MATING DESIGNS IN TREE IMPROVEMENT

Abstract

Tree improvement enhances the value of tree species by selecting the most desirable trees, breeding or mating the selected trees, and evaluating the resulting progeny. The effectiveness of the tree breeding programs depends upon the effective mating design (Surendran et al., 2003). The primary objective of mating design is to determine the genetic variance based on the correlation between the relatives and how they are used for variation into various genetic components using the second degree of statics. The choice of breeding strategy is significantly influenced by mating design (Van Buijtenen 1986; Bridgwater and Franklin, 1985). Mating designs are usually adopted to achieve the goals like providing information to evaluate parents, estimating genetic gains and genetic parameters, establishing a base population suitable for subsequent cycles of selection, and being cost-effective (Fins et al., 1992). In all mating designs, the individuals are randomly selected or chosen and crossed to produce progenies that are related to one another as full or half siblings (Nduwumuremyi et al., 2013). No single mating design will be most effective for achieving all the objectives (Zobel and Talbert, 1984). The type of information obtained from the testing program will depend on the mating designs. The breeder must choose a design that provides the necessary genetic information. The complexity of the mating design and the necessity to maintain complete pedigree records both affect the economic cost of mating design. Although various mating techniques have been developed, only a small number of them have been optimized for tree or crop improvement (Awata et al., 2018).

Keywords: Tree improvement, breeding or mating, resulting progeny

I. INTRODUCTION

Improvement means increasing the yield as well as the quality of any material. Increasing yield means an increase in productivity and it is very important as forest cover is reducing with the increase in the demand for forest products. To overcome this bridge gap, tree improvement is an important tool that increases the productivity of forests to a greater extent.

Tree Improvement is the increase in the yield and quality of wood products in a short period by combining silviculture management (more yield) and control of parentage (superior quality). There are two other related terms to tree improvement: Forest Genetics and Tree Breeding. The former term is defined as the genetic study of the heredity and variation of inherited characteristics of forest trees whereas the later term is the application of genetic, reproductive biology, and economic principles to the genetic improvement and management of forest trees.

Trees in general are selected, based on their phenotypic superiority for planning in the seed orchard. Once parents are selected, their genetic worth is tested by mating them in any fashion and their genetic worth is established. Or we can say that, tree improvement increases the value of a tree species by 1) Selecting the most desirable trees from natural stands or plantations, 2) Breeding or mating these select trees. 3) Testing the resulting progeny.

Mating design refers to a technique of crossing, that is used to create progenies of certain kinds that can be used to anticipate the genetic worthiness of their parents (Surendran *et al.,* 2003). Alternatively, the term “mating designs” refers to the methods used by trees to mate and produce progeny. This creates a progeny population and gives information for further testing programs.

II. FACTORS INFLUENCING THE CHOICE OF MATING DESIGNS

1. Some Factors are taken into Consideration while Selecting a Mating Design (Acquaah, 2012):

- Objectives of the experiment (breeding or genetic studies)
- Type of pollination (Self or cross-pollinated)
- Type of cross (natural or artificial)
- Type of pollen dispersal (wind or insect)
- Presence of male sterility system
- Size of population

III. OBJECTIVES OF MATING DESIGNS

2. The Following are the Broad Objectives of a Mating Design:

- Progeny testing
- Estimation of variance components
- Estimation of genetic gains
- Estimation of heritability
- Creation of base population

- Determination of combining abilities

3. **Progeny Testing:** In the context of progeny testing, the mating design can provide information for evaluating the parents. It involves choosing parents based on the performance of their offspring. The best way to assess the breeding value of chosen parents in seed orchards is to raise offspring in a way that makes it possible to estimate the genetic worth of the parents. The genetic values of a parent that can be measured from the progeny test are: variance, heritability, general combining ability and specific combining ability (Surendran *et al.,* 2003). This will help breeders to separate the parents whose phenotypic superiority had resulted due to growing in a good environment from those that are superior because they have a good phenotype.

4. **Estimation of Variance Components:** The selection of parents depends upon the degree of inheritance to perform a specific role in the tree improvement programs. The components of variance are separated as follows:

   Phenotypic variance (PV) = Genotypic variance (GV) + Environmental variance (EV) Environmental variance can be obtained by the analysis of variance based on the experimental design of the field. According to Fisher (1918), Genotypic variance can be divided into three components *i.e.,* Additive, Dominance, and Epistasis variances.

5. **Additive Variance:** refers to the component that results from variations between two homozygotes of a gene, for example, AA and aa.

   - **Some Features of the Additive Variance:**
     - It is fixable *i.e.;* it fixes the average effect of the genes present on all the segregating loci
     - Additive genes indicate a lack of dominance i.e., intermediate expression
     - Measure of additive gene action
     - It responds to selection
     - A measure of additive variance is GCA

6. **Dominance Variance:** this arises due to the deviation of heterozygotes (Aa) from the average effect of the two homozygotes (AA and aa).

   - **Some Features of Dominance Variance:**
     - It is not fixable
     - It is due to intra-allelic interactions
     - Measure of dominance gene action
     - It is associated with heterozygosity
     - It is the main cause of heterosis

7. **Epistasis Variance:** results from the interaction between two or more genes.

   - **Some Features of Epistasis Variance:**
     - It is due to inter-allelic interactions.
     - It is of three types viz., Additive x Additive (interaction of AA and BB); Additive x Dominance (AA x Bb, Aa x BB); Dominance x Dominance (Aa x Bb).

8. **Gene Action:** The act or mode of expression of genes in a genetic population is referred to as gene action. It is of two types: 1) Additive gene action 2) non-additive gene action

9. **Additive Gene Action**
   - It involves joint effects of additive variance and additive x additive type of epistasis.
   - Mode of action is **additive** (fixable).

10. **Non-Additive Gene Action**

    - It includes dominance variance and additive x dominance, and dominance x dominance types of epistasis.
    - Mode of action is **non-additive** (non-fixable).

IV. ESTIMATION OF GENETIC GAINS

1. **Genetic Gain** is the increase in average genetic value or average phenotypic value within a population as a result of selection within the population during generations of breeding. The best way to estimate the progress made in a tree improvement program is to compare the relative performance of the improved and unimproved population by the same test. All the mating designs have an in-built mechanism to provide the expected and realized genetic gains due to genetic tests by using mating design (Surendran *et al.,* 2003).

2. **Estimation of Heritability:** Heritability is the portion of the total variance that may be due to genetic factors. It is of two types: broad sense and narrow sense heritability

   - **Broad Sense Heritability:** (Lush,1940) It is the ratio of total genetic variance to total phenotypic variance. Parental and segregating material can be used to estimate the broad sense heritability. It is useful in choosing the elite types from the homozygous population.
     $(h^2) = V_g/V_p \text{ X } 100$
     If it is high then characters are least influenced by the environment

   - **Narrow Sense Heritability:** (Smith, 1952) It is the ratio of additive genetic variance to the total phenotypic variance. It requires crossing in a definite fashion. It is useful in the selection of elite types from segregating material.
     $(h^2) = V_a/V_p \text{ X } 100$
     Characters are governed by additive gene action, if it is high.

     Estimation of narrow-sense heritability is most important because it throws light on the nature of the population as well as the dependence upon the traits for transmission in the subsequent generation. It can be utilized for predicting the efficacy of selection and provides an understanding of how various traits will respond under selection pressure.

V. CREATION OF BASE POPULATION

1. **Base Population:** act as a source material from which subsequent selections can be obtained. To satisfy this objective, the mating design must first permit co-ancestry

management i.e., use controlled mating and keep complete pedigree records. Secondly; the selected design must produce sufficient numbers of families and individuals to maintain desired selection differential (the difference between the mean phenotypic value of the selected population and to mean phenotypic value of the original population). To fulfill the second objective is difficult when parents of unknown breeding values mated together to provide the base population for the next cycle of selection. In this instance, it is important to make sufficient numbers of crosses per parent so that there is a reasonable probability that it will have been mated with at least one average or a better parent. Thus, it may be possible to select progenies only from parents with good breeding values rather than from mating between parents with good and poor breeding values.

2. **Estimation of Combining Abilities:** The ability of an organism to transmit genetic superiority to its offspring is known as combining ability. It is of two types: General and Specific combining abilities

3. **General Combining Abilities:** it is a mean performance of a parent in a series of cross combinations, which will be determined from the performance of F_1 progeny. It is estimated by half-sib mating. It has a relationship with a narrow sense heritability. It is due to additive genetic variation and additive x additive type of gene interaction. It denotes combining ability of genotypes especially inbred with various testers. It helps in the identification and selection of the best genotypes to use in hybridization, as a parent.

4. **Information on GCA can be Used for:**

   - Choosing the best parents for seed orchard
   - Choosing parents of progeny for future genetic improvement programs

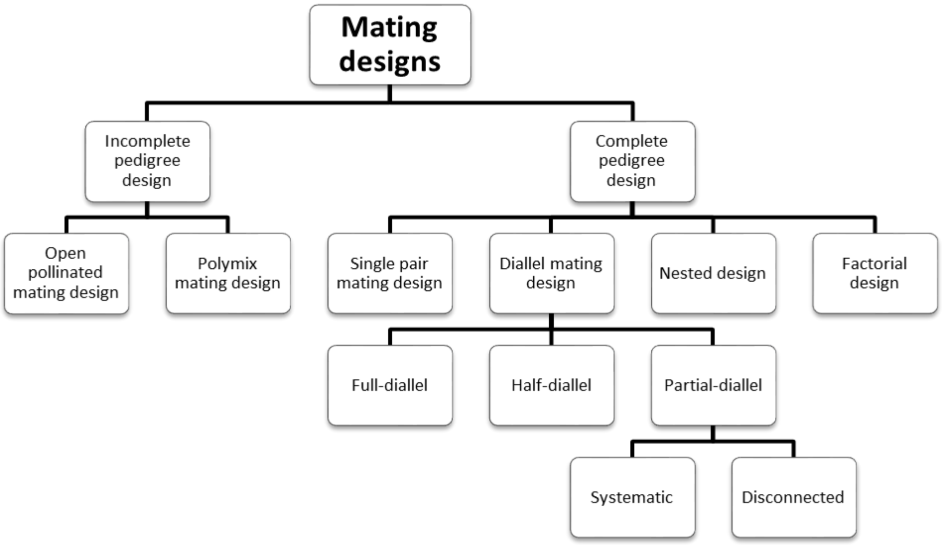
5. **Specific Combining Abilities:** it is the performance of F_1 progeny in a particular combination that ultimately tells upon specific parents to produce such a cross or simply it is the performance of parents in specific combinations. It is estimated by full-sib mating. It has a relationship with heterosis. It is due to dominance genetic variation and all three types of gene interactions. It also helps in the identification and hence selection of best cross combinations *i.e.,* those with the desired output. When we see that an inbred line combines well in any cross, it is because of a specific combining ability. Identification of higher SCA results in the production of superior hybrids and such hybrid combinations can be identified through a mating design.

After deciding on the breeding program's goals, there are two more key decisions to be taken *i.e.,* the choice of mating design to create a progeny population, and the choice of experimental design to be followed in the field. There are large numbers of experimental designs available. But generally, complete randomized design and the randomized complete block design are used in breeding programs because they are cheap, simple, and can be applied in the field without any difficulty as compared with other complex designs. Breeders must choose a design that provides necessary genetic information and at the same time, it should be cost effective. The economic cost of mating design is also determined by the complexity of mating design and the need to keep complete pedigree records.

VI. CLASSIFICATION OF MATING DESIGNS

Mating designs are classified into two main categories i.e., Incomplete pedigree design and Complete pedigree design

1. **Incomplete Pedigree Design:** In this, only one parent is known for any given progeny and further classified into two categories viz., Open-pollinated mating design and poly mix mating design.



2. **Open Pollinated Mating Design:** In this, open pollination is used to allow tree mating at random. Female parents may provide open-pollinated seeds. Seed collection may be from the plus tree growing in natural stands or plantations and from genotypes in seed orchards. If we collect seeds from seed orchards so it is advisable that seed orchards must have heavy seed production because pollination characteristics may be differed in young seed orchards as compared to fully productive seed orchards (Mandal and Gibson, 1998). At a young age only, a few clones produce most of the pollen therefore, seeds collected from young orchards may have only a limited number of pollen parents.

- **Advantages**
  - Easiest and least expensive
  - GCA can be estimated
  - Helps in the estimation of heritability values
  - Advanced generation selection can be made
  - Helps in rouging of genetically inferior trees
  - Used to rapidly test particular trees
  - Component of variance or covariance for females gives reliable estimates of ¼ D (additive genetic variance)

- **Disadvantages**
  - Limited utility for the future generation
  - Possibility of selfing

  - SCA cannot be estimated
  - Inbreeding depression
  - Lack of complete pedigree

3. **Poly Mix Mating Design:** It is also known as **poly cross** and sometimes **top cross** mating design. In this design, a few trees are chosen to serve as the male parents, and pollen from both parents is collected in equal quantity and mixed. The pollen mixture is then administered to the female parents. In order to ensure that female parents are pollinated by a diverse group of other parents, a lot of pollen is usually added to the mixture. There should be a minimum of 10 male parents chosen (Mandal and Gibson, 1998).

   - **Advantages**
     - GCA can be estimated
     - Helpful in estimating the realized and expected gains from additive genetic variation
     - Provides heritability and breeding values of female parents involved in the pollen mix
     - Except for open-pollinated mating design, less expensive than other mating designs
     - Reliable estimates of ¼ D (additive genetic variance) can be obtained by the component of variance or covariance

   - **Disadvantages**
     - SCA cannot be estimated
     - Breeding value may be biased due to non-random pollination by pollens included in the mix because pollens of some clones are more viable than that of others and it can result in an erroneous estimate of GCA
     - Advanced generation selection is difficult

4. **Complete Pedigree Design:** In this, the pedigree of both the male and female parents is known. So, it is possible to predict the performance of progenies based on their ancestral inheritance. It is further classified as follows:

5. **Single Pair Mating Design:** In this design, each parent can only be mated to another member of the population once. In the given example, even several parents who can be used as either males or females are mated in a single pair fashion and produces 4 crosses *viz.,* 1x2, 3x4, 5x6, 7x8. If the goal is to create a population for the selection of individuals for a new seed orchard or use in continuous breeding, this design performs especially well (Surendran *et al.,* 2003). Single pair mating with genetically proven parents will be useful in a breeding program to produce populations for advanced generation selection.

Male Parents									
	Clones	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Female Parents	**1**	-	x	-	-	-	-	-	-
	2	-	-	-	-	-	-	-	-
	3	-	-	-	x	-	-	-	-
	4	-	-	-	-	-	-	-	-
	5	-	-	-	-	-	x	-	-
	6	-	-	-	-	-	-	-	-
	7	-	-	-	-	-	-	-	x
	8	-	-	-	-	-	-	-	-

- **Advantages**
  - Easy to carry out
  - SCA can be estimated
  - Provide estimates of heritability
  - Creates a maximum number of unrelated families
  - It involves a minimum number of crosses
  - Component of variation among full-sib family means can be used to estimate ½ D
  - Helps in the maintenance of large and effective population size

- **Disadvantages**
  - It requires an even number of trees all time
  - GCA cannot be estimated
  - Not suitable for rouging seed orchards

6. **Diallel Mating Design:** The diallel term was introduced by Schmidt (1919). Diallel design is a very useful design that is used to produce crosses for the evaluation of genetic variances. Diallel cross-refers to all possible combinations of crosses. It is further classified into three types: complete, half, and partial diallel mating design

7. **Full Diallel Mating Design:** In this, each parent is crossed to all others in every combination including, self, direct, and reciprocal crosses. Reciprocal crosses are two matings involving two parents in which, in the first mating, the first parent is used as a female, the second as the male; whereas in the second mating, the second parent is used as a female and the first parent is used as a male. It involves n^2 number of combinations where n is the number of parents (Zobel and Talbert, 1984). efficient as full diallel but is mostly used as it creates fewer crosses than full diallel. For example, 8 parents are involved in a cross that produces 36 hybrids including selfed parents.

Male Parents									
	Clones	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Female Parents	**1**	x	x	x	x	x	x	x	x
	2	x	x	x	x	x	x	x	x
	3	x	x	x	x	x	x	x	x

	4	**x**	**x**	**x**	**x**	**x**	**x**	**x**	**x**
	5	**x**	**x**	**x**	**x**	**x**	**x**	**x**	**x**
	6	**x**	**x**	**x**	**x**	**x**	**x**	**x**	**x**
	7	**x**	**x**	**x**	**x**	**x**	**x**	**x**	**x**
	8	**x**	**x**	**x**	**x**	**x**	**x**	**x**	**x**

- **Advantages**
  - Helpful to create the maximum number of unrelated families
  - Helpful in the estimation of all genetic parameters
  - Provides good estimates of GCA and SCA values
  - Component of variance for GCA estimates is ¼ D and that of SCA estimates is ¼ H
  - Dominance type of gene action is possible
  - It contributes to the knowledge of heterotic system
  - Provide knowledge of quantitative traits

- **Disadvantages**
  - Very cumbersome to apply
  - Produces a very large number of crosses
  - Very time consuming
  - Very costlier
  - Hardly used in progeny testing

8. **Half Diallel Mating Design:** In this, each parent is mated to every other parent only once as a male parent only. This design is similar to full diallel except that reciprocal cross is not made and sometimes self. The number of crosses will be n(n-1)/2 when self-parents does not involve in the cross. This design is not as efficient as full diallel but is mostly used as it creates fewer crosses than full diallel. For example, 8 parents are involved in a cross that produces 36 hybrids including selfed parents.

		Male Parents							
Female Parents	**Clones**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
	1	**X**	-	-	-	-	-	-	-
	2	**X**	**X**	-	-	-	-	-	-
	3	**X**	**X**	**X**	-	-	-	-	-
	4	**X**	**X**	**X**	**X**	-	-	-	-
	5	**X**	**X**	**X**	**X**	**X**	-	-	-
	6	**X**	**X**	**X**	**X**	**X**	**X**	-	-
	7	**X**	**X**	**X**	**X**	**X**	**X**	**X**	-
	8	**X**	**X**	**X**	**X**	**X**	**X**	**X**	**X**

- **Advantages**
  - It is the best to design for forest species
  - Helpful in the estimation of GCA, SCA, and genetic parameters
  - Component of variation for GCA estimates is ¼ D and that of SCA estimates is ¼ H
  - Cost-effective in comparison to full diallel design

- **Disadvantages**
  - Not as effective as full diallel
  - Number of crosses is still large and requires extra care in handling the crosses

Griffing (1956) developed four main methods of diallel mating design. The choice among the four methods depends on the inbreeding depression of the parents.

Method 1: Full diallel crosses including parents and reciprocals ($n=p^2$)

	Males					
	Clones	**1**	**2**	**3**	**4**	**5**
Females	**1**	**1x1**	**2x1**	**3x1**	**4x1**	**5x1**
	2	**1x2**	**2x2**	**3x2**	**4x2**	**5x2**
	3	**1x3**	**2x3**	**3x3**	**4x3**	**5x3**
	4	**1x4**	**2x4**	**3x4**	**4x4**	**5x4**
	5	**1x5**	**2x5**	**3x5**	**4x5**	**5x5**

Method 2: Full diallel crosses with no parents ($n=p(p-1)$)

	Males					
	Clones	**1**	**2**	**3**	**4**	**5**
Females	**1**	**-**	**2x1**	**3x1**	**4x1**	**5x1**
	2	**1x2**	**-**	**3x2**	**4x2**	**5x2**
	3	**1x3**	**2x3**	**-**	**4x3**	**5x3**
	4	**1x4**	**2x4**	**3x4**	**-**	**5x4**
	5	**1x5**	**2x5**	**3x5**	**4x5**	**-**

Method 3: Half diallel crosses including parents and no reciprocals ($n=p(p+1)/2$)

	Males					
	Clones	**1**	**2**	**3**	**4**	**5**
Females	**1**	**1x1**	**-**	**-**	**-**	**-**
	2	**1x2**	**2x2**	**-**	**-**	**-**
	3	**1x3**	**2x3**	**3x3**	**-**	**-**
	4	**1x4**	**2x4**	**3x4**	**4x4**	**-**
	5	**1x5**	**2x5**	**3x5**	**4x5**	**5x5**

Method 4: Half diallel crosses with no parents and no reciprocals (n=p(p-1)/2)

	Males					
	Clones	**1**	**2**	**3**	**4**	**5**
Females	**1**	**-**	**-**	**-**	**-**	**-**
	2	**1x2**	**-**	**-**	**-**	**-**
	3	**1x3**	**2x3**	**-**	**-**	**-**
	4	**1x4**	**2x4**	**3x4**	**-**	**-**
	5	**1x5**	**2x5**	**3x5**	**4x5**	**-**

9. **Partial Diallel Mating Design:** In this design, only a few of the necessary crosses are made meaning that not all parents are mated. This design may exist in a variety of conformations (Braten, 1965). There is a systematic way of mating individuals and this way is discussed in two types of partial mating design viz., Systematic or progressive and disconnected diallel mating design.

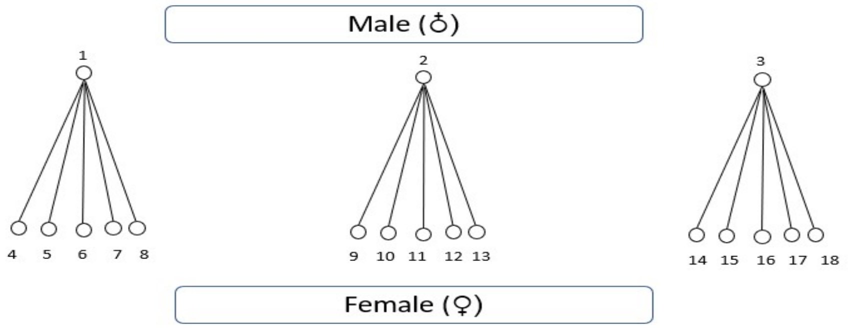
10. **Systematic or Progressive Mating Design:** In this design, crosses are created that fall along specific diagonals. The selection of the diagonals ensures that no parent participates in more than a few crosses. It reduces the involvement of a single parent in a large number of crosses and creates a maximum number of unrelated crosses. It estimates GCA for each parent and SCA for a part of possible combinations. The component of the variance for GCA estimates is ¼ additive and for SCA it is ¼ nonadditive variance (Zobel and Talbert, 1984).

	Male parents												
	Clones	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Female parents	**1**		**x**	**x**					**x**	**x**	**x**		
	2			**x**	**x**					**x**	**x**	**x**	
	3				**x**	**x**					**x**	**x**	**x**
	4					**x**	**x**					**x**	**x**
	5						**x**	**x**					**x**
	6							**x**	**x**				
	7								**x**	**x**			
	8									**x**	**x**		
	9										**x**	**x**	
	10	**x**										**x**	**x**
	11	**x**	**x**										**x**
	12	**x**	**x**	**x**									

11. **Disconnected Mating Design:** In this design, parents are separated into small groups of 5 to 10 tree, and within each group, diallel or half-diallel matings are performed. The number of crosses reduced in this design. Helpful in the estimation of GCA and SCA values. This design is less costly than a full diallel design. For example, 12 parent breeding population has been divided into two groups involving six parents each and these parents have been mated in half diallel fashion excluding self-crosses and resulting in 30 populations as shown below

		Male Parents											
	Clones	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Female Parents	**1**		x	x	x	x	x						
	2			x	x	x	x						
	3				x	x	x						
	4					x	x						
	5						x						
	6												
	7								x	x	x	x	x
	8									x	x	x	x
	9										x	x	x
	10											x	x
	11												x
	12												

12. **Nested Design:** This design is also known as hierarchical mating design. In this design, group of parents of one sex are mated to members of the other sex. It was first developed by maize corn breeders to estimate variance components. It is also called North Carolina Design I. It is a control-pollinated design that has been used in forest trees (Surendran *et al.,* 2003). In the figure, 1,2, and 3 are males of rarer sex and each is mated to five different female parents.



- **Advantages**
  - ➢ This design applies to agricultural crops
  - ➢ GCA value can be estimated
  - ➢ Components of variance among parental groups of male estimates ¼ additive variance and ¼ dominance variance
  - ➢ Easy and less costly

- **Disadvantages**
  - ➢ Generates a small number of unrelated families
  - ➢ Not suitable for advanced-generation breeding programs
  - ➢ GCA is only available to those who are of the rarer sex

13. **Factorial Design:** Members of one sex cross with many members of the other sex in all possible ways in this design (Mandal and Gibson, 1998). Males and females are different

but they crossed in all combinations and males are designated as “testers” while females are as “lines” that’s why this design is known as the “Line X Tester” design. Tester is a genotype that is used to identify superior germplasm and that’s why this is also designated as a “Tester” design. The line X tester design permits the evaluation of the general combining abilities of lines crossed to a set of testers as well as the general combining abilities of the latter (Kempthorne, 1957). This design was first studied or used at North Carolina State University, US, and named “North Carolina Design II”. It is very useful for progeny testing programs because breeding values can be estimated for all genotypes in the population which is being tested.

Male Parents						
Female Parents	**Clones**	**1**	**2**	**3**	**4**	**5**
	6	**x**	**x**	**x**	**x**	**x**
	7	**x**	**x**	**x**	**x**	**x**
	8	**x**	**x**	**x**	**x**	**x**
	9	**x**	**x**	**x**	**x**	**x**
	10	**x**	**x**	**x**	**x**	**x**
	11	**x**	**x**	**x**	**x**	**x**
	12	**x**	**x**	**x**	**x**	**x**

- **Advantages**
  - Useful in progeny testing program
  - GCA and SCA can be estimated
  - Component of variance among male and female groups estimates ¼ D and for male and female, it estimated ¼ H.
  - Helps in the estimation of heritability values
  - Helpful to estimate the realized and expected gains from additive and non-additive genetic variance

- **Disadvantages**
  - Produces a small number of unrelated families
  - The number of testers will determine the maximum number of parents that may be chosen for the subsequent generation.

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