters, the varimax rotated factor matrices of F_1 , E_2 , backcross and selfed backcross diallel sets were factorially analysed for two locations. The results of analysis of variance are given in Table 80. Significance of mean squares for principal factors (F) and Characters (C) (upper part of Table 80) suggests that the number of factors required to explain the variability in the data varies with the number and the degree of expression of the characters under study. This is also indicated by significant F x C interaction, which implies that the differences between the contributions of different characters to factor loadings vary with the number of principal components. Significant inter-location effects (L) indicate differences in scores on the characters related to different principal components at different locations. Significance of the second order interaction, L x F x C, may be considered as interaction of the L x F with C, L x C with F, or of F x C with L. Since L x C is not significant, indicating that characters do not vary with locations, the L x F x C interaction may be interpreted in the light of L x F and F x C interactions alone. In the first case, L x F x C indicates that after pooling the sum of squares

TABLE 80

Factorial analysis of variance of factor loadings of varimax rotated factor matrices of F1, F2, backcross and selfed backcross diallel sets over two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	0.23868	0.23868	5.15589*
Principal factors (F)	4	2.73528	0.68382	14.77165**
L x F	4	2.39790	0.59947	12.94968**
Generations (G)	3	0.07528	0.02509	0.54210
L x G	3	0.08975	0.02991	0.64629
F x G	12	0.54642	0.04503	0.97284
L x F x G	12	0.19273	0.01606	0.34695
Characters (C)	9	1.60613	0.20068	4.33507**
L x C	9	0.76141	0.08460	1.82754
F x C	36	22.47183	0.62421	13.48413**
G x C	27	0.54033	0.02001	0.43230
L x F x C	36	7.44184	0.20671	4.46545**
L x G x C	27	0.91759	0.03398	0.73413
F x G x C	108	12.82314	0.11837	2.56482**
Error (L x F x G x C)	108	4.99961	0.04629	-
Locations	1	0.23868	0.23868	1.76766
Principal factors	4	2.73528	0.68382	5.06437**
L x F	4	2.39790	0.59974	4.43972**
Error	390	52.66000	0.13502	-

* Significant at 5% level
 ** Significant at 1% level

for characters into error sum of squares, the values of factor loadings vary at each location, and in the second case, it shows that the score of factor loadings on each character varies with the number of principal factors, considered independently of locations. Similarly, significant $F \times G \times C$ interaction may be interpreted considering the interactions of $F \times G$ with C , $F \times C$ with G and $G \times C$ with F . Since $F \times G$ and $G \times C$ are non-significant, the significance of $F \times G \times C$ in the presence of a significant $F \times C$ means that different factor loadings are carried by characters when averaged over generations.

Generations do not seem to have any effect on the factor loadings nor do they show interaction with principal factors, locations and characters. When the sum of squares for generations are pooled into error (lower part of Table 80), the location effects are not significant but the principal components are, with significant $L \times F$ interactions. It follows, therefore, that though on the average there is no significant location effect, the $L \times F$ interaction is significant. Thus the contributions of different factor loadings on different characters at different locations are not the same.

The factorial analysis of variance on weighted values for general combining abilities over four generations and two locations is given in Table 81. Individual GCA's were standardized by dividing each value of a particular character by the GCA, averaged over four generations and two locations, for that character. The aim of such standardization preceding *factorial ANOVA* was to normalize the scales for different characters. For example, heading data were taken in number of days,

TABLE 81

Factorial analysis of variance of general combining ability
over four generations and two locations.

Source of variation	D.F.	Sum of squares	Mean squares	F ratio
Locations (L)	1	1.71959	1.71959	1.15079
Parents (P)	4	2.54764	0.63691	0.42623
L x P	4	1.11852	0.27963	0.18713
Generations (G)	3	4.27284	1.42428	0.95316
L x G	3	1.78580	0.59526	0.39837
P x G	12	6.27137	0.52261	0.34975
L x P x G	12	3.89558	0.32463	0.21725
Error	360	537.93774	1.49427	-
Locations (L)	1	1.71959	1.71959	1.88320
Parents (P)	4	2.54764	0.63691	0.69752
L x P	4	1.11852	0.27963	0.30624
Generations (G)	3	4.27284	1.42428	1.55981
L x G	3	1.78580	0.59526	0.65191
P x G	12	6.27137	0.52261	0.57234
L x P x G	12	3.89558	0.32463	0.35552
Characters (C)	9	12.69835	1.43315	1.56952
L x C	9	8.39985	0.93331	1.02213
P x C	36	91.33239	2.53701	2.77942***
G x C	27	21.10522	0.78167	0.85606
L x P x C	36	192.26447	5.34067	5.84888***
L x G x C	27	21.24818	0.78696	0.86185
P x G x C	108	92.07365	0.85253	0.93366
Error (L x P x G x C)	108	98.61607	0.91311	-

***Significant at 0.1% level

plant height was measured in centimeters, yield per plant, weight of seeds per spike and 1000-kernel weight were expressed in grams, and number of tillers per plant, number of spikelets per spike and number of seeds per spike were scored as counts. Thus by dividing the GCA of each character by its mean over two locations, the scale differences were removed but the inter-location differences were preserved.

The first part of Table 81 shows a three-way layout analysis of general combining abilities where locations, parents and generations have been treated as main effects. None of the mean squares showed significance. This means that parental lines did not differ in their general combining abilities over the two locations in any generation of the diallel cross. When the characters were introduced as a fourth main effect by analyzing the normalized GCA's in a four-way factorial layout (second part of Table 81), the mean squares for $P \times C$ and $L \times P \times C$ interaction were significant. This suggests that the combining ability values for different characters vary with the number of parents and locations.

It is interesting to note that after introducing characters as separate effects, the mean squares, either for generations or any of the interactions involving generations, were not significant. This indicates that generations do not affect GCA's for any characters in question. The significance of $P \times C$ and $L \times P \times C$ interactions on the other hand provides the possibility for comparing which of the parental lines for their relative adaptability is more

TABLE 82

Analysis of variance of Parkland GCAs' regression
upon Ellerslie GCAs' regression for each of the parental lines

Parent	Source of variation	D.F.	Sum of squares	Mean squares	Regression coefficient
Marquis	Due to regression	1	157.5731	157.5731***	b = 0.9416
	Due to error	8	1.8675	0.2334	
Chinook	Due to regression	1	138.6222	138.6222***	b = 1.1118
	Due to error	8	1.3375	0.1671	
Khush-hal	Due to regression	1	62.7426	62.7426***	b = 1.0769
	Due to error	8	4.2024	0.5253	
Ciano	Due to regression	1	60.1872	60.1872***	b = 1.1163
	Due to error	8	1.0378	0.1297	
Inia	Due to regression	1	75.7396	75.7396***	b = 0.8821
	Due to error	8	0.4692	0.0586	

***Significant at 0.1% level.

adaptive. For this purpose the GCA's for all the characters (averaged over all generations) at Parkland were regressed for each of the parental lines upon those at Ellerslie. The regression coefficients and the sums of squares due to regression and error partitioned for each cultivar are given in Table 82. It may be pointed out that unweighted GCA's (original values) were used in regression analysis since the effect of change in the degree of expression of one character relative to the other can be studied regardless of the unit of scale used. Significance of mean squares due to regression (Table 82) indicates that for every unit of change in GCA's at Ellerslie there is a corresponding proportional change for the corresponding GCA's at Parkland.

The genetic components of variation (from unadjusted treatment means) D , F and H_1 were considered themselves as variables and factorially analysed over generations and locations in order to study their consistency over the two environments. Before performing the factorial ANOVA, the values of genetic components for each character were standardized at each location. Thus, each D value was divided by the V_{OLO} for the same character, generation and location. Similarly, F 's were divided by their corresponding mean covariances (W_{OL01} in F_1 diallel, W_{OL02} in F_2 and backcross diallels and W_{OL03} in the selfed backcross diallel) and H_1 's by their respective mean variances (V_{1L1} in F_1 diallel, V_{1L2} in F_2 and backcross diallels and V_{1L3} in the selfed backcross diallel). Thus, for example, the F for number of tillers per

TABLE 83

Factorial analysis of variance of genetic components of variation over generations and locations. The sum of squares are respectively partitioned for D , H_1 and F .

Component	Source of variation	D.F.	Sum of squares	Mean squares	F ratio
D	Locations	1	0.14331	0.14331	1.10820
	Generations	3	0.03167	0.01055	0.08164
	Location x Generation	3	0.07301	0.02433	0.18820
	Error	72	9.31106	0.12932	
H_1	Locations	1	10.38381	10.38381	7.77135***
	Generations	3	2.16681	0.72227	0.54056
	Location x Generation	3	1.10966	0.36688	0.27458
	Error	72	96.20391	1.33616	
F	Locations	1	15.78510	15.78510	7.34709***
	Generations	3	7.28304	2.42768	1.13021
	Location x Generation	3	0.43955	0.14651	0.06821
	Error	72	154.65565	2.14799	

***Significant at 0.1% level

plant at Ellerslie in the selfed backcross diallel set of Table 78 was divided by the corresponding V_{OLO3} from Table 77 (at Ellerslie) as follows: $-0.4873 \div 0.6890 = -0.7072$.

The process of standardizing the scale is analogous to Allard's technique, where prior to factorial ANOVA, each variance and covariance was divided by V_{OLO} of the respective block for that character (Allard 1956; Crumacker and Allard 1962). In the present study additive [D], dominance [H_1] and additive x dominance [F] components are subsequently considered separately and analysed independently for their stability over generations and locations. The reciprocals of the variances of the parents of the array mean variances and of the array mean covariances were used as weights in standardizing the values of D 's, H_1 's and F 's respectively. The use of these different multipliers in normalizing the scale effects preserved the order of magnitude of respective parameters. The factorial ANOVA on the weighted values of D 's, H 's and F 's is given in Table 83. The results show that additive effects of the genes (component D) are the same for two locations. Dominance gene effects (component H_1) and additive x dominance effects (component F) differ significantly at the two locations. On the whole, generations do not seem to affect the values of genetic components of variation. Significant mean squares for locations with respect to H_1 and F raises the question of the heterogeneity of location effects on the parameters in different generations. To answer this, the unweighted values of D 's, H_1 's and F 's at Parkland were respectively regressed for each generation upon those of Ellerslie, and

TABLE 84

Analysis of variance of regression of genetic components of variation of Parkland upon those of Elersdale for each generation.

Component	Generation	Source of variation	D.F.	Mean squares	F value	
Additive Component [D]	F ₁ diallel	Due to regression	1	228657.5229	4578.6540***	r = 0.9990
		Due to error	8	49.9399		b = 1.0658
F ₂ diallel	F ₂ diallel	Due to regression	1	227792.7663	3549.9323***	r = 0.9998
		Due to error	8	64.1682		b = 1.0603
Backcross diallel	Backcross diallel	Due to regression	1	228207.7135	4597.8009***	r = 0.9990
		Due to error	8	49.6341		b = 1.0630
Dominance Component [H ₁]	F ₁ diallel	Due to regression	1	229319.4236	4251.7073***	r = 0.9990
		Due to error	8	53.9429		b = 1.0642
F ₂ diallel	F ₂ diallel	Due to regression	1	1532.9315	81.7304***	r = 0.9534
		Due to error	8	18.7562		b = 0.8233
Backcross diallel	Backcross diallel	Due to regression	1	2001.8299	391.1351***	r = 0.9398
		Due to error	8	5.1180		b = 1.3637
Selfed back-cross diallel	Selfed back-cross diallel	Due to regression	1	2619.8306	74.1992***	r = 0.9500
		Due to error	8	35.3087		b = 2.4385
Additive x dominance Component [F]	F ₁ diallel	Due to regression	1	412.1566	39.0566***	r = 0.9109
		Due to error	8	10.5528		b = 1.0623
F ₂ diallel	F ₂ diallel	Due to regression	1	812.9743	80.8326***	r = 0.9538
		Due to error	8	10.0575		b = 0.4664
Backcross diallel	Backcross diallel	Due to regression	1	1190.1414	31.2178***	r = -0.8921
		Due to error	8	38.1237		b = -1.4409
Selfed back-cross	Selfed back-cross	Due to regression	1	40.3149	2.8143	r = 0.5100
		Due to error	8	14.3248		b = 0.3220
		Due to regression	1	8.6977	0.8605	r = 0.3098
		Due to error	8	10.1077		b = 0.3603

***Significant at 0.01% level

the sum of squares of deviations were partitioned into variation due to regression and remainder (error). Extremely high variance ratios (Table 84) for the parameters D and H_1 , and close agreements between the coefficients of correlation and regression, both in sign and magnitude, indicate stability of these parameters over the two locations. The case of parameter F is rather confusing. The diallels based on backcross and selfed backcross generations show a lack of correspondence between F values at the two locations (variance ratio for regression non-significant). This may be ascribed to a change of relationship between additive and dominance gene effects ($F = Edh$) caused by altered environmental conditions. A more drastic relational change is that between the F_1 and F_2 generations of the diallel sets ($r = 0.95$, $b = 0.47$ and $r = -0.89$, $b = -1.44$, respectively). It is rather difficult to think of a logical explanation for this reversed relationship.

Since, on the whole, generation did not significantly affect the genetic components of variation, their estimates were obtained by solving, least-square-wise, the following system of linear equations, where the known terms, i.e., the array variances and covariances for a given generation were obtained by using adjusted treatment means from analysis of variance as a partially balanced lattice design:

$$\text{(Parents):} \quad D + E - V_{OLO} = d_1$$

$$F_1 \text{ diallel:} \quad (1/2)D - (1/4)F + (1/5)E - W_{OLO1} = d_2$$

TABLE 65

Components of genetic variation obtained from statistics based on adjusted treatment means for ten characters over four generations at two locations.

Character	σ^2	F	H_1	H_2	E
Onset-of-heading	6.1134 ± 0.7633** 0.6775 ± 2.7613**	9.2001 ± 1.7249** 11.7477 ± 6.2167	11.6377 ± 3.1176** 24.7571 ± 11.2393	15.6197 ± 2.7703** 21.4853 ± 10.6215	1.2710 ± 0.7546 2.7420 ± 2.7299
Final heading	7.9905 ± 1.4377** 7.6683 ± 3.7577	15.6700 ± 3.2479** 10.2621 ± 0.4667	16.0634 ± 5.0675** 26.9443 ± 15.2940	12.6612 ± 5.2157* 18.3367 ± 13.6368	3.6999 ± 1.4237 3.6684 ± 3.7147
Heading-upon	0.1776 ± 0.1172** 0.2777 ± 0.2762**	0.5307 ± 0.1111* 1.7011 ± 0.1767**	1.2307 ± 0.5612 4.6736 ± 0.3155**	0.9446 ± 0.5304 3.4230 ± 0.2660**	0.1134 ± 0.1163** 0.4755 ± 0.0773**
Plant height	49.1349 ± 194.5003 15.5347 ± 354.1527	237.1360 ± 436.5302 -336.9360 ± 732.1192	-124.3556 ± 792.1164 -274.4798 ± 321.1500	-26.7551 ± 766.2176 86.9170 ± 177.9948	329.6360 ± 192.3059 324.0950 ± 320.8911
Number of tillers per plant	0.1566 ± 0.3331* 3.4403 ± 0.1271**	1.1345 ± 1.2587 1.9009 ± 0.2671**	-1.6911 ± 2.1710 6.3136 ± 0.5175**	-1.9535 ± 1.9158 5.3106 ± 0.4614**	1.9733 ± 0.5273** 0.2227 ± 0.1257
Number of spikelets per spike	0.7525 ± 0.1522** 0.1191 ± 0.6715	1.1351 ± 0.3436* 0.7397 ± 0.1667	0.8665 ± 0.6287 1.3766 ± 0.1882**	0.6613 ± 0.5006 1.3117 ± 0.1333**	0.5284 ± 0.1527** 0.1653 ± 0.0926**
Number of seeds per spike	12.9117 ± 3.2257* 9.7701 ± 1.9713	15.9223 ± 7.3939 14.5569 ± 2.1133**	26.5635 ± 13.3331 45.6831 ± 4.1977	17.6712 ± 11.6634 19.6795 ± 9.7429**	13.6969 ± 3.2364** 0.2603 ± 1.0165
Weight of seeds per spike	0.6137 ± 0.9227** 0.6194 ± 0.6377**	0.6146 ± 0.6836** 0.7369 ± 0.6163**	-0.6113 ± 0.6185 0.0219 ± 6.0291	-0.0191 ± 0.6974** 0.9664 ± 0.6359	0.0259 ± 0.0625** 0.0170 ± 0.0070**
1000-kernel weight	5.6133 ± 1.2255** 9.243 ± 3.6167*	7.6471 ± 2.9262** 16.2759 ± 6.8136*	11.9483 ± 5.2734 12.2269 ± 12.2769	7.9756 ± 4.7070 11.6570 ± 10.9468	3.9345 ± 1.2568* 2.6562 ± 2.9424
Yield per plant	1.9202 ± 0.7331* -1.1375 ± 0.1945**	3.6622 ± 1.6130 -1.9421 ± 0.4463**	4.9964 ± 2.7668 -4.3292 ± 0.7930**	3.3320 ± 2.5918 -3.4464 ± 0.7671**	2.5752 ± 0.7660** -2.3649 ± 0.1926**

The first heading under each column refers to Lillerello and the second to Parkland.
* Significant at 5% level.
** Significant at 1% level.

F₂ diallel:

$$(1/4)D - (1/4)F + (1/4)H_1 + (3/5)E + V_{1L1} = d_3$$

$$(1/4)D - (1/4)F + (1/4)H_1 - (1/4)H_2 + (1/10)E - V_{0L1} = d_4$$

$$(1/2)D - (1/3)F + (1/5)E - W_{0L02} = d_5$$

$$(1/4)D - (1/8)F + (1/16)H_1 + (3/5)E - V_{1L2} = d_6$$

$$(1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2$$

$$+ (1/10)E - V_{0L2} = d_7$$

Backcross
diallel:

$$(1/2)D - (1/8)F + (1/5)E - W_{0L02} = d_8$$

$$(1/4)D - (1/3)F + (1/16)H_1 + (2/5)E - V_{1L2} = d_9$$

$$(1/4)D - (1/8)F + (1/16)H_1 - (1/16)H_2$$

$$+ (7/100)E - V_{0L2} = d_{10}$$

Selfed backcross
diallel:

$$(1/2)D - (1/16)F + (1/5)E - W_{0L03} = d_{11}$$

$$(1/4)D - (1/16)F + (1/32)H_1 + (2/5)E - V_{1L3} = d_{12}$$

$$(1/4)D - (1/16)F + (1/32)H_1 - (1/32)H_2$$

$$+ (7/100)E - V_{0L3} = d_{13}$$

In this system of equations $d_i, i=1, 2, \dots, 13$ denotes the difference between the expected and observed values of the i th statistic. The environmental component of variation (E) was accounted for by using the multiplier $(1/2)$ when F_1 and F_2 generations, and $(1/4)$ when backcross and selfed backcross generation diallel sets were considered (Hayman 1953). The solutions of this system of equations for the various components of variation are shown in Table 85. Error terms were calculated in a manner usual to the unweighted least square solution, i.e. as $\pm (\sum_k \sum_l c_{kl}^2 / DF)^{1/2}$, where c_{ii} is the appropriate term on the main diagonal of the variance-covariance matrix of the coefficients,

TABLE 86

Estimates of genetic parameters from diallel analysis
of adjusted treatment means for ten characters over four generations at two locations.

Character	$(H_1 + D) / 2$	$(H_2 + 3H_1)$	$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	Heritability
Onset-of-heading	1.4763*	0.1921*	2.9621*	0.3969
	1.6751	0.2169	2.3189	0.2689
Final heading	2.3455*	0.1750*	3.8012*	0.3674
	1.6396	0.2164	2.4948	0.2420
Heading-span	1.8545	0.1627	3.9580	0.1145
	2.8931*	0.1856*	3.2920*	0.1027
Plant height	2.1990	0.0344	0.1188	0.0308
	4.1365	-0.0810	-0.4922	0.0109
Number of tillers per plant	1.5543	0.3559	46.3456	0.0764
	2.1175*	0.2102*	1.9999*	0.2125
Number of spikelets per spike	1.0660	0.1446	5.7672	0.2935
	2.6639	0.2362*	1.6100	0.0960
Number of seeds per spike	1.7276	0.1642	2.8599	0.1366
	2.3135	0.1545	2.7392	0.2312
Weight of seeds per spike	0.9016	0.4225	3.7901	0.1941
	1.1099	0.6669	23.2235	0.2679
1000-kernel weight	1.5144	0.1727	3.0116	0.2020
	1.4222	0.1489	4.1330	0.4026
Yield per plant	1.6622	0.1667	3.7498	0.1327
	1.9770*	0.1091	0.3842	-0.1855

*First heading under each column refers to El Dorado and the second to Parkland
*The parameters involved are significantly different from zero (Table 85)

and $L.F. = 13 - 5 = 8$ (thirteen equations, five fitted parameters). For one set of paradoxical results (significant negative values of D , H_1 and H_2 for yield per plant at Parkland), the source of error could not be determined.

The proportional estimates of genetic parameters obtained from Table 85 are given in Table 86. The data indicate that all characters are inherited as over-dominant traits at both locations, except for weight of seeds per spike at Ellerslie which showed nearly complete dominance, i.e. $(H_1 \div D)^{1/2} = 1$. Moreover $[(1/4DH_1)^{1/2} + F] \div [(1/4DH_1)^{1/2} - F] > 1$ in all cases, except for plant height at both locations and yield per plant at Parkland, suggests strongly a preponderance of dominant genes in the parents. When valid, $(H_2 \div 4H_1)$ was found to be less than 0.25, indicating thus a certain degree of numerical asymmetry of alleles with positive and with negative effects at loci showing dominance. Heritability values in all cases were low, the maximum being 40.26% (1000-kernel weight at Parkland).

The results of Table 86 when compared with those of Tables 20, 39, 60 and 79 show the effect of the adjustment factor characteristic of incomplete block designs. In the latter Tables, where genetic parameters have been estimated from analyses of F_1 , F_2 , backcross and selfed backcross diallel sets of unadjusted treatment means (treated as randomized block design), the values of $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$ and $[(1/4DH_1)^{1/2} + F] \div [(1/4DH_1)^{1/2} - F]$ show a wide range of variation from partial dominance to overdominance, from a fully symmetrical distribution of alleles with positive and negative effects to strong

TABLE 87

Analysis of variance of regression of genetic components of variation at Parkland upon those at Ellerslie averaged over generations for all characters.

Component of variation	Source of variation	D.F.	Sum of squares	Mean squares	Coefficients of correlation & regression
Additive component [D]	Due to regression	1	228499.9514	228499.9514**	b = 1.0633
	Due to error	8	432.9894	54.1236	r = 0.9990
Dominance component [H ₁]	Due to regression	1	1561.3878	1561.3878**	z = 1.3188
	Due to error	8	65.5032	8.1879	r = 0.9796
Additive x Dominance Component [F]	Due to regression	1	306.8222	306.8222**	b = 1.0430
	Due to error	8	100.9412	12.6176	r = 0.8674
Additive component [D]	Due to regression	1	197.6459	197.6459**	b = 0.3825
	Due to error	8	90.3328	11.2916	r = 0.7579
Dominance component [H ₁]	Due to regression	1	76528.1655	75528.1655**	b = 1.4230
	Due to error	8	345.5664	43.1958	r = 0.9997
Additive x Dominance Component [F]	Due to regression	1	137604.3889	137604.3889**	b = 2.6663
	Due to error	8	963.3961	120.4245	r = 0.9964

The first part of the table refers to unadjusted treatment means (treated in randomized block design) and the second part refers to adjusted treatment means from partially balanced lattice design.

**Significant at 1% level

asymmetry, and from equal to unequal proportions of dominant to recessive alleles in the parents. Table 86 on the other hand shows that these ratios, especially those for valid parameters (* in Table 85), are more stable over characters since over-dominance in inheritance, asymmetry of alleles at loci exhibiting dominance, and inequality in the proportions of dominant and recessive alleles are constant features of the concerned characters.

The regression analysis of genetic components of variation D , H_1 and F for Ellerslie and Parkland, obtained first from unadjusted treatment means (randomized block design) averaged over generations, and then from adjusted treatment means of Table 85, is given in Table 87. The purpose of this analysis was to see whether there is concordance between the values of parameters evaluated from the data at the two locations separately. The results given in Table 87 show a good agreement in this respect between locations. Parameters D and F evaluated from array variances and covariances from unadjusted treatment means show the same rates of change from character to character at the two locations ($b = 1$). For H_1 this change is $b = 1.32$ at Parkland for unit change at Ellerslie. With adjustment of treatment means the situation is changed, so that for unit change at Ellerslie there is a change of $b = 0.38$ for D and $b = 2.67$ for F at Parkland. The corresponding change for H_1 is less pronounced ($b = 1.32$) without adjustment as compared to $b = 1.42$ with adjustment.

The relationships between the two locations in regard to changes in D , H_1 and F for the various characters are shown graphically

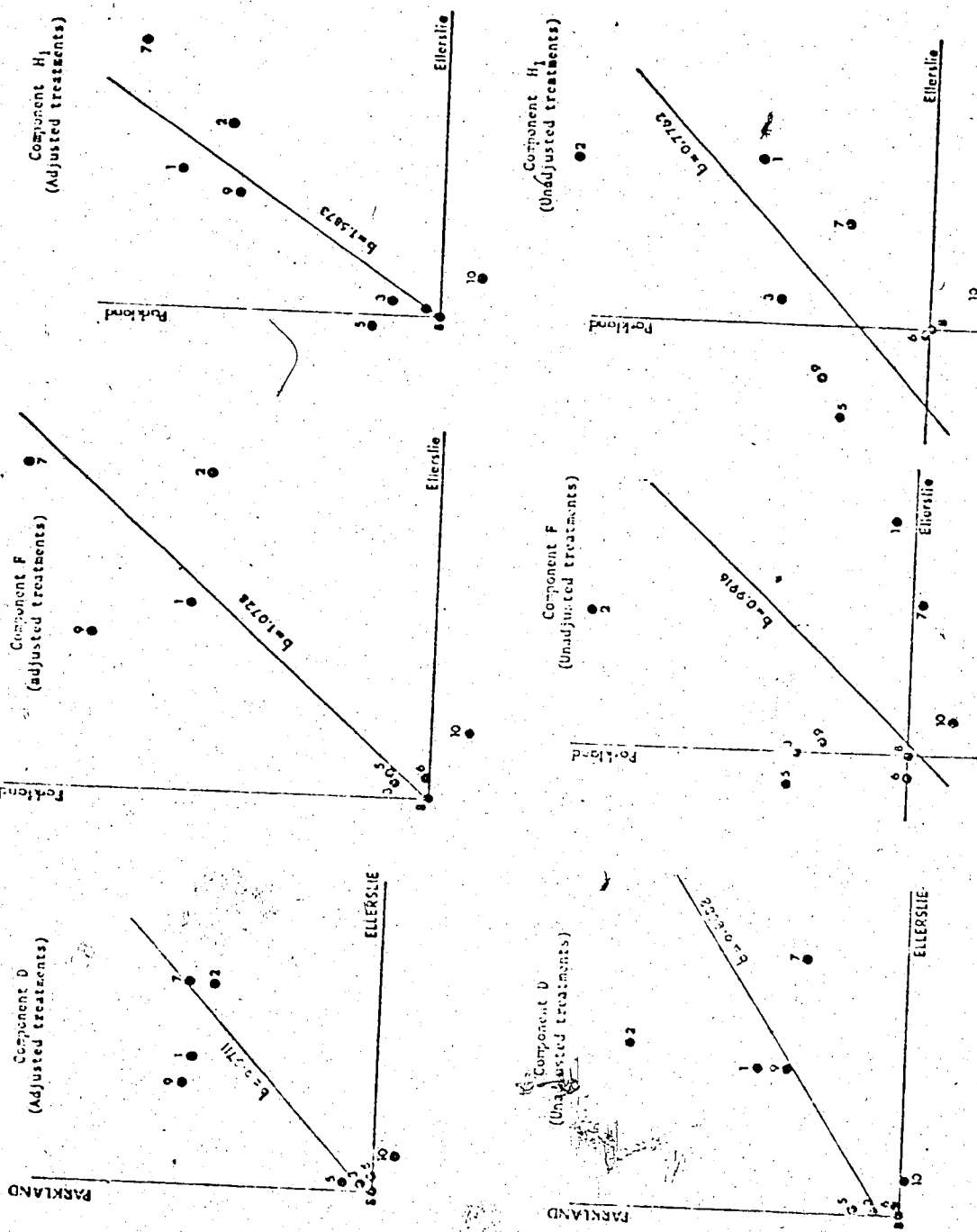


Figure 81. Regression of genetic components of variation at Parkland upon those at Ellerslie for all the characters except plant height. Solid circles refer to regression intercepts for different characters.

in Figure 81. The scatter of the intercept points around the regression lines shows that there are considerable discrepancies between the two locations. The points of intercepts for plant height are not shown in the graphs because of very high values of the components which far exceeded the boundaries of the graphs. Therefore the coefficients of regression were recalculated excluding plant height. It is rather difficult to determine either from the regression analysis of Table 87 or from the graphs whether and by how much the use of adjusted treatment means has improved the estimates of the parameters. Hence it is not possible to assess the parametric relationships within and between the characters and within and between the locations or environments. Nevertheless, looking at the graphs of the parameters derived beginning with the adjusted treatment means, one would be rather strongly inclined to conclude that the adjustment of means has considerably improved the degree of concordance between the two locations with respect to parameters.

DISCUSSION

The F_1 , F_2 , backcross and selfed backcross generations of five parent diallel cross of common wheat (*Triticum aestivum* L.) were grown in 1972 at two locations and the data obtained was analysed with respect to correlation between the characters, principal factors, general and specific combining abilities, genetic components of variation and environmental effects. The experimental design used was a partially balanced triple lattice. However, most of the analyses were carried out both as a complete randomized block design and as a lattice design. The results obtained are discussed in sequel.

Correlation and factor analyses. Among the characters considered in this study, yield of grain per plant is agronomically the most important. Therefore the knowledge of its correlation with other characters is of importance from a theoretical and a practical point of view. The results of the correlation analyses of F_1 , F_2 , backcross and selfed backcross diallel sets are given in Tables 2, 21, 42, and 61. These results show that early maturing entries have produced high yields and the late maturing ones low yields of grain per plant. As expected, there was a positive correlation between yield per plant and most of its subcharacters or components. A strong positive association was found to exist between the subcharacters, number of tillers per plant, weight of seeds per spike and 1000-kernel weight with yield per plant. The components, number of spikelets per spike and number of seeds per spike were not correlated with yield at either location in F_1 (Table 2) but were

positively correlated in the other generations of diallel cross either at both locations (Table 21) or at one of them (Tables 42 and 61). There was no correlation between yield and plant height.

The degree of expression of metrical characters (phenotypes) depends both on the genotypic constitution of the parents and the environmental conditions under which the experimental materials are grown. Therefore the comparison of results obtained by various researchers using different sets of parents and carried out under different environmental conditions lead only to non-related or loosely-related general information. For example, Lee and Kaltsikes (1973) working with durum wheat in Winnipeg have found that the characters days-to-maturity and yield per plant were positively correlated in both the F_1 and the F_2 generations of a 10 x 10 diallel cross, whereas in the present study of all the generations of diallel cross the correlation was negative. On the other hand, Hsu (1970) has found that in the F_1 generation of a five-parent diallel cross of common wheat there was no correlation between anthesis date (final heading) and yield per plant, a result similar to that found in the present case at Parkland. Although Hsu has conducted his study in Edmonton, the two experiments were spaced in time, and except for Inia, the parental lines used were different. The significant positive association of yield per plant with its components found in this study was also observed in the works of Johnson and Schmidt (1968), Smoczek (1969), Lebsock and Amaya (1969), Hsu and Walton (1970), Kaltsikes and Lee (1971), Lee and Kaltsikes (1973) and Chebib *et al*' (1973). The absence of correlation between plant height

and yield per plant in the present study was also observed by Kaltsikes and Lee (1971) and Chebib *et al* (1973). These results are in disagreement with those of some other experiments [Lebsock and Amaya (1969), Kaltsikes and Larter (1970) and Lee and Kaltsikes (1973)].

The relationship between individual character is rather complicated. Therefore the data were subjected to factor analysis. This analysis provides information on contributions of independent variables relative to those of dependent ones. The results of the factor analysis of F_1 , F_2 , backcross and selfed backcross data obtained for two locations are shown in Tables 3, 22, 43 and 62, and the principal factors have been interpreted earlier. The first principal factor, *lateness*, has negative loading for yield per plant and the highest positive loading for onset-of-heading and final heading. This confirms the conclusion arrived at earlier, that the majority of late-heading entries have produced low grain yields per plant. The degree of expression of heading-span was found to be correlated with final heading but not with onset-of-heading. It was not correlated with yield in F_1 and F_2 but was positively associated with it in backcross and selfed backcross data. This inconsistency suggests that heading-span is not one of the characters affecting yield per plant. In fact the factor analyses based on the F_1 , F_2 backcross and selfed backcross diallel sets have revealed positive factor loadings for heading-span and negative ones for yield. It follows therefore that positive correlations of heading-span with yield per plant at Parkland in the backcross and selfed backcross diallel sets does not necessarily imply

a cause-and-effect relationship, and may in fact be attributed to strong environmental influence upon particular entries of the diallel table.

The second principal factor, termed differently in different generations, carried the highest loadings for number of spikelets per spike, number of seeds per spike and weight of seeds per spike except the backcross diallel at Barkland (Table 43), for which plant height had the highest loading. A similar situation was observed with respect to principal factors 3, 4 and 5 which had their highest loadings from different characters in different generations of the diallel cross. Thus it appears that different factors operate differently in different populations (generations) though they share the same gene pool.

Combining ability analyses. The results of the analyses of data for general and specific combining abilities with respect to the characters considered have shown that the parents with high GCA's do not necessarily produce hybrids with high SCA's. The comparisons of GCA's with SCA's for all the generations and characters are collected in Table 83. Of all the comparisons, eighty to be exact, 84% constitute cases in which high SCA's are associated with one or both parents having low GCA's, and vice versa. These observations are in agreement with those reported by Crumpacker and Urquhart (1962), Fonseca (1965), Brown *et al* (1966), Gyawalli *et al* (1968) and Singh *et al* (1969) in wheat. Analogous results have been observed by Larson (1941) in tomatoes, and

TABLE 6B

Summary of the results of general and specific combining ability analyses showing that the hybrids with highest SCA's are associated with parents of low GCA's and vice versa.

	Onset-of-heading		Final heading		Heading-span		Plant height		Number of tillers per plant			
	F1	F2	B0	B1	F1	F2	B0	B1	F1	F2	B0	B1
*Both parents with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
Hybrid with highest SCA	++	++	++	++	++	++	++	++	++	++	++	++
Both parents with low GCA	--	--	--	--	--	--	--	--	--	--	--	--
Both parents with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
One parent with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
Both parents with low GCA	--	--	--	--	--	--	--	--	--	--	--	--
Number of spikelets per spike												
	Number of spikelets per spike		Number of seeds per spike		Weight of seeds per spike		1000-kernel weight		Yield per plant			
	F1	F2	B0	B1	F1	F2	B0	B1	F1	F2	B0	B1
*Both parents with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
Hybrid with highest SCA	++	++	++	++	++	++	++	++	++	++	++	++
Both parents with low GCA	--	--	--	--	--	--	--	--	--	--	--	--
Both parents with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
One parent with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
Both parents with low GCA	--	--	--	--	--	--	--	--	--	--	--	--
Both parents with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
One parent with high GCA	++	++	++	++	++	++	++	++	++	++	++	++
Both parents with low GCA	--	--	--	--	--	--	--	--	--	--	--	--

(+) and (-) signs indicate, respectively, affirmation and contradiction of the statements.
 The first location of (+) or (-) refers to maternal and the second to paternal.
 (*) sign characteristic of the location shows disagreement of the proposition made in the text.
 F1, F2 B0 and B1 refer to P₁ P₂, backcross and selfed backcross generations of diallel set.

by Walker (1963), Chang (1967), Soomro (1967), Baluch and Soomro (1969) and Soomro and Baluch (1969) in cotton. On the other hand Kime (1950) and Hawkins *et al.* (1965) working with cotton have found that GCA and SCA were positively correlated so that the present results are in contradiction to their reports.

Significant variances of general and specific combining abilities for a particular character denote, respectively, the importance of additive and non-additive gene effects for that character. If the variance for specific combining ability for a particular character is significant and that for general combining ability is not, selection for the character will be on the basis of SCA. On the other hand, high SCA variances associated with a particular parent, even if it has high GCA, reflect an inconsistency in the performance of that parent with respect to the particular character (Griffing, 1956) and indicate that the hybrids involved with that parent would perform poorer than would be expected on the basis of their specific combining abilities. It follows therefore that in combining ability screening tests a pedigree selection procedure would be expected to screen out the strains with considerably larger SCA variances.

In the present studies variances of general combining ability were generally larger than those of specific combining ability for all characters, and diallel-set generations at both locations (Tables 5 to 14, 24 to 33, 45 to 54 and 64 to 73). There were a few cases where the estimates of SCA variances were higher than those for GCA's, but the magnitudes of their differences were negligible. This

would indicate a high consistency of performance of the parental lines an observation which may also be generally verified by their general combining ability values (Tables 4, 23, 44 and 63), and more specifically from the results of Table 82. The significance of variances for general and specific combining abilities were examined from Tables 15, 34, 55 and 74. In general, the mean squares for GCA were significant for all characters except heading-span and yield per plant at one or both the locations. Such significances of GCA mean squares are not uncommon in wheat (Brown *et al* 1966, Fonseca 1965, Paroda and Joshi 1970a, Parodi *et al* 1970 and Bitzer *et al* 1971). Mean squares for SCA were significant only for a few characters.

It may be pointed out that a high general combining ability for some characters as for example onset-of-heading and final heading may not be desirable under certain circumstances. High GCA for these characters implies lateness, so that when selecting for earliness, lines with the lowest GCA's must therefore be given priority. In the present study Ciano and Inia had the lowest GCA's for heading data, and consequently selection from their progenies is expected to result in early lines. Plant height is another character for which the selection of wheat cultivars with low GCA's may be desirable.

Diallel cross analysis. The analysis of variance of diallel tables according to Hayman (1954a) gave a component significances (for additive gene effects) in all generations of the diallel cross (Tables 16, 35, 56 and 75) for all the characters except heading-span and yield per plant

(Tables 16 and 35) and yield per plant (Tables 56 and 75). These results corresponded to those for general combining ability in ANOVA's (Tables 15, 34, 55 and 74). Thus Hayman's a component and Griffing's GCA are analogous. Genetic components of variation for each generation of the diallel cross have shown values ranging from non-significance to high significance. The only paradoxical ones are the negative but significant D 's and H_1 's of Tables 19, 38, 59 and 78, which may be ascribed to high environmental variation. Such unexpected values are not uncommon (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) in biometrical genetics. The interpretation of genetic parameters in such cases becomes questionable.

Proportional values of the estimates of genetic parameters viz., $(H_1 \div D)^{1/2}$, $(H_2 \div 4H_1)$, $[(4H_1)^{1/2} \div F] : [(4H_1)^{1/2} - F]$ and $[H^2/H_2]$ for characters studied in different generations of the diallel cross ranged from partial dominance to over-dominance, from complete symmetry to strong asymmetry in distribution of genes with positive and negative effects in the parents, from equal proportions of dominant and recessive genes in the parents to a preponderance of dominants or recessives, and from high to low numbers of gene groups controlling a particular character. Heritability estimates also showed a wide range of values, from -0.1129 (yield per plant, Table 39) to +1.085 (onset-of-heading, Table 79), indicating in this example, a complete lack of heritability for yield and an extremely high heritability for earliness. Quite low heritability estimates of yield in wheat have been reported by a number of researchers (Wiebel 1956, McNeal 1960,

Kronstad and Foot 1964, Johnson *et al* 1966, and Paroda and Joshi 1970, 1970a).

Genotype-environment interaction. The assessment of genetic and environmental components of variation with respect to a character depends upon the gene pool involved and the non-hereditary factors constituting the environment in which the experimental material is grown. The choice of statistical approach varies with the type of data available and the object of the study. In this study factorial ANOVA and regression analysis (Mather, 1951) were used to assess the degree of discordance between identical sets of materials grown at two locations with respect to factor loadings for the various characters, general combining abilities of the parents and the main genetic components of variation.

The factor loadings on various characters seemed to be different for the two locations (Table 80). The effect of generations on factor-loading scores for different characters was negligibly small. In fact none of the interactions involving generation were significant. This finding contradicts that of Lee and Kaltsikes (1973) who found discrepancies between their F_1 and F_2 diallel factor analyses with respect to the factor loading scores on various characters. They attributed these generation differences to a considerable difference in plot size for the two generations, and difference in planting techniques viz., space-planting for F_1 diallel and solid planting for F_2 diallel. In the present case, though plot size, planting techniques and experimental

set up was the same, nevertheless, the environmental conditions at the two locations were quite different. In spite of significant inter-location effects, different generations proved to be fairly homogeneous with regard to factor loadings.

In the factorial ANOVA for general combining abilities of the four generations of the diallel cross and the two locations (Table 81) it was found that the GCA values were more or less the same. However, when characters were treated separately in the analysis (ANOVA assumed single observation per cell), GCA's differed between locations. These results indicate that parents did not differ in GCA's over the two locations when their GCA's were averaged over all characters, but they certainly did when considered individually for each character. The response of each variety with respect to additive gene effects was studied after averaging the GCA's of a cultivar over four generations of the diallel cross and regressing the estimates obtained at one location upon those of the other. In the analysis of variance for regression (Table 82) the inter-location effects were found to be homogeneous for each variety. In other words, the GCA's for the two locations were concordant. The variances for general and specific combining ability also did not differ significantly at the two locations. Moreover, the conspicuous feature of the combining ability analysis was the high consistency with which the GCA variances were higher than the corresponding SCA variances at both locations. This in fact shows the stability of cultivars over locations according to Griffing's (1956) enunciation.

The stability of genetic components of variation, viz., D , H_1 and F was assessed over the two locations through *factorial ANOVA*. The results indicated (Table 83) that there was no significant difference between locations for any component. Moreover, the generations, on the whole, did not affect these parameters at either location. But when the estimates of one component for Parkland were regressed upon those of Ellerslie it was found that the selfed backcross generation of the diallel cross was affecting the component F . This constituted a significant change in the relationship between additive and dominance gene effects in the progeny of the backcrosses. Moreover the estimates of the F component for the two locations were correlated differently in the F_1 and F_2 generations (+ r and - r respectively). It is rather difficult to think of a logical explanation for this change of relationship between additive and dominance gene effects [$\Sigma(d) \times \Sigma(h)$] in two generations of the same diallel set.

The occurrence of significant negative values for genetic components of variation was an unexpected feature of diallel cross analysis for which a satisfactory interpretation is lacking. Such values have been reported in a number of instances (Mather 1949, Wright 1952, Newell 1970 and Holmes 1972) but a logical explanation for their occurrence has not been given. The frequency of their occurrence appear to be too high to be attributed to chance.

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APPENDIX I

Origin, parentage and varietal description
of five cultivars of wheat used in diallel study

- Variety: Marquis
Origin: Central Experimental Farm, Ottawa, Canada
Parents: Hard Red Calcutta x Red Fyfe
Growth habit: Spring
Plant height: 110 - 120 cms.
Spike: Mid-long, fusiform with apical awns; beaks short, acute
Kernel: Dark red, hard, ovate-truncate
- Variety: Chinook
Origin: Central Experimental Farm, Ottawa, Canada
Parents: Thatcher x S-615-11
Growth habit: Spring
Plant height: 110 - 125 cms.
Spike: Fusiform, mid-long, short apical awns, white glumes with mid-wide beaks
Kernel: Red, hard, short to mid-long, oval
- Variety: Khush-hal
Origin: Agricultural Research Institute, Peshawar, Pakistan
Parents: Local white x Standard Desi
Growth habit: Spring
Plant height: 80 - 90 cms.
Spike: White, fluffy, awned, white pubescent glumes with mid-wide beaks
Kernel: Amber colored, soft, mid-long, oval
- Variety: Ciano-67
Origin: National Institute of Agricultural Research, Mexico
Parents: Pitic 62-Chris 'Sib' x Sonora 64
Growth habit: Spring
Plant height: 85 - 95 cms.
Spike: White, bearded; fusiform
Kernel: Hard red, medium size
- Variety: Inia-66
Origin: National Institute of Agricultural Research, Mexico
Parents: Lerma Rojo 64 x Sonora 64
Growth habit: Spring
Plant height: 100 - 110 cms.
Spike: White, bearded, fusiform
Kernel: Hard, red, medium-long

APPENDIX-II

NUMERICAL DESIGNATIONS OF THE PARENTS AND THEIR
CROSSES USED IN THE DIALLEL ANALYSES

1. (KxCH)F22	46. (CHxI)I1	91. I-PARENT	136. KI(CxK)	181. (Cxx)F2
2. (Ixx)I1	47. C-PARENT	92. (Cxx)C1	137. (KxCH)M1	182. (Ixx)F22
3. I1(IxC)	48. (Cxx)F22	93. CHO(KxCH)	138. (Cxi)F2	183. CHO(CHxC)
4. (KxH)F22	49. (CHxI)CHO	94. CHI(CxCH)	139. IO(Kxi)	184. (Ixx)I1
5. (IxC)I1	50. (Kxi)I1	95. C1(Cxx)	140. CO(Kxx)	185. (CHxC)C1
6. (Cxi)F22	51. (CHxi)F2	96. (Ixx)I1	141. (CHxK)F1	186. IO(Ixx)
7. CHI(KxCH)	52. C1(IxC)	97. (Ixx)CHI	142. (IxC)C1	187. IO(CHxi)
8. (Ixx)F2	53. (Kxx)KO	98. M1(Cxx)	143. M1(Ixx)	188. (Kxx)CO
9. M-PARENT	54. (Kxi)MO	99. (Cxx)CHI	144. CO(Kxx)	189. (Ixx)F1
10. KI(KxCH)	55. MO(KxC)	100. (Cxx)F2	145. (CHxC)F2	190. (Kxi)IO
11. (Cxi)C1	56. (Kxi)F22	101. CO(IxC)	146. KO(Ixx)	191. CO(Kxx)
12. (Kxx)MO	57. IO(IxC)	102. KI(Kxi)	147. (Cxx)C1	192. (Cxx)CO
13. KI(CHxK)	58. (Kxx)CO	103. (Kxx)KO	148. (Cxx)F22	193. (Kxx)F1
14. (CHxx)CHI	59. (CHxx)F2	104. (Kxx)F22	149. KO(Cxx)	194. (CHx)CHO
15. C1(CHxC)	60. CHI(CHxK)	105. (Kxx)CHO	150. (Kxi)F1	195. (Ixx)IO
16. K-PARENT	61. (CHxC)F22	106. C1(Kxx)	151. (Kxi)F2	196. (Ixx)IO
17. (Ixx)KI	62. MO(CHxi)	107. CH-PARENT	152. CHI(KxCH)	197. CHO(KxCH)
18. CHI(CHxK)	63. (Kxx)F2	108. C1(Kxx)	153. CO(KxCH)	198. KI(Kxx)
19. (KxCH)F2	64. MO(Ixx)	109. (CHxK)CHI	154. (Kxi)MO	199. IO(Ixx)
20. CHI(CHxC)	65. (Ixx)CHO	110. (Kxx)MO	155. MO(Kxx)	200. (Kxx)MO
21. (Kxx)M1	66. (Kxi)F22	111. M1(KxCH)	156. KO(Kxx)	201. I1(CHxi)
22. I1(Ixx)	67. (Cxx)MO	112. (Cxi)M1	157. (CHx)CHO	202. (Kxi)O
23. C1(CxCH)	68. (Cxi)CO	113. (Cxx)F2	158. (Cxx)F1	203. (Cxx)CO
24. (KxC)F2	69. (KxC)C1	114. (CHx)CHO	159. KI(Ixx)	204. (Ixx)F1
25. (Kxx)F22	70. (Cxx)CHO	115. (Ixx)F1	160. (Ixx)CO	205. (CHx)F1
26. (Ixx)F22	71. M1(Kxx)	116. (CHx)KO	161. (Cxx)M1	206. I1(Ixx)
27. (CHxC)CHI	72. KO(Kxi)	117. (CHxi)F22	162. CO(Kxx)	207. KO(KxCH)
28. CHI(CHxi)	73. (CHxi)CHI	118. (Ixx)IO	163. CHO(CHxC)	208. MO(Kxi)
29. I1(Kxi)	74. (Kxi)KI	119. I1(Kxi)	164. (Kxi)KI	209. (Ixx)IO
30. (Ixx)CHI	75. (Kxi)IO	120. M1(Kxi)	165. CO(CHxi)	210. (CHx)F22
31. F1(KxC)	76. (CHxi)M1	121. (Kxx)C1	166. M1(Kxx)	211. (CHxi)IO
32. (Cxi)I1	77. (Cxx)C1	122. (Ixx)M1	167. CO(Kxx)	212. CHO(KxCH)
33. (Cxx)F1	78. (CHxx)F22	123. CHI(CHxC)	168. (Cxx)F1	213. KI(Kxx)
34. CHI(Ixx)	79. IO(Kxi)	124. (Kxi)KI	169. (Kxx)F2	214. (Cxi)O
35. (CHxC)CO	80. (Kxx)F2	125. (Cxi)F1	170. IO(KxCH)	215. (Kxi)F1
36. MO(Kxx)	81. MO(Kxx)	126. MO(Kxx)	171. KI(Kxx)	216. (Cxx)F1
37. (Ixx)F2	82. (KxCH)KI	127. (Kxx)M1	172. (Ixx)F2	217. MO(Kxi)
38. (CHx)KI	83. IO(Cxi)	128. I1(Ixx)	173. (Cxi)F1	218. KO(Ixx)
39. (Ixx)KO	84. (Kxx)F2	129. (Kxi)F2	174. MO(KxCH)	219. CO(Kxi)
40. (Kxx)F1	85. (Cxx)F1	130. CO(CHxC)	175. (Cxx)F22	220. (Kxx)F1
41. (Kxi)F1	86. (CHxi)MO	131. (Ixx)F2	176. (CHxi)F1	221. (Cxx)CO
42. (Kxi)F22	87. (Ixx)F22	132. (Kxx)F1	177. (Kxi)I1	222. (Kxi)IO
43. (Cxx)F2	88. CHO(Ixx)	133. C1(Cxi)	178. (Kxx)CHI	223. (KxCH)F1
44. (CHxC)CHO	89. (Kxx)KI	134. (Cxx)F22	179. I1(Cxi)	224. (KxCH)KO
45. (Kxi)MO	90. (Ixx)F22	135. C1(Kxx)	180. (Kxx)KO	225. (CHxi)F1

NOTE: M=Marquis, CH=Chinook, K=Kinch-hal, C=Ciano-67 and I=Inia-66.

For any two varieties, for example 'C' and 'K', above mentioned combinations could be explained as follows:

(Cxx)F1 = F₁ hybrid.
 (Kxx)F1 = Reciprocal F₁ hybrid.
 (Cxx)F2 = F₂-generation hybrid.
 (Kxx)F2 = Reciprocal F₂ hybrid.
 (Cxx)F22 and its reciprocal are the F₂'s repeated second time in each replication to complete the requirements of the 15x15 partially balanced lattice design.

(Cxx)CO = Back cross-1.
 CO(Cxx) = Reciprocal back cross.
 (Cxx)KO = Back cross-2.
 K(Cxx) = Reciprocal back cross-2.
 (Cxx)C1 = Selfed generation of (Cxx)CO.
 C1(Cxx) = Reciprocal of (Cxx)C1.
 (Cxx)KI = Selfed generation of (Cxx)KO.
 KI(Cxx) = Reciprocal of (Cxx)KI.

APPENDICES III TO XXII

Unadjusted treatment means (original data) of all the entries with respect to ten quantitative characters at two locations.

The numbers in the first row of each block are the code numbers of entries and those in the second row are the mean values of the corresponding entries listed in Appendix II.

APPENDIX VI Plant height at Ellerslie

181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
72,500	87,900	105,310	85,050	58,950	71,310	85,530	82,260	86,410	89,350	107,000	101,240	101,210	95,350	74,210
76,540	76,270	110,130	91,210	103,470	111,370	89,920	67,610	74,670	101,320	75,850	112,160	108,400	75,210	106,820
87,350	89,750	89,570	74,520	71,590	74,340	123,140	71,640	75,210	96,570	111,520	71,710	81,510	82,440	102,160
96,930	81,890	79,170	114,920	83,900	104,270	94,210	114,530	102,640	91,230	109,320	79,220	104,520	125,310	120,460
101,750	105,530	74,810	87,060	120,020	115,370	155,530	87,380	102,740	69,240	92,670	102,050	74,920	91,500	92,850
95,030	94,240	106,700	81,310	86,160	74,270	112,010	71,520	129,050	81,450	82,770	77,350	77,670	65,010	74,760
70,700	75,420	116,060	81,520	82,420	76,840	117,850	124,940	105,570	74,820	75,140	76,140	76,140	92,140	94,730
81,200	115,210	88,940	91,620	79,120	74,500	126,230	76,270	74,110	114,830	84,710	74,270	131,120	71,140	84,650
86,880	85,140	94,150	105,710	129,670	101,700	131,000	114,170	69,270	71,270	101,170	107,430	87,350	74,420	101,410
90,010	70,320	68,720	93,670	71,120	71,570	124,270	71,370	117,120	71,550	70,340	104,760	83,160	112,730	84,620
102,850	80,700	70,120	82,750	85,470	74,800	67,100	87,010	99,010	85,730	74,110	77,110	82,570	84,710	87,150
89,200	85,970	66,300	87,400	74,210	92,100	73,420	82,010	71,710	101,010	69,010	82,010	81,010	84,010	81,010
67,130	101,290	68,310	67,740	91,320	11,270	89,070	85,570	72,410	85,510	71,710	75,410	102,420	72,120	82,720
104,030	74,310	101,770	77,750	105,910	91,500	75,840	75,970	81,440	34,800	102,120	86,770	78,320	71,220	74,120
77,750	89,520	70,910	64,170	97,400	104,470	72,440	74,770	111,110	92,570	111,040	82,810	92,100	72,470	81,110

196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
104,160	79,220	100,150	112,410	81,340	74,510	104,110	101,110	101,160	82,710	75,440	89,010	71,410	111,310	111,310
89,090	71,410	81,150	103,840	99,120	114,210	74,440	115,540	101,670	74,120	74,110	102,170	74,410	101,010	89,410
124,420	82,070	112,100	111,740	63,420	101,710	127,750	103,290	51,140	74,740	112,110	102,110	102,110	74,110	101,110
69,670	66,160	71,530	104,440	110,150	112,270	110,010	87,690	101,110	112,010	107,010	77,410	11,410	101,110	107,110
73,520	112,240	103,730	124,770	60,640	95,170	87,070	101,110	101,110	101,110	101,110	101,110	101,110	101,110	101,110
87,430	74,560	78,100	10,510	107,410	121,270	111,110	111,110	111,110	111,110	111,110	111,110	111,110	111,110	111,110
75,030	95,700	104,830	91,111	94,440	91,310	84,110	74,720	11,410	42,520	71,110	81,110	70,110	64,110	71,110
72,520	90,150	82,440	107,160	72,790	71,010	104,620	94,240	71,510	91,010	84,110	71,110	71,110	71,110	71,110
71,190	104,450	74,510	74,940	102,440	92,110	122,110	74,110	101,110	74,110	104,110	101,110	101,110	101,110	101,110
87,120	115,150	101,450	111,410	111,110	91,110	70,110	70,110	111,110	111,110	111,110	111,110	111,110	111,110	111,110
103,120	101,710	72,150	71,550	83,150	93,110	72,110	81,110	71,110	71,110	71,110	71,110	71,110	71,110	71,110
88,540	103,110	77,240	87,110	111,110	87,110	87,110	87,110	87,110	87,110	87,110	87,110	87,110	87,110	87,110
12,040	94,110	104,010	101,110	81,110	74,110	91,110	94,110	74,110	79,110	111,110	91,110	74,110	74,110	74,110
113,670	72,400	74,570	71,110	94,110	95,640	111,070	101,110	104,110	74,640	111,110	72,470	104,110	104,110	104,110
81,070	102,640	79,440	111,420	86,910	75,150	94,640	91,690	77,110	95,420	71,640	94,640	87,490	101,240	84,110

211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
81,270	119,430	111,270	93,150	81,110	71,110	102,260	81,110	102,110	71,110	87,110	74,110	101,210	74,240	74,210
104,100	80,040	111,040	96,450	94,910	110,140	108,110	87,110	84,110	104,110	102,110	101,110	101,110	101,110	101,110
74,340	90,690	74,920	81,740	81,910	74,720	117,110	74,420	79,110	97,110	47,440	101,110	104,440	74,110	84,110
87,120	75,440	101,110	105,410	73,720	115,410	127,240	74,110	74,110	83,240	121,110	111,110	85,070	101,070	114,920
113,110	91,740	75,720	81,620	114,110	91,110	104,110	81,110	112,420	90,590	114,110	111,110	91,110	102,110	124,070
110,110	107,010	117,010	91,110	74,440	127,110	74,110	87,110	111,110	82,110	94,710	111,110	124,110	114,110	75,650
116,530	77,070	84,440	77,420	111,110	74,740	74,740	111,110	101,110	101,110	101,110	101,110	101,110	101,110	101,110
80,110	77,040	104,010	74,240	118,110	104,110	104,110	104,110	104,110	104,110	104,110	104,110	104,110	104,110	104,110
91,110	102,240	102,110	84,970	117,070	111,110	101,110	101,110	101,110	101,110	101,110	101,110	101,110	101,110	101,110
71,610	74,810	100,160	99,540	91,240	104,070	94,240	74,110	74,110	74,110	74,110	74,110	74,110	74,110	74,110
81,900	71,110	101,110	112,760	97,110	102,110	74,640	84,840	74,110	81,110	124,040	111,110	74,110	101,110	87,080
97,040	100,640	104,110	91,110	125,160	75,110	84,240	74,110	74,110	74,110	74,110	74,110	74,110	74,110	74,110
88,540	88,110	94,920	77,760	114,110	81,740	111,110	74,740	72,110	91,110	74,740	84,320	109,540	84,740	84,010
83,520	91,740	77,120	111,620	92,520	97,690	71,520	74,750	91,610	92,210	215,110	94,110	125,910	74,110	104,440
94,810	92,840	90,980	115,220	79,320	101,230	87,320	87,780	120,490	119,270	91,750	82,240	94,720	81,170	81,170

APPENDIX VII Number of tillers per plant at Ellerslie

TABLE 1. NUMBER OF TILLERS PER PLANT

(Rows)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	12,320	9,700	10,400	11,500	12,000	9,700	9,700	12,500	11,400	12,500	11,700	9,800	10,000	11,500	12,500
2.	700	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	10,200	10,300	11,100	11,000	9,700	10,300	8,300	9,700	10,200	10,700	6,200	11,000	12,300	9,000	12,500
4.	10,500	12,000	12,800	10,500	10,900	9,700	9,700	11,500	11,500	7,400	8,500	9,200	12,100	8,400	12,600
5.	11,700	9,100	10,300	11,500	11,700	11,700	10,900	11,674	6,444			11,500	7,900	11,700	11,100
6.	15,600	11,500	11,100	12,100	11,200	11,200	11,200	11,200	11,200	11,200	11,200	12,100	14,100	11,200	11,400
7.	10,900	11,500	10,100	12,100	11,200	9,700	12,100	12,100	11,200	11,200	11,200	11,200	12,100	14,100	11,200
8.	10,200	14,000	9,800	10,100	9,100	9,200	12,500	12,500	11,800	9,500	4,700	11,300	9,000	12,000	12,000
9.	10,200	11,400	11,100	10,200	9,400	10,100	1,200	12,100	12,600	6,000	10,400	9,600	11,300	12,200	13,100
10.	12,500	9,000	9,000	10,500	9,400	8,250	8,700	9,000	9,000	9,700	12,500	11,400	12,100	11,200	10,600
11.	9,400	9,400	8,700	7,400	200	200	200	200	200	200	200	200	200	200	200
12.	10,400	9,100	10,100	8,400	9,700	11,800	7,300	9,700	12,100	9,400	11,500	11,600	11,700	12,400	8,400
13.	9,600	8,200	9,800	8,100	10,100	13,000	7,000	12,100	9,200	9,100	7,700	4,600	9,100	7,600	7,500
14.	10,100	9,400	12,200	6,400	9,100	9,100	8,400	9,400	8,400	8,400	8,400	9,300	9,300	7,500	8,400
15.	9,200	9,100	11,100	7,900	8,100	9,700	7,000	8,800	12,100	4,400	11,900	9,400	9,400	8,700	9,700

TABLE 2.

(Rows)	18	29	88	59	74	89	104	119	134	149	154	179	194	209	224
1.	10,300	9,700	9,100	11,400	10,100	9,700	11,200	8,500	12,200	11,500	12,200	11,300	11,300	12,200	9,800
2.	11,800	12,900	11,200	9,400	11,000	15,700	9,700	9,200	11,300	1,400	12,100	13,400	12,100	11,100	12,400
3.	15,100	12,600	12,700	11,000	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700
4.	13,200	9,500	8,500	9,100	11,700	10,700	11,200	11,200	9,100	11,200	11,200	11,200	11,200	11,200	11,200
5.	13,600	14,100	11,200	10,100	10,400	12,900	12,100	12,100	11,900	12,100	11,300	11,300	11,300	11,300	11,300
6.	11,800	10,600	11,400	12,700	14,700	14,900	12,100	11,500	12,100	11,700	14,200	11,300	12,200	9,800	12,400
7.	10,900	11,500	11,700	11,700	15,400	15,200	11,400	11,200	4,200	12,200	12,500	9,200	9,200	9,200	11,200
8.	14,100	16,200	13,200	14,300	11,700	11,700	12,700	11,200	14,400	12,200	15,400	12,100	11,200	11,500	11,600
9.	9,700	11,300	12,000	12,700	12,200	11,700	12,200	12,200	14,700	12,400	11,400	11,400	11,400	11,400	11,400
10.	12,900	12,600	15,200	9,100	11,400	14,100	12,100	11,400	11,400	11,400	11,400	11,400	11,400	11,400	11,400
11.	13,100	9,100	13,100	9,400	11,400	11,400	11,400	11,400	9,200	9,000	9,000	9,000	9,000	9,000	11,400
12.	9,700	15,900	9,400	11,200	11,200	13,700	11,200	11,200	12,400	14,700	11,200	11,200	11,200	11,200	11,200
13.	11,700	12,100	14,100	11,700	11,100	8,400	11,500	12,700	7,400	11,400	11,900	9,400	9,700	8,500	11,800
14.	14,900	11,200	10,800	12,700	12,100	11,200	12,100	11,200	11,200	11,200	11,200	11,200	11,200	11,200	11,200
15.	15,700	10,100	11,100	15,400	12,200	10,700	12,100	10,200	11,100	9,700	16,500	11,200	11,200	11,200	8,100

TABLE 3.

(Rows)	85	59	72	67	121	115	124	143	157	172	115	149	213	2	16
1.	8,700	11,600	12,600	12,400	11,500	11,500	11,100	12,100	14,700	11,100	11,100	11,100	11,100	11,100	11,100
2.	12,100	14,500	15,100	12,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700
3.	12,200	11,600	10,100	15,400	11,400	8,500	12,200	11,000	9,900	11,400	11,400	11,400	11,400	11,400	11,400
4.	12,800	12,400	12,700	11,000	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700
5.	15,000	11,900	11,100	14,700	11,100	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700
6.	16,100	11,700	16,300	11,100	10,400	12,400	12,100	11,400	12,000	12,100	12,100	12,100	12,100	12,100	12,100
7.	15,500	14,400	11,900	12,900	15,400	14,800	12,300	12,300	11,500	11,500	11,500	11,500	11,500	11,500	11,500
8.	17,400	14,000	17,500	11,700	14,200	13,700	14,900	15,700	12,400	11,200	15,700	14,900	15,700	15,700	15,700
9.	10,500	14,700	11,200	15,100	12,400	12,700	15,100	11,200	11,200	11,200	11,200	11,200	11,200	11,200	11,200
10.	14,200	12,700	12,100	10,100	14,100	14,900	11,300	11,900	13,900	11,900	15,000	11,900	11,900	11,900	11,900
11.	11,100	9,100	12,400	14,700	11,700	14,900	16,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700
12.	10,400	11,100	12,900	12,200	11,400	9,100	12,100	11,500	7,700	11,700	11,700	11,700	11,700	11,700	11,700
13.	10,500	10,700	13,100	11,500	12,700	11,400	12,800	11,700	10,400	9,400	11,100	11,100	11,100	11,100	11,100
14.	11,800	11,400	11,600	12,600	12,100	11,500	12,900	11,300	9,900	11,600	11,100	11,100	11,100	11,100	11,100
15.	11,900	12,400	9,600	12,400	11,700	11,500	12,700	9,700	12,400	10,800	9,400	12,200	9,400	12,700	10,600

APPENDIX VIII Number of spikelets per spike at Ellerslie

REPLICATE		NUMBER OF SPIKELETS PER SPIKE														
(1000)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1.	11,511	12,000	10,113	10,100	13,700	10,400	15,411	11,500	10,733	12,111	10,100	11,667	12,101	11,733	10,400	
2.	11,667	12,700	10,400	12,467	12,433	14,733	12,967	12,200	12,467	12,567	10,467	11,667	11,667	10,167	10,167	
3.	11,333	12,000	11,933	11,567	11,633	12,400	10,733	10,233	10,167	11,133	11,267	11,267	11,267	11,267	11,267	
4.	10,333	11,333	11,633	10,133	10,167	11,100	11,200	10,233	11,233	11,233	11,233	11,233	11,233	11,233	11,233	
5.	10,300	11,567	11,733	10,500	11,467	10,567	10,567	10,567	11,975	11,133	12,045	11,200	11,975	11,975	11,200	
6.	10,667	11,933	11,733	11,133	10,767	10,767	10,767	10,767	11,200	11,200	11,200	11,200	11,200	11,200	11,200	
7.	10,733	12,433	10,667	11,733	11,400	11,133	11,533	11,533	11,533	11,533	11,533	11,533	11,533	11,533	11,533	
8.	10,400	11,933	10,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	
9.	12,667	11,733	11,200	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	
10.	11,300	12,700	11,400	10,767	12,400	10,200	10,200	10,200	11,200	11,200	11,200	11,200	11,200	11,200	11,200	
11.	12,257	12,633	10,433	11,167	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	
12.	11,167	12,267	11,500	11,500	11,700	10,133	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	11,700	
13.	11,300	11,233	11,467	11,267	10,200	11,433	12,167	11,567	11,567	11,567	11,567	11,567	11,567	11,567	11,567	
14.	11,167	12,567	10,200	11,500	10,433	11,267	10,433	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	
15.	11,100	11,267	10,500	11,533	12,567	10,567	11,933	10,933	11,933	11,933	11,933	11,933	11,933	11,933	11,933	
REPLICATION 2																
1.	11,511	11,733	10,567	11,633	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	
2.	11,957	11,633	10,296	12,433	11,700	10,200	10,200	10,200	10,200	10,200	10,200	10,200	10,200	10,200	10,200	
3.	11,400	12,167	12,733	10,133	11,767	10,133	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	
4.	12,833	11,867	12,067	12,433	11,200	12,467	12,467	12,467	12,467	12,467	12,467	12,467	12,467	12,467	12,467	
5.	12,633	11,633	11,133	11,767	11,833	11,833	11,833	11,833	11,833	11,833	11,833	11,833	11,833	11,833	11,833	
6.	12,733	11,600	12,133	11,133	11,433	10,433	12,133	12,133	12,133	12,133	12,133	12,133	12,133	12,133	12,133	
7.	12,300	11,467	11,100	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	11,467	
8.	12,267	11,975	12,200	11,133	11,267	12,433	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	11,267	
9.	11,333	10,711	11,067	12,267	11,633	10,933	11,633	11,633	11,633	11,633	11,633	11,633	11,633	11,633	11,633	
10.	12,133	11,267	11,267	11,700	11,100	11,667	12,200	11,467	12,367	10,233	11,957	12,600	11,957	12,600	11,957	
11.	10,733	11,267	10,467	11,933	11,700	10,200	11,667	10,233	11,133	10,200	11,200	10,200	11,200	11,200	11,200	
12.	11,033	10,333	12,933	10,167	10,167	10,167	10,167	10,167	10,167	10,167	10,167	10,167	10,167	10,167	10,167	
13.	11,033	11,100	11,267	11,167	11,100	11,067	11,100	11,100	11,100	11,100	11,100	11,100	11,100	11,100	11,100	
14.	11,333	10,467	10,500	11,296	11,633	11,533	12,433	12,267	10,767	10,000	11,133	10,400	10,133	11,267	10,133	
15.	11,967	12,700	11,167	10,233	10,267	10,400	10,167	10,733	11,733	12,600	10,267	11,567	11,433	11,567	11,433	
REPLICATION 3																
1.	11,300	11,133	11,100	11,267	10,467	12,433	10,167	11,567	11,567	11,567	11,567	11,567	11,567	11,567	11,567	
2.	10,267	10,133	11,733	10,733	11,133	11,633	10,957	10,167	11,233	11,233	11,233	11,233	11,233	11,233	11,233	
3.	10,767	10,800	10,400	11,900	11,767	12,400	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	11,133	
4.	12,400	10,900	10,400	11,900	11,133	10,433	10,133	10,133	10,133	10,133	10,133	10,133	10,133	10,133	10,133	
5.	10,567	11,167	11,667	10,833	10,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	
6.	11,500	11,100	10,400	11,033	11,100	10,233	11,767	11,500	10,267	10,267	10,267	10,267	10,267	10,267	10,267	
7.	10,400	10,433	11,400	10,400	11,133	11,400	10,533	12,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	
8.	10,167	11,667	11,167	11,167	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	
9.	11,067	11,700	10,700	10,267	10,767	11,100	11,100	11,100	11,100	11,100	11,100	11,100	11,100	11,100	11,100	
10.	10,000	11,633	11,267	10,200	11,167	11,633	10,167	11,633	11,633	11,633	11,633	11,633	11,633	11,633	11,633	
11.	11,033	11,567	11,800	11,467	10,100	11,100	10,733	11,433	10,733	10,733	10,733	10,733	10,733	10,733	10,733	
12.	11,067	11,667	11,533	10,400	11,167	12,167	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	11,667	
13.	10,933	11,667	10,300	10,633	10,633	11,667	10,267	11,167	11,167	11,167	11,167	11,167	11,167	11,167	11,167	
14.	10,300	10,233	11,533	11,100	10,167	10,500	10,700	11,200	10,033	11,567	11,667	10,767	11,267	11,267	11,267	
15.	10,000	10,967	11,767	11,100	10,767	10,167	10,267	10,833	10,400	11,233	11,267	10,433	10,533	10,233	11,267	

APPENDIX X Weight of seeds per spike at Ellerslie

(lb./ac)	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115
1.	1,077	2,061	3,456	2,617	1,806	2,165	2,028	1,665	2,367	1,793	1,803	1,793	1,535	1,711	2,359
2.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
3.	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
4.	1,557	1,817	1,752	1,410	1,901	1,966	2,271	1,550	1,710	1,559	2,358	1,817	1,374	1,660	1,856
5.	1,776	1,256	1,705	1,356	1,897	1,869	2,126	1,616	1,531	1,966	1,557	1,819	1,703	1,519	1,501
6.	1,492	2,161	1,651	1,162	1,427	1,822	2,216	1,666	2,025	1,522	1,699	1,627	2,132	1,519	1,762
7.	2,297	1,383	1,867	1,812	1,822	2,366	1,132	1,619	1,919	1,721	1,993	1,512	1,510	1,322	1,612
8.	1,676	1,796	1,916	2,329	1,622	1,687	1,735	1,937	1,442	1,563	1,725	1,918	1,249	1,457	2,262
9.	1,751	1,697	1,561	1,513	1,466	1,715	1,571	1,619	1,677	1,563	1,754	1,627	1,765	1,561	1,579
10.	1,547	1,523	2,227	1,993	1,749	1,993	1,615	1,656	1,707	1,319	1,699	1,718	1,197	1,716	1,513
11.	1,677	1,401	1,755	1,115	1,522	1,176	1,561	1,761	1,912	1,524	1,796	1,881	1,756	1,629	1,319
12.	1,656	1,714	1,576	1,158	1,576	1,725	1,715	1,523	1,586	1,579	1,523	1,525	1,845	1,523	2,017
13.	1,627	1,613	1,876	1,171	1,847	1,727	1,656	2,295	1,613	1,655	1,958	1,947	1,519	1,761	1,679
14.	1,213	1,351	1,695	1,662	1,524	1,576	1,129	1,613	1,572	1,747	1,456	1,157	1,529	1,764	2,012
15.	1,353	1,245	1,699	1,559	1,662	1,661	1,479	1,673	1,122	1,173	1,527	1,632	1,467	1,626	1,573
PLOT 10-2															
1.	1,689	1,255	1,253	1,376	1,659	2,375	1,778	1,673	1,916	1,387	1,975	1,763	1,255	2,496	1,742
2.	1,537	1,424	1,685	1,552	1,695	1,926	2,101	1,736	2,172	1,673	2,133	1,331	1,679	1,625	1,715
3.	1,999	1,578	1,627	1,769	1,602	2,112	2,299	1,670	2,022	1,556	1,912	1,793	2,045	1,724	1,742
4.	1,872	2,133	2,799	1,625	1,628	1,739	1,652	1,714	1,727	1,716	1,659	1,645	1,695	1,562	1,576
5.	2,262	1,064	1,873	1,517	1,896	1,731	2,162	1,662	1,555	1,734	1,671	1,375	1,801	1,763	2,411
6.	2,123	1,513	1,567	2,121	1,674	1,631	1,513	1,624	1,667	1,611	1,719	1,562	1,226	2,044	1,716
7.	1,341	1,636	1,991	1,691	1,657	1,616	1,572	2,026	1,542	1,625	1,627	1,717	1,651	1,714	2,115
8.	2,221	1,795	1,872	1,319	1,566	1,678	1,552	1,672	2,124	1,376	1,526	1,699	1,721	1,322	2,119
9.	2,317	1,476	1,743	1,623	1,632	1,526	1,556	1,646	1,778	1,626	1,625	1,611	1,697	1,627	1,401
10.	1,627	1,572	1,765	1,552	1,549	1,545	1,443	1,702	1,625	1,655	1,631	1,658	1,575	1,825	2,112
11.	1,712	1,612	1,639	1,697	1,692	1,747	1,519	1,656	1,571	1,573	1,506	1,676	1,676	1,537	1,720
12.	1,825	1,622	1,205	1,511	1,779	1,625	1,513	2,275	1,110	2,097	1,576	1,569	1,661	1,721	1,661
13.	1,913	1,617	1,660	1,721	2,022	1,733	1,542	1,613	1,762	2,031	1,574	1,619	1,577	1,562	1,813
14.	1,518	1,662	1,911	1,626	1,220	1,511	1,479	1,656	2,076	1,726	1,526	1,121	1,755	1,922	1,751
15.	1,666	1,654	1,556	1,666	2,105	1,662	1,211	1,662	1,897	1,873	1,230	1,516	1,539	1,619	1,211
PLOT 10-3															
1.	1,669	1,515	1,925	1,775	2,079	1,295	1,102	1,762	1,795	1,519	1,625	2,254	1,496	1,762	1,655
2.	1,696	2,075	1,726	1,515	2,259	1,719	1,649	1,887	2,076	2,078	2,122	1,646	1,762	1,615	2,012
3.	2,297	1,627	2,673	1,516	2,119	2,172	1,792	2,214	1,993	2,000	2,508	1,891	1,935	1,969	1,675
4.	1,795	2,218	1,629	1,716	1,922	1,721	1,667	1,729	2,155	1,734	1,949	1,612	2,167	1,616	1,612
5.	1,359	2,026	1,710	1,613	1,755	1,763	1,659	1,628	1,612	1,763	1,725	1,723	1,212	1,756	1,711
6.	1,712	1,513	1,650	1,412	1,759	1,740	1,649	1,166	1,627	1,665	1,669	1,571	1,763	1,726	1,617
7.	1,575	1,670	2,241	1,559	1,522	1,769	1,767	1,551	2,211	1,710	1,706	1,549	1,717	1,726	1,706
8.	1,927	1,719	1,364	2,260	1,645	1,571	1,756	1,669	1,776	2,136	1,659	1,664	1,618	1,655	2,276
9.	2,112	1,819	1,676	1,659	2,162	1,711	1,767	1,759	1,672	1,734	2,097	1,655	1,825	2,073	2,199
10.	1,940	1,578	1,575	1,558	1,733	1,716	1,523	1,925	1,919	1,661	1,662	1,621	1,705	1,511	1,559
11.	2,019	1,696	1,692	1,623	1,696	1,682	1,513	1,651	2,266	1,977	1,696	1,711	2,126	2,096	1,717
12.	1,571	1,511	1,781	1,549	1,711	1,652	2,062	1,926	1,557	1,667	1,110	1,729	1,761	1,712	1,611
13.	1,627	1,369	1,616	1,610	1,620	1,666	1,491	1,766	1,922	1,762	1,761	1,561	2,014	1,346	1,526
14.	1,870	1,572	1,369	1,750	1,930	1,567	2,025	1,971	1,719	1,415	1,616	1,929	1,561	1,669	1,719
15.	1,603	1,610	1,620	1,658	1,670	1,683	1,655	1,930	1,576	1,692	2,043	1,916	1,616	1,529	1,666

APPENDIX XI 1000-kernel weight at Ellerslie

APPENDIX XI-1. 1000-KERNEL WEIGHT														
(Bucks)	187	188	189	190	191	192	193	194	195	196	197	198	199	200
1.	88.360	87.459	87.369	87.513	88.267	88.260	88.671	88.764	89.358	89.455	89.305	89.455	89.353	89.772
2.	89.621	89.059	89.059	89.082	89.359	89.566	89.389	89.312	89.811	89.513	89.723	89.227	89.28	89.29
3.	89.236	89.769	89.581	89.463	89.503	89.688	89.553	89.418	89.627	89.65	89.586	89.187	89.420	89.821
4.	89.567	89.855	89.177	89.727	89.516	89.599	89.440	89.516	89.55	89.55	89.55	89.57	89.57	89.57
5.	89.354	89.558	89.421	89.351	89.201	89.585	89.651	89.668	89.565	89.627	89.672	89.472	89.187	89.188
6.	89.213	89.173	89.216	89.667	89.330	89.193	89.582	89.519	89.764	89.367	89.387	89.273	89.216	89.216
7.	89.266	89.811	89.519	89.262	89.423	89.229	89.377	89.98	89.623	89.648	89.713	89.101	89.053	89.232
8.	89.737	89.589	89.519	89.549	89.548	89.713	89.541	89.359	89.577	89.660	89.227	89.261	89.471	89.589
9.	89.225	89.508	89.432	89.732	89.178	89.189	89.562	89.567	89.522	89.628	89.265	89.250	89.250	89.377
10.	89.419	89.425	89.478	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472
11.	89.731	89.667	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478
12.	89.743	89.309	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478	89.478
13.	89.627	89.648	89.529	89.772	89.370	89.135	89.276	89.557	89.373	89.915	89.711	89.441	89.238	89.564
14.	89.728	89.344	89.181	89.571	89.720	89.47	89.128	89.443	89.949	89.251	89.722	89.573	89.217	89.479
15.	89.523	89.363	89.725	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472	89.472
APPENDIX XI-2. 1000-KERNEL WEIGHT														
(Bucks)	201	202	203	204	205	206	207	208	209	210	211	212	213	214
1.	89.216	89.525	89.701	89.564	89.314	89.213	89.997	89.793	89.325	89.626	89.173	89.358	89.823	89.555
2.	89.747	89.581	89.651	89.538	89.313	89.440	89.223	89.675	89.103	89.622	89.153	89.163	89.373	89.278
3.	89.672	89.812	89.674	89.665	89.627	89.627	89.627	89.627	89.627	89.627	89.627	89.627	89.627	89.627
4.	89.521	89.223	89.571	89.571	89.571	89.571	89.571	89.571	89.571	89.571	89.571	89.571	89.571	89.571
5.	89.147	89.523	89.181	89.313	89.661	89.712	89.559	89.442	89.315	89.915	89.471	89.448	89.245	89.573
6.	89.523	89.575	89.518	89.778	89.492	89.124	89.450	89.277	89.139	89.695	89.556	89.316	89.617	89.423
7.	89.731	89.523	89.645	89.651	89.456	89.100	89.505	89.724	89.699	89.643	89.385	89.157	89.840	89.512
8.	89.710	89.643	89.477	89.249	89.705	89.318	89.315	89.441	89.511	89.571	89.443	89.443	89.615	89.595
9.	89.326	89.885	89.478	89.150	89.249	89.275	89.027	89.572	89.442	89.396	89.395	89.353	89.623	89.704
10.	89.704	89.622	89.570	89.148	89.403	89.223	89.611	89.439	89.259	89.226	89.251	89.181	89.222	89.573
11.	89.346	89.343	89.525	89.181	89.458	89.453	89.453	89.616	89.252	89.252	89.712	89.658	89.517	89.115
12.	89.343	89.328	89.354	89.210	89.543	89.222	89.222	89.222	89.222	89.222	89.222	89.222	89.222	89.222
13.	89.774	89.267	89.379	89.152	89.774	89.774	89.774	89.774	89.774	89.774	89.774	89.774	89.774	89.774
14.	89.528	89.151	89.487	89.296	89.179	89.451	89.113	89.219	89.212	89.479	89.571	89.722	89.172	89.172
15.	89.739	89.345	89.224	89.675	89.227	89.452	89.972	89.665	89.266	89.253	89.325	89.481	89.241	89.356
APPENDIX XI-3. 1000-KERNEL WEIGHT														
(Bucks)	215	216	217	218	219	220	221	222	223	224	225	226	227	228
1.	89.713	89.579	89.542	89.116	89.219	89.183	89.791	89.751	89.665	89.709	89.387	89.258	89.273	89.296
2.	89.551	89.211	89.171	89.171	89.243	89.135	89.224	89.517	89.409	89.493	89.329	89.115	89.696	89.718
3.	89.464	89.517	89.172	89.718	89.216	89.173	89.255	89.920	89.190	89.573	89.189	89.123	89.392	89.416
4.	89.851	89.783	89.506	89.205	89.477	89.181	89.428	89.256	89.571	89.682	89.613	89.288	89.218	89.205
5.	89.154	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181	89.181
6.	89.577	89.499	89.523	89.512	89.553	89.553	89.553	89.553	89.553	89.553	89.553	89.553	89.553	89.553
7.	89.245	89.249	89.317	89.242	89.582	89.443	89.161	89.164	89.168	89.269	89.672	89.278	89.322	89.318
8.	89.326	89.197	89.553	89.816	89.228	89.181	89.577	89.572	89.705	89.557	89.523	89.291	89.417	89.318
9.	89.159	89.876	89.202	89.217	89.582	89.727	89.123	89.116	89.455	89.896	89.118	89.400	89.362	89.296
10.	89.427	89.167	89.600	89.316	89.493	89.490	89.655	89.697	89.160	89.165	89.328	89.011	89.386	89.571
11.	89.216	89.219	89.320	89.515	89.515	89.515	89.515	89.515	89.515	89.515	89.515	89.515	89.515	89.515
12.	89.370	89.558	89.448	89.157	89.169	89.169	89.169	89.169	89.169	89.169	89.169	89.169	89.169	89.169
13.	89.320	89.180	89.260	89.310	89.200	89.689	89.779	89.616	89.271	89.180	89.615	89.076	89.228	89.360
14.	89.125	89.115	89.167	89.475	89.500	89.216	89.466	89.102	89.458	89.117	89.520	89.105	89.027	89.119
15.	89.437	89.525	89.683	89.653	89.993	89.297	89.128	89.788	89.916	89.293	89.667	89.183	89.279	89.318

APPENDIX XII Yield per plant at Ellerslie

REPLICATION 1																	
(0101)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	
1.	20.010	13.910	16.140	22.970	21.432	17.581	13.556	13.670	15.172	17.733	15.478	12.317	15.513	16.733	16.103		
2.	12.247	11.896	15.951	16.670	16.845	13.225	11.716	16.570	15.949	15.074	16.119	16.177	15.511	13.349	12.445		
3.	12.612	13.550	15.513	13.754	16.931	16.135	14.951	12.710	219	220	221	222	223	224	225		
4.	11.727	16.453	17.140	13.781	17.710	15.785	14.736	12.676	13.311	12.508	16.281	10.773	16.172	12.912	18.402		
5.	16.037	8.417	15.155	11.023	14.148	15.496	23.134	22.147	13.054	14.553	15.254	15.281	12.374	17.030	11.692		
6.	19.545	15.469	12.526	10.622	16.642	12.951	15.110	18.263	18.235	17.137	15.926	15.132	13.700	13.131	11.915		
7.	21.035	17.378	15.016	16.612	16.779	10.748	13.965	20.540	17.273	15.213	15.550	16.810	22.014	16.473	18.405		
8.	13.153	16.750	13.478	16.762	13.726	12.523	14.522	21.774	13.217	16.618	13.659	12.918	13.958	16.073	17.483		
9.	13.782	16.239	13.517	11.169	10.230	10.653	8.450	12.204	12.231	13.548	15.544	13.058	12.576	13.812	17.127		
10.	11.674	11.982	12.554	15.617	13.507	12.813	10.423	12.568	2.0	9.053	13.167	12.552	12.550	12.645	12.116		
11.	9.544	10.004	11.515	8.025	12.142	9.447	9.225	15.511	11.751	8.272	13.012	3.181	4.140	8.455	11.241		
12.	10.145	13.119	11.583	7.123	14.243	12.613	10.705	11.114	13.573	11.552	12.664	12.843	11.923	13.111	12.114		
13.	13.032	17.187	17.624	12.470	14.456	16.722	8.211	16.727	11.755	8.440	17.775	11.113	11.728	12.211	11.258		
14.	8.046	11.520	16.711	1.522	10.343	9.743	13.149	11.745	12.432	11.456	12.572	11.711	11.195	10.214	15.458		
15.	13.402	9.938	18.776	4.171	12.116	12.197	15.049	17.610	11.052	12.978	11.832	11.673	11.245	11.249	12.557		
REPLICATION 2																	
1.	11.304	11.297	10.155	11.355	13.542	16.157	15.135	12.952	11.219	12.192	16.356	11.357	13.241	15.193	16.118		
2.	12.540	18.333	15.252	11.631	15.249	16.778	10.123	12.722	16.754	12.812	16.526	15.745	11.276	15.529	13.524		
3.	15.745	14.592	15.545	11.731	10.624	19.771	14.271	14.251	15.491	17.440	20.156	21.373	17.635	21.671	17.113		
4.	17.218	14.531	11.950	11.455	14.626	11.724	18.195	13.475	11.525	13.539	15.221	12.333	13.051	17.111	16.256		
5.	21.312	15.443	14.195	23.072	15.023	12.574	17.557	14.172	15.458	11.414	22.554	17.171	15.6	20.9	21.6		
6.	16.918	12.857	14.289	17.155	18.434	16.154	17.975	13.231	18.125	13.742	18.113	12.723	11.253	14.328	16.710		
7.	8.774	11.050	11.614	12.229	17.711	16.256	12.195	15.447	11.621	11.000	14.104	12.227	17.248	15.210	17.673		
8.	15.927	21.325	14.271	14.750	24.195	18.043	15.814	14.743	22.007	14.373	18.249	19.643	14.231	11.774	20.200		
9.	14.423	13.324	16.444	15.777	17.738	15.744	14.213	14.745	16.169	11.210	15.528	20.117	11.712	12.417	15.632		
10.	13.907	18.020	15.619	11.949	12.176	18.615	11.135	13.249	15.493	15.971	21.304	17.150	16.717	16.011	22.645		
11.	17.953	10.404	19.142	16.733	14.996	14.558	15.743	14.962	11.745	14.244	17.113	14.322	14.2	20.9	22.2		
12.	13.275	19.254	13.430	12.140	14.442	15.462	23.644	25.819	19.075	17.372	12.291	14.522	15.054	18.127	17.074		
13.	15.721	12.751	10.640	16.719	14.555	12.711	14.348	8.431	9.249	13.329	12.700	11.218	11.520	14.444	15.423		
14.	11.425	12.738	13.239	15.454	11.717	14.155	15.647	19.421	14.548	13.358	15.492	21.727	13.155	11.744	12.135		
15.	13.354	12.165	11.714	11.019	15.153	17.824	12.193	11.192	13.119	14.568	15.054	16.152	14.525	13.122	12.920		
REPLICATION 3																	
1.	17.441	17.426	16.490	17.418	22.527	24.181	22.277	19.319	15.475	20.748	16.427	17.282	27.147	22.214	15.482		
2.	24.842	15.515	15.134	21.058	21.569	17.512	13.116	20.872	18.131	13.275	19.118	22.259	12.131	13.431	14.752		
3.	22.594	11.521	17.403	24.523	14.243	11.149	16.419	19.370	17.145	15.505	14.915	14.152	11.928	16.185	18.118		
4.	27.076	22.997	16.527	14.120	17.018	20.476	16.155	19.737	18.572	23.434	17.917	17.221	21.714	22.124	14.830		
5.	11.108	17.902	21.006	21.777	21.542	19.585	27.216	14.654	16.133	19.445	19.127	21.319	15.139	21.515	14.383		
6.	15.179	13.262	21.872	17.643	14.010	21.213	14.466	19.174	13.279	14.843	14.521	15.245	12.292	13.274	15.043		
7.	14.055	14.392	17.720	14.814	11.251	11.773	18.217	18.317	23.287	15.281	17.688	15.287	21.113	14.545	13.747		
8.	28.240	19.800	20.872	17.115	15.131	17.974	21.419	28.927	19.359	14.132	14.758	14.823	17.771	19.231	14.713		
9.	14.915	21.034	21.911	14.074	24.581	18.757	11.211	11.147	13.124	22.111	19.115	15.226	11.155	24.935	22.774		
10.	13.207	15.968	15.947	17.548	10.027	13.289	13.218	15.125	10.549	22.011	20.189	15.757	21.183	14.103	15.718		
11.	14.816	15.198	15.648	15.347	17.695	21.102	24.331	19.770	17.014	20.225	21.837	20.111	17.127	16.792	20.495		
12.	11.361	19.911	11.832	17.091	15.016	14.153	15.769	15.137	14.746	18.915	12.151	14.720	15.710	23.812	23.920		
13.	13.219	13.101	15.769	17.774	13.016	13.204	16.715	14.194	19.124	14.270	13.148	16.610	12.740	12.681	13.260		
14.	14.445	20.732	14.216	14.650	15.803	15.803	16.211	16.491	13.157	16.622	18.140	17.022	15.124	12.136	17.720		
15.	9.610	15.049	9.867	15.638	20.569	15.720	16.553	16.966	10.720	15.013	16.558	14.263	15.532	19.170	24.554		

APPENDIX XV Heading-span at Parkland

APPENDIX XV

(Block)	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195
1.	11,000	8,000	5,000	5,000	8,000	8,000	10,000	8,000	5,000	10,000	10,000	10,000	10,000	10,000	10,000
2.	12,000	9,000	6,000	6,000	9,000	9,000	11,000	9,000	6,000	11,000	11,000	11,000	11,000	11,000	11,000
3.	9,000	9,000	5,000	5,000	10,000	9,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000
4.	8,000	8,000	9,000	9,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000
5.	7,000	11,000	9,000	9,000	8,000	8,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
6.	6,000	8,000	8,000	8,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000
7.	8,000	6,000	3,000	3,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000
8.	6,000	12,000	6,000	6,000	10,000	10,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
9.	9,000	7,000	9,000	7,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
10.	8,000	9,000	7,000	7,000	5,000	5,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
11.	6,000	5,000	8,000	8,000	4,000	4,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000
12.	9,000	8,000	8,000	8,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000	10,000
13.	9,000	10,000	8,000	8,000	9,000	9,000	9,000	9,000	9,000	9,000	9,000	9,000	9,000	9,000	9,000
14.	8,000	5,000	12,000	7,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
15.	6,000	5,000	3,000	3,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000	8,000

APPENDIX XV

1.	10,000	7,000	9,000	5,000	12,000	6,000	5,000	5,000	9,000	7,000	6,000	8,000	4,000	4,000	7,000	8,000
2.	6,000	5,000	8,000	4,000	3,000	7,000	6,000	3,000	7,000	5,000	5,000	7,000	5,000	7,000	5,000	5,000
3.	11,000	9,000	5,000	5,000	8,000	9,000	7,000	9,000	10,000	8,000	5,000	11,000	11,000	9,000	10,000	7,000
4.	9,000	8,000	7,000	3,000	5,000	7,000	5,000	5,000	11,000	5,000	8,000	8,000	8,000	8,000	8,000	8,000
5.	8,000	6,000	8,000	8,000	10,000	6,000	5,000	5,000	5,000	8,000	6,000	5,000	5,000	5,000	5,000	7,000
6.	5,000	9,000	10,000	4,000	5,000	9,000	8,000	7,000	8,000	3,000	5,000	11,000	11,000	11,000	11,000	11,000
7.	6,000	5,000	6,000	5,000	7,000	8,000	10,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000	11,000
8.	6,000	8,000	7,000	5,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000
9.	7,000	7,000	10,000	11,000	10,000	7,000	5,000	7,000	8,000	8,000	8,000	9,000	9,000	9,000	9,000	7,000
10.	8,000	8,000	8,000	10,000	8,000	7,000	9,000	8,000	11,000	8,000	10,000	10,000	10,000	10,000	10,000	10,000
11.	7,000	5,000	7,000	9,000	8,000	7,000	8,000	9,000	5,000	5,000	9,000	5,000	3,000	6,000	7,000	7,000
12.	5,000	9,000	6,000	5,000	5,000	5,000	5,000	5,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000	7,000
13.	5,000	5,000	6,000	5,000	9,000	9,000	8,000	8,000	10,000	7,000	5,000	5,000	5,000	9,000	8,000	9,000
14.	11,000	8,000	7,000	4,000	7,000	4,000	11,000	10,000	5,000	8,000	5,000	5,000	8,000	8,000	8,000	8,000
15.	12,000	6,000	6,000	12,000	14,000	6,000	6,000	7,000	11,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000

APPENDIX XV

1.	2,000	3,000	5,000	6,000	10,000	5,000	5,000	6,000	9,000	8,000	9,000	7,000	7,000	9,000	5,000
2.	6,000	6,000	6,000	7,000	4,000	5,000	6,000	5,000	5,000	5,000	6,000	5,000	7,000	6,000	6,000
3.	5,000	6,000	11,000	12,000	16,000	16,000	18,000	18,000	20,000	21,000	5,000	5,000	5,000	5,000	6,000
4.	5,000	5,000	5,000	4,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
5.	5,000	7,000	5,000	5,000	5,000	6,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
6.	7,000	7,000	6,000	8,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
7.	7,000	7,000	5,000	5,000	11,000	11,000	14,000	14,000	17,000	17,000	17,000	17,000	17,000	17,000	17,000
8.	6,000	5,000	7,000	5,000	7,000	5,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000
9.	8,000	7,000	5,000	5,000	6,000	6,000	7,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000
10.	5,000	6,000	5,000	7,000	8,000	6,000	6,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
11.	7,000	5,000	5,000	20,000	22,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000	12,000
12.	6,000	5,000	7,000	16,000	17,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000	6,000
13.	5,000	6,000	6,000	7,000	8,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
14.	8,000	5,000	8,000	6,000	6,000	5,000	6,000	6,000	5,000	5,000	5,000	5,000	5,000	5,000	5,000
15.	7,000	5,000	3,000	7,000	8,000	6,000	6,000	5,000	7,000	8,000	8,000	8,000	8,000	8,000	8,000

APPENDIX XVII Number of tillers per plant at Parkland

PERMANENT PLOT DATA

(Block)	193	192	191	190	189	188	187	186	185	184	183	182	181	180	
1.	15,400	12,200	13,100	12,400	16,000	11,200	12,200	12,400	11,100	11,700	11,400	13,700	193	193	194
2.	12,800	12,100	14,400	14,100	13,100	16,100	12,700	23	28	25	25	27	28	29	30
3.	12,500	16,700	16,100	14,500	13,600	13,200	17,000	210	218	221	222	222	224	224	225
4.	18,600	11,500	12,000	13,000	15,600	18,500	12,400	15,700	12,200	13,400	12,100	12,100	57	58	59
5.	15,467	13,100	13,600	12,900	11,200	15,000	10,400	13,500	16,800	13,100	12,400	15,200	117	116	119
6.	15,400	12,400	12,400	14,300	10,400	12,400	11,700	11,000	11,200	12,100	14,200	16,700	12,000	13,100	13,100
7.	10,200	13,100	14,100	12,200	8,200	10,500	16,800	11,100	14,200	11,000	13,100	12,400	12,400	13,400	13,400
8.	15,100	14,200	13,300	10,700	12,500	18,400	11,700	11,900	14,100	12,400	14,200	10,100	72	73	74
9.	11,700	11,100	12,400	12,700	11,200	11,600	14,600	12,100	15,900	12,400	11,700	11,800	142	143	144
10.	15,300	17,100	10,400	11,400	11,700	11,700	10,300	10,300	13,400	13,100	11,400	11,900	14,100	12,100	13,400
11.	17,100	14,200	13,100	11,100	11,100	12,400	15,400	12,900	13,500	13,400	13,400	13,500	16,400	14,200	14,500
12.	18,500	12,100	15,700	14,200	15,700	15,200	11,400	11,300	11,300	12,600	14,400	11,300	87	83	85
13.	16,300	15,700	13,100	17,400	12,500	15,100	11,300	13,900	14,400	14,500	14,500	14,700	147	145	142
14.	18,900	13,000	14,400	12,700	13,200	12,600	13,200	11,000	11,900	15,100	14,500	11,400	12,100	15,100	15,200
15.	14,700	13,300	11,400	15,400	16,400	15,200	13,700	12,500	13,400	14,200	13,600	13,700	15,100	10,550	15,200

REPLICATES

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.
13,700	9,200	11,100	15,100	10,400	11,700	13,400	11,200	15,100	9,200	11,500	9,200	11,500	9,200	11,100
15,300	11,100	12,600	12,100	12,400	11,600	11,200	13,500	9,000	12,400	10,700	16,200	14,100	10,100	11,300
16,400	15,100	11,000	14,000	11,100	10,100	12,400	11,500	12,000	11,100	10,100	11,200	11,200	11,200	11,400
15,700	12,900	11,400	12,400	14,400	12,200	12,100	17,000	11,200	12,000	12,000	12,000	12,000	12,000	12,000
11,500	12,100	10,200	17,700	12,700	12,900	4,500	14,500	12,700	12,100	14,100	12,100	8,700	12,000	12,500
9,400	13,200	16,500	12,400	13,400	11,400	13,700	15,900	13,100	11,400	14,100	11,200	11,100	14,100	11,500
11,600	11,300	9,700	12,800	14,100	11,400	11,400	9,500	11,000	12,000	12,000	11,400	11,200	11,200	11,200
11,400	14,200	9,100	9,400	11,200	8,400	11,200	9,500	9,500	12,400	12,400	11,700	11,400	11,200	12,000
9,100	17,100	10,300	12,600	10,300	10,100	10,400	13,100	9,000	9,000	9,000	11,200	9,500	10,100	11,400
22,467	23,444	17,100	19,222	13,500	11,000	12,700	9,400	12,500	13,400	13,400	17,000	17,000	17,000	17,000
12,600	13,400	8,100	7,100	1,000	9,400	12,100	10,400	10,200	8,500	15,200	6,200	11,100	9,000	12,400
9,100	12,200	11,100	11,100	6,100	12,700	9,000	11,000	9,100	12,100	11,400	8,500	12,100	13,400	12,700
14,300	14,700	13,100	14,100	14,100	10,200	14,700	19,500	16,400	11,700	15,500	14,400	12,500	13,400	14,100
19,200	12,100	11,000	9,900	12,000	11,400	13,400	12,400	15,100	10,100	12,100	11,900	11,400	11,500	12,400
15,800	11,100	11,100	14,800	11,200	10,400	12,400	13,400	9,500	10,400	10,400	10,400	10,400	10,400	12,700

REPLICATES

1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.
15,100	14,100	15,000	14,100	15,100	11,500	16,400	11,500	12,000	5,700	11,300	14,200	11,500	14,100	14,600
11,000	13,400	15,400	12,400	11,700	13,400	11,200	12,400	12,100	11,100	14,000	13,000	17,000	12,700	11,100
13,200	11,700	8,100	16,000	12,400	9,500	13,000	11,100	11,100	202	216	6	19	11	67
195	209	223	12	25	40	54	68	82	96	110	124	138	152	166
11,100	11,200	14,000	12,000	11,000	15,100	12,100	14,600	12,100	9,500	14,100	14,200	13,100	12,100	13,200
15,300	15,100	9,400	10,700	12,000	7,400	11,200	12,700	14,400	9,100	15,700	11,667	10,400	12,500	13,000
14,700	12,700	12,200	9,700	8,100	13,200	11,100	13,100	11,600	10,400	9,400	9,700	14,100	13,600	13,600
20,600	12,400	11,900	14,000	11,900	10,400	10,400	14,400	11,900	13,400	14,400	11,400	9,700	11,200	8,700
15,100	14,400	12,000	9,900	14,500	12,100	10,600	9,200	12,700	10,800	15,500	11,700	11,400	11,400	11,000
9,500	12,400	11,100	11,100	4,500	10,400	11,400	12,000	8,400	9,900	11,500	8,700	12,100	9,500	11,100
15,700	10,800	12,100	10,400	11,100	10,400	10,400	10,400	11,900	10,700	8,000	12,000	11,400	11,400	12,200
165	179	193	207	221	235	249	263	277	291	305	319	333	347	361
9,700	12,400	13,100	8,400	11,200	10,444	11,300	12,100	11,700	13,100	12,100	12,100	10,400	14,100	16,100
120	134	148	162	176	190	204	218	232	246	260	274	288	302	316
11,400	9,700	13,000	13,200	9,700	10,300	11,900	11,900	12,700	12,700	12,700	12,700	12,700	12,700	12,700
30	44	58	72	86	100	114	128	142	156	170	184	198	212	226
75	89	103	117	131	145	159	173	187	201	215	229	243	257	271
9,375	11,400	12,600	8,400	10,700	11,400	11,400	10,300	9,889	10,063	10,500	11,200	12,100	13,400	11,300
210	224	238	252	266	280	294	308	322	336	350	364	378	392	406
13,100	11,100	10,100	11,400	11,200	12,400	11,200	10,400	13,400	10,100	12,500	10,100	10,100	10,000	11,200

APPENDIX XIX Number of seeds per spike at Parkland

Plot	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1.	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115
2.	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130
3.	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145
4.	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
5.	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175
6.	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190
7.	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205
8.	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220
9.	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235
10.	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250
11.	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265
12.	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
13.	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295
14.	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310
15.	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325
16.	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
17.	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355
18.	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370
19.	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385
20.	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
21.	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415
22.	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430
23.	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445
24.	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460
25.	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475
26.	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490
27.	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505
28.	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520
29.	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535
30.	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550
31.	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565
32.	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580
33.	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595
34.	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610
35.	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625
36.	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640
37.	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655
38.	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670
39.	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685
40.	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700
41.	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715
42.	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730
43.	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745
44.	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760
45.	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775
46.	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790
47.	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805
48.	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820
49.	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835
50.	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850
51.	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865
52.	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880
53.	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895
54.	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910
55.	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925
56.	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940
57.	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955
58.	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970
59.	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985
60.	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000

