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DEVELOPMENT OF HIGH YIELDING DOUBLE CROSS MAIZE HYBRIDS USING 9 X 9 DIALLEL METHOD

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Abstract

Diallel analysis is one of the methods to develop and evaluate F1 and F2 hybrid crosses for desirable parameters based on mode of gene actions. The experiment entitled "Development of high yielding double cross F1 maize hybrids utilizing 9 x 9 full diallel method" was selected and conducted at Bacha Khan University Agriculture Research Farm during Kharif season 2021-22.Eight F1 Maize hybrids and one open pollinated variety of sweet corn were crossed in all possible combinations and produced 72 double crosses F¬1 hybrids including reciprocals and compared with 9 parents. Experiment was laid out in a partial lattice square design with 9 blocks having 9 entries each with three replications. After analyzing the data on the following parameters: Days to 50% Anthesis, Days to 50% Silking, Days to 50% Anthesis Silking Interval (ASI), Height of Cob, Plant Height and Grain Yield; significant differences were observed among the double cross F1 hybrids for almost all of the parameters with the exception of the parameters: Number of cobs, Plant height, cob diameter and cob length. The traits having significant results were further subjected to genetic analysis for finding mode of gene actions, genetic components of variation and heritabilities of significant parameters. Highly significant variations were observed for all genetic components using Hayman's approach regarding grain yield, which indicated presence of additive (A), dominance (B), directional dominant (B1), non-symmetrical genes distribution. Significant values of maternal (C) and reciprocal effects (D) for all parameters indicated retesting of A and B effects to make them non-significate for having no maternal and reciprocal effects.

The Wr-Vr graph showed that the regression line cuts the y-axis above the origin for all parameters. This is an indication that partial dominance type of gene action is controlling the traits under study. The value for broad sense heritability was larger than narrow sense heritability for parameters: (days to 50% tasseling, days to anthesis, days to silking, ASI and grain yield). This indicated that main role was played by non-additive genes in the expression of these parameters.

Component of variation for days to 50% tasseling, days to silking and height of cob, pointed out that GCA variance was greater than SCA variance indicating the importance of additive gene effects for the control of the trait. While, Components of variance for ASI, days to 50% anthesis and grain yield indicated that SCA variance was greater in magnitude than GCA variance giving a greater estimate of variance due to dominant effects. Minimum Days to 50% Anthesis was noted for 6 x 5 (55 days), whereas minimum days to 50% tasseling was observed for 9 x 2, 1 x 5 and 1 x 10 (54 days). Minimum ASI was noted for 2 x 4, 6 x 6, 5 x 8, 4 x 1, 5 x 9, 5 x 2, 7 x 6, 7 x 10 (3 days). F1 (1 x 4, 1 x 7, 1 x 8, 1 x 10, 2 x 1, 2 x 5, 2 x 6, 4 x 10, 6 x 2, 6 x 8, 6 x 7, 6 x 10, 7 x 1, 7 x 5, 7 x 10, 8 x 7, 8 x 9, 8 x 10, 9 x 1, 9 x 2, 9 x 6, 9 x 7, 10 x 1) gave maximum grain yield. Further suggested that the above mentioned crosses should be utilizing in the coming breeding programs for more desire improvement from all angles (qualitative and quantitative).

Keywords: *Combining ability, Heterosis study, Gene action, Heritability, Inbreeding depression.*

Introduction

Maize or corn (*Zea mays* L.) is a diploid species belongs to group poaceae. It is verdant on majority of the members of the globe because of its extensive changeable and maximum productivity [1]. Maize is grown as dual season crop. It prefers cross pollination due to its male and female flowers orientation. Maize can be successfully grown in almost all the zones of the world and could be a potential crop for the developing nations. It can be grown from with range of latitude from 500 N to 400 S and with altitude up to 3300 meters Total above the sea level [2].

Total area under maize crop was 118 million hectares with 785 million metric tons worldwide production. Area of 1130 thousand hectares with average grain yield of 4053 kgha^{-1} were recorded in Pakistan. Major growing areas in Khyber Pakhtunkhwa are Peshawar, Swabi, Mardan, Swat and D.I. Khan and Charsadda [3].

Perhaps the majority of constantly accustomed mating scheme in plants study is the diallel mating design as it is a superior source to detect behavior of producers in crosses. The diallel lay out was useable implications if dissect and translated truly. There are n^2 crosses are produced between parents, including reciprocals. Due to heavy data manipulation and laboriousness less than 20 parents include in the mating design. Main focus in diallel analysis is on estimation of overall commix capability (GCA) backwash of their parents and specific commix capability (SCA) effects for specific crosses of the parents [4].

The diallel mating scheme might be the maximum regularly used mating layout in plant studies and is an exceptional scheme to decide how mother and father carry out in crosses. The diallel mating layout has many beneficial functions if analyzed and interpreted correctly. As the call implies, n 2 crosses are produced among n dad and mom, consisting of reciprocals. Because of the logistics in generating and comparing the crosses among dad and mom, the range of mother and father covered with inside the diallel mating layout typically consists of much less than 20 mother and father. Usually, the primary emphasis is to estimate the relative trendy combining capacity (GCA) results of the dad and mom in crosses and particular combining capacity (SCA) consequences for unique crosses of the mother and father. The development of a brand new range with excessive yield is the precise goal of all Maize breeders. The first step in a success breeding software is to choose suitable mother and father. Diallel evaluation offers a scientific method for the detection of suitable mother and father and crosses advanced in phrases of the investigated tendencies. It additionally enables plant breeders to pick the maximum green choice approach via way of means of permitting them to estimate numerous genetic parameters. In carried out breeding programs, the estimation of the GCA and SCA results may be very informative with inside the assessment of inbred strains in hybrids. Another example of powerful use of the diallel crossing designs is to assess cultivars in crosses to discover feasible new heterotic groups. The mother and father and crosses are evaluated to estimate GCA and SCA outcomes and heterocyst of the parent's vs crosses. Other combos and analyses may be used relying crop species and goals of the investigator. Estimates of genetic results are suitable for maximum diallel mating systems, however frequently investigators choice to increase estimation to consist of genetic additives of variance and heritability. The idea of GCA and SCA turned into brought through Sprague and Tatum (1942) and its mathematical modeling changed into set approximately through Griffing (1956) in his classical paper alongside the diallel crosses. The price of any populace relies upon on its ability and it's combining cap potential in crosses [5]. The usefulness of those ideas for the characterization of an inbred in crosses were an increasing number of famous some of the maize breeders feel the previous few decades. Diallel crosses were broadly utilized in genetic studies to research the inheritance of critical trends amongst a fixed of genotypes. These have been devised, specifically, to research the combining capacity of the parental traces for the cause of identity of advanced mother and father to be used in hybrid improvement programs. Analysis of diallel information is generally performed in line with the strategies of Griffing (1956) which partition the overall variant of diallel information into GCA of the mother and father and SCA of the crosses. A diallel is easy to control in maize and components critical statistics approximately the studied populations for numerous genetic parameters [6] Recently weather extrude and value of maize hybrids are main troubles in maize production. Unprecedented rain fall and abrupt warmth because of weather alternate purpose heavy loss to the maize crop grown with inside the final season at Charsadda. Farmers of the locality additionally can't come up with the money for the excessive price of hybrid seed. In addition, availability of excellent seed additionally a prime difficulty with inside the region. So, to deal with all of the triumphing problems in maize, diallel mating layout having nine x nine crosses of F1hybrids to provide double pass hybrids were selected for the studies observe. Major recognition might be on investigating the GCA of the parental lines in order to become aware of advanced dad and mom to be used in hybrid development programmers, so as to have broader adaptability and suitable resistance for extraordinary weather extrude.

1.1 Aim

The overall aim of this study is Agriculture sustainability at Charsadda.

1.2 Objectives

I. To check well known and unique combining capacity.

II. To check heritability amongst crosses and parental hybrids.

III. To estimate heterocyst amongst parents and crosses.

IV. To choose pleasant acting hybrids for double cross maize hybrids production.

METHODOLOGY

The study entitled "development of high yielding double cross maize hybrids utilizing 9x9 diallel method" was conducted at Bacha Khan Agriculture research farm (BARF) Charsadda during Kharif season 2021-22. The experiment comprised of two phases. During first phase of experiment different genotypes namely white1, white2, white4, yellow hybrid1, yellow hybrid2, yellow hybrid3, yellow hybrid4, and variety 'white' sweet corn were sown and crossed in 9 x 9 diallel fashion. During second phase, experimental material comprised of 9 x 9 diallel crosses was laid out in partial lattice square design in three replication. Each candidate maize hybrid was planted in single row with 5 meter length having row to row distance of 75 cm, respectively. Plot area was 1 × 5 × 0.75 m (3.75 m^2) for each entry in the experiment. The experiment was planted in July, 2022. All the agronomic practices were carried out during crop growing season. Data were recorded on 11 quantitative parameters using five randomly selected plants in each plot.

2.1 Plan of work

Phase I

Collection of material from CCRI

Phase II

Crossing of genotypes in a diallel manner.

Phase III

Sowing of diallel crosses along with parental hybrids and checks.

Phase IV

Data collection and data organization

Phase V

Data analysis and thesis write up.

Computation of data were carried out by R language utilizing analysis of variance for partial lattice square design and then exposed hem to genetic analysis including GCA, SCA, and heritability.

RESULTS AND DISCUSSION

3.1 Analysis of variance

Analysis of variance (ANOVA) carried out for the subsequent parameters which confirmed widespread variations at p < 0> 0.05) have been recorded (Table 1).

3.2 Days to 50% Tasseling

The ANOVA effects showed highly substantial versions for days to 50 % tasseling which found out genetic variations some of the genotypes for days to 50 % tasseling. Plant breeders prefer genetic variability many of the genotypes for the development of crop flora. [7] Found out comparable effects for days to 50% tasseling. Mean information depicted that days to 50% tasseling have been ranged from fifty four to sixty one days from sowing to 50% tasseling. Minimum days have been recorded for the F1 crosses: 9x2, 1 x 5 and 1 x 10 i.e. 54 days. Maximum days have been taken with the aid of using the pass Parent four (sixty one days). As the genotypes: 1 x 5, 9 x 2 and 1 x 10 had minimum days for 50% tasseling indicated earliness genes that's the fine sing for breeders and can be applied with inside the breeding software for drought susceptible regions in addition to sickness susceptible regions.

3.3 Days to 50% Anthesis

The ANOVA outcomes proven a notably sizable versions for days to 50% anthesis some of the genotypes indicated the provision of first rate genetic variations a few of the dad and mom and crosses for the studied parameter days to 50% anthesis. They additionally discovered minimal days for maize pass concerning days to 50% Antes is (fifty five days) and located most days (sixty eight). Similar outcomes for this person in maize have been displayed with the aid of using [9] Mean information depicted that days to 50% Anthesis have been ranged from fifty five to sixty eight days from sowing date. Minimum days turned into recorded for go 6 x five (fifty five days). Maximum days became taken with the aid of using the go four x eight (sixty eight days). The pass 6 x 5 has the genes for earliness and may be applied with inside the breeding software for drought susceptible regions in addition to sickness susceptible regions.

3.4 Days to 50% Silking

The ANOVA consequences showed highly widespread versions for the parameter days to 50 % silking. The genotypes found out genetic variations some of the crosses and mother and father for the times to 50 % silking. Highly sizeable version the various mother and father and F2 populace in Maize for the person days to 50% silking have been additionally determined with the aid of using [10] Mean statistics depicted that days to 50% silking had been ranged from fifty seven to sixty one days from sowing (Table 2). Minimum days had been recorded for crosses 1 x 8, 1 x 10, 1 x 2, 1 x 5 and 1 x 6 (fifty seven days). Maximum days changed into taken through the determine 4 x 4 (sixty five days). The genotypes 1 x 8, 1 x 10, 1 x 2, 1 x 5 and 1 x 6 had the genes for earliness and will be applied with inside the breeding software.

3.5 Anthesis silking c programming language (ASI)

The ANOVA confirmed especially tremendous versions a few of the genotypes found out genetic variations for the parameter anthesis silking c programming language (ASI). For Plant breeder’s variability is needed for genetic development of crop vegetation. Earliness for the studied parameter is the maximum appealing person for plant breeders this look at confirmed variant amongst mother and father and crosses for this reason indicated the presence of genetic variability. For this parameter our outcomes are settlement with the fulfillment of [11]

They additionally discovered minimal days for maize genotypes concerning anthesis silking c language (ASI) three days. Mean statistics depicted that anthesis silking c programming language (ASI)have been ranged from three to eleven days (Table 2) Minimum days have been recorded for crosses 2 x 4, 6 x 6, 5 x 8, 4 x 1, 5 x 9, 5 x 2, 7 x 6, 7 x 10 (three days). Maximum days have been taken through the crosses 8 x 10, 10 x 2 (eleven days). The crosses2 x 4, 6 x 6, 5 x 8, 4 x 1, 5 x 9, 5 x 2, 7 x 6, 7 x 10 have the genes for earliness and may be applied with inside the breeding software for drought susceptible regions in addition to sickness susceptible regions.

3.6 Plant peak (cm)

The ANOVA confirmed no full-size version a number of the genotypes for the studied parameter plant peak (cm), but no vast variations for the studied parameter discovered genetic similarities most of the genotypes. For Plant breeders variability is needed for genetic development of crop plant life however for the parameter plant peak the ANOVA confirmed similarities most of the genotypes. Current research is the compliance with [88] who documented comparable findings for plant peak in Maize crop. Mean statistics depicted that plant height were ranged from 154 to 264 cm from the floor of earth (Table 2). Minimum peak have been recorded for crosses 7 x 1, nine x 2 (154 cm). Maximum peak become taken via way of means of the go nine x four (264 cm). The crosses 7 x 1, 9 x 2 have the genes for to govern the peak of plant and might be applied with inside the breeding software for gale (thane) regions and drought susceptible. Plant peak is one of the extra essential trait which desires breeder's consideration. Plant breeders deliver desire to such germless that have genes for dwarf due to the fact they face up to lodging.

3.7 Height of cob (cm)

The ANOVA confirmed exceedingly considerable versions some of the mother and father and crosses found out genetic version for the studied parameter peak of cob. Breeders supply desire to the ones germless that have the cob placed on mid due to the fact if the cob is down close to earth the animals without problems devour the cob and if the cob placed on pinnacle then they without problems lodging. They additionally discovered minimal peak for maize genotypes concerning peak of cob (eighty one cm). The pronounced effects of [12] are comparable with us. Mean statistics depicted that cob height were ranged from eighty one to 126 cm from the floor of the earth. Minimum top changed into recorded for pass 7 x 10 (eighty one cm). Maximum peak turned into taken via way of means of the determine 1 x 1 (126 cm). The go 7 x 10 has the genes for to manipulate the peak of cob and the discern 1 x 1 has the genes for the peak of cob and can be applied with inside the breeding software.

3.8 Diameter of cob (cm)

The ANOVA confirmed non-large version many of the genotypes for the have a look at parameter, Diameter of cob (cm) but non-large variations for the studied parameter discovered genetic similarities the various genotypes. For Plant breeders variability is needed for genetic development of crop vegetation however for the parameter diameter of cob the ANOVA confirmed similarities some of the genotypes. The diameter of cob is without delay share to yielding as a result yield boom may be the end result of excessive diameter of cob. The said consequences of [13] are identical with us. Mean information depicted that diameter of cob were ranged from three to eight cm (Table 2). Minimum diameter have been recorded for crosses nine x 2, 6 x 7, and six x four (three cm). Maximum diameter had been taken through the genotypes 10 x 6, 6 x 6, and 1 x 2 (eight cm). Cob diameter is one of the extra crucial trait which desires breeder's consideration. Plant breeders provide choice to such germless that have genes for excessive cob diameter.

3.9 Cob duration (cm)

The ANOVA confirmed non-enormous version some of the genotypes for the studied parameter cob duration (cm), but non-extensive variations for the studied parameter found out genetic similarities a number of the genotypes. Cob duration is the maximum vital individual they may be without delay have an effect on the grain yield. Also said comparable outcomes. Mean statistics depicted that cob period have been ranged from 14 to 21 cm (Table 2). Minimum top have been recorded for crosses 8 x 1, 9 x 8, 9 x 2, 5 x 4, 4 x 8 (14 cm). Maximum peak become taken via way of means of the figure 8 x 8 (21 cm). Cob duration is one of the extra crucial man or woman for plant breeders. The figure eight x eight has the genes for excessive cob period and can be applied with inside the breeding software.

3.10 Number of cobs in step with access

The ANOVA outcomes decided similarity a number of the dad and mom and crosses for the studied parameter range of cobs in step with access, but non-extensive variations for the studied parameter found out genetic similarities a number of the genotypes. When the quantity of cobs will increase that is the high quality sign for breeder to choose fine dad and mom or crosses for breeding software. [92] Also have comparable findings. Mean information depicted that Number of cobs in step with access, have been ranged from 18 to 21 (Table 2). Minimum wide variety of cobs have been recorded for crosses 2 x 9, 4x 8, 2 x 1, 8 x 7, 7 x 8(18). Maximum range of cobs have been taken with the aid of using the crosses 1 x 2, 1 x 10, 6 x 9,7 x 4,5 x 10,9 x 9,8 x 8(21).The quantity of Cobs in step with access is one of the extra essential parameter which desires breeders consideration. Plant breeders provide choice to such genotypes that have most wide variety of cobs and can be applied with inside the breeding software.

3.11 Grain yield (Kg ha-1)

The ANOVA outcomes showed highly widespread versions for the studied parameter grain yield (gm). The genotypes found out genetic variations for the studied parameter. Plant breeders prefer genetic variability some of the genotypes for the development of crop plant life. Grain yield is one of the maximum crucial parameter for breeders at some point of breeding software excessive yielding strains deciding on for subsequent generation. In my effects the crosses confirmed superiority on his mother and father. Variation sensible applicable consequences have been additionally stated via way of means of [14]. Mean records depicted that Grain yield (gm) had been ranged from 2565 to 11862kg. Minimum Grain yield (gm) changed into recorded for the pass: five x 7(2565). Maximum Grain yield (gm) turned into taken with the aid of using the pass 2 x 10 (11862). As the move 2 x 10 have the genes for excessive yielding they can be applied with inside the breeding software.

3.12 DIALLEL ANALYSIS

Parameters displaying sizeable genotypic variations in evaluation of variance (Hayman's 1953) have been subjected to diallel evaluation as non-sizeable variations screen that environmental version play a dominant function over genotypic version at the same time as diallel evaluation is used to training session genetics of the crop exploiting genotypic variability. Some parameters confirmed non-sizeable versions (Table-1) so diallel evaluation became achieved on all parameters except (Number of cobs according to access, Cob duration, Diameter of cob, Plant top).

3.13 Grain yield

Highly extensive variations amongst genotypes for grain yield (Table-1) allowed intending for whole diallel evaluation (Table-three). Component ‘a’ became tremendous indicating the presence of additive variant. Items dominant version (b) directional dominant ‘b1’ and particular gene results ‘b3’ have been tremendously big. The giant price of object ‘b2’ indicated presence of symmetrical gene distribution. Significant values of objects maternal impact ‘c’ and reciprocal impact ‘d’ required retesting for ‘a’ and ‘b’ respectively decreasing them from tremendous to non-large displaying the impact of maternal consequences and reciprocal outcomes over additive version and dominant variant respectively.

3.14 Days to 50% tasseling

Analysis of variance following Hayman’s (1953) for days to 50% tasseling (Table-four) discovered that the object ‘a’ (measures additive gene impact) become fairly massive and accounted for a better percentage of the whole version. The ordinary dominance component ‘b’ , ‘b1’ and b3 turned into fantastically massive indicating presence of dominance and directional dominance although ‘b2’ turned into particularly substantial indicating crucial position of precise genes the various dad and mom and governing the trait. Significant maternal (c) and reciprocal (d) confirmed the presence of maternal and paternal outcomes.

3.15 Days to 50% anthesis

Diallel evaluation for days to 50% anthesis (Table-five) depicted that objects ‘b’ and ‘b3’ changed into huge displaying significance of dominant gene consequences with particular genes governing the trait. Items ‘a’ additive gene outcomes ‘b1’ directional dominance ‘b2’ symmetrical gene distribution some of the dad and mom have been good sized. Item ‘c’ maternal outcomes objected’ reciprocal outcomes turned into sizable.

3.16 Days to 50% silking

Diallel evaluation for days to 50% silking (Table-6) confirmed vast ‘a’ , ‘b’ , ‘b1’ , ‘b2 , ‘b3’ , ‘c’ and ‘d’ gadgets indicating presence of dominant gene outcomes with symmetrical distribution of genes some of the mother and father respectively. Significant values for objects ‘a’ , ‘b1’ , ‘b3’ , ‘c’ and ‘d’ indicated presence of additive gene outcomes.

3.17 Anthesis silking interval (ASI)

Data Subjected to diallel evaluation for anthesis silking interval (ASI) (Table-7) found out massive ‘a’, ‘b’ and ‘b2’ gadgets indicating the presence of each additive and dominant gene consequences with symmetrical distribution of genes the various mother and father. Directional dominance and precise genes movement have been defined with the aid of using tremendous values of 'b1' and 'b2' gadgets. Item 'c' turned into full-size displaying presence of maternal outcomes. Significant cost of' indicated significance of reciprocal consequences.

3.18 Height of cob (cm)

Diallel evaluation of variance for peak of cob (cm) (Table-eight) found out that 'an' object turned into tremendous indicating presence of additive gene results at the trait. The additives 'b', 'b2', and 'b3' have been substantial displaying presence of dominant gene outcomes, symmetry of gene distribution a number of the dad and mom and significance of precise genes, respectively. Item 'c' shows the presence of maternal consequences become sizable. Item's' became sizeable discovered the consequences of reciprocal.

3.19 COMBINING ABILITY ANALYSIS

Traits displaying enormous genotypic version in evaluation of variance have been in addition subjected to partitioning into version because of widespread combining cap potential (GCA), precise combining capacity (SCA) and reciprocal results. The respective outcomes have been computed in line with Griffin (1956).

3.20 Days to 50% tasseling

Analysis of variance of mixing cap potential for days to 50% tasseling found out that imply squares because of GCA, SCA and reciprocal outcomes have been particularly giant (Table-nine). [94] Reported enormous imply squares most effective because of GCA for days to 50% tasseling whilst [95] said enormous GCA in addition to SCA suggest squares. Component of version (Table-10) mentioned that GCA variance become extra than SCA variance indicating the significance of additive gene outcomes for the manager of the trait. Similar effects had been additionally mentioned through [15].

3.21 Days to 50% Anthesis

Analysis of variance of mixing cap potential for days to 50% anthesis confirmed that version because of GCA, SCA and reciprocal consequences turned into pretty tremendous (Table-nine). The effects are in conformity with [16] who additionally suggested considerable GCA, SCA results for the trait at the same time as [17] said large reciprocal outcomes. Computations of variance additives (Table-10) found out that SCA variance become more than GCA variance displaying much less percentage of additive variant. This is according with (16).

3.22 Days to 50% Silking

Highly widespread variations had been located because of GCA, SCA and reciprocal results for days to 50% silking (Table-nine).Significant GCA, SCA and reciprocal results had been additionally mentioned via way of means of [18]. Components of variant (Table-10) found out very excessive price for version because of GCA indicating excessive percentage of additive version. The effects are supported with the aid of using findings of (17).

3.23 Anthesis silking interval (ASI)

Highly vast imply squares because of GCA, SCA and reciprocal have been recorded for anthesis silking interval (ASI) (Table-nine). These outcomes are dedication with the findings of [99] who said huge GCA, SCA and reciprocal results for trait. Components of variance (Table-10) indicated that SCA variance turned into more in significance than GCA variance giving a more estimate of variance because of dominant results. [19] Reported dominant and additive genetic consequences.

3.24 Height of cob (cm)

Mean squares discovered exceedingly extensive variations because of standard, unique combining cap potential and reciprocal consequences (Table-nine). Results get aid from the findings of [101] who said widespread GCA results at the same time as [20] mentioned sizable SCA outcomes and huge SCA in addition to GCA consequences had been said through [21]. Computation of variance (Table-10) additives found out very excessive cost for version because of GCA indicating excessive percentage of additive version. Non additive manage of genes had been stated through [22].

3.25 Grain yield (gm)

It is clear from (Table-nine) that imply squares because of GCA, SCA and reciprocal consequences have been fantastically considerable. Significant GCA and SCA suggest squares were stated via way of means of [105] at the same time as great outcomes because of GCA were stated via way of means of [106], but sizable SCA results simplest were said through [23]. Variance of additives discovered (Table-10) extra percentage of SCA variance suggesting dominant gene outcomes over the trait. Additive outcomes for the trait have been said through [24].

3.26 Heritability for studied parameter

3.27 Days to 50% Tasseling

High h2was calculated for days to 50% tasseling (Table-eleven). The price for large feel heritability (0.40) turned into large than slender feel heritability (0.10). Table-eleven found out that the times to 50% tasseling changed into significantly govern via way of means of non-additive genes. The results from our examine are according with the effects of [25]. The Wr-Vr graphical evaluation pertaining days to 50% tasseling indicates that regression line cuts the y-axis above the beginning. This is a sign that partial dominance kind of gene movement is controlling the trait beneath Neath have a look at. Maximum quantity of dominant genes has been cited in mother and father which can be close to the foundation. The farthest dad and mom include most quantity of recessive genes. Only figure become nearly with inside the middle of regression line. Thus it has intermediate variety of dominant and recessive genes (Fig four.1).

3.28 Days to 50% Anthesis

Higher heritability estimates have been discovered for days to 50% anthesis. Maximum price 0.27 turned into mentioned for huge feel heritability, at the same time as slender feel heritability became recorded at 0.10 (Table-eleven). The indicated that fundamental position became performed via way of means of non-additive genes with inside the expression of this parameter. [26] Also attained comparable effects with inside the feel of h2for this trait.

For the man or woman days to 50 % anthesis it's been observed that trait is managed with the aid of using non-additive kind of gene movement i.e. partial dominance. This has been tons clean through inspecting the regression line which cuts the y axis above the foundation. (Fig-four.2). Parents confirmed most variety of dominant genes as their function is close to the starting place. Whereas dad and mom have recessive genes because it turned into farthest from starting place. And blended fashion of dominant and recessive genes had been stated as those have been found in nearly middle of regression line. Likewise the graphical evaluation of the parameter days to 50 % anthesis depict that this individual has over dominant kind of gene motion. This may be judged with the aid of using the regression line which cuts the Wr higher the foundation. It displays the non-additive kind of gene motion.

3.29 Days to 50% Silking

Analysis for days to 50% silking found out that huge feel heritability 0.50 turned into better in comparison to slender feel heritability 0.27. Clearly indicated the involvement of non-additive genes (Table-eleven). [27] Attained comparable outcomes for the parameter days to 50% silking. The graphical expression Wr-Vr for the trait days to 50 % slinking confirmed partial dominance kind of gene motion. Because regression line cuts the Wr above the starting place. This depicts epistasis i.e. involvement of intermingling or interplay of genes (Fig- 4.3). The scattering of the mother and father over regression line shows that there has been enough variety with inside the genotypes. Maximum variety of dominant genes changed into because of its closest role to the foundation. Being farthest from the starting place most numbers of recessive genes have been proven in mother and father.

3.30 Anthesis silking interval (ASI)

It is found out from (Table-eleven) that the position of non-additive gene movement turned into distinguished in for anthesis silking interval because the vast feel heritability confirmed 0.forty six changed into greater than slim experience heritability 0.20 . According to [28] non-additive genes movement turned into concerned significantly with inside the expression of this trait. In Wr-Vr graphical evaluation concerning anthesis silking interval (ASI) non-additive kind of gene movement i.e. partial dominance has been determined. The regression line cuts the y-axis above the beginning. All dad and mom had been scattered over regression. This suggests that statistics recorded for this determine aren't homogenous. Hence for in addition evaluation concerning this trait may be proceeded.

3.31 Height of cob (cm)

The expression of trait peak of cob (cm) relies upon non-additive gene motion as turned into indicated through excessive 0.fifty eight large experience heritability in comparison to 0.24 (Table-eleven). Similar consequences have been additionally recorded through [29]. For the trait like top of cob the inheritance of genes fashion has been stated as over partial dominance because of interception of regression line above the starting place. Hence non additive kind of epistasis is controlling this trait. (Fig-4.5). The role of the parameters at the regression line display that supply cloth is of numerous nature i.e. it has enough heterogeneity and may be preceded for similarly evaluation.

3.32 Grain yield (gm)

High price of wide feel heritability 0.56 for the trait grain yield (gm) became glaring from (Table-eleven). While slim feel heritability 0.07 turned into a whole lot lower. This conformed the contribution of non-additive gene movement for the trait grain yield (gm). Our consequences are in keeping with locating of [30], who discovered the position of wide feel heritability in inheriting the person.

Probing into Wr-Vr graphical evaluation for the parameter grain yield (gm) the mode of gene movement changed into partial dominance (Fig-4.6). The discern elucidates that regression line cuts above the starting place. Partial dominance is likewise a demonstration of the involvement of epistasis. So it's also a non-additive kind of gene movement that controlling the yield traits. All mother and father aren't clustering over regression line. The dispersion of the genotypes depicts that the fabric used has enough range

Table- 1 Mean squares for different agronomic characters and CV.

Trait	Replication	Error	%CV
Days to 50% Tasseling	37.00	14.28	6.7
Days to 50% Anthesis	18.54	3.10	2.7
Days to 50% Silking	25.58	16.39	6.8
Anthesis silking interval (ASI)	2.79	0.63	15.2
Plant height (cm)	63.02	2621.78	24.5
Height of cob (cm)	10.85	281.81	16.8
Diameter of cob (cm)	0.014	0.27	11.1
Cob length (cm)	0.01	5.97	13.8
Number of cobs per entry	0.61	1.21	5.5
Grain yield (gm.)	347511	56495	3.3

Table-2 Range values of the studied parameters

S.No.	Parameters	Minimum	Maximum
1	Days to 50% Tasseling	54	61
2	Days to 50% Anthesis	55	68
3	Days to 50% Silking	57	61
4	Anthesis silking interval (ASI)	3	11
5	Plant height (cm)	154	264
6	Height of cob (cm)	81	126
7	Diameter of cob (cm)	3	8
8	Cob length (cm)	14	21
9	Number of cobs per entry	18	21
10	Grain yield (gm)	2565	11862

Table-3. The mean squares and degrees of freedom for the analysis of variance of 9 x 9 diallel for grain yield (gm.).

Item	Df	SS	MS	F
A	8	1989911	248739	5.59**
B	36	53660580	1490572	3.35**

b1	1	909483	909483	2.04**
b2	8	744337	93042	2.09**
b3	27	52006761	1926176	4.33**
C	8	937311	117164	2.63**
D	28	5348257	191009	4.29**
Total	242	11676779		

Table-4. The mean squares and degrees of freedom for the analysis of variance of 9 x 9diallel for days to 50 % tasseling.

Item	**Df**	**SS**	**MS**	**F**
A (additive effect)	8	271	33.9	20.53**
B (dominance effect)	36	270762	7521.2	4558.42**
b1 deviation of the F_1's from the mid-parental values	1	7	6.8	4.12**
b2 mean dominance deviation of the F_1's from the mid-parental values within each array differs over arrays	8	51	6.4	3.86**
b3 dominance deviation that is unique to each F_1	27	270704	10026.1	6076.60**
C the average maternal effects of each parental line	8	65	8.2	4.94**
D reciprocal effects not attributed to c	28	185	6.6	4.0**
Total	242	879		

Table-5. The mean squares and degrees of freedom for the analysis of variance of 9 x 9diallel for days to 50% Anthesis.

Item	**Df**	**SS**	**MS**	**F**
A	8	93	11.6	8.39**
B	36	352303	9786.2	7081.73**
b1	1	9	9.2	6.68**

b2	8	20	2.5	1.83^{ns}
b3	27	352274	13047.2	9441.52**
C	8	79	9.8	7.10**
D	28	159	5.7	4.11**
Total	242	654		

Table-6. The mean squares and degrees of freedom for the analysis of variance of 9 x 9 diallel for days to 50% silking.

Item	**Df**	**SS**	**MS**	**F**
A	8	292	36.5	288.42**
B	36	296201	8227.8	64966.98**
b1	1	7	7.3	57.51**
b2	8	63	7.9	61.99**
b3	27	296131	10967.8	86602.14**
C	8	213	26.7	210.45**
D	28	350	12.5	98.73**
Total	242	922		

Table-7. The mean squares and degrees of freedom for the analysis of variance of 9 x 9 diallel for anthesis silking interval (ASI)

Item	Df	SS	MS	F
A	8	62.66	7.832	86.07**
B	36	2398.45	66.624	732.14**
b1	1	1.56	1.556	17.10**
b2	8	14.44	1.805	19.83**
b3	27	2382.45	88.239	969.68**
C	8	57.19	7.148	78.55**
D	28	92.81	3.315	36.42**
Total	242	247.66		

Table-8. The mean squares and degrees of freedom for the analysis of variance of 9 x 9 diallel for height of cob (cm).

Item	Df	SS	MS	F
A	8	23.32	2.916	409.44**
B	36	1833.29	50.925	7151.46**
b1	1	3.70	3.697	519.22**
b2	8	2.53	0.317	44.47**
b3	27	1827.05	67.669	9502.87**
C	8	9.23	1.154	162.03**
D	28	37.41	1.336	187.65**
Total	242	87.49		

Figure-1 **Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for days to 50 tasseling.**

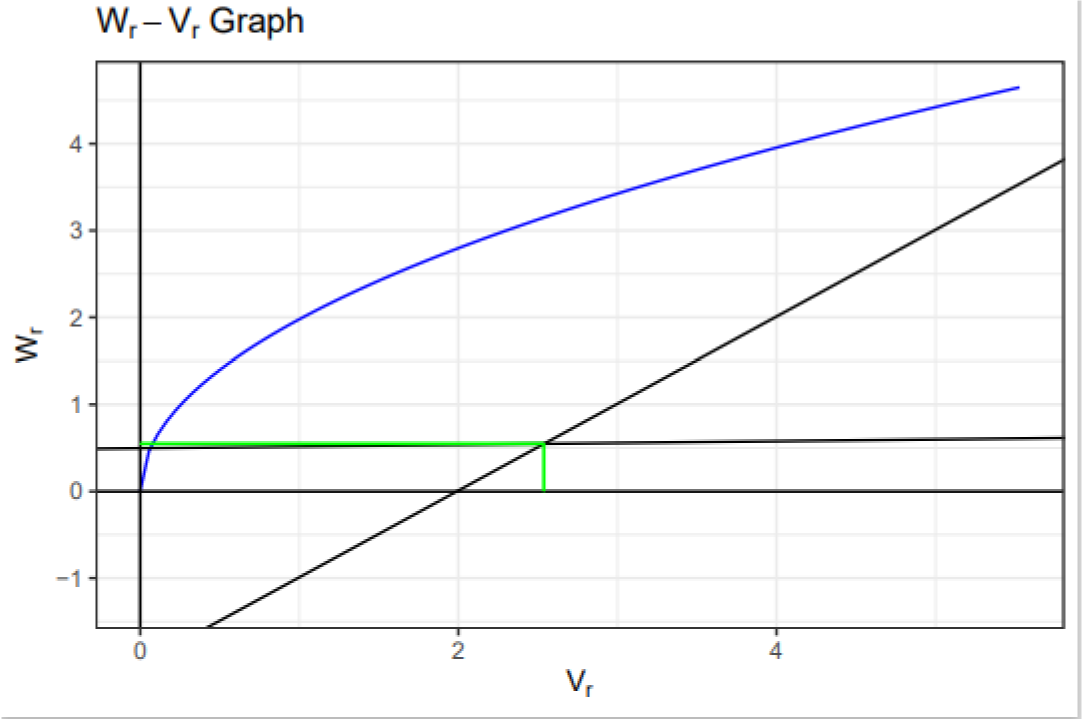

Figure-2 **Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for days to 50 anthesis.**

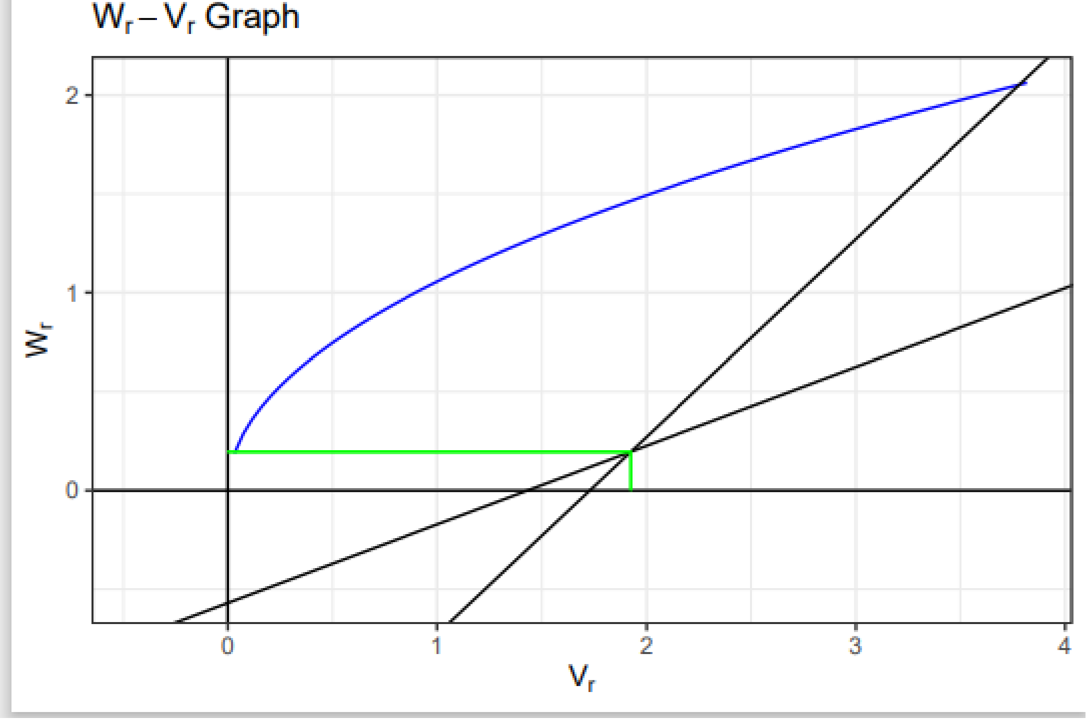

Figure-3 Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for days to 50 silking.

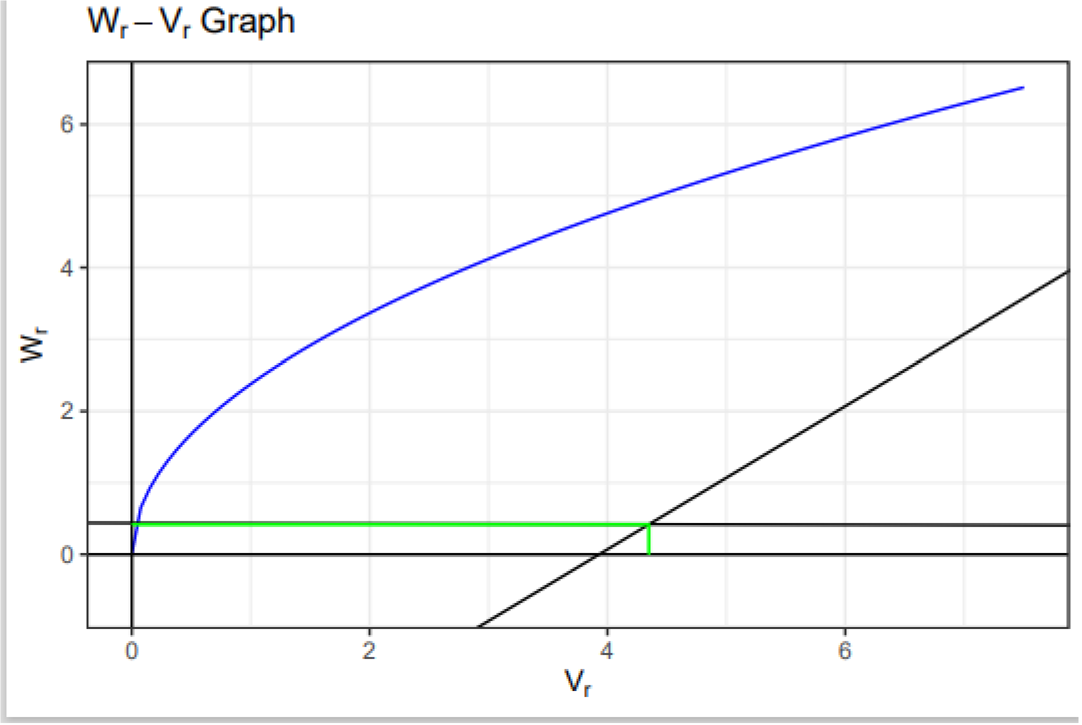

Figure-4 Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for anthesis silking interval (ASI).

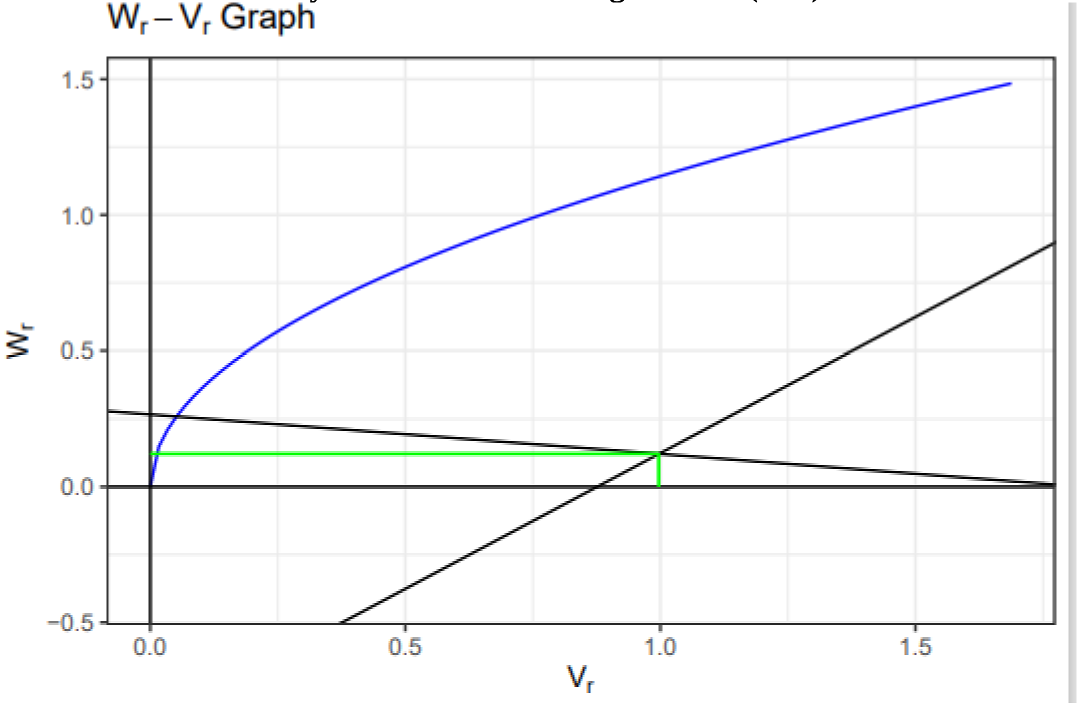

Figure-5 **Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for height of cob (cm).**

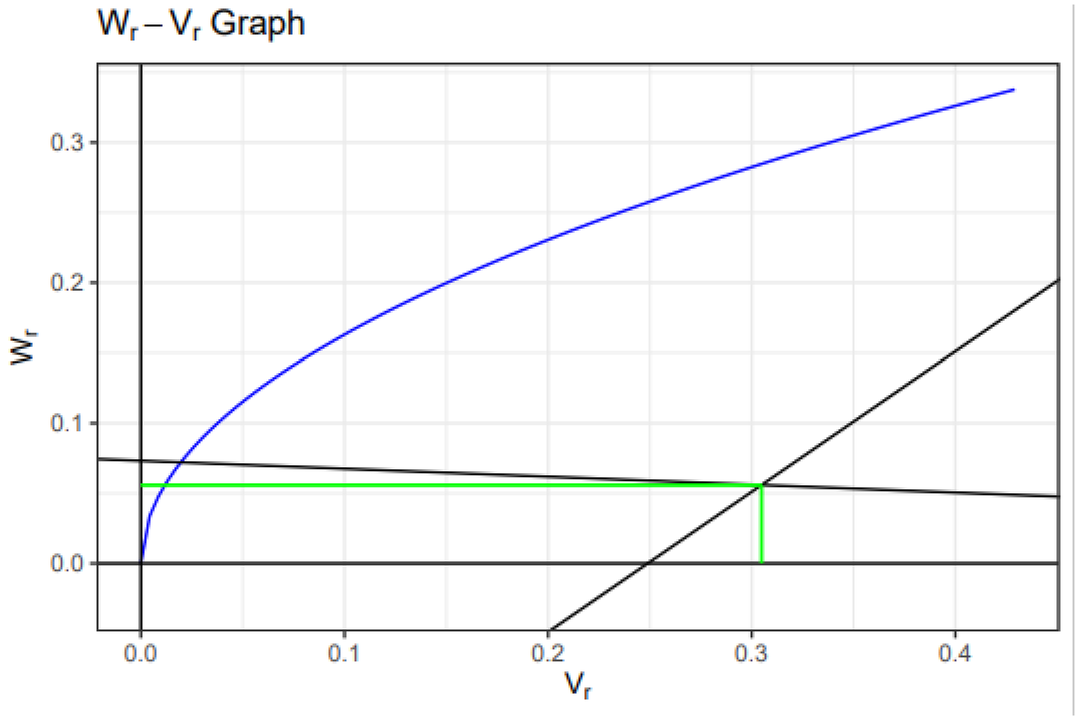

Figure-6 **Covariance and variance (Wr, Vr) regression graph of the 9 x 9 diallel analysis for grain yield (gm.).**

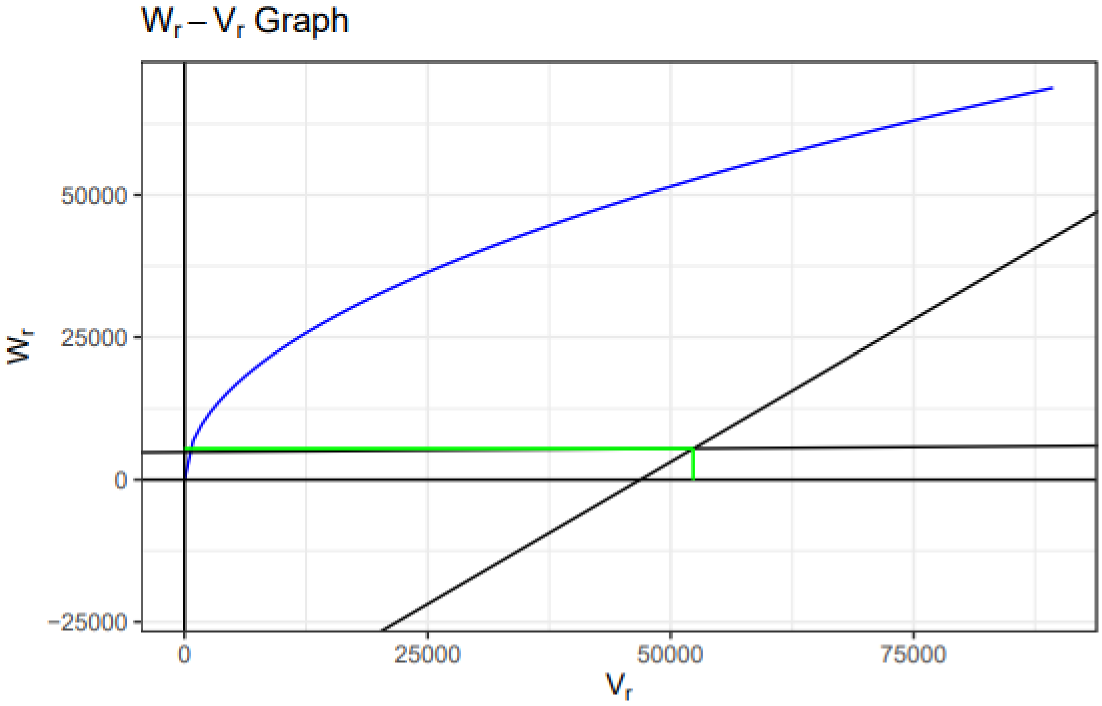

Table-9 Analysis of variance for combining ability in 9 Maize genotypes and their all possible crosses.

Trait	GCA (d.f. = 8)	SCA (d.f. = 36)	Reciprocal (d.f. = 36)	Error (d.f. = 160)
Days to 50% Tasseling	11.29**	1.35**	1.73**	0.55
Days to 50% Anthesis	3.86**	1.27**	1.65**	0.46
Days to 50% Silking	12.17**	1.72**	3.91**	0.04
Anthesis silking interval (ASI)	2.61**	0.53**	1.04**	0.03
Height of cob (cm)	1277.19**	276.05**	374.44**	0.00
Grain yield (gm.)	82913**	46043**	43650**	0

Table-10 Estimates of components of variation for general combing ability (g), specific combing ability (s), reciprocal effects (r), environment (e), additive gene effect (a) and dominant gene effect (d) for the parameters studied.

Trait	G	S	R	E	a	d
Days to 50% Tasseling	0.55	0.44	0.59	0.54	1.10	0.44
Days to 50% Anthesis	0.14	0.45	0.59	0.46	0.28	0.45
Days to 50% Silking	0.58	0.93	1.93	0.04	1.16	0.93
Anthesis silking interval (ASI)	0.11	0.28	0.50	0.03	0.23	0.28
Height of cob (cm)	5.58	1.53	1.87	3.09	1.11	1.53
Grain yield (gm.)	2.08	2.55	2.18	1.48	4.16	2.55

Table-11 Heritability and gene action for studied parameter.

Parameters	h^2(b.s)	h^2(n.s)	Additive variance	Phenotypic variance
Days to 50% Tasseling	0.40	0.29	1.10	3.79
Days to 50% Anthesis	0.27	0.10	0.28	2.71
Anthesis silking interval (ASI) **Days to 50% Silking**	0.46	0.20	0.23	1.10
Height of cob (cm)	0.58	0.24	111.65	452.03
Grain yield (gm.)	0.56	0.07	4166.69	52192.68
Days to 50% Silking	0.50	0.27	1.16	4.15

Table-12 General combining ability (diagonal), specific combing ability (above diagonal)and reciprocal effects of Anthesis silking interval(ASI)

	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6	Cross 7	Cross 8	Cross 9
Cross 1	0.7263374	-1.0411523	0.4588477	-0.81893004	0.47736626	0.069958848	0.77366255	-0.07818930	0.27366255
Cross 2	0.8333333	0.1522634	-0.8004115	0.08847737	0.71810700	-0.189300412	0.01440329	-0.50411523	0.34773663
Cross 3	1.0000000	0.1666667	-0.5144033	0.08847737	0.21810700	-0.522633745	0.18106996	0.16255144	0.51440329
Cross 4	1.8333333	1.8333333	-0.5000000	-0.40329218	-0.72633745	0.199588477	-0.09670782	0.55144033	0.23662551
Cross 5	0.5000000	0.5000000	0.0000000	-0.83333333	-0.03292181	-0.004115226	-0.30041152	-0.31893004	0.19958848
Cross 6	0.3333333	-1.5000000	-0.5000000	-0.33333333	0.50000000	0.207818930	-0.54115226	0.44032922	-0.70781893

Cross 7	2.0000000	0.3333333	-0.1666667	0.00000000	-0.16666667	-0.166666667	0.17078189	0.14403292	-0.50411523
Cross 8	0.0000000	0.0000000	0.0000000	-0.50000000	0.00000000	0.000000000	0.00000000	0.02263374	-0.02263374
Cross 9	0.3333333	-0.5000000	0.0000000	-0.16666667	0.83333333	0.500000000	0.33333333	0.00000000	-0.32921811

Standard error for days to 50% anthesis silking interval

Standard error	Values
S.E. (r_{ij}-r_{kl})	0.03
S.E. (g_i)	0.12
S.E. (s_{ii})	0.09
S.E. (s_{ij})	0.04
S.E. (r_{ij})	0.16
S.E. (g_i-g_j)	0.15
S.E. (s_{ii}-s_{ji})	0.14
S.E. (s_{ii}-s_{ij})	0.12
S.E. (s_{ii}-s_{jk})	0.11
S.E. (s_{ij}-s_{jk})	0.13
S.E. (s_{ij}-s_{kl})	0.11

Table-13 General combining ability (diagonal), specific combing ability (above diagonal) and reciprocal effects of days to 50% anthesis.

	Cross 1	**Cross 2**	**Cross 3**	**Cross 4**	**Cross 5**	**Cross 6**	**Cross 7**	**Cross 8**	**Cross 9**
Cross 1	-0.4485597	-1.0329218	-0.9773663	-0.2366255	0.57818930	-0.3662551	1.28189300	-0.12551440	0.57818930
Cross 2	-0.6666667	0.5514403	1.1893004	-0.7366255	-0.25514403	0.6337449	0.44855967	0.70781893	0.07818930
Cross 3	-0.3333333	1.5000000	0.8292181	0.9855967	-0.36625514	-1.4773663	-0.49588477	0.26337449	-0.53292181
Cross 4	-0.5000000	-1.0000000	0.6666667	0.2551440	1.54115226	0.5967078	-0.08847737	-0.66255144	-0.95884774
Cross 5	-0.3333333	0.1666667	0.6666667	1.3333333	-0.05967078	0.2448560	-1.27366255	-1.18106996	-0.14403292
Cross 6	0.0000000	2.0000000	1.5000000	1.3333333	1.00000000	-0.1152263	-0.38477366	0.04115226	0.07818930
Cross 7	0.1666667	0.6666667	0.3333333	0.5000000	-0.66666667	1.1666667	-0.59670782	-0.14403292	-0.27366255
Cross 8	-0.1666667	2.0000000	1.1666667	0.6666667	0.16666667	-0.6666667	0.00000000	-0.18930041	-0.01440329
Cross 9	-1.1666667	-0.3333333	1.0000000	0.0000000	0.50000000	0.3333333	1.16666667	0.83333333	-0.22633745

Standard error for days to 50% anthesis

Standard error	**Values**
S.E. (r_{ij}-r_{kl})	0.44
S.E. (g_i)	1.76
S.E. (s_{ii})	1.25
S.E. (s_{ij})	.40
S.E. (r_{ij})	0.66

S.E. (g_i-g_j)	2.47
S.E. (s_{ii}-s_{ji})	2.33
S.E. (s_{ii}-s_{ij})	2.14
S.E. (s_{ii}-s_{jk})	1.86
S.E. (s_{ij}-s_{jk})	1.74
S.E. (s_{ij}-s_{kl})	1.98

Table-14 General combining ability (diagonal), specific combing ability (above diagonal) and reciprocal effects of days to 50% silking

	Cross 1	**Cross 2**	**Cross 3**	**Cross 4**	**Cross 5**	**Cross 6**	**Cross 7**	**Cross 8**	**Cross 9**
Cross 1	-1.0102881	0.7325103	-1.360082	0.2139918	0.2695473	-0.2489712	0.4176955	-0.24897119	0.30658436
Cross 2	-2.0000000	0.5082305	1.954733	-1.3045267	-1.0823045	0.8991770	0.2325103	1.06584362	-0.37860082
Cross 3	-1.5000000	1.3333333	1.434156	0.1028807	-0.6748971	-0.3600823	-0.5267490	-0.52674897	-0.30452675
Cross 4	-2.3333333	2.3333333	2.000000	1.0267490	2.0658436	0.0473251	-0.4526749	-1.28600823	-0.89711934
Cross 5	-0.5000000	0.3333333	0.000000	2.3333333	-0.1954733	0.2695473	-0.7304527	-0.39711934	-0.67489712
Cross 6	-0.3333333	3.3333333	2.000000	2.0000000	0.0000000	-0.5102881	0.4176955	-0.24897119	0.63991770
Cross 7	-1.6666667	0.6666667	0.500000	0.5000000	-1.0000000	0.8333333	-0.5102881	-0.08230453	0.13991770
Cross 8	0.5000000	2.3333333	1.666667	1.5000000	-0.1666667	-1.0000000	-0.8333333	-0.67695473	-0.19341564
Cross 9	-0.3333333	0.5000000	0.500000	-0.5000000	-0.5000000	-0.5000000	1.0000000	1.50000000	-0.06584362

Standard error	**Values**
S.E. ($r_{ij}-r_{kl}$)	0.05
S.E. (g_i)	0.23
S.E. (s_{ii})	0.16
S.E. (s_{ij})	0.18
S.E. (r_{ij})	0.08
S.E. (g_i-g_j)	0.32
S.E. ($s_{ii}-s_{ji}$)	0.30
S.E. ($s_{ii}-s_{ij}$)	0.28
S.E. ($s_{ii}-s_{jk}$)	0.24
S.E. ($s_{ij}-s_{jk}$)	0.22
S.E. ($s_{ij}-s_{kl}$)	0.25

Standard error for days to 50% silking

Table-15 General combining ability (diagonal), specific combing ability (above diagonal) and reciprocal effects height of cob (cm)

	Cross1	Cross2	Cross3	Cross4	Cross5	Cross6	Cross7	Cross8	Cross9
Cross1	11.29383	1.939506	5.439506	2.206173	-4.038272	-11.649383	10.706173	-7.660494	0.3950617
Cross2	-14.00000	-6.183951	5.717284	-12.516049	16.339506	-25.371605	-2.116049	8.717284	4.6728395
Cross3	18.70000	-9.700000	-12.183951	9.583951	-19.660494	-7.871605	-7.316049	0.917284	10.7728395
Cross4	10.40000	-12.400000	4.300000	-5.450617	-13.893827	21.395062	-5.149383	1.183951	0.4395062
Cross5	29.30000	21.200000	13.600000	-16.900000	-2.906173	24.250617	11.406173	6.739506	-12.2049383
Cross6	1.70000	-15.500000	-5.200000	-14.400000	-5.200000	10.704938	4.695062	11.428395	13.4839506
Cross7	19.90000	11.800000	11.600000	14.900000	-7.400000	14.500000	-5.650617	-10.016049	-8.1604938
Cross8	-2.90000	6.600000	-4.600000	-19.600000	-17.100000	-7.000000	5.000000	7.916049	-7.5271605
Cross9	-7.50000	-5.700000	-5.600000	-20.600000	-19.100000	-17.200000	5.200000	-18.000000	2.4604938

Standard error for height of cob

Standard error	Values
S.E. ($r_{ij}-r_{kl}$)	8.21
S.E. (g_i)	3.28
S.E. (s_{ii})	2.34
S.E. (s_{ij})	2.61
S.E. (r_{ij})	1.23
S.E. (g_i-g_j)	4.61
S.E. ($s_{ii}-s_{ji}$)	4.35
S.E. ($s_{ii}-s_{ij}$)	3.99
S.E. ($s_{ii}-s_{jk}$	3.48
S.E. ($s_{ij}-s_{jk}$)	3.26
S.E. ($s_{ij}-s_{kl}$)	3.69

Table-16 General combining ability (diagonal), specific combing ability (above diagonal) and reciprocal effects of grain yield (gm.)

	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6	Cross 7	Cross 8	Cross 9
Cross 1	103.8519	75.70370	75.59259	35.70370	-154.740741	10.48148	-162.62963	-74.07407	288.259259
Cross 2	-76.0000	-52.14815	-59.40741	181.70370	259.259259	-232.51852	-81.62963	99.92593	-186.740741
Cross 3	20.0000	-37.00000	-78.03704	146.59259	-3.851852	-35.62963	-26.74074	91.81481	30.148148
Cross 4	7.0000	109.00000	-32.00000	-93.14815	-80.740741	74.48148	10.37037	-59.07407	-50.740741
Cross 5	57.0000	43.00000	-28.00000	-72.00000	27.296296	83.03704	46.92593	134.48148	226.814815
Cross 6	-4.0000	-207.00000	-210.00000	-393.00000	38.000000	33.07407	162.14815	-145.29630	104.037037

Cross 7	208.0000	83.00000	-4.00000	58.00000	59.000000	-34.00000	66.18519	157.59259	-9.074074
Cross 8	-115.0000	-157.00000	-55.00000	-259.00000	-85.000000	-363.00000	181.00000	30.62963	-153.518519
Cross 9	-33.0000	86.00000	241.00000	109.00000	145.000000	98.00000	136.00000	-214.00000	-37.703704

Standard error for grain yield (gm.)

Standard error	**Values**
S.E. (r_{ij}-r_{kl})	2.19
S.E. (g_i)	8.78
S.E. (s_{ii})	6.25
S.E. (s_{ij})	6.98
S.E. (r_{ij})	3.29
S.E. (g_i-g_j)	1.23
S.E. (s_{ii}-s_{ji})	1.16
S.E. (s_{ii}-s_{ij})	1.06
S.E. (s_{ii}-S_{jk})	9.31
S.E. (s_{ij}-s_{jk})	8.71
S.E. (s_{ij}-s_{kl})	9.87

CONCLUSION

All the developments have been analyzed to decide large variations amongst genotypes. The tendencies discovered tremendous consequences have been similarly subjected to genetic evaluation for the have a look at of genetic additives of variation, gene motion, combining cap potential and heritability the usage of the strategies of Mather and jinks (1982), Hayman (1954) and Griffing (1956).

All the parameters confirmed large effects besides quantity of cobs, Plant height, Cob diameter and cob period for which confirmed non-giant variations.

The following conclusions may be drawn from the existing take a look at:

• Analysis of variance showed especially widespread variations amongst genotypes besides 4 parameters.

•Grain yield parameter confirmed first-class consequences for crosses. Crosses confirmed superiority on his parents.

• The pleasant yield values and a number of its additives have been received through the diallel pass (1 x 4, 1 x 7, 1 x 8, 1 x 10, 2 x 1, 2 x 5, 2 x 6, 4 x 10, 6 x 2, 6 x 8, 6 x 7, 6 x 10, 7 x 1, 7 x 5, 7 x 10, 8 x 7, 8 x 9, 8 x 10, 9 x 1, 9 x 2, 9 x 6, 9 x 7, 10 x 1).

• Maximum kernel yield and a number of the maximum critical additives exhibited with the aid of using the reciprocal crosses.

• Parents given above possessed the first-rate standard combiner for kernel yield and all of its additives.

• The diallel crosses participated with figure confirmed the quality reciprocal combiner in the direction of growing kernel yield and maximum of its additives.

• The reciprocal pass possessed the first-class precise combiner for kernel yield and nearly all of its additives.

• The probabilities of maternal results for all studied characters had been manifestly observed undoubtedly or negatively in reciprocal crosses.

• The controlling of non-additive gene motion changed into found glaringly in nearly all the studied characters of their inheritance.

•Grain yield found out fine and big correlation with different parameters.

RECOMMENDATIONS

ACCORDING TO OUR OUTCOMES ON THIS STUDY, THE SUBSEQUENT POINTERS MAY BE LAID:

• Further and complementary breeding packages are desires for this crop to provide a few appropriate hybrids for Khyber Pakhtunkhwa specifically district Charsadda, and development in genetic development of the yielding capacity of maize hybrids can be try via such yield associated characters.

• Attempting to attain new genetic substances via inbred strains and types from unique reasserts and introducing them to breeding packages that allows you to enhancing maize productiveness in our region.

• It recommends that district Charsadda region is higher to develop for the duration of spring season due to the suitability of the environmental situation of this place to provide a suitable yield.

- Results acquired confirmed that maximum of the created crosses own a very good yield capacity, survival to climatically situations winning in district charsadda.

- According to my effects crosses confirmed superiority on his parents for grain yield I advise to formers to provide his personal seeds via diallel double cross hybrid.

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