UNIT- VII

**Genetic Composition of Cross Pollinated Crops**

Tapash Dasgupta

Professor. & Dean

School of Agriculture and Rural Development

IRDM Faculty Centre,

Ramakrishna Mission Vivekananda Educational and Research Institute,

Narendrapur, Kolkata- 700103.

E-mail: dean.irdm@gmail.com

Shyam Chandra Ghosh

Ph.D. Scholar, GPB

Department of Genetics and Plant Breeding

School of Agriculture and Rural Development

IRDM Faculty Centre,

Ramakrishna Mission Vivekananda Educational and Research Institute,

Narendrapur, Kolkata- 700103.

E-mail: shyamghoshgpb@gmail.com

**ABSTRACT**

Plants ‘where fertilization taken place with the foreign pollen during the reproduction system which promoted or governed by different morphological, physiological, biochemical trait which is under control of the genetic architect of the genome of the species or varieties in cross pollination system. Phenotypic out- look of any genotype is the natural expression of the cumulative pooled effect of all the traits and expressed either monogenic, oligogenic and polygenic in nature. Cross pollinated allogemous genetic composition is heterozygous and homogeneous in nature, which is followed random mating, mutation, migration, selection and genetic drift. In a panmictic population or Mendelian population, genetic architecture by means of genotypic or genic or allelic frequencies remain constant in nature in the population under principles of Hardy –Weinberg law. Gene action may be mainly additive in nature with their allelic combinations and expression. Perponderance, additive gene action in the trait preferable is to improve the trait with the means of selection per se general combining ability (GCA) specially in self-pollinated crops and on the other hand’ non-additive gene action per se specific combining ability (SCA) is helpful in the hybrid breeding for the improvement of the trait of interest mainly in cross pollinated crops. Breeding of cross pollinated crops may be succeeded with heterosis or population improvement breeding techniques due to the presence of heterozygosis in the natural population and heterosis may be achieved with the crossing of homozygous and homogeneous inbred lines which leads to Heterosis due to regaining the heterotic combination.

**Key Words:** Additive, Crops, Dominance, Genetics, Mutation, Random Mating, Selection**.**

**Introduction:**

The genetic organization of cross –pollinated crops is different from that of the self –pollinated crops because of difference in reproductive structure and evolutionary history. Homozygosity is the normal state at each locus for self –pollinated crops. Inbreeding does not lead to loss of vigour and fecundity and some appearance of morbid and lethal forms in ovule cover. On the other hand, although few homozygous the loci may exist in cross-pollinated crops, most of the loci are heterozygous. Natural populations of allogamous crops are heterozygous in nature. Practically, every individual carries deleterious recessive genes shielded by favorable dominant alleles. Upon inbreeding, these deleterious recessive genes become homozygous and manifest adverse effect on their carriers. The extent of adverse effects, upon inbreeding, is a function of number of harmful recessive genes carried by the plant before inbreeding. Because, in most of the cross –pollinated crops homozygous individuals are weaker, heterozygosity must be restored in the end product of any breeding programme. The end product could be homogeneous (as in case of single cross hybrids) or heterogeneous (as in double cross, three way cross hybrids, synthetics and composites) Dabholkar, (2006).

Population genetic effects of cross fertilization:

A Population derived with cross fertilization, consisting of a mixture of plants with a homozygous or heterozygous (complex) genotype. In addition, the effects of a special form of the cross-fertilization *i.e.* panmixies, are considered. It is shown that continued panmixis leads sooner or later to a genotypic composition which is completely determined by the allele frequencies. Allele frequencies do not change in course of the generations, but the haplotypic and genotypic composition may change considerably. The allelic frequency change in a population, which was described by Bos and Caligari (2008) for diploid and autotetraploid crops.

**Allogamy**

Transfer of pollen grains from the anther of one plant to the stigma of another plant is called allogamy or cross pollination. This system is generally leaded the out-breeding. Allogamy leads to heterozygosity in the locus and allelic combination. Such species develop heterozygous balance and exhibit significant inbreeding depression on selfing, which has negative impact on the traits and phenotypic appearance.

These are the several mechanisms lead to cross pollination followed by cross fertilization. The most important one are;

**Dioecy** *i .e*. male and female gamates are produced by different plants.

Asparagus- *Asparagus officinalis* L.

Spinach - *Spinacia olerecea* L.

Papaya - *Carica papaya* L

Date Palm - *Phoenix dactylifera* L.

**Monoecy,** *i.e*. male and female gametes are produced by separate flowers but found on the same plant.

Banana- *Musa species*

Oil Palm- *Elaies guineensis*

Fig- *Ficus carica* L.

Coconut – *Cocos nucifera* L.

Maize- *Zea may* L.

Cucumber - *Cucumber sativus* L.

In musk melon (*Cucumis melo*) most varieties show andromonoecy, *i.e*. the plants produce both staminate flowers and bisexual flowers, whereas others varieties are monoecious.

**Protandry**, *i.e*. the pollen is released before receptiveness of the stigma.

Leek – *Allium porrum* L.

Onion – *Allium cepa* L.

Carrot- *Daucus carrot* L.

Sisal- *Agave sisalana* Perr.

**Protogyny-** *i.e.* the stigma is receptive before the pollen is released.

Tea – *Camellia sinensis* L. O. Kuntze.

Avacado – *Persea americana* Miller

Walnut- *Juglans nigra* L.

Pearl millet - *Pennisetum typhoides*. Rich.

**Self- incompability** is a physiological barrier preventing normal pollen gains fertilizing eggs produces by the same plants.

Cacao- *Theobroma cacao* L.

Citrus- *Citrus spp*.

Tea- *Camellia sinensis* L. O. Kuntze.

Robusta Coffee- *Coffea canephora* Pierre ex Froehner

Sugar beets – *Beta Vulgaris* L.

Cabbage- *Brassica olerecea* spp.

Rye- *Secale cereal* L.

**Flower morphology:**

Fig – *Ficus carica* L.

Primrose- *Primula veris* L.

Common buckwheat – *Fagopyrum esculentum* Moench.

Table-1. List’ Cross Pollinated Crops

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Crops | | Scientific Name | Chromosome (2n) | Chromosome (x) | Genome Size |
| **Cross Pollinated Seed Propagated Crops** | Corn/Maize | *Zea mays* | 20 | 10 | 2.5bbp |
| Pearlmillet | *Pennisetum glaucum* | 14 | 7 | 1.76gbp |
| Niger | *Guizotia abyssinica* | 30 | 15 | 153793bp |
| Radish | [*Raphanus raphanistrum subsp. sativus*](https://en.wikipedia.org/wiki/Raphanus_raphanistrum) | 18 | 9 | 402mbp |
| Cabbage | *Brassica oleracea var. capitata* | 18 | 6 | 659.83mb |
| Sunflower | *Helianthus annuus* | 34 | 17 | 3.5gbbp |
| Sugarbeet | *Beta vulgaris* | 18 | 9 | 714-758mb |
| Castor | *Ricinus communis* | 20 | 10 | 320mb |
| Spinach | *Spinacia oleracea* | 12 | 6 | 989mb |
| Onion | *Allium cepa var. cepa* | 16 | 8 | 16 Gb |
| Garlic | *Allium sativum* | 16 | 8 | 16.24Gb |
| Turnip | *Brasica rapa subsp. Rapa* | 20 | 10 | 518 Mbp |
| Squash | *Fragaria vesca* | 14 | 7 | 500Mb |
| Maskmelon | *Cucumis sativus* | 17 | 7 | 454Mb |
| Watermelon | *Citrullus lanatus* | 22 | 11 | 46.18Gb |
| Cucumber | *Cucumis sativus* | 12 | 6 | 367Mbp |
| Pumpkin | *Cucumis moschata* | 20 | 10 | 271.4Mb |
| Coconut | *Cocos nucifera L.* | 32 | 16 | 2.42Gbp |
| Carrot | *Daucus carota L.* | 18 | 9 | 480Mb |
| Oilpalm | *Elaeis guineensis* | 32 | 16 | 1.8GB |
| MORINGA | *Moringa oleifera* | 28 | 14 | 315Mb |
| **Cross Pollinated Vegetative Propagated** | Sugarcane | *Saccharum officinarum* | 80 | 10 | 10Gb |
| Coffee | *Coffea arabica L* | 44 | 11 | 1300Mb |
| Cocoa | *Theobroma cacao* | 20 | 10 | 5.624Mb |
| Tea | *Camelia sinensis* | 30 | 15 | 3.8-4.0 Gb |
| Apple | *Malus x domestica* | 34 | 17 | 750Mb |
| Grapes | *Vitis vinifera* | 38 | 19 | 500mb |
| Almond | *Prunus dulcis* | 16 | 8 | 240 Mb |
| Strawberries’ | *Fragaria virginiana* | 56 | 7 | 708-720 Mb |
| Pine Apple | *Ananas comosus* | 28 | 7 | 526 Mb |
| Banana | *Musa sp.* | 33 | 11 | 523 Mb |
| Cashew | *Anacardium occidentale* | 42 | 21 | 488Mb |
| Cassava | *Manihot esculenta* | 36 | 18 | 770Mb |
| Rubber | *Hevea brasiliensis* | 36 | 18 | 969.72 Mb |
| **Often Cross Pollinated** | Sorghum/Bajra | *Sorghum bicolor* | 20 | 10 | 700Mb |
| Red Gram, Arhar | *Cajanus cajan* | 22 | 11 | 833.07 Mb |
| Soyabean | *Glycine max* | 40 | 20 | 1.1-1.15 Gb |
| Cowpea | *Vigna unguiculata* | 22 | 11 | 641 Mb |
| Groundnut | *Arachis hypogaea* | 40 | 10 | 2.7 Gb |
| Indian Mustard | *B.juncea* | 36 | 18 | 153483bp |
| Saflower | *Carthamus tinctorius* | 24 | 12 | 1.p7 Gb |
| Cotton | *G. hirsutum* | 26 | 13 | 2.5Gb |

Source: www.ncbi.nlm.nih.gov

Effect with regards to the haplotypic and genotypic composition of a population developed by means of panmixis is called panmictic population.

**Genetic Consequence of Cross Pollination**: Cross-pollination preserves and promotes heterozygosity in a population. The Cross-pollinated species are highly heterozygous and show mild to severe inbreeding depression and a considerable amount of heterosis. The breeding methods in such species aim at improving the crop species without reducing heterozygosity to an appreciable degree. Usually, hybrid or synthetic varieties are the aim of breeder wherever the seed production of such varieties is economically feasible (Mukharjee, 2018).

**Often Cross-Pollinated Species:**

Frequent, cross-pollination creates and maintenance of tremendous, amount of genetic variability, chiefly because of high amount, heterozygosity in population, Reddy (2018).

1. Each variety is a highly random pollinated population usually maintained at genetic equilibrium in an absence of selection.
2. An immense amount of genetic variability floats in crops at both intra and inter population level due to frequent random gene flow among genotypes.
3. Role of dominance is potential to release of recessive alleles on selfing.
4. A high degree of panmixia (random population) leads to rapid non –discrimination of population characteristics.
5. Reduction of genetic correlations among progenies.
6. Cross pollinated species show severe to high inbreeding depression and high Heterosis (George, 2012)
7. Hybridization between two inbreeds usually leads to recovery of vigour lost by inbreeding.

In nature, plants exist according to the law of nature and their foot print exists through reproduction. It is the part, a life cycle and plant produces itself by means’ seeds or propagules which are the product of pollination and fertilization process or vegetative reproduction and remains same as the unique by means of unique genetic program already existed in the genome or genotype of the plants. And some time generate some variance due to artificial selection, mutation or migration.

Cross-pollinated crops are highly heterotic due to free inter mating among their plants and inclination founds heterozygous balance. A random mating population means each individual of the population has equal opportunity of mating with any other individuals of that population. The random mating population is also known as "Mendalian population" or "panmictic population". A panmictic population may be having a gene pool consisting of all the gametes produced by the population. Thus the gene pool may be defined as the sum total of all the genes present in a population.

During pollination in which the pollen from [anther](https://www.biologyonline.com/dictionary/anther) of a [flower](https://www.biologyonline.com/dictionary/flower) is transferred to the [stigma](https://www.biologyonline.com/dictionary/stigma) of a flower of another plant, the system is called cross pollination. In flowering plants, [fertilization](https://www.biologyonline.com/dictionary/fertilization) occurs through pollination, *i.e*. the transfer of pollen from the [anther](https://www.biologyonline.com/dictionary/anther) to the [stigma](https://www.biologyonline.com/dictionary/stigma) of a plant. The pollen contains the male gametes (sperm cells) that are transferred into the female gametophyte (*i.e*. ovules of flowering plants and the cones of coniferous plants) via the pollen tube. In regard to pollination, the ovum may be fertilized either by cross-pollination or by self-pollination. Cross-pollination refers to the mode of fertilization wherein the sperm from the pollen (from the anther) of a plant is transferred to the stigma of the flower of another plant. In cross-pollination, new genotypes are produced more than in self-pollination. It helps to augment genetic diversity. It also reduces inbreeding depression, *i.e.* when the biological fitness in a given population is reduced as a result of inbreeding. Thus, it helps reduce the probability of a plant species producing offspring subject to disease or genetic disadvantages due to unfavorable recessive alleles. The more diverse the genes or [allele](https://www.biologyonline.com/dictionary/allele)s in the gene pool, the better they are protected against extinction and more adaptable to the various climatic situation.

**Theoretical and Biological fundamentals in Plant Breeding:**

In plant breeding, quantitative genetics help breeder to interpret the data and draw the productive conclusion from the observations and in the quantitative productive decision from the work done, Simmonds (1984), Baker (1984), suggested that quantitative genetics principles were key to maximizing the efficiency of plant breeding programme by adding a priori comparisons between selection schemes and guiding decisions on allocation of testing resources on population sizes needed to maintain the long term selection gains. On the other hand, Dudley (1997) suggested quantitative genetic theory, had immediate practical uses in choosing appropriate parent for breeding crosses for weighting among line and within –line selection during in-breeding, for designing efficient recurrent selection schemes, and for appropriately weighting DNA marker information in marker assisted selection programme.

Theoretically, earlier non expert people are expert in practical plant breeding historically, (Allard 1960). Some ways in which quantitative genetic and a population genetic theory has been useful in plant breeding include:

1. The estimation of the relative importance of genotypic (G), G x E , and environmental (E) effect on phenotype(P);
2. The estimation of heritability (h2) and prediction of gain from selection;
3. The estimation of genetic co-relations and co-related changes under selection;
4. The design of efficient evaluation and selection schemes based on optimal allocation of resources;
5. Understand changes in partitioning of genetics variance among and within lines at different levels of inbreeding; and
6. Understanding the effects of population size and mating system on inbreeding and genetic drift; and
7. Understanding of the effect of different methods of population maintenance on genetic variability in the germplasm.

Table 2. General intra –population improvement methods,

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Selection Method | Generations per cycle | Progenies | | Expected Progress\* |
| Evaluated | Used for recombination |
|  | Intra population selection schemes | | |  |
| Mass Selection | 1 | Individual plants | Individual Plants | (k(1/2)ó2/A)/ ópm |
| Half –sib progeny test, | 3 | Half- sibs | S1’s | (k(1/2)ó2/A)/ óphs |
| Half sib test, | 2 | Half -sibs | Half sibs | (k(1/4)ó2/A)/ óphs |
| Half sib test, | 2 | Full- sibs | Full sibs | (k(1/2)ó2/A)/ ópfs |
| S1 progeny test | 3 | S1’s | S1’s | (k(ó2A+C))/ ó2ps |

\*Based on Empig et al. (1972) and Sprague (1966).

k = Selection differential in standard units

ó2A = Additive genetics variance

ó2pm , ó2phs, ó2pfs, ó2ps are the phenotypic standard deviations for mass selection , half-sib, full-sib and self- progenies respectively.

**Hardy Weinberg Law**:

The Hardy Weinberg law may be defined as the gene and genotypic frequencies in a Mandelian population remain constant generation in a random mating population after generation if there is no selection, mutation, migration or random drift persisted.

The law was suggested by Hardy in 1908 in England and Weingberg , in 1909 in Germany independently.

Table 3. Genotypic and Allelic Frequency in a random mating population for single locus

|  |  |  |  |
| --- | --- | --- | --- |
| Random Mating Population/Mendelian Population | | | |
| Genotype | AA | Aa | aa |
| Frequency | P2 | 2pq | q2 |

p2 + 2pq + q2 = 1

(p + q )2 = 1

p+ q = 1

Where, A= allele, a= allele

p and q is the frequency of the allele, A and a.

Table 4. Consequences of random mating of genotypes in a Mendelian population

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Mating | Frequency of Mating | Frequency of progeny from the mating | | |
| AA | Aa | aa |
| AA x AA | p2 + p2= p4 | p4 |  |  |
| AA x Aa | 2(p2 x 2pq) = 4p3q | 2p3q | 2p3q |  |
| AA x aa | 2(p2 x p2) = 2p2q2 |  | 2p2q2 |  |
| Aa x Aa | (2pq x 2pq)= 4p2q2 | p2q2 | 2p2q2 | p2q2 |
| Aa x aa | 2(2pq x q2)= 4pq3 |  | 2pq3 | 2pq3 |
| aa x aa | q2 x q2 = q4 |  |  | q4 |

The frequency of the progeny from a mating is deduced by a simple logic.

The frequency of progeny with AA genotype would be,

= p4 + 2p3q +p2q2  ( p2 is taken as common, since p2 + 2pq +q2 = 1)

= p2(p2 +2pq +q2)

= p2

Similarly, the frequency of aa progeny would be,

= p2q2 + 2pq3 + q4

= q2(p2+2pq+q2) (q2 is taken as common, since p2 + 2pq +q2 = 1)

=q2

And the frequency of Aa progeny would be,

= 2p3q + 2p2q2 + 2pq3

= 2p3q + 4p2q2 + 2pq3

= 2pq(p2+ 2pq+q2) (2pq is taken as common, since p2 + 2pq+ q2= 1)

= 2pq

**Factors disturbing equilibrium in populations:**

Migration, mutation, selection and random drift are called as evolutionary force due to by which create the change in allelic or genic frequency in a population.

**Migration:**

Migration may be defined as a movement of individual from one population to another population and participate in the reproduction with the population. Therefore, migration changes the genic frequency with allelic contribution in the population and may change the existing alleles.

Consequences:

1. The migration change directly the population variability and magnitude depend upon the number of individuals migrated in an original population.
2. Migration may be represented as inter-varietal crossing, poly-crossing etc.

**Mutation:**

Mutation may be defined as the sudden and heritable change of a character or trait of an organism or individual and which is due to the structural change of the concerned gene.

Consequences:

1. It is the ultimate variation source present in the biological system.
2. Mutation may be due to new allele not present in the population or my change, the frequencies of the existing alleles.
3. Mutation rate is generally around 10-6 .
4. Mutation is very much useful in the crop improvement program.
5. Many varieties have been developed with mutagenic treatment.
6. Most of the mutation is lethal.

**Random Drift:**

Random drift or genetic drift may be defined as a random change in gene frequency due to sampling error.

Consequences:

1. Random drift is more importance in small population because sampling error is more effective in the smaller population then larger population.
2. Ultimate result of random drift is that frequency of the allele of a gene becomes zero and that of the other allele become one.
3. Allelic frequency one, is the fixed in the population.
4. If allelic frequency becomes one then the population becomes homozygous.
5. Phenotypic dissortative mating may be use in this case.

**Inbreeding:**

Mating between two individuals of their common ancestry is call inbreeding.

Consequences:

1. Inbreeding reduces the heterozygosity or heterozygous combination and increase the homozygosis or homozygous combinations.
2. In diocious and monocious species where selfing is restricted, reducing the heterozygosity *i.e.* 1/(2N-1) per generation.
3. Rate of homozygosity is equal to or 1/2N , where N is the number of plant in a population per generation in monoecious or hermaphrodite species.

**Selection:**

Selection may be defined as choosing or giving a chance to participate in mating with the desirable quality or trait of an individual by choice to produce better population over the population with better genetic makeup and performance.

1. In selected random parting population allelic combination would be either AA or aa.
2. Selected random mating population’s selection differential would be (=s) >1.
3. Fitness of a genotype may be defined as its reproduction rate in-relation to other genotype.
4. Selection only changes the frequency, rather than eliminate the allele.
5. Selection is highly effective in a random mating population to increase or decrease the frequency of allele but unable to either fix or eliminate the alleles.
6. On selection tentatively population size would be at least 1000 and selection to be done 5% means at least 50 plants/ individuals this is called permissible selection intensity.
7. Progress under selection of quantitative trait depends on presence, non-additive gene action, high heritability and selection intensity.

The effect of selection on quantitative characters can be measured in terms of change in the genetic properties of population, such as means, variances and co-variances. In case of selection, the standard deviation (SD) or standard error (SE) is used as selection index. In maintenance breeding, selection of plants within the range of mean +- SD is normally used for nuclear seed production, Reddy (2016).

**Selection Intensity**: Selection intensity may be defined as the number of genotypes selected for a base population i.e. 5 plants selected out of 100 than 5 is the selection intensity and it may be presented as percent (%) e.g. 5%.

**Selection Differential**: Selection differential may be defined as the difference from the selected percentage mean over the population mean performance of a trait (s).

µ0= mean of initial population

µ1= mean of individuals selected as parents

Therefore, selection differentials (S) = µ0- µ1.

The selection differential (S) magnitude is depended upon the variability exited in the initial or base population over the variability of selected parents.

**Selection Response**: Selection response may be defined as the phenotypic mean performance of the selected percentages progeny’s phenotypic mean over the base population’s phenotypic mean performance.

µ0= mean of initial population

µ1= mean of individuals selected as parents

µ2= mean of offspring of selected parents.

µ2 - µ0= Selection Response(R).

**Heritability**: In general, heritability may be defined as the proportion of total variability that is due to genetic causes, or the relation of genotypic variance to the total variance. It is a good index of the transmission of characters from the parent to their offspring, Falconer, (1960).

**Types of Heritability**: Depending upon the components of variance used as numerator in the calculation, heritability is two type *viz.* broad sense heritability and real sense heritability or narrow sense heritability (Lush, 1940).

**Broad Sense heritability**: it is the ratio of genotypic variance to total or phenotypic variance.

H= . ó2g/ó2p  or Genotypic variance / Phenotypic variance.

**Real sense or narrow sense heritability:** It is the ratio of additive or fixable genetic variance over the phenotypic variance.

H= . ó2A/ó2P  or Additive genetic variance / Phenotypic variance.

Heritability plays important role in the selection highly heritable or fixable or additive variance based elite genotype from the segregating population in the crop improvement programme.

According to Johanson *et al* . (1955a), heritability value is categorized as follows:

Low <30 %, Moderate = 30-60% and High > 60%.

**Co-Heritability**: Analysis of covariance permits an estimation of co-heritability for the related traits.

Co-heritability between characters x and y = ógxy/ ópxy \* 100.

Where, ógxy = Genotypic covariance

ópxy = Phenotypic covariance

On the other hand, heritability may be defined as the ratio of additive genetic variance to phenotypic variance.

h2= VA/VP

h2 is stand for the heritability, VA = additive variance andVP = phenotypic variance.

An equivalent meaning of the heritability is the regression of breeding value on phenotypic value.

h2= bAP = VA/PA

Covariance of cov.AP = VA

P= A + R

Where, P= Phenotypic value, A= Additive Value and R= Environmental, Dominance and Interaction value.

The correlation between a breeding value and a phenotypic value, rAP, is equal to the square root of the heritability.

rAP =  bAP . óP/óA = h2 1/h= h

Breeding value, a phenotype on phenotypic value may be presented as its phenotypic value and the heritability.

On the other hand, therefore, A (expected) = h2P = Breeding Value.

**Genetic Advance**: Genetic advance may be defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population *i.e.* an original population. The expected genetic gain or advance under selection is estimated by following the method suggested by Johanson *et al.* (1955a).

Genetic Advance (GA) = . ó2g/ó2p  x K or . = ó2g/ó2p  x óp x K

Where, ó2g = Genotypic variance

ó2p = Phenotypic variance

K = Phenotypic standard deviation

óp = Selection differential at a particular level of selection intensity, which takes into account the mean phenotypic value of the selected families.

The range of genetic advances as per mean as suggested by Keerthana *et al*. (2019).

Low < 10%, Moderate = 10-20% , High= > 20.

Heritability and genetic advance are important selection parameters. Heritability along with genetic advance is more useful in predicting the genetic gain under selection, Johanson *et al,* (1955a).

1. High heritability with a high genetic advance indicates the preponderance of additive gene action.
2. High heritability with a low genetic advance indicates the non-additive gene action.
3. Low heritability with a high genetic advance indicates the additive gene action.
4. Low heritability with a low genetic advance indicates that the trait is a trait is highly influence by environmental factor and selection would be inefficient.

**Gene action and breeding methods in the cross pollinated crops:**

1. **Non –Additive Gene Action**: In the presence of non-additive gene action, heterosis breeding and population improvement by recurrent selection to be carried out for the specific combining ability (SCA) per se combination and parentage for the trait.
2. **Additive and Non- Additive**: In the presence of both type of gene action population improvement by reciprocal recurrent selection to be carried out for the trait and genotypes.

**The System of Mating**: The breeding methods involved to change the genetic composition of a population are mainly a selection and mating system.

**Selection** *i.e.* identify and reselecting the individual which to would give better performance in a future generation prospective purpose congenial to a growing environment.

**Mating System** *i.e*. pollination and nature of fertilization is to produce the breeding population or develop new variety.

**Matting may be classified as:**

**Random Mating:** *i.e*. each female gamete is equally likely to unite with gamete, and the rate of reproduction of each genotype is equalizing when there is no artificial selection.

Consequences;

a) Gene frequencies remain constant,

b) Variance for the character remains constant, and

c) The correlation between relatives and prepotency does not change.

1. However, in breeding populations some form of selection is practiced; such as a mating system is known as random mating with selection. Further, the mating is usually not completely random since differences in flowering time, a position of plants in the field, prevalent wind’ direction, etc. limit the randomness of mating.
2. Random mating with selection changes the mean of character, and increases the frequency of allele for which selection is induced.
3. It would tend to increase the variance when a selection is in favour of a rare allele, but would tend to reduce it when the character is highly heritable, and is governed by one or few genes, whereas for the polygenic trait with low heritability variance also changes at lower the rate on selective mating.
4. In random mating with small population lead to inbreeding and genetic drift increasing the homozygosity. Random mating is useful in plant breeding in several ways, *e.g*. progeny testing, production and maintenance of synthetic and composite varieties, production of polycross progeny, etc.

**Genetic Assortative Matting:**

Genetic assertive mating is commonly known as inbreeding when matting occurs between more closely related ancestries than in random mating.

**Consequences:**

1. Increases homozygosity and reduces heterozygosity.
2. Due to self-fertilization characters becomes toward fixed.
3. Due to rapid inbreeding, breeding population become large and need selection to maintain the population on better handling.
4. Genetic variability increased rapidly in the population but in case of an interbreeding ultimate variability reduces to zero.
5. Under selection, genetic variability reduced rapidly in the population and when a line selected genetic variability is very small or zero.
6. The prepotency of individuals increases under inbreeding.
7. Prepotency is the property of an individual to produce progeny which is similar to each other and parent.
8. Generally, prepotency is affected by homozygosity, dominance, epistasis and linkage.
9. An individual completely homozygous for all the dominant alleles would be the most prepotent.
10. Genetic assertive mating is used to develop and maintenance of both partial and complete inbreeds.

**Genetic Disseortive matting**: *i.e*. when less closely related ancestries are mated is called as genetic dissortive mating.

**Consequences:**

1. Non relatives are crossed.
2. Inter varietal or inter species cross are crossed.
3. These individuals belong to different population.
4. It’s similar to migrated population.
5. In this mating system homozygosity is reduced and heterozygosity is increased.

**Phenotypic assortative matting:**

Mating between individuals those are phenotypically more similar than would be expected under random mating is called phenotypic assortative mating.

**Consequences:**

1. Divide the population in two extreme phenotypes.
2. Increase homozygosity.
3. Genetic variability also increases by both extreme phenotypic population developments.
4. The prepotency increases due to development of increase in homozygosity.
5. Dominance and non additive gene actions reduce the effect of phenotypic assortative mating.
6. Mating system is used in the isolation of extreme phenotypes.

**Phenotypic dissortative matting**:

Mating between phenotypically dissimilar individuals belong to the same population is refered to as phenotypic dissortative mating.

**Consequences:**

1. It is useful in the maintenance or to increase the heterozygosity.
2. Population variance may decrease due to the production of intermediate phenotypes.
3. It reduces the prepotency due to increase in heterozygosity.
4. It is useful on making population stable.
5. Progeny row, in such mating would be more superior to parentages.
6. It may be used on the maintenance of the small population variability due to inbreeding reduction.

**Conclusion:**

Genetic composition of cross pollinated crops give us an immense exposure to understand the genetics inside of the cross pollinated crops and genetic consequences insight of the out-breeding and maintaining the genotypic genic and allelic frequencies under heterotic out crossing in a population generation after generation. Cross pollinated crops are heterozygous and homogeneous in nature. Cross pollinated crops follows the role of nature, naturally by means of out crossing. In general, variability is more exited in the cross pollinated crops due to natural out crossing or random mating in the population. Breeder’s point of view, crop improvement could be carried out with hybridization and population improvement breeding techniques in the cross pollinated species as per their genetic architecture and nature of genetic transmission and expression.

**References:**

1. Allard, R. W. 1960. Principles of Plant Breeding. Wiley, New York.
2. Bos, I and Caligari, P. 2010. Selection methods in plant breeding 2nd edition, p. 7-32.
3. Dabholkar, A. R., 2006. General plant Breeding, Concept Publishing Company, New Delhi.
4. Dudley, J. D.1997. Quantitative genetics and plant breeding. Advances in agronomy. 59:1-23.
5. Empig, L.T.,; Gardner, C. O. and Compton, W. A. 1972. Theoretical gains for different population improvement procedures. MP 26 (Revised) University of Nebraska, College of Agriculture, The Agricultural Experimentation Station.
6. Falconer, D. S and Mackey, T. F. C. 1960. Introduction to quantitative genetics. Pearson Education Ltd.
7. George, A. 2012. Principles of Plant Genetics and Breeding. Wiley. USA.
8. Hallod, J. B, 2006. USDA ARS Plant Science Research Unit, North Carolina State University. Plant Breeding: The Arnel R. Halauer International Symposium. Edited Lamkey , K. R and Lee, Michael, Plant Breeding. Blackwell Publishing Lqtd.. P-127.
9. Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of phenotypic and genotypic correlation in soybean and their implication in selection. Agronomic Journal, 47: 477- 482.
10. Keerthana, K.., Chitra, S., Subramanian, A., Nithila, S., Elangovan, M., 2019. Studies on genetic variability un finger millets L. genotypes under sodic conditions, Electronic Journal of Plant Breeding, 10(2), 566-569.
11. Lush, J. L. 1940. Intrusive collection of regression of offspring on dams asa method of estimating heritability of characters. Proc. Am. Soc. Anim. Prod. 33: 293-301.
12. Mukherjee, B. K. 2018. Concept and methods: cross –pollinated crops. Chopra, V. L. Plant Breeding theory and practice. New India Publishing Agency, New Delhi.
13. Nandarajan, N. Manivannan, N. and Gunasekaran, M. 2016.Quantative genetics and biometrical techniques in plant breeding.Kalyani Publishers, Ludhiana, India.
14. Reddy, V. R. P. 2018. Key Note on Genetics and Plant Breeding. Daya Publishing House, New Delhi.
15. Simmonds, N. W. 1984. Gene Manipulation and Plant Breeding. 637-654. Proceeding of the 16th Stalder Genetics Symposium. University of Missouri Agricultural Experiment Station, Columbia.
16. Singh, B. D, 2001. Plant Breeding: Principles and Methods. Kalyani Publishers, Ludhiyana.
17. Spague, G. F. 1966. Quantitative Genetics in Plant Breeding. In Plant Breeding, Ed. K. J. Frey, Iowa State University Press, Ames, Iowa, USA, pp 315-354.