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DEVELOPMENT OF HIGH YIELDING AND RESILIENCE TO CLIMATE CHANGE DOUBLE CROSS MAIZE HYBRIDS UTILIZING 8 X 8 DIALLEL METHOD

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Article Info

Abstract

Diallel analysis is one of the methods used to evaluate F1 and F2 hybrid crosses for desirable parameters based on mode of gene actions. The experiment entitled “Development of high yielding and resilience to climate change double cross maize hybrids utilizing 8 x 8 full diallel method” was selected and conducted at Bacha Khan University Agriculture Research Farm during Kharif season 2022-24. Eight F1 Maize hybrids were crossed in all possible combinations and produced 72 double Crosse F¬1 hybrids including reciprocals and compared with 8 parents. Experiment was laid out in a partial latticlattice square design with 8 blocks having 8 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-significant for having no maternal and reciprocal effects.

Keywords:
High Yielding Maize, Climate Resilience, Double Cross Hybrids, Diallel Analysis, Maize Breeding

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 within the range of latitude from 500 N to 400 S and at an altitude up to 3300 meters 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 dissected and translated truly. There are n2 crosses are produced between parents, including reciprocals. Due to heavy data manipulation and laboriousness less than 20 parents are 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 [5].

Plant breeders focus on genetic evaluation of the hobby tendencies due to the fact that they lead in the direction of a higher knowledge of the genetic dating among crossed lineages. Therefore the diallel mating layout is beneficial in predicting the first-rate mixtures among parents and segregating populations [6]. In this context numerous plant scientists proposed the idea of diallel pass as there aggregate of genetic variability due crosses amongst all parents in all mixtures. The genetic systems ought to be wonderful and allotted in heterotic organizations offering not unusual place trends in the group, and divergent among heterotic businesses. The diallel go technique allows to estimate beneficial genetic parameters to pick genitors for hybridization, because the identity of gene motion of individual control [7]. It additionally lets in to pick out the fine male or woman discern that allows you to provide the most heterotic expression for hybrids. Maize breeders have goal of enhancing new range having excessive yield. The first degree in a successful breeding software is to select suitable parents. Then choice of right approach like use of the diallel mating designs which compare cultivars to discover new heterotic combos [8]. Parents are evaluated primarily based totally on estimates of mixing competencies and heterotic effect. Other mixtures and analyses may be used relying crop species and goals of the investigator. Investigators additionally encompass different additives of variance and heritability with estimation of genetic effects [9].

Heterosis works as a primary device for advanced manufacturing of vegetation with inside the shape of F1 hybrids. Plant breeders have extensively exploited and used heterocyst in boosting up yield of many vegetation. Therefore, the heterotic research can offer the idea for the exploitation of precious hybrid mixtures with inside the destiny breeding packages and their business usage. Hybrid maize manufacturing has been effectively utilized by the grower in every area. The presence of enough hybrid power is an essential prerequisite for a hit manufacturing of hybrid varieties. Several studies employees have said prevalence of heterocyst in giant portions for grain yield and its diverse additives in diverse F1 maize populations. [10] Estimated heterocyst in maize hybrids and their parental inbred strains for grain yield and its additives and said heterocyst 167% for grain yield and 85% for different trends, at the same time as 53% for harvest index. [11] Conducted test for heterocyst and inheritance of plant peak, ear peak, leaves plant-1, cob length, traces cob, seeds line -1, one hundred-grain weight and grain yield. Most of trends had a nice and significant (P ≤0.01) heterocyst. [12] Estimated heterocyst for plant and ear top in maize. Average heterocyst for the plant and ear heights have been 33.3% and 61.9%, respectively. [18] Reported heterocyst for grain yield ranged 129% to114% [13].

Heterocyst yield became 6.1 t ha-1; for yield become 22.0%, starting from 12.2% to 51.9% reported heterocyst for yield, plant peak, ear top, ear length, kernel rows ear-1, kernels row-1, one hundred kernel weight and grain yield. Estimated heterocyst and mixing capacity for grain yield and its contributing characters in diallel pass in maize. The maximum percent of heterocyst for grain ear-1 over MP and BP had been observed. Heterotic outcomes of various levels in unique crosses of maize grain yield and different trends i.e. maturity, plant peak, ear peak, kernels ear-1 , 1000-grain weight and grain yield kg ha-1 have additionally been suggested by [14]. The hybrid hasve to be advanced each quantitatively in addition to qualitatively. Therefore, the prevailing research have been undertaken to estimate the heterocyst and hetero beltiosis results in maize. The maximum essential element in hybrid formation is the choice germplasm of the fundamental populace forming in order to decide the provision of advanced determine. Parents derived from advanced genetic germplasm with a great agronomic male or female can have excessive widespread combining general combining abilities potential (GCA) and excessive particular combining abilities (SCA). To collect excessive-yielding varieties, we want combining cap potential figure statistics, each popular combining cap potential (GCA) and unique combining capacity (SCA). Diallel crosses is aan extensively used technique for understanding the cap potential of mixing every character in a pass. This technique is used to discover which parent have the ability for use in crosses packages to provide new progressed varieties. Diallel evaluation is the evaluation of a fixed of crosses acquired from an aggregate of figure's (n) figure to supply the alleged genetic and GCA and SCA parameters [15].

Specific combining capacity (SCA) is the contribution of an inbred line to hybrid overall performance in a move with a precise inbred line, in terms of its contributions in crosses with an array of targeted inbred traces. Specific combining cap potential (SCA) is the distortion of the crossover look of the inbred line with any other inbred line to GCA. The capacity of positive mixtures (SCA) is vital for generating hybrid varieties. The final aim of plant breeding is to expand cultivars which have constantly proper overall performance for the number one tendencyies of interest. Primary trends will range amongst crop species over time, however the final aim stays the same. To obtain this aim, it's far crucial that plant breeders use all the data and strategies which might be at their disposal. Many of the tendencies which are crucial in cultivar improvement are quantitative. Although development were made in cultivar improvement in maximum crop species feel the rediscovery of Modalism, similarly genetic development requiresd extra facts at the inheritance of the number one tendencyies and institutions with different trends wanted in stepped forward cultivars. Quantitative geneticists believed they may decorate breeding strategies if the inheritance of quantitative trends turned into higher understood. Generally, the fundamental standards have been widely wide-spread and integrated with the formerly used breeding techniques [16]. Because of very extensive usage of maize, the principle aim of all maize breeding applications is to achieve new inbreeds and hybrids to be able to outperform the prevailing hybrids with appreciatione to some of trends. In operating in the direction of this aim, unique interest is paid to grain yield because it is most the maximum vital agronomic characteristic. In order to achieve this aim Tthe diallel mating scheme might be the mostmaximum regularly used mating layout in plant studies and is an exceptional scheme to decide how female and male 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 parents, consisting of reciprocals. Because of the logistics in generating and comparing the crosses among parents, the range of female and male covered with inside the diallel mating layout typically consists of much less than 20 parents. Usually, the primary emphasis is to estimate the relative trendy combining capacity (GCA) results of the parents in crosses and particular combining capacity (SCA) consequences for unique crosses of the male and female. The development of a brand new range with excessive yield is the precise goal of all Maize breeders. The first step in a a success breeding software is to choose suitable male and female. Diallel evaluation offers a scientific method for the detection of suitable male and female 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 male and female 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 [17]. The usefulness of those ideas for the characterization of an inbred in crosses were an increasing number of famous some of the maize breeders feltel 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 male and female 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 male and female SCA of the crosses. A diallel is easy to control in maize and components critical statistics approximately the studied populations for numerous genetic parameters [18] recently weather extrude and value of maize hybrids are mainare 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 afford excessive price of hybrid seed. In addition, unavailability of excellent seed is a prime difficulty in cultivation the region. So, to deal with all of the triumphing problems in maize cultivation, diallel mating layout having nine x nine crosses of F1hybrids to provide double pass hybrids were selected for the studies to observe. Major recognition might be on investigating the GCA of the parental lines in order to become aware of advanced parents to be used in hybrid development programs, so as to have broader adaptability and suitable resistance for extraordinary weather conditions.

1.1 Aim

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

1.2 Objectives

- **I.** Assessment of general and specific combining ability.
- **II.** Assessment of heritability among crosses and parental hybrids.
- **III.** Estimation of heterosis.
- **IV.** Selection of best performing hybrids for double cross maize hybrids production.
- **V.** Selection of high yielding double cross hybrids.

METHODOLOGY

1.2.1.1 The study entitled "development of high yielding and resilience to climate change double cross maize hybrids utilizing 8 x 8 full diallel method" was conducted at Bacha Khan Agriculture research farm (BARF) Charsadda during Kharif season 2022-24. 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 white were sown and crossed in 8 x 8 diallel fashion. During second phase, experimental material comprised of 8 x 8 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 m2) 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.

Data was noted and subjected to statistical analyses on the given parameters.

Following agronomic parameters were recorded for analysis.

2.2. Agronomic Parameters

1. Days to tasseling at 50%

Days for tasseling, when reached at 50% were noted, from the date of sowing.

2. Days to anthesis at 50%

Days for anthesis, when 50% plants reached shed pollen, were written from the sowing date.

3. Silking at 50%

Silking data was taken in days from sowing until 50% of ears showed silks.

4. Pollen shed silking interval

The data was collected as the difference between the date of 50% silking and the date of 50% to pollen shedding from the date of sowing with the given formula:

Difference between Anthesis Silk interval = (days to 50% silking – days to 50% anthesis)

5. Plant Stature (cm)

Plant stature of five randomly selected plants was determined by measuring the height from the soil surface to the base bearing the flag leaf using a measuring rod. The recorded measurements in centimeters.

6. Cob height (cm)

Five random plant height measurements, in centimeters, taken from the ground level to the base node bearing the top ear for each plant.

7. Cob girth (cm)

Measurements were obtained using a Vernier caliper to determine the diameter of five randomly selected cobs in centimeters.

8. Cob size (cm)

Cob length was measured from randomly selected of five cobs in centimeter from tip to end of the cob with the help of a common ruler.

9. Number of cobs per entry

The number of plants per entry will be counted under field conditions.

10. Grain yield (gm.)

Per hectare grain yield will be calculated, after ears harvested at full crop maturity, using the following equation [19].

$$\text{Grain yield} = \frac{\text{Fresh wt.} \times (100 - \text{Grain Moisture content}) \times 0.80 \times 10{,}000}{(100-12) \times 3.75\ \text{m}^2}$$

0.80 = Shelling coefficient

3.75 = Area of sub plot per entry

10,000 = Area of hectare in square meters

(100 – 12) = storage moistur

To determine gene action, genetic components of variation, general and specific combining abilities and broad and narrow sense heritability, the methods of Mather and Jinks (1982), Hayman (1954) and Griffing (1956) approaches were used [20].

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.

CHAPTER NO 4

RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance (ANOVA) carried out for the subsequent parameters which confirmed considerable variations at $p < 0> 0.05$) among all studied parameters. (Table 1).

4.1.1. Days to 50% Tasseling

The ANOVA results showed highly significant variations for days to 50 % tasseling which revealed genetic differences among the genotypes for days to 50 % tasseling. Plant breeders prefer genetic variability among the genotypes for the improvement of crop plants. [1, 2] revealed similar results for days to 50% tasseling.

Mean data depicted that days to 50% tasseling were ranged from 54 to 61 days from sowing to 50% tasseling. Minimum days were recorded for the F1 crosses: 9 x 2, 1 x 5 and 1 x 10 i.e. 54 days. Maximum days were taken by the cross Parent 4 (61 days). As the genotypes: 1 x 5, 9 x 2 and 1 x 10 had minimum days for 50% tasseling indicated earliness genes which is the positive sing for breeders and could be utilized in the breeding program for drought prone areas as well as disease prone regions.

4.1.2. Days to 50% Anthesis

The ANOVA results demonstrated a highly significant variations for days to 50% anthesis among the genotypes indicated the availability of decent genetic differences among the parents and crosses for the studied parameter days to 50% anthesis. They also observed minimum days for maize cross regarding days to 50% Antesis (55 days) and observed maximum days (68). Similar results for this character in maize were displayed by [21]

Mean data depicted that days to 50% Anthesis were ranged from 55 to 68 days from sowing date. Minimum days was recorded for cross 6 x 5 (55 days). Maximum days was taken by the cross 4 x 8 (68 days). The cross 6 x 5 has the genes for earliness and could be utilized in the breeding program for drought prone areas as well as disease prone regions.

4.1.3. Days to 50% Silking

The ANOVA results showed highly significant variations for the parameter days to 50 % silking. The genotypes revealed genetic differences among the crosses and parents for the days to 50 % silking. Highly significant variation among the parents and F2 population in Maize for the character days to 50% silking were also found by [22]

Mean data depicted that days to 50% silking were ranged from 57 to 61 days from sowing (Table 2). Minimum days were recorded for crosses 1 x 8, 1 x 10, 1 x 2, 1 x 5 and 1 x 6 (57 days). Maximum days was taken by the parent 4 x 4 (65 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 could be utilized in the breeding program.

4.1.4. Anthesis silking interval (ASI)

The ANOVA showed highly significant variations among the genotypes revealed genetic differences for the parameter anthesis silking interval (ASI). For Plant breeder's variability is required for genetic improvement of crop plants. Earliness for the studied parameter is the most attractive character for plant breeders this study showed variation among parents and crosses thus indicated the presence of genetic variability. For this parameter our results are agreement with the achievement of [23]

They also observed minimum days for maize genotypes regarding anthesis silking interval (ASI) 3 days. Mean data depicted that anthesis silking interval (ASI) were ranged from 3 to 11 days (Table 2) Minimum days were 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 (3 days). Maximum days were taken by the crosses 8 x 10, 10 x 2 (11 days). The crosses 2 x 4, 6 x 6, 5 x 8, 4 x 1, 5 x 8, 5 x 2, 7 x 6, 7 x 10 have the genes for earliness and could be utilized in the breeding program for drought prone areas as well as disease prone regions.

4.1.5. Plant height (cm)

The ANOVA showed non-significant variation among the genotypes for the studied parameter plant height (cm), however non-significant differences for the studied parameter revealed genetic similarities among the genotypes. For Plant breeders variability is required for genetic improvement of crop plants but for the parameter plant height the ANOVA showed similarities among the genotypes. Current investigation is the compliance with [6] who documented similar findings for plant height in Maize crop.

Mean data depicted that plant height were ranged from 154 to 264 cm from the surface of earth (Table 2). Minimum height were recorded for crosses 7 x 1, 9 x 2 (154 cm). Maximum height was taken by the cross

9 x 4 (264 cm). The crosses 7 x 1, 9 x 2 have the genes for to control the height of plant and could be utilized in the breeding program for gale (thufane) areas and drought prone. . Plant height is one of the more important trait which needs breeder's consideration. Plant breeders give preference to such germplasms which have genes for dwarf because they resist lodging.

4.1.6. Height of cob (cm)

The ANOVA showed highly significant variations among the parents and crosses revealed genetic variation for the studied parameter height of cob. Breeders give preference to those germplasms which have the cob located on mid because if the cob is down near to earth the animals easily eat the cob and if the cob located on top then they easily lodging. They also observed minimum height for maize genotypes regarding height of cob (81 cm). The reported outcomes of [8] are similar with us.

Mean data depicted that cob height were ranged from 81 to 126 cm from the surface of the earth. Minimum height was recorded for cross 7 x 10 (81 cm). Maximum height was taken by the parent 1 x 1 (126 cm). The cross 7 x 10 has the genes for to control the height of cob and the parent 1 x 1 has the genes for the height of cob and could be utilized in the breeding program.

4.1.7. Diameter of cob (cm)

The ANOVA showed non-significant variation among the genotypes for the study parameter, Diameter of cob (cm) however non-significant differences for the studied parameter revealed genetic similarities among the genotypes. For Plant breeders variability is required for genetic improvement of crop plants but for the parameter diameter of cob the ANOVA showed similarities among the genotypes. The diameter of cob is directly proportion to yielding hence yield increase will be the result of high diameter of cob. The reported outcomes of [23] are same with us.

Mean data depicted that diameter of cob were ranged from 3 to 8 cm (Table 2). Minimum diameter were recorded for crosses 9 x 2, 6 x 7, and 6 x 4 (3 cm). Maximum diameter were taken by the genotypes 10 x 6, 6 x 6, and 1 x 2 (8 cm). Cob diameter is one of the more important trait which needs breeder's consideration. Plant breeders give preference to such germplasms which have genes for high cob diameter.

4.1.8. Cob length (cm)

The ANOVA showed non-significant variation among the genotypes for the studied parameter cob length (cm), however non-significant differences for the studied parameter revealed genetic similarities among the genotypes. Cob length is the most important character they are directly affect the grain yield. [24] Also reported similar results.

Mean data depicted that cob length were ranged from 14 to 21 cm (Table 2). Minimum height were recorded for crosses 8 x 1, 9 x 8, 9 x 2, 5 x 4, 4 x 8 (14 cm). Maximum height was taken by the parent 8 x 8 (21 cm). Cob length is one of the more important character for plant breeders. The parent 8 x 8 has the genes for high cob length and could be utilized in the breeding program.

4.1.9. Number of Cobs Per Entry

The ANOVA results determined similarity among the parents and crosses for the studied parameter number of cobs per entry, however non-significant differences for the studied parameter revealed genetic similarities among the genotypes. When the number of cobs increases this is the positive signal for breeder to select best parents or crosses for breeding program. [25] Also have similar findings.

Mean data depicted that Number of cobs per entry, were ranged from 18 to 21 (Table 2). Minimum number of cobs were recorded for crosses 2 x 9, 4 x 8, 2 x 1, 8 x 7, 7 x 8(18). Maximum number of cobs were taken by 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 number of Cobs per entry is one of the more important parameter which needs breeders consideration. Plant breeders give preference to such genotypes which have maximum number of cobs and could be utilized in the breeding program.

4.1.10. Grain Yield (Kg ha-1)

The ANOVA results showed highly significant variations for the studied parameter grain yield (Kg ha-1). The genotypes revealed genetic differences for the studied parameter. Plant breeders prefer genetic variability among the genotypes for the improvement of crop plants. Grain yield is one of the most important parameter for breeders during breeding program high yielding lines selecting for next generation. In my results the crosses showed superiority on his parents. Variation wise relevant results were also reported by [26].

Mean data depicted that Grain yield (gm) were ranged from 2565 to 11862 kg. Minimum Grain yield (gm) was recorded for the cross: 5 x 7(2565). Maximum Grain yield (gm) was taken by the cross 2 x 10 (11862). As the cross 2 x 10 have the genes for high yielding they could be utilized in the breeding program.

4.1 DIALLEL ANALYSIS

Parameters showing significant genotypic differences in analysis of variance (Hayman's 1953) were subjected to diallel analysis as non-significant differences reveal that environmental variation play a dominant role over genotypic variation while diallel analysis is used to work out genetics of the crop exploiting genotypic variability. Some parameters showed non-significant variations (Table-1) so diallel analysis was performed on all parameters except (Number of cobs per entry, Cob length, Diameter of cob, Plant height)

4.2.1 Grain Yield.

In the context of grain yield, there were notable and statistically significant variations observed among the different genotypes, as indicated in Table-1. These significant differences allowed for a comprehensive diallel analysis, as shown in Table-3. The analysis revealed the presence of additive variation, as denoted by the significant component 'a'. Additionally, the variations related to dominance ('b'), directional dominance ('b1'), and specific gene effects ('b3') were highly significant. The significant value of item 'b2' indicated a symmetrical distribution of genes. Furthermore, the influence of maternal effects ('c') and reciprocal effects ('d') was found to affect the additive and dominant variations, respectively, reducing their significance.

4.2.2. Days To 50% Tasseling

Days to 50% tasseling: For the trait of days to 50% tasseling, the analysis of variance, following Hayman's (1953) approach as presented in Table-4, demonstrated that the item 'a', which measures additive gene effects, was highly significant and accounted for a substantial portion of the total variation. The overall dominance component ('b'), along with its directional dominance ('b1') and specific gene effects ('b3'), showed high significance, indicating the presence of dominant gene effects and directional influences. Moreover, the highly significant value of 'b2' indicated the importance of specific genes among the parents, governing this particular trait. The presence of maternal effects ('c') and reciprocal effects ('d') was also significant, suggesting the influence of both maternal and paternal factors.

4.2.3. Days To 50% Anthesis

Days to 50% anthesis: In the diallel analysis for days to 50% anthesis (Table-5), the significant items were 'b' and 'b3', signifying the importance of dominant gene effects with specific genes governing this trait. The additive gene effects ('a'), directional dominance ('b1'), and symmetrical gene distribution among the parents ('b2') were all found to be significant. Additionally, the presence of maternal effects ('c') and reciprocal effects ('d') showed significance, suggesting the influence of both maternal and paternal factors on this trait.

4.2.4. Days To 50% Silking

Diallel analysis conducted on days to 50% silking (Table-6) revealed the presence of significant effects for 'a,' 'b,' 'b1,' 'b2,' 'b3,' 'c,' and 'd' items. These significant values suggest the involvement of dominant gene effects, indicating the presence of genes with symmetrical distribution among the parents.

4.2.5. Anthesis Silking Interval (ASI)

A diallel analysis was performed on the data related to the anthesis silking interval (ASI) (Table-7). The results indicated significant contributions from additive and dominant gene effects, as evidenced by the significant values of 'a', 'b', and 'b2' items. The genes were distributed symmetrically among the parents. The presence of directional dominance and specific gene actions was explained by the significant values of 'b1' and 'b2' items. Furthermore, the significant value of 'c' indicated the presence of maternal effects, while the importance of reciprocal effects was highlighted by the significant value of 'd'.

4.2.6. Height of Cob (Cm)

Diallel analysis of variance was performed on the height of the cob (cm) in Table-8. The results indicated that the 'a' factor was statistically significant, suggesting the presence of additive gene effects on the trait. Additionally, the components 'b', 'b2', and 'b3' were found to be significant, indicating the presence of dominant gene effects, symmetry of gene distribution among the parents, and the importance of specific genes, respectively. The 'c' factor indicated significant maternal effects, while the 'd' factor revealed significant reciprocal effects.

4.3. COMBINING ABILITY ANALYSIS

Griffing's method, proposed by George E. Griffing in 1956, is a commonly employed technique for partitioning the genetic variation in quantitative traits within plant breeding experiments. This method enables the estimation of the effects of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects on the traits of interest.

4.3.1 Days to 50% Tasseling

Analysis of variance of combining ability for days to 50% tasseling revealed that mean squares due to GCA, SCA and reciprocal effects were highly significant (Table-9). [94] Reported significant mean squares only due to GCA for days to 50% tasseling while [95] reported significant GCA as well as SCA mean squares.

Component of variation (Table-10) pointed out that GCA variance was greater than SCA variance indicating the importance of additive gene effects for the control of the trait. Similar results were also reported by [27].

4.3.2 Days to 50% Anthesis

Analysis of variance of combining ability for days to 50% anthesis showed that variation due to GCA, SCA and reciprocal effects was highly significant (Table-9). The results are in conformity with [28] who also reported significant GCA, SCA effects for the trait while [29] reported significant reciprocal effects.

Computations of variance components (Table-10) revealed that SCA variance was greater than GCA variance showing less proportion of additive variation. This is in accordance with (30).

4.3.3 Days to 50% Silking

Highly significant differences were observed due to GCA, SCA and reciprocal effects for days to 50% silking (Table-9).Significant GCA, SCA and reciprocal effects were also reported by [31].

Components of variation (Table-10) revealed very high value for variation due to GCA indicating high proportion of additive variation. The results are supported by findings of (32).

4.3.4 Anthesis Silking Interval (ASI)

Highly significant mean squares due to GCA, SCA and reciprocal were recorded for anthesis silking internal (ASI) (Table-9). These results are commitment with the findings of [33] who reported significant GCA, SCA and reciprocal effects for trait.

Components of variance (Table-10) indicated that SCA variance was greater in magnitude than GCA variance giving a greater estimate of variance due to dominant effects. [34] Reported dominant and additive genetic effects.

4.3.5 Height of cob (cm)

Mean squares revealed highly significant differences due to general, specific combining ability and reciprocal effects (Table-9). Results get support from the findings of [35] who reported significant GCA effects while [102] reported significant SCA effects and significant SCA as well as GCA effects were reported by [36].

Computation of variance (Table-10) components revealed very high value for variation due to GCA indicating high proportion of additive variation. Non additive control of genes have been reported by [37].

4.3.6 Grain Yield (Gm)

It is evident from (Table-9) that mean squares due to GCA, SCA and reciprocal effects were highly significant. Significant GCA and SCA mean squares have been reported by [105] while significant effects due to GCA have been reported by [106], however significant SCA effects only have been reported by [38].

4.4. Heritability for Studied Parameter

4.4.1 Days To 50% Tasseling

High h2 was calculated for days to 50% tasseling (Table-11). The value for broad sense heritability (0.40) was larger than narrow sense heritability (0.10). Table-11 revealed that the days to 50% tasseling was greatly govern by non-additive genes. The outcomes from our study are in accordance with the results of [40].

4.4.2 Days to 50% Anthesis

Higher heritability estimates were revealed for days to 50% anthesis. Maximum value 0.27 was noted for broad sense heritability, while narrow sense heritability was recorded at 0.10 (Table-11). The indicated that main role was played by non-additive genes in the expression of this parameter. Also attained similar results in the sense of h2for this trait.

4.4.3 Days to 50% Silking

Analysis for days to 50% silking revealed that broad sense heritability 0.50 was higher as compared to narrow sense heritability 0.27. Clearly indicated the involvement of non-additive genes (Table-11). Attained similar results for the parameter days to 50% silking.

4.4.4 Anthesis Silking Interval (ASI)

It is revealed from (Table-11) that the role of non-additive gene action was prominent in for anthesis silking interval as the broad sense heritability showed 0.46 was more than narrow sense heritability 0.20

4.4.5 Height of Cob (cm)

The expression of trait height of cob (cm) depends upon non-additive gene action as was indicated by high 0.58 broad sense heritability as compared to 0.24 (Table-11

The observed trend in the inheritance of the height trait in corn cobs indicates partial dominance and non-additive epistasis, as evidenced by the regression line intercepting above the origin (Fig-4.5). This suggests that the expression of the trait is not solely governed by the individual effects of genes, but rather by the complex interactions between them. The positioning of the parameters on the regression line further indicates that the source material is diverse, displaying sufficient heterogeneity. This diversity makes it suitable for further analysis and investigation.

4.4.6 Grain Yield (gm)

High value of broad sense heritability 0.56 for the trait grain yield (gm) was evident from (Table-11). While narrow sense heritability 0.07 was much lower. This conformed the contribution of non-additive gene action for the trait grain yield (gm).

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	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 8 x 8 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

Table-4. The mean squares and degrees of freedom for the analysis of variance of 8 x 8 diallel 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 the 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

Table-5. The mean squares and degrees of freedom for the analysis of variance of 8 x 8 diallel 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

Table-6. The mean squares and degrees of freedom for the analysis of variance of 8 x 8 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

Table-7. The mean squares and degrees of freedom for the analysis of variance of 8 x 8 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

Table-8. The mean squares and degrees of freedom for the analysis of variance of 8 x 8 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		

* Significant ($P \leq 0.05$)

** Highly significant ($P \leq 0.01$)

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
Anthesissilking 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

* Significant (P ≤ 0.05)

** Highly significant (P ≤ 0.01)

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

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 6 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 5, 1 x 7, 1 x 8, 1 x 7, 2 x 1, 2 x 5, 2 x 6, 4 x 4, 6 x 2, 6 x 8, 6 x 7, 6 x 2, 7 x 1, 7 x 5, 7 x 1, 8 x 7, 8 x 9, 8 x 3, 8 x 1, 9 x 2, 9 x 6, 3 x 7, 5 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 CharsddaCharsadda, 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 charsaddaCharsadda.
- 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 move hybrid.

CHAPTER NO 7

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