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Review paper

Common mating design for Hybrid development

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Mating design is the most important design that used in the production of offspring in plant breeding. The different forms of mating designs are used by plant breeders and geneticists for target purpose. Selection of good mating design is very critical for getting success in plant breeding. Plant breeders were using different mating designs and arrangements for the purpose of producing progenies. The mating designs are playing a crucial role with the main objectives of obtaining genetic information and get base population for the development of plant cultivars. In conventional crop improvement program, choice of mating design and genetic materials are the key to successes to develop the appropriate plant cultivars. Selection of mating design is affected by several factors that may include time, space, objectives of the study and other related problems. Mating design is needed to analysis variance in offspring's of crop plants and evaluates the effects of gene action. It is also developed to estimate combining abilities of crop plants to formulate the appropriate breeding strategies. The knowledge of combining ability is very critical to determine the breeding procedure to improve the desirable traits. There is possibility to improve parents through selection, when the general combining ability to specific combining ability is greater than unity and the breeding procedure is designed heterosis breeding to improve the desirable traits when the general combining ability to specific combining ability is less than unity. Gene actions are estimated and analyzed using different mating designs as genetic expressions to devise crop improvement programs. To broaden genetic bases of the population, hybridization with use of mating is very critical to improve the required desirable traits.

Key Words: Mating Design; Hybrids; Dominance; Additive Gene; Combining Ability

INTRODUCTION

Mating designs are principles involved in arranging different cross combinations and altering the genetics of plants to satisfy human needs (Sansern *et al*., 2010). Mating designs are procedural cross between crop plants to develop progenies and determine type gene actions involved in inheritance of traits. Different mating designs have been using by breeders and geneticists for the development of improved varieties for desirable characteristics (Mumtaz et *al*., 2015). Genetic variation is a key component in broadening gene pools in any given crop population and is critical to the success of yield improvement program. The original intent of developing these designs was to estimate additive and dominance variance genetic parameters. The different types and extent of gene actions (additive, dominance and epistatic) genetic variances are determined by using mating design during hybrid development.

Mating designs are used to estimate combining abilities of parental populations involved in making crosses and determine the type of gene actions operating in the inheritance of the traits under investigation (Khan *et al*., 2009). Nowadays, mating designs are playing pivotal role in the development of best performing and superior genotypes in different arrangements and cross combinations through altering the genetics of crops to meet the increasing demand for the improved technologies (Jampatong *et al*., 2010). Population development and hybridization are important for improvement of both quantitative and qualitative traits of different crops and are determined by proper selection of mating designs as well as the parents to be mated. Mating designs were developed to estimate different genetic components of variation. Based on information generated through mating

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designs, methods were developed to predict performance of hybrids and populations, and identify breeding methods designed to utilize different types of gene actions.

Combining ability analysis is very important in identifying potential inbred parents that can be used for producing hybrids. Combining ability also help in elucidating the nature and magnitude of different types of gene action governing the expression of quantitative characters of economic importance (Pal and Prodhan, 1994). In biometrical genetics, two types of combining abilities are considered i.e. general combining ability (GCA) and specific combining ability (SCA). General combining ability refers to the average performance of the genotype in a series of hybrid combinations and is a measure of additive gene action, whereas specific combining ability is the performance of a parent in a specific cross in relation to general combining ability (Ali *et al*., 2014). The true knowledge of the estimates of general and specific combining ability may be useful in selecting the choice of parents in a breeding program. General combining ability (GCA) of the parents and specific combining ability (SCA) of the hybrids are used to enlighten the nature of gene action concerned in the inheritance of traits (Ishaq M and Raziuddin, 2016).

General combining ability (GCA) is directly related to the breeding value of a parent and is associated with additive genetic effects, while specific combining ability (SCA) is the relative performance of a cross that is associated with non-additive gene action, predominantly contributed by dominance, epistasis, or genotype × environment interaction effects (Rojas and Sprague, 1952; Falconer and Mackay, 1996). Therefore, both GCA and SCA effects are important in the selection or development of breeding populations (Viana and Matta, 2003). Combining ability analysis is one of the powerful available evaluation tools to estimate the combining ability variance and effects for selecting the desirable parents and crosses for exploitation of heterosis.

For successfully achieved in the development of desirable genotypes, selecting appropriate parents and mating design is mandatory. But, selection of mating designs are affected by crossing used, type of pollination, type of pollen dissemination, the presence of male sterility system and the size of population desired. Genetic diversity is estimated by mating design based on the objectives of the investigation, space, time and biological limiting factors (Saif-ul-malook *et al*., 2014). Mating design is mainly offering information on genetic variances, generating genetic population as a basis for improvement, developing potential genotypes and estimating genetic gain (Acquaah, 2012). Using any specific mating design is to tackle any plant breeding related research questions like; are genetic variability significant? how much of the variation is heritable or due to environment? and what types of gene(s) influence significance?

Mating design allows for the production of large number of crosses to widen the genetic base of the population for efficient and effective improvement. Genetic variance analyses like genetic advances, combining ability, heterosis, heritability, correlation and regression analyses, generation mean analysis, stability analysis and gene action are the most used in addressing various research questions (Mumtaz *et al*., 2015). In order to achieve the hypothesized objectives, the interpretation of the results should match the mating design in plant breeding experiment (Nduwumuremyi *et al*., 2013). The primary and ultimate goal of plant breeders and geneticists are to generate superior improved crop plants by using different mating design in different arrangements. This also enables breeders to identify genotypes with best performance depending on the performance of the produced progenies.

Breeders and geneticists have used different mating designs for development of improved genotypes of plants (Mumtaz *et al*., 2015). By using mating design, different genetic components of variation are studied to estimate quantitative characters. For the success of improvement, appropriate mating design should be used to produce best progenies (Singh *et al*., 1993). Plant breeders are highly concerned in the improvement of crops through hybridization and the selection of superior parents is very significant for yield and other desirable traits. Therefore, the objective of the review was to understand common mating designs for identification of different genetic variations and to design the appropriate breeding program for further improvement.

MATING DESIGN

Mating design is schematic cross between two groups of plants made to produce progenies in plant breeding that is concerned in agriculture and bio-science. Plant breeder need to quantify additive and non-additive components of genetic variances in order to determine appropriate selection methods to improve quantitative characteristics. However, the choice of a mating design for estimating genetic variances should be dictated by the objectives of the study, time, space, cost and other biological limitations. Therefore, various mating designs can be used by plant breeders to estimate genetic parameters in populations. In plant breeding, various mating designs and arrangements are used by breeders and geneticists to generate improved plants (Khan *et al*., 2009). One of the concerns of plant breeders in improving crops through hybridization is the choice of superior parents for yield and other desirable traits and that combine well upon crossing. Mating designs are used to estimate combining abilities of parental populations involved in making crosses and to determine the type of gene actions operating in the inheritance of the traits under investigation.

Hence, combining ability studies, besides providing information of the nature of gene action, also enables

classification of selected parental material with respect to breeding behavior. With a progress in biometrical genetics, several techniques are suggested for the estimation of combining ability. The main purposes of using mating designs are: to inform breeders with vital information on the genetic control of the character under investigation; and to generate breeding population(s) that can be utilized as a source population for the selection and development of potential genotypes (Sharma JR, 1995). These purposes enable the breeder to choose an appropriate breeding strategy, thereby evaluating the genetic progress that can be expected for a given selection intensity (Hill *et al*., 1997). Thus, selection of a mating design for the development of progenies and their evaluation depends on its efficiency in estimating variance components (Falconer DS, 1989).

Major Mating Designs in Plant Breeding and Genetics

Mating design refers to the procedure of producing the progenies in plant breeding. Plant breeders and geneticists; theoretically and practically use different form of mating designs and arrangements for targeted purpose. Thus, several studies (Griffing, 1956; Acquaah, 2012) described and contrasted different mating designs and six types of mating designs have been described so far: bi-parental progenies (BIP), poly-cross, Top-cross, North Carolina (I, III, III), Diallel (I, II, III, and IV) and Line x tester design. In all mating designs, the individuals are taken randomly and crossed to produce progenies which are related to each other as half-sibs or full-sibs.

Bi-Parental Mating

The bi-parental design is called paired crossing design and is reported to be the simplest mating design (Mather and Jinks, 1982). In this design, the breeder selects a large number of plants (n) at random and cross them in pairs to produce 1/2n full-sib families (Acquaah, 2012). Bi-parental mating is also called paired crossing design. The mating design provides opportunity for creating variability with minimum effort and cost (cross-pollinated species) and also provides information needed to determine whether the variation within a population is significant for a long term selection program (Hallauer *et al*., 2010). However, the design cannot give information on the type of genetic variation. Bi-parental mating design involves pairs of individuals chosen randomly from a random mating population then mated. Normally, individual pairs of plants can be crossed reciprocally to produce progenies which can be bulked for evaluation across environments. Many crosses are required to allow accurate measurements and adequate interpretations relative to the reference population. If n parents are used the total number of crosses = n/2 (Mahalingam, A *et al.*, 2011). The merits of bi-parental design are (i) it provides information on additive and dominance components of genetic variance; (ii) it is useful in selecting breeding procedure for genetic improvement of polygenic characters.

$P_1 \times p_2$	$P_3 \times p_4$	$P_5 \times p_6$	$P_7 \times p_8$	$P_{xi} \times p_{xj}$
FS_1	FS_2	FS_3	FS_4	FS_x

Figure 1: Schematic presentation of biparental progeny development

Bi-parental mating is helpful for creating variability and determines the relative importance of genetic components of variance (additive and dominance components of variance) as well as expected response to selection of a trait in formulating and effective breeding program for its genetic improvement. It is the simplest design in which a number of P plants are paired off at random to give ½P families. The parents are mated only once in pairs. The P parents generate ½ P full-sib families (Mather and Jinks, 1982). Statistically, if r plants per progenies families are evaluated, the variation within (w) and between (b) families may be analyzed as follows:

Table 1: Analysis of variance for biparental mating design

Source of variation	Df	MS	EMS
Between families	$(\frac{a}{b}$ n-1)	MS_1	$\sigma^2w+r\,\sigma^2b$
Within families	$\frac{a}{b}$ n(r-1)	MS_2	σ^2w
Total	$\frac{a}{b}$ nr-1	-	-

Source: Acquaah (2012)

Where: n and r refer to the number of parents and plants sampled within each cross respectively; $\sigma^2 b$ is the covariance of full-sibs ($\sigma^2 b$=Cov FS=$^1/_2 V_A$ + $^1/_4$ V_D + V_{EC}) = $^1/_r$ (MS1-MS2) and $\sigma^2 w$ = [σ^2_G - Cov FS] + σ^2_{EW} =$^1/_2 V_A$ +$^3/_4$ V_D + V_{EW} = MS^2; is the environmental source of variation for variance within the crosses. When you assume that dominance effects are zero, then $\sigma^2 b$ = $^1/_2 V_A$ and $\sigma^2 w$ = $^1/_2 V_A$ + V_{EW}.

Poly-cross Design

A polycross is a mating arrangement for interpollinating a group of cultivars or clones using natural hybridization in an isolated crossing block (Falconer and Mackay, 1996). The term polycross means progeny from a line that was subjected to out-crossing with other selected lines growing within the same nursery. This design is for intermating a group of cultivars by natural crossing in an isolated block. If an isolation block is not available, hand-crossing is required and the entries must be planted to facilitate the required interpollinating. The mating design is often used for generating synthetic cultivars and may be used for recombining selected entries or families in recurrent selection programs. The design provides equal opportunity for each and every clone or parent to naturally cross with each other in the block such that self-pollination is prevented (Saladaga, 1989).

However, to achieve this objective, a proper design in the polycross block is critical. It provides an equal opportunity for each entry to be crossed with every other entry. It is critical that the entries be equally represented and randomly arranged in the crossing block (Falconer and Mackay, 1996).

The polycross design has an advantage of producing synthetic cultivars, recombining selected genotypes in the recurrent selection procedure and evaluating the general combing ability of the parent genotypes (Sleper and Poehlman, 2006; Acquaah, 2012).

The general combining abilities estimated are basically for maternal parents and the variations measured in a progeny can be partitioned into within and between maternal parents (Falconer and Mackay, 1996) and consequently, general combining ability helps in estimating heritability. The mean performance of the progenies of any female parent in the polycross is used to determine the variance components and consequently the general combining ability (Wrinkle and Weber, 1986).

Table 2: ANOVA table of Polycross design with many replications

Sources	Df	MS	Expected mean square	Variance components
Progenies	*g-1*	M_1	$\sigma^2_e + r\,\sigma^2_{prog}$	σ^2_{prog} = Cov (HS) = $\frac{1+F}{4}\sigma^2_A$
Blocks	*r-1*	M_2	-	-
Error	*(g-1)(r-1)*	M_3	σ^2_e	$\sigma^2_e = \sigma^2$

Source: Wrinkle and Weber (1986)

The variance component σ^2_{prog} is an estimate of $\frac{1+F}{4}$ σ^2_A; when the parents are non-inbred, F= zero. It is convenient to use Polycross design in cross-pollinated species when evaluating a large number of genotypes. The selection is then applied based on half-sib progeny means.

Top Cross Design

Top cross refers to a mating between a selection, line, clone and a common pollen parent which may be a variety, inbred line or single cross. The selected plants are crossed with a common tester(s) of known performance, generally in open pollination. The tester parent should have well known genetic background; either narrow- or broad-based testers (Aly *et al*., 2013). The top cross mating scheme involves the crossing of a number of selections, lines, or clones to a common parent (tester) which may be a cultivar, an inbred line, a single cross etc., where the tester is the same for each mating. Because a common tester is used for all crosses, all progeny families produced are half-sibs; therefore, top cross mating design permits the evaluation of GCA for the group of lines, clones, or selections involved in the crosses. The top cross mating design is mainly used in cross-pollinated crops such as maize where it is commonly an inbred-cultivar cross. Additionally, the design is used for initial evaluations of breeding potentials in new maize accessions (Stuber, 2004).

Top cross has been fairly widely used for preliminary evaluation of combining ability of new inbred lines (Mosa, 2010).

The possible numbers of crosses are n x 1, given n number of inbreds. Top cross progenies yield only GCA information, not SCA.

It is a simple and efficient system of screening inbred lines for combining ability before pairing inbreds in single-cross yield trials.

This design is probably the simplest model of mating design that can provide preliminary rapid screening of genetic stocks as it involves the lowest crossing load and simple statistical analysis (Mosa, 2010).

Table 3: Analysis of variance for top cross progenies

Source of variation	Df	Mean Squares	Expected Squares	Mean	Variance of relatives
Progenies	g -1	M_1	$\sigma^2 e + r\sigma^2_{prog}$		σ^2_{prog} = CovHS = [(1+F)/4] σ^2A
Blocks	r -1	M_2	-		-
Error	g – 1)(r – 1)	M_e	σ^2e		$\sigma^2e = \sigma^2$

Source: Wrinkle and Weber (1986)

The variance component σ^2_{prog} is an estimate of $\frac{1+F}{4}\sigma^2_A$ calculated from $\sigma^2_{prog} = V(m_1) + V(m_2)$, when the parents are non-inbred, F= zero

North Carolina Design

North Carolina design is one of the most useful mating designs for estimation of genetic variance and crop selection. The mating design produces large number of progenies and is also useful for self-pollinated crops with multiple flowers. North Carolina design has three different mating schemes and these include NC Design I, NC Design II and NC Design III respectively (Hallauer *et al*., 2010).

North Carolina Design I:

NC Design I is adequate only for estimating genetic variance of a reference population which is assumed to be a random mating population and is in linkage equilibrium (Comstock and Robinson, 1952). It is a very popular multipurpose design for both theoretical and practical plant breeding applications (Acquaah, 2012). It is commonly used to estimate additive and dominance variances as well as for the evaluation of full- and half-sib recurrent selection. It requires sufficient seed for replicated evaluation trials, and hence is not of practical application in breeding species that are not capable of producing large amounts of seed. It is applicable to both self- and cross-pollinated species that meet this criterion. NC Design I is a hierarchical design with non common parents nested in common parents (Acquaah, 2012). The NCI has advantage over biparental and polycross designs, because it gives three statistics compared with only two in the polycross and biparental (Kearsey and Pooni, 1996).

Table 4: Format of the ANOVA table for North Carolina design I

Source	Df	MS	Expected MS
Sets	(s-1)		
Replications in sets	s(r-1)		
Males in sets	s(m-1)	M_1	$\sigma^2_e + k\sigma^2_p + rk\sigma^2_f + rkf\sigma^2_m$
Females in males in sets	sm(f-1)	M_2	$\sigma^2e + k\sigma^2p + rk\sigma^2_f$
Reps x Females	s(mf-1)(r-1)	M_3	$\sigma^2_e + k\sigma^2_p$
Residual	smfr(k-1)	M_4	σ^2e
Total	smfrk-1		

Source: Comstock and Robinson (1952).

North Carolina Design II:

In this design, each member of a group of parents used as males is mated to each member of another group of parents used as females. It is used to evaluate inbred lines for combining ability (Le Clerg, 1966). The design is most adapted to plants that have multiple flowers, so that each plant can be used repeatedly as both male and female. Blocking is used in this design to allow all mating involving a single group of males to a single group of females to be kept intact as a unit (Acquaah, 2012). The design is essentially a two-way ANOVA in which the variation may be partitioned into difference between males (m) and females (f) and their interaction. This design also allows the breeder to measure not only GCA but also SCA (Acquaah, 2012). However, the NCII is not providing test of epitasis or G x E interaction (Kearsey and Pooni, 1996). In North Carolina II, every progeny family has half sib relationships through both common male and common female. This is accomplished by systematic crossing program in which n_1 male and n_2 female are mated in all possible combinations to give n_1n_2 progeny families. It is therefore a rectangular mating design, unless $n_1=n_2$. Reciprocal crosses may be carried out to analyze maternal effects (Hill, 2010).

Table 5: Format of the ANOVA table for North Carolina Design II

Source	Df	Expected MS
Sets	s-1	
Replications in sets	S(r-1)	
Between males	S(m-1)	$\sigma^2_W + r\sigma^2_{m\ x\ f} + rf\sigma^2_m$
Between females	S(f-1)	$\sigma_{2W} + r\sigma^2_{m\ x\ f} + rm\sigma^2_f$
Males x females	s(m-1) (f-1)	$\sigma^2_W + r\sigma^2_{\ m\ x\ f}$
Plots within replications	S(mf-1)(r-1)	σ^2_W
Total	Srmf-1	

Source: Le Clerg (1966)

North Carolina Design III:

In this design, a random sample of F_2 plants is backcrossed to the two inbred lines from which the F_2 was descended. It is considered the most powerful of all the three NC designs (Comstock and Robinson, 1952). However, it was made more powerful by the modifications made by Kearsey and Jinks that add a third tester not just the two inbreds (Acquaah, 2012). The two parental lines act as testers against which F_2 are assessed. The parents being progenitors of the F_2, are very special testers because F_2 is segregating at all loci for which the testers differ but for no other loci (Kearsey and Pooni, 1996). The F_2 population is reference population for mating NCIII (Hallauer *et al*., 2010). The modification is called the triple test cross and is capable of testing non-allelic (epistatic) interactions, which the other designs cannot, and also capable of estimating additive and dominance variance (Acquaah, 2012). The analysis of this design may be divided into two parts, the first part supplies a test for epistasis, and the second assesses the significance and provides estimates of the additive and dominance components of variation. The NCIII is a special case of NCII, therefore the ANOVA is similar to that of the NCII although it differs in one special feature; the two testers are not a random sample from any population but are two very particular lines, the progenitor of the F_2.

Table 6: Format of the ANOVA table for the North Carolina design III

Source	Df	MS	Ems
Replications	(r-1)		
Parents/Testers (T)	1	MS_T	$\sigma^2_W + r\sigma^2_{Tm} + mrk^2_T$
F_2 (m)	m-1	MS_m	$\sigma^2_W + 2r\sigma^2_m$
T x M	m-1	MS_{Tm}	$\sigma^2_W + r\sigma^2_{Tm}$
Within FS families	(r-1)(2m-1)	MS_W	σ^2_W
Total	2mr-1		

Source: Comstock and Robinson (1952)

Diallel design

A complete diallel mating design is one that allows the parents to be crossed in all possible combinations (Begna, T, 2020), including selfs and reciprocals. This is the kind of mating scheme required to achieve Hardy-Weinberg equilibrium in a population (Acquaah, 2012). The diallel is the most used and abused of all mating designs in obtaining various genetic information (Hallauer *et al*., 2010). Much of its abuse could probably be due to the presence of two models for diallel analysis; random and fixed models (Griffing, 1956). A random model involves parents that are random members of a random mating population. A random model is useful for estimating GCA and SCA variances.

In contrast, when parents are considered fixed effects, the aim is to measure the GCA effect for each parent and the SCA effect for each pair of parents. A complete diallel mating design is one that allows the parents to be crossed in all possible combinations (Begna, T, 2020), including selfs and reciprocals. This is the kind of mating scheme required to achieve Hardy-Weinberg equilibrium in a population (Acquaah, 2012). The most frequently used methods in the diallel analysis are Griffing's (1956) diallel procedures. Griffing (1956) suggested four different diallel methods for use in plants: 1) Method 1 (full diallel): parents, F_1 and reciprocals, 2) Method 2 (half diallel): parents and F_1's, 3) Method 3: F_1's and reciprocals, 4) Method 4: F_1's. The number of progenies generated from each method is different, the number of progeny families (pf) for methods 1 through 4 is: $pf = n^2$, $pf = 1/2n\ (n + 1)$, $pf = n\ (n-1)$ and $pf = 1/2n\ (n-1)$, respectively (Acquaah, 2012). These four methods have been widely used to study the patterns of inheritance of different traits in many crops.

This mating design provides information on GCA and SCA (Griffing, 1956). However, the fixed model of method 3 or 4 is the most appropriate for obtaining unbiased estimates of combining abilities and gene action. This method is most suitable when there are no genotypic reciprocal effects (Griffing, 1956). The most of the

problems arising with diallel crosses are essentially due to experimental design such that analysis of data is complex (Johnson and King, 1998). A relatively larger GCA/SCA variance ratio demonstrates importance of additive genetic effects and a lower ratio indicates predominance of dominance and/or epistatic gene effects. GCA and SCA effects for individual lines are calculated only when the overall analysis shows that mean squares for GCA and SCA are significant. There are four diallel mating design that widely used in genetics and breeding.

Method I or full diallel design:

The method I or full diallel design consisted by parents, one set of F_1's and reciprocal F_1's. The system gives n^2 genotypes (Griffing, 1956).

Table 7: Skeleton of ANOVA for method I diallel design

				Expected mean squares	
Source	Df	SS	MS	Model I	Model II
GCA	p-1	S_g	M_g	$\sigma^2 + 2p(\frac{1}{p-1})\Sigma g_i^2$	$\sigma^2 + 2(\frac{p-1}{p})\sigma^2_g + 2p\,\sigma^2_g$
SCA	p(p-1)/2	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)}\Sigma\Sigma s_{ij}^2$	$\sigma^2 + 2(\frac{p2-p+1}{p2})\sigma^2_s$
Reciprocal eff.	p(p-1)/2	S_r	M_r	$\sigma^2 + 2(\frac{2}{p(p-1)})\Sigma\Sigma r_{ij}^2$	$\sigma^2 + 2\,\sigma^2_r$
Error	m	S_e	M_e	σ^2	

Source: Griffing (1956)

Method II or half diallel design: This method includes parents and one set of F_1's without reciprocals F_1's. This design gives *p (p+1)/2* genotypes.

Table 8: Analysis of variance for method II

				Expected mean squares	
Source	Df	SS	MS	Model I	Model II
GCA	p-1	S_g	M_g	$\sigma^2 + (2+p)(\frac{1}{p-1})\Sigma g_i^2$	$\sigma^2 + \sigma^2_s + (p+2)\,\sigma^2_g$
SCA	p(p-1)/2	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)}\Sigma\Sigma s_{ij}^2$	$\sigma^2 + \sigma^2_s$
Error	M	S_e	M_e	σ^2	

Source: Griffing (1956)

Method III: In this method, one set of F_1's and the reciprocals are included. This mating design gives rise to *a = p (p-1)* different number of genotypes. As for methods I and II, also it has both fixed and random effect models.

Table 9: Skeleton of ANOVA of Diallel method III

				Expected mean squares	
Source	Df	SS	MS	Model I	Model II
GCA	p-1	S_g	M_g	$\sigma^2 + 2p(p-2)(\frac{1}{p-1})\Sigma g_i^2$	$\sigma^2 + 2\,\sigma^2_s + 2(p-2)\,\sigma^2_g$
SCA	p(p-3)/2	S_s	M_s	$\sigma^2 + \frac{2}{p(p-3)}\Sigma\Sigma s_{ij}^2$	$\sigma^2 + 2\,\sigma^2_s$
Reciprocal eff.	p(p-1)/2	S_r	M_r	$\sigma^2 + 2(\frac{2}{p(p-1)})\Sigma\Sigma r_{ij}^2$	$\sigma^2 + 2\,\sigma^2_r$
Error	M	S_e	M_e	σ^2	σ^2

Source: Griffing (1956)

Method IV: In this method, only one set of F_1's are included. It is the most common of the diallel crossing systems. There are *a = p (p-1)/2* different genotypes evaluated. As for other diallel methods, there are two models.

Table 10: Skeleton of ANOVA for Diallel method IV

				Expected mean squares	
Source	Df	SS	MS	Model I	Model II
GCA	p-1	S_g	M_g	$\sigma^2 + (p-2)(\frac{1}{p-1})\Sigma g_i^2$	$\sigma^2 + 2\,\sigma^2_s + (p-2)\,\sigma^2_g$
SCA	p(p-3)/2	S_s	M_s	$\sigma^2 + \frac{2}{p(p-3)}\Sigma\Sigma s_{ij}^2$	$\sigma^2 + 2\,\sigma^2_s$
Error	M	S_e	M_e	σ^2	σ^2

Source: Griffing (1956)

Table 11: Skeleton of ANOVA for Line x Tester Design

			Expected mean squares	
Source	Df	MS	Model I	Model II
Replication	r-1			
Lines	m-1	M1	$\sigma^2 + rf\frac{1}{m-1} + \Sigma g_i^2$	$\sigma^2 + V_{sca} + rf_{gca(m)}$
Testers	f-1	M2	$\sigma^2 + rm\frac{1}{f-1} + \Sigma g_j^2$	$\sigma^2 + rV_{sca} + rm_{gca(m)}$
Line X Tester	(m-1)(f-1)	M3	$\sigma^2 + r[\frac{1}{(m-1)(f-1)}] + \Sigma\Sigma s_{ij}$	$\sigma^2 + rV_{sca}$
Error	(r-1)(mf-1)	M4	σ^2	σ^2

Source: Sharma (2006)

Line × Tester Design

Line x tester is basically an extension of top cross design in the sense that instead of one tester as used in top cross, more than ones testers are used under L x T mating design. This design involves hybridization between lines (f) and wide based testers (m) in one-to-one fashion generating f x m = fm hybrids (Sharma, 2006). It is the simplest mating design that provides both full-sibs and half-sibs simultaneously as opposed to top-cross which provides only half-sibs. It provides SCA of each cross, and it is not providing GCA of lines only but of the testers also, as liner and tester both are different sets of genotypes (Sharma, 2006). In addition, it is used in estimating various types of gene actions important in the expression of quantitative traits (Rashid *et al*., 2007). Line × tester analysis is one of the most powerful tools for predicting the general combining ability (GCA) of parents and selecting of suitable parents and crosses with high specific combining ability (SCA) (Rashid *et al*., 2007).

The line x tester mating design is helpful for estimating the nature and magnitude of gene action controlling quantitative traits. Line × tester is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations.

It provides information on gene effects in controlling inheritance of traits of interest and helps in selecting the parents to be included in cultivar improvement or hybridization programs. It is the best way to test the value of a germplasm and identify the best parents to produce superior hybrids (Mindaye *et al*., 2016). Line × tester analysis evaluates the general combining and specific combining abilities in both self and cross-pollinated crops (Kempthorne, 1957) and identifies superior parental genotypes and hybrids in terms of traits involved in studies (Ahuja and Dhayal, 2007). Line x tester design is the best analysis for estimating general combining ability, specific combining ability and various types of gene actions (Fahmi *et al*., 2017).

The line x tester analysis method is used to breed both self and cross-pollinated plants and to estimate favorable parents and crosses and their general and specific combining abilities (Aslam *et al*., 2014).

CONCLUSION

In plant breeding program, creation of genetic variability is the most fundamental and pre-requisite step to improve crop plant through hybridization. Genetic variation is created through inter-specific hybridization, mutation, polyploidy and recombination. Among these, hybridization is the most relevant to increase genetic variation for success of crop improvement program. To generate useful genetic materials, selection of appropriate mating design and parents are the keys to the successful of plant breeding procedures. Crosses are developed through hybridization from the selected superior parents for desirable traits like yield and other related traits. Originally, the primary intent of mating designs was to estimate genetic variance components like additive, dominance and epistatic variances of genetic parameters.

Combining ability is the ability to combine parents among each other during hybridization process to transmit desirable genes to the next generation. There are two major different combining ability types; variance due to general combining ability and variance due to specific combining ability. Mating design is very critical in estimation of combining ability and determination of gene actions involved in the inheritance of traits. Several mating design and arrangements are used to develop improved crop plants in plant breeding program by breeders and geneticists.

Both additive and non-additive genetic components are determined and quantified to make appropriate selection methods to improve quantitative characteristics. In order to produce best and superior progenies, various mating design can be used accordingly.

Generally, mating designs are developed to estimate and determine the type and quantity of genetic components for improving the crop plant through devising the right breeding procedures. Therefore, selection of mating design is necessary to make further improvement and success of plant breeding schemes. Population genetic variance can be described in terms of general and specific combining ability variances which could further be partitioned into

additive and non-additive components of variation.

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