

A Review on Mating Designs

Aamer Mumtaz¹, Fareeha Zafar¹, *Saifulmalook¹, Amar Shehzad¹¹Department of Plant Breeding and Genetics, University of Agriculture Faisalabad*Corresponding author email: aamer3002@gmail.com, saifulmalookpbg@gmail.com

Abstract: Selection of good mating design is necessary for getting success in plant breeding. Choice of mating designs depends upon several factors i.e., objective of study, time, space and other biological problems or limitations. For production of different progenies and achievement of their objectives, plant breeders used different mating designs and arrangements. In all mating designs crossing is done in half sibs and full sib methods by taking individuals randomly. In this review the aim is to highlight the method, merits and demerits of ten mating designs which are path coefficient analysis, Generation mean, Bi-parental mating, Line Tester design, Correlation, Diallel analysis, Partial Diallel analysis, Triple test cross, Combing ability, Triallel and quadriallel analysis and Discriminant function technique.

[Aamer Mumtaz, Fareeha Zafar, Saifulmalook, Amar Shehzad. **A Review on Mating Designs**. *Nat Sci* 2015;13(2):98-105]. (ISSN: 1545-0740). <http://www.sciencepub.net/nature>. 15

Keywords: Path coefficient analysis, progenies, Generation mean, Parameters, mating

Introduction:

Various mating designs were used by plant breeders and geneticist for improvement of plants. For getting success in plant breeding, the selection of good mating design and parents is necessary (Khan *et al.*, 2009 and Malook *et al.*, 2014abcd). Several factors affects the choice of mating desings such as the type of crossing to be used (Artificial or natural), type of pollination (Self or cross pollinated), type of pollen dissemination (Insect or wind), the purpose of project (For genetic or breeding studies), the presence of male sterility system and the size of population required. Mating design have four main importance, (1) Information on genetic control of character, (2) As a basis for selection and development of best varieties, to generate a breeding population, (3) Estimation of genetic gain, (4) Information for evaluation of parents used in breeding program (Acquaah, 2012, Abass *et al.*, 2014 and Malook *et al.*, 2015). For experiments plant breeders used two types of designs, mating and experiment design.

Mating designs were developed to study quantitative characters. With the help of these designs different genetics components of variation are estimated. All plant breeder and geneticists used mating design for two ways (1) Theoretical and (2) Practical (Sing *et al.*, 2004).

These designs used in different forms for target purpose. The choice of mating design to estimated genetic diversity depends upon use of objective of study, time .space and other biological problems or limitations. A suitable mating design is necessary for successful plant breeding schemes (Khan *et al.*, 2009 and Malook *et al.*, 2014ef).

By the use of mating design, breeders crossed randomly to producing progenies which related to each other as (1) Half-sib and (2) Full-sib.

Analysis of variance is a successful tool to measure genetic diversity in crop improvement to estimate components of variance's and its mean. Number of mating design is used for number of best producing progenies by breeders and geneticists in plant breeding programmed for their success and improvement to next generations (Singh, 1993).

We obtained many parts of breeding by use of these designs that is (1) Progeny trials, mapping populations, (2) Realized selective response and correlated selective response, (3) Changes in progenies generation to generation for breeding purpose, (4) To get information about inheritance of important characters, (5) Develop one or more type of progeny by recombination's, half-sib, full-sib and test crosses etc. (6) Evaluate progeny in set of environment.

Number of mating designs were used to estimate genetic diversity for crop improvement, like as path coefficient analysis, diallel mating design, Line \times tester, generation mean analysis, bi-parental cross, stability analysis, heritability and genetic advance, Combing ability, heterosis and inbreeding depression, gene action in plant breeding, triple test cross analysis and correlation in plant breeding population etc. (Singh, 1993; Mumtaz *et al.*, 2014 and Amin *et al.*, 2014ab). The detail of some mating designs are discussed in this study.

1. Path coefficient analysis:

Path analysis is a method to cause correlation of two variables (independent variable on dependent variable) to measure direct or indirect effects. Path

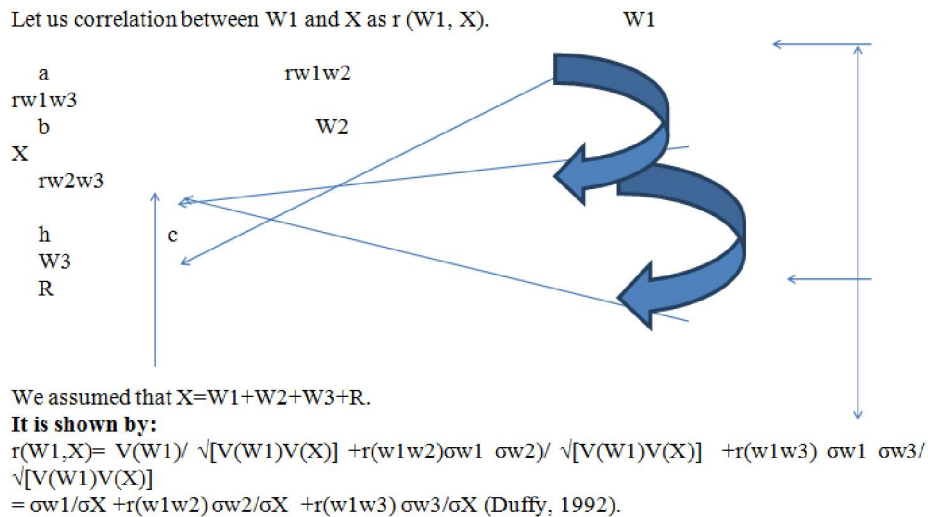
analysis is a standard partial regression coefficient on the effects. Path analysis determined yield components by help of breeders (Cole and Preacher, 2014)

Path analysis is three types:

First is Phenotypic: It is the all possible phenotypic correlation coefficients among given traits. Second is genotypic: It is all possible genotypic correlation coefficients among given traits. Environmental paths: It is all possible environmental correlation coefficients among given traits.

The phenotypic and genotypic are commonly used in breeding. Computation of path has three steps. First is direct effect: It is straight effect of independent variable on dependent variable. Second is indirect effect: It is the effect of independent variable on dependent one or other independent character. Third is residual effect: It is other possible independent variables which were not included in given traits.)

For example: If Y is effect and X is causes. The path analysis the cause W to the effect X. its is denoted by $(w1 \rightarrow X)$ is $\sigma w1 / \sigma x$.



Interpretation of results:

(1) If correlation between yield and character by the effect of direct. Gave true relation between it and selected trait will be rewarding for yield improvement. (2) If correlation is due to indirect effect through another component character. Such trait will be lived in yield improvement. (3) If direct effect is positive and high but cause is negative then direct effect for such trait used to reduce the undesirable indirect effect. (4) If residual effect is high or moderate, selected beside of character which contributed to yield (Duffy, 1992).

Different merits of path analysis are (1) Path analysis is a method to understand association of two variables by effect and cause. (2) It shows positive effect by direct and negative effect by indirect of such traits used to yield improvement. (3) It provides superior genotype from breeding population (Lleras, 2005).

Various demerits of path analysis are (1) Path analysis is design to deal with additive effect to variable and its applications for non-additive effect to variable so may be wrong result occur. (2) Its computation is very complex (Lleras, 2005).

2. Generation mean analysis:

Generation mean analysis is a biometrical technique depend on mean value of 6 different populations i.e. parents (P1, P2) there .F1, F2, and back crosses B1 and B2 to estimation of genetic components of variations.

It provides information about presence and absence of epistasis besides of estimation of additives and dominance variations and effect. Analysis is based on first order of statistics. Graphical analysis is not applicable. Combing ability is not possible. It is free from genetically assumptions. Their requirements depend on two crop seasons for developed test material (Kearsey and Pooni, 1996).

It provides three models for the estimation of genetic components.

First is six parameter: Its provide information about mean analysis of 6 parameters', d ,h, I ,j and l (Haq *et al.*, 2013). Second is five parameters: It based on five population for analysis that is P1,P2,F1,F2 and F3 generation of crosses and its parameter's is m, d, h, I and l (Yadav and Singh, 2011). Third is three parameters: Its provide information about three population its parameters is m, d and h (Abbasi *et al.*, 2014 and Mustafa *et al.*, 2014ab).

This techniques evaluate lesser number of parents at a time as compared to partial diallel and line×tester analysis.

Some important steps for generation mean analysis is (1) To make a cross by selection of parents, (2) Making back cross and raising F1.

Evaluation of material is done by following methods

(1) Biometrical analysis, (2) Epistasis test and (3) Estimation of gene effect and variance.

Interpretation of result:

(1) If additive genetic variance is high it should be placed on mass selection in self-pollinated species and synthetic breeding in cross pollinated species. (2) If dominance or over dominance variance is predominant, the objective is to developed hybrid for commercial purpose. (3) If epistasis variance is high it should be placed on selection of families and lines. (4) If all genetic components are in equal magnitude in population improvement programme and in composite it should be used to developed superior lines with desirable genes material (Kearsey and Pooni, 1996).

Some merits of generation mean analysis are:

(1) Analysis is possible if un-replicated data in population, (2) It depends on first order of statistics, (3) Some estimation is very useful like genetic advance, heritability, heterosis and inbreeding depression (Hallauer *et al.*, 2010).

Some demerits of generation mean analysis are (1) Limited number of crosses at a time of six population involved in evaluation of each crosses, (2) It requires additional crop seasons (Hallauer *et al.*, 2010).

3. Bi-parental cross

It allows crossing of randomly selected plants from F₂ or subsequent generation in a definite fashion. Two mating programmed like half-sib and full-sib progenies (Acquaah, 2012).

Important steps of bi-parental cross are

(1) Selection of parents, (2) Make original cross (3) F1 and F2 population grown, (4) Making crossing in F2 (5) Evaluation of crosses, (6) Biometrical analysis,

Bi-parental cross have 3 type of design (Comstock and Robinson, 1952): North Carolina design 1, North Carolina design 2, North Carolina design 3.

i. North Carolina design 1:

Each male mated to different group of female. It has set of 'f' crosses where f is female plants. Variance between males provides an estimate of additive variance. If variance between female it provide dominance and additive variance estimation. It is influenced by maternal effects.it require 10 to 12 time more area. It is a least powerful design. It involve F₂ plant in crossing. Variance id divided between two fractions, male and female (Acquaah, 2012).

ANOVA(Acquaah, 2012):

Source of variance	Degree of freedom	Mean square	Expected mean square
Sets	s-1		
Replication set	s(r-1)		
Male set	s (m-1)	M1	VE= rVf+ rVm
Female set	sm (f-1)	M2	VE + rVF
Error	S(mf-1) (r-1)	M3	VE
Total	Smfr-1		

ii. North Carolina design 2:

Each male is mated with same group of female. It has mf set of crosses in which 'm' is male and 'f' is female plant. Due to male and female variance it provides additive effects. It also provides dominance variance if male × female variance (Acquaah, 2012 and Sarfaraz *et al.*, 2014). It also influenced by

maternal effects (Hill, *et al.*, 1998). It requires 2 to 4 time more area. It is an intermediate design which involved F2 plants in crossing. Variance is divided in three fractions due to males and females and due to male × female cross (Acquaah, 2012). It does not provide epistasis test or G×E interaction (Kearsey and Pooni, 1996).

ANNOVA (Kearsey and Pooni, 1996)

Source of variance	Degree of freedom	Mean square	Expected mean squares
Sets	s-1		
Replication	S (r-1)		
Males	S (m-1)	M1	VE + rVfm + rfVm
Females	S (f-1)	M2	VE+ rVfm + rmVf
Male×female	S(m-1)(f-1)	M3	VE + rVfm
Error	S(mf-1)(r-1)	M4	VE
Total	Smfr-1		

iii. North Carolina design 3:

Each male is mated to both inbred parents of original cross. It consists of 2m cross where m is number of male. It is capable of testing epistasis, additive and dominance variances. This is more

powerful design and involves F2, F1 and P2 plants during crossing. Variance is divided into two fraction due to male and due to male×female (Acquaah, 2012). It is also called as triple test cross because a third tester is included in this (Hill *et al.*, 1998).

ANOVA(Hallauer *et al.*, 2010):

Source of variance	Degree of freedom	Mean square	Expected mean square
Set	s-1		
Replication	S(r-1)		
Inbred line	S		
Male set (N)	S(n-1)	M1	VE+2rVm
Male×female set	S(n-1)	M2	VE+rVml
Error	S(2n-1)(r-1)	M3	VE
Total	2nsr-1		

Some merits of NCD are (1) Improvement of both self and cross pollinated species. (2) It is suitable as breeding procedure for genetic improvement. (3) Bi-parental creating heterozygosity (Sun *et al.*, 2012).

Some demerits of NCD are (1) Its cross is more complex, (2) It does not provide information about epistasis variance. (3) It is not suitable for segregating population of three ways, double and multiple crosses (Sun *et al.*, 2012)

4. Line × tester analysis:

A common parent is used in crossing with several lines. Parents are selected from germplasm in

which some parents selected as male and some as female parents. Each male is cross with each female. It is good method or technique to evaluate germplasm lines and combine ability variance and its effects (Sharma, 2006).

In crossing plane, each male crossed with each female but each male should not be crossed with each other as well as male also. If ten lines and five testers are used, fifty crosses for evaluation (Sharma 2006). It is also helpful in estimating gene actions of quantitative traits (Rashid *et al.*, 2007).

Female parents	Male parents				
	M1	M2	M3	M4	M5
F1	X	X	X	X	X
F2	X	X	X	X	X
F3	X	X	X	X	X
F4	X	X	X	X	X
F5	X	X	X	X	X
F6	X	X	X	X	X
F7	X	X	X	X	X
F8	X	X	X	X	X
F9	X	X	X	X	X
F10	X	X	X	X	X

Main features of lines × tester analysis are (1) In this technique mf crosses is needed in which 'm' is male and 'f' is female. if 10 female and 5 male parents then fifty crosses should be obtained (2) It can provide information about germplasm lines (3) It is analysis is simple then others designs in breeding programmed (4) Both first and second order of statistic involves (Sharma 2006).

Characters of a good tester are (1) Broad genetic base (2) Wider adaptability (3) Low yield potential (4) Low performance of other traits (Sharma 2006).

Some merits of Line × Tester analysis are (1) By this technique selection of desirable parents and breeding procedure by measuring genetic

components of variance (2) Good method to estimate of germplasm lines. (3) Heterosis, heritability and genetic advance also be estimated (Sharma 2006).

Some demerits of line × Tester analysis are (1) Does not estimation of epistasis variance, (2) In this technique each parents have not opportunity to mate with other parents (Sharma 2006).

5. Correlation

Correlation is used to find degree and direction of relationship between two or more variable, so it is also correlate mutual relationship between two or more variables. It is represented by 'r'. Three types of correlation (Bahmankar *et al.* 2014):

First is simple correlation (association between two variables). It is also three types: Phenotypic: it is directly observed and estimated from phenotypic variance and co variance. Genotypic: It is a heritable and heritable association between two variables and estimated from genotypic variance and co variance. Environmental: It is due to environmental effect and estimated from error variance and co variance.

Second is partial correlation: It is estimation of correlation between two variables by effect of third variable. It is denoted by $r_{12.3}$. Third is multiple correlation: Correlation of two or more independent variables on dependent variable. It is represented by R .

Some imitations of correlation are (1) sometime provide misleading result (2) Sometime correlations become zero between two variables having linear relationship (Bahmankar *et al.* 2014).

6. Diallel cross

It allows mating of selected plant in all possible combination (Schlegel, 2010).

There are two types of diallel cross

(1) Full diallel : (Full diallel with parents and Full diallel without parents.) (Griffing, 1956).

(2) Half diallel: (Half diallel with parents and half diallel without parents.) (Griffing 1956).

Diallel cross analysis involve these steps (1) Involve all possible single crosses among 'n' parents $N(n-1)/2$, (2) Calculation is complex, (3) Results have high precision, (4) Help in choice of parents and breeding procedures, (5) May included direct and reciprocal crosses (6) Sampling of cross is not required, (7) 10 to 12 parents can be evaluating (7) Planting arrangement for diallel by unpaired parents and paired parents (8) Graphical analysis is also possible. (Vr-Wr graph) (9) It is called mating design (Acquaah, 2012: Griffing 1956, Hayman and Jinks, 1977).

Some merits of diallel cross are (1) Each parents have equal chance for mating and recombine with other parents (2) If F2 population is required then inbreeding depression also worked out (3) Evaluation of single crosses in term of genetic component of variance (Nduwumuremyi *et al.*, 2003).

Some demerits of diallel cross are (1) By hand its analysis is complex (2) Limited number of parents can be test at a time.

7. Partial diallel analysis:

It is a method of analysis in which a part of all possible crosses from a diallel analysis. It is also called fractional diallel. More parents can be evaluate at a time of test. In plant breeding it is commonly used for evaluation of parents in term of combine ability (Viana *et al.*, 1999).

Complete diallel involve all possible single crosses among 'n' parents. i.e. $(n-1)/2$.

Partial analysis: It involve $ns/2$ crosses where 'n' and 's'=number of parents and sample crosses.

Its calculation is complex. (1) Only one type analysis (2) It have only one method of combine ability (3) It Includes direct crosses (4) Sampling of crosses is needed (5) Evaluate more parents than diallel. (6) Help in choice of parents and breeding procedures (Viana *et al.*, 1999).

Some merits of partial diallel analysis is: (1) Estimated heritability, genetic advance and heterosis. (2) Can be used with open pollinated species having male sterility (Viana *et al.*, 1999).

Some demerits of partial diallel analysis is: (1) Each parent has not opportunity to mate and recombine every other parent (Viana *et al.*, 1999).

8. Triple test cross analysis:

It allows crossing of randomly selected F₂ plants with both inbred plant and their F₁. This technique provides information about absence and presence of epistasis beside additive and dominance variance (Bakheit *et al.* (2001).

It has following Steps:

- Making single cross
- Raising F₁ progeny
- Making back crosses
- Evaluation of material
- Biometrical analysis.

Triple test cross analysis involves F₂, F₁, P₁ and P₂ generation of a single cross to develop test material. It require three crop seasons for genetic material. It is a more difficult analysis than generation mean analysis. In this analysis test of epistasis is possible. IT has only one model of analysis (Zhu and Zhang, 2007).

Some merits of triple test cross analysis are (1) It provides independent estimation of additive genetic variance and dominance variance (Zhu and Zhang, 2007).

Demerit of triple test cross is that it is used only some crop so it can't be commonly used in breeding and its main problem is choice of contrasting pair of inbred lined to get better result (Zhu and Zhang, 2007).

9. Combining ability:

It is the ability of a genotype to transmit superior performance to its crosses. It is of two types (Griffing 1956).

It is of two types (1) General combining ability: It is average performance of genotype in a series of hybrid combinations. It measures additive gene action and (2) Specific combining ability: It is performance of parents in specific crosses.

It has these Steps: (1) Selection of genotype (2) Making single cross (3) Evaluation of material

Biometrical analysis

Combine ability and heritability, both are useful for plant breeders. The general combining ability variance provides estimate of additive genetic variance which is required for the estimation of narrow sense heritability (Griffing 1956).

Combine ability and heterosis: The specific combine ability variance is used to measure of dominance variance. If heterosis is very high for a specific cross and observation made are true for an economic character like yield. it is possible to utilized commercial hybrid (Griffing 1956).

10. Triallel and quadriallel analysis

Triallel analysis is the analysis of all possible three way crosses among selected parents. It is equal to $n(n-1)(n-2)/2$.

Main steps are (1) Making single crosses (2) Making three way crosses (3) Evaluation of material (4) Biometrical analysis.

Merit of triallel analysis is, it provide reliable information about components of epistasis variance.

Demerit of triallel analysis is, it require two cropping seasons for experimental genetic material.

Quadriallel analysis is the analysis of all possible double crosses among selected parents .it is $n(n-1)(n-2)(n-3)/8$ (Rawlings and Cockerham, 1962).

Main steps of triallel and quadriallel analysis are (1) Making single crosses (2) Making double crosses (3) Evaluation of material.

Merit of quadriallel analysis is, it provides superior double cross hybrid especially in cross pollinated crops (Rawlings and Cockerham, 1962).

Demerit of quadriallel analysis is: It is cost able experiment to made number of crosses in this design because it needed one extra season of crop (Rawlings and Cockerham, 1962).

11. Discriminant function technique:

This technique is used for development of selection on various character combinations where plant breeder indirectly selects the genetic material in yield. This character is linear combination character associated with yield (Klecka, 1980).

It has three type of selection such as (1) Classical: It estimates desirable and undesirable genotypes in selection process. First time applied for plant by smith 1936. (2) Restricted: It helps to improve all sets of plant keeping value of other character and theses character some time single or may be double character. First time purposed by Kemthorne and Nordskog in 1959 (3) General (modification the experiment of smith by Johansson and Hanson in 1957. In this type traits are depend on average statistics for several population

Computation steps are (1) Calculation of weight coefficient (2) Genetic advance (3) Relative efficiency.

It measures efficiency of various linear character combinations in their selection process. Analysis of variance and covariance is involved. It should be help to estimation of yield (Klecka, 1980).

Some merits of discriminate function technique is (1) Provide information about yield (2). Applied on both population parental and segregating population (Klecka, 1980).

Some demerits of discriminate function technique is (1) Selectable indication is more comple (2) Selection is useful in single plant not in family (Klecka, 1980).

Conclusion

The choice of suitable mating design is very important for success of any experiment. For suitable choice any design types, its merits and demerits must have known. Each mating design has its own significance, merits and demerits according to conditions of experiment i.e., space, time, objectives of study and problems. For example path coefficient analysis is done for measuring correlation between a dependent and an independent variable. If information about presence and absence of epistasis besides of estimation of additives and dominance variations and effects is to be checked generation mean analysis is used. If crossing of randomly selected plants from F_2 or subsequent generation in a definite fashion is needed the bi-parental design is used. If the effect of tester is to be checked with different lines then line \times tester design is used. If degree and direction of relationship between two or more variable is to be checked then correlation is used. If crossing of all plants in all possible combinations is needed then diallel analysis is used and if part of all possible combinations are needed then partial diallel analysis is used and Discriminate function technique is used for development of selection on various character combinations where plant breeder indirectly selects the genetic material in yield. This study in detail describes the functions, merits and demerits of different mating designs which are necessary for success of any experiment.

References:

1. Aamer Mumtaz, Hafeez Ahmad Sadaqat, Saif-ul-malook, Abdul Subhan Nazik and Hafiz Mehboob 2014. Genetic behavior of quality traits in Brassica rapa. *Vegetose*, 27 (3): 139-145.
2. Abass H. G., A. Mahmood, Q. Ali, Saif-ul-Malook, M. Waseem and N.H. Khan. 2014. Genetic variability for yield, its components and quality traits in upland cotton (*Gossypium hirsutum* L.) *Nature and Science*, 12: 31-35.

3. Abbasi S. Baghizadeh A. Mohammadi-Nejad G. and Nakhoda B. (2013). Annual Review and Research in Biology 4(24): 3636-3644.
4. Acquaah G. (2012). Principles of plant genetics and breeding. 2nd ed. Wiley-Blackwell, Oxford.
5. Amin W., Saif-ul-malook, S. ashraf and Amir Bibi. 2014b. A review of screening and conventional breeding under different seed priming conditions in sunflower (*Helianthus annuus* L.) Nature and Science, 12: 23- 37.
6. Amin,W., Saif-ul-malook, A. Mumtaz, S. ashraf, H. M. ahmad, K. Hafeez¹, M. Sajjad and A. Bibi. 2014a. Combining ability analysis and effect of seed priming on seedling traits in Sunflower (*Helianthus annuus*). Report and Opinion, 6: 19-30.
7. Bakheit B. R. Ismil A.A. El-Shimy A.A. and Sedk F.S. (2001). Tiple test cross analysis in four sesame crosses (*Sesamum indicum* L.). Journal of Agricultural Science 137: 185-193.
8. Cole D.A. and Preacher K.J. (2014). Manifest Variable Path Analysis: Potentially Serious and Misleading Consequences Due to Uncorrected Measurement Error. Psychological Methods 19(2): 300–315.
9. Comstock, E. and Robinsonh, H.F. (1952). The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. Biometry 4: 254-266.
10. Duffy J.R. (1992). Path analysis. Clinical Aphasiology 21: 47-57.
11. Griffing B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Sciences 9: 463-493.
12. Hallauer A.R, Carena M.J. and Filho J.B.M. (2010). Quantitative genetics in maize breeding. Iowa state university press, Ames, Iowa.
13. Hallauer, A.R., Carena M.J. and Filho J.B.M. (2010). Quantitative genetics in maize breeding. 6th ed. Springer, Iowa, USA.
14. Hanson W.D. and Johnson H.W. (1957). Methods of calculating and evaluating a general selection index obtained by pooling information from two or more experiments. Genetics 42: 421-432.
15. Haq M.I.U. Ajmal, S. Kamal N. Khanum S. Siddique M. and Kiani M.Z. (2013). Generation Mean Analysis for Grain Yield in Maize. Journal of Animal and Plant Sciences 23(4): 1146-1151.
16. Hayman K. and Jinks J.I. (1977). Introduction to Biometrical Genetics. Chapaman and Hall. London, (1st Edition).
17. Hill J. Becker H.C. and Tigerstedt P.M.A. (1998). Quantitative and ecological aspects of plant breeding. Chapman and Hall, UK, Lond
18. Kearsy M.J. and Pooni H.S. (1996). The Genetical Analysis of Quantitative Traits. Chapman and Hall, 1st edition, London, pp 46.
19. Kempthorne O. and Nordskog, A. W. (1959). Biometry. 15 : 10.
20. Khan S.A. Ahmad H. Khan A. Saeed M. Khan S.M. and Ahmad B. (2009). Using line x tester analysis for earliness and plant height traits in sunflower. Journal of Plant Breeding and Genetics 01(03): 117-129.
21. Klecka W.R. (1980). Discriminanat Analysis. Beverley Hills: Sage.
22. Lleras C. (2005). Path analysis. Encyclopedia of social measurement, Volume 3, Elsevier Inc.
23. Mumtaz A., Sadaqat, H.A., Saifulmalook, Nazik, A.S. and Ahmad, H.M. 2014. Genetic Behavior of Quality Related Traits in *Brassica rapa* L. Vegetos 27(3): 139-145.
24. Mustafa G., Ehsanullah, Saif-ul-Malook, E. Ahmad,M. Sarfaraz, S. A. Qaisarani andM. K. Shahbaz. 2014. Yield attributes and productivity of various Bt and non Bt cotton varieties in Faisalabad environment. Nature and Science, 12(11): 92-103.
25. Mustafa G., Ehsanullah, Saif-ul-Malook, M. Sarfaraz, M.K. Shahbaz , U.Chopra and Q. Ali .2014. A review of production for various Bt and non Bt cotton varieties in Pakistan. Nature and Science, 12: 81-91.
26. Nduwumuremyi A. Tongoona P. and Habimana S. (2013). Mating Designs: Helpful Tool for Quantitative Plant Breeding Analysis. Journal of Plant Breeding and Genetics 01 (03): 117-129.
27. Rashid M., Cheema A.A. and Ashraf M. (2007). Line x tester analysis in Basmati rice. Pakistan Journal of Botany 39: 2035-2042.
28. Rawlings J.O. and Cockerham C.C. (1962). Analysis of double cross hybrid populations. Biometry 18: 229-244.
29. Saif-ul-Malook and M. Ahsan. 2014a. Maize Stress Breeding and Genetics: Combining Ability Analysis for Maize Breeding. LAP LAMBERT Academic Publishing, GmbH & Co. Vol. pp: 1- 121.
30. Saif-ul-malook, M. Ahsan and Q. Ali. 2014b. Genetic Variability and Correlation Studies among Morphological Traits of *Zea mays* under Normal and Water Stress Conditions. Persian Gulf Crop Protection. 3(4): 15-24.
31. Saif-ul-malook, M. Ahsan, Q. Ali and A. mumtaz. 2014c. Genetic variability of maize genotypes under water stress and normal conditions. Researcher, 6: 31 – 37.

32. Saif-ul-malook, M. Ahsan, Q. Ali, A. Mumtaz. 2014d. Inheritance of yield related traits in maize under normal and drought condition. *Nature and Science*, 12: 36 – 49.
33. Saif-ul-malook, Qurban ali, Muhammad Ahsan, Aamer Mumtaz and Muhammad Sajjad. 2014f. An overview of conventional breeding for drought tolerance in *Zea mays*. *Nature and Science*, 12: 7-22.
34. Saif-u-Malook. 2015. Mutation breeding approach to breed drought tolerant maize hybrids. *International Journal of Biosciences*. 6(2): 427-436.
35. Sarfaraz M., Wasi-Ud-Din, Muhammad Sajjad, Muhammad Wajid, Saif-ul-Malook, Muhammad Khalid Shabaz, Hafiz Mahboob Ahamed and Hafiz Salman Saeed. 2014. Effect of Planting Time and Nitrogen Levels on various yield Components of Sunflower (*Helianthus annuus* L.). *Nature and Science*, 12(12): 19-28.
36. Schlegel R.H.J. (2010). Dictionary of plant breeding. 2 ed. CRC Press, Taylor & Francis Group, Boca Raton.
37. Sharma J.R. (2006). Statistical and biometrical techniques in plant breeding. 1 ed. New Age International. New Delhi. India.
38. Singh P. (1993). Biometrical Techniques in Plant Breeding. Kayani Publishers, India.
39. Singh R.K. Pooni H.S. Singh M. and Bandopadhyaya A. (2004). Mating Designs and Their Implications for Plant Breeding IN Plant Breeding pp. 523-534.
40. Smith H. and Fairfield. (1936). Investigations on analysing yield of wheat varieties. 1-111.” MS. in the custody of C.S. and I.R., Australia
41. Sun Z. Li H. Zhang L. and Wang J. (2012). Estimation of recombination frequency in biparental genetic populations. *Genetical Research* 94: 163–177.
42. Viana J.M.S. Cruz C.D. and Cardoso A. A. (1999). *Genetics and Molecular Biology* 22(4):591-599.
43. Yadav H.K. and Singh S.P. (2011). Inheritance of quantitative traits in opium poppy (*Papaver somniferum* L). *Genetika* 43(1): 113 -128.
44. Zhu C. and Zhang R. (2007). Efficiency of triple test cross for detecting epistasis with marker information. *Heredity* 98:401-410.

2/10/2015