



Review Article

FUNDAMENTAL OF GENETIC COMPOSITION OF CROSS-POLLINATED CROPS

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Received: February 14, 2023; Revised: May 15, 2023; Accepted: May 18, 2023; Published: May 30, 2023

Abstract: Plants where fertilization takes place with the foreign pollen during the reproduction system which is promoted or governed by different morphological, physiological, biochemical traits which are under control of the genetic architecture of the genome of the species or varieties in a cross-pollination system. Phenotypic out-look of any genotype is the natural expression of the cumulative pooled effect of all the traits and is expressed either monogenic, oligogenic, and polygenic in nature. Cross-pollinated genetic composition is heterozygous and homogeneous in nature, which is followed by 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. Preponderance, additive gene action in the trait is preferable 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, cross-pollinated crops may be succeeded with heterosis or population improvement breeding techniques due to the presence of heterozygosity in the natural population and the heterosis may be achieved with the crossing of homozygous and homogeneous inbred lines which leads to the heterosis due to regaining the heterotic combination.

Keywords: Additive, Crops, Dominance, Genetics, Mutation, Random Mating, Selection

Citation: Ghosh S.C. and Dasgupta T. (2023) Fundamental of Genetic Composition of Cross-Pollinated Crops. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 15, Issue 5, pp.- 12363-12368.

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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 loci 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 the homozygous and manifest adverse effect on their carriers. The extent of adverse effects, upon inbreeding, is a function of a 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 ways cross hybrids, synthetics and composites [1].

Population and genetic effects of cross fertilization

A population derived with cross fertilization, consisting of a mixture of plants with homozygous or heterozygous genotypes. In addition, the effects of a special form, ispanmixis due to cross-fertilization. It has been found that continued panmixis leads to a genotypic composition which is fully determined by the allele frequencies available in a population. Allele frequencies do not change in course of the generations, whereas the haplotypic and genotypic composition may change considerably. The allelic frequency may change in a population, which was described for diploid and autotetraploid crops species [2,3].

Allogamy: The system in which pollen grains are transferred from one plant to another plant's stigma is called pollination and fusion of germinated pollen and ovule is called fertilization and entire the events is called allogamy. This type of plants is called allogamous plants. This system is generally leads 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 several mechanisms lead to cross pollination followed by cross fertilization. These are as followed;

Dioecy: Condition where, male and female gametes are produced by different plants.

Asparagus- *Asparagus officinalis* L

Spinach - *Spinacia oleracea* L

Papaya - *Carica papaya* L

Date Palm - *Phoenix dactylifera* L.

Monoecy: Condition here, male and female gametes are produced by separate flowers but found on the same plant.

Banana- *Musa species*,

Oil Palm- *Elaeis guineensis*

Fig- *Ficus carica* L

Coconut – *Cocos nucifera* L

Maize- *Zea mays* L

Cucumber - *Cucumis sativus* L.

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

Table-1 List' Cross Pollinated Crops

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

Table-2 General intra-population improvement methods [8,9]

Selection Method	Generations per cycle	Progenies		Expected Progress [8,9]*
		Evaluated	Used for recombination	
Intra population selection scheme				
Mass Selection,	1	Individual plant	Individual Plant	$(k(1/2)\delta^2/A)/\delta pm$
Half –sib progeny test,	3	Half- sibs	S _i 's	$(k(1/2)\delta^2/A)/\delta ps$
Half sib test,	2	Half -sibs	Half sibs	$(k(1/4)\delta^2/A)/\delta ps$
Half sib test,	2	Full- sibs	Full sibs	$(k(1/2)\delta^2/A)/\delta ps$
S ₁ progeny test	3	S _i 's	S _i 's	$(k(\delta^2A+C))/\delta^{2ps}$

k = Selection differential in standard units, δ^2A = Additive genetics variance

δ^2pm , δ^2ps , δ^2ps , δ^2ps are the phenotypic standard deviations (PSD) for mass selection, half-sib, full-sib and self-progenies respectively.

Protandry: Condition here, the pollen is released before receptiveness of the stigma.

Leek – *Allium porrum* L

Onion – *Allium cepa* L

Carrot- *Daucus carota* L

Sisal- *Agave sisalana* Perr.

Cacao- *Theobroma cacao* L

Citrus- Citrus species

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

Robusta Coffee- *Coffea canephora* Pierre ex Froehner

Sugar beets – *Beta vulgaris* L.

Cabbage- *Brassica oleracea* species

Rye- *Secale cereal* L.

Protogyny: Condition here, the stigma is receptive before the pollen is released.

Tea – *Camellia sinensis* L. O. Kuntze

Avocado – *Persea americana* Miller

Walnut- *Juglans nigra* L

Pearl millet -*Pennisetum typhoides*.

Flower morphology: Condition here, due to organization of the floral morphology lead to cross pollination and fertilization.

Fig – *Ficus carica* L.

Primrose- *Primula veris* L.

Common buckwheat – *Fagopyrum esculentum* Moench.

Effect with regards to the haploidgenotypic composition of a population developed by means of panmixis called panmictic population.

Self- incompatibility: Condition here, is a physiological barrier preventing normal pollen gains fertilizing eggs produces by the same plants.

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. Usually, hybrid or synthetic varieties are the aim of breeder wherever the seed production of such varieties is economically feasible [4].

Often Cross-Pollinated Species

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

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 [6].
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 a 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 intermating among their plant population and inclination towards heterozygous balance. A random mating population means each individual of the population has equal opportunity, mating with any other individuals of that population. The random mating population is also known as "Mendelian population" or "panmictic population". The panmictic population may be having a gene pool consisting of all the gametes produced by the population whereas; the gene pool may be defined as the sum total of all the genes present in a population [5].

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 was suggested that quantitative genetics principles play key role on maximizing the efficiency of plant breeding programme by adding a priori comparisons between selection schemes and guiding decisions on allocation of testing resources here, population sizes need to maintain during long term selection gains. On the other hand, was 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, on designing efficient recurrent selection schemes, and for appropriately weighting DNA marker information in a marker assisted selection programme [18].

Theoretically, earlier non expert people are expert in practical plant breeding historically [7]. Naturally, the quantitative genetic and a population genetic theory' has been useful in plant breeding include as:

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 (h^2) and a prediction of genetic 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 germplasms.

Hardy Weinberg Law

The Hardy Weinberg law may be defined as the gene and genotypic frequencies in a Mendelian population remain constant, in a generation of a random mating population after generation; does not act the selection, mutation, migration or random drift. The law was suggested individually by Hardy in 1908 in England and Weinberg in 1909 in Germany.

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

Random Mating Population/Mendelian Population			
Genotype	AA	Aa	aa
Frequency	P^2	$2pq$	q^2

$$p^2 + 2pq + q^2 = 1$$

$$(p + q)^2 = 1$$

$$p + q = 1$$

Where, A= allele, a= allele

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

Table-4 Mendelian population in Random mating gene and allele frequencies

Mating	Frequency of Mating	Frequency of progeny from the mating		
		AA	Aa	aa
AA x AA	$p^2 + p^2 = p^4$	p^4		
AA x Aa	$2(p^2 \times 2pq) = 4p^3q$	$2p^3q$	$2p^3q$	
AA x aa	$2(p^2 \times q^2) = 2p^2q^2$		$2p^2q^2$	
Aa x Aa	$(2pq \times 2pq) = 4p^2q^2$	p^2q^2	$2p^2q^2$	p^2q^2
Aa x aa	$2(2pq \times q^2) = 4pq^3$		$2pq^3$	$2pq^3$
aa x aa	$q^2 \times q^2 = q^4$			q^4

The frequency of progeny with AA genotype would be,

$$= p^4 + 2p^3q + p^2q^2 \quad (p^2 \text{ is taken as common, since } p^2 + 2pq + q^2 = 1)$$

$$= p^2(p^2 + 2pq + q^2)$$

$$= p^2$$

Similarly, the frequency of aa progeny would be,

$$= p^2q^2 + 2pq^3 + q^4$$

$$= q^2(p^2 + 2pq + q^2) \quad (q^2 \text{ is taken as common, since } p^2 + 2pq + q^2 = 1)$$

$$= q^2$$

And the frequency of Aa progeny would be,

$$= 2p^3q + 2p^2q^2 + 2pq^3$$

$$= 2p^3q + 4p^2q^2 + 2pq^3$$

$$= 2pq(p^2 + 2pq + q^2) \quad (2pq \text{ is taken as common, since } p^2 + 2pq + q^2 = 1)$$

$$= 2pq$$

Factors disturbing equilibrium in populations

Migration, mutation, selection and random drift are called as the evolutionary force due to by which create the change in allele and gene or both frequencies in a population.

Migration

Migration may be defined as a movement of individual from one population to another population and participate in the reproduction of 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 an 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 in the population or may change, the existing alleles the frequencies.

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 or selection pressure.

Consequences

1. Random drift is more importance in small population because sampling error.
2. Ultimate result of random drift is a frequency of the allele of a gene becomes zero and 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 assortative 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 $1/2N$, where N is the number of plant.

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. Genotypic fitness is a reproduction rate of a 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.
 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 a 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 \pm SD is normally used for nuclear seed production [10].

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).

μ_0 = mean of initial population

μ_1 = mean of individuals selected as parents

Therefore, selection differentials (S) = $\mu_0 - \mu_1$.

The selection differential (S) magnitude is depended upon the variability existed 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 (%) phenotypic mean of a progeny over the base population's phenotypic mean performance.

μ_0 = mean of initial population

μ_1 = mean of individuals selected as parents

μ_2 = mean of offspring of selected parents.

$\mu_2 - \mu_0$ = Selection Response(R).

Heritability: In general, heritability may be defined as genotypic variance over the phenotypic variance. It is a good index of the transmission of characters from the parent to their offspring [11].

Types of heritability: Depending upon the components of variance used as numerator in the calculation, heritability may be grouped in two categories viz. broad sense heritability and real sense heritability or narrow sense heritability [12].

Broad sense heritability: It is the ratio of genotypic variance to total phenotypic variance.

$H = \sigma^2_g / \sigma^2_p$ 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.

$H = \sigma^2_A / \sigma^2_P$ or Additive genetic variance / Phenotypic variance.

Heritability plays an 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 (9), heritability value is categorized as follows:

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

Co-heritability: Analysis of covariance may be defined as an estimation of co-heritability for related traits.

Co-heritability of between two characters like for, x and y = $\sigma_{gxy} / \sigma_{pxy} \times 100$.

Where, σ_{gxy} = Genotypic covariance

σ_{pxy} = Phenotypic covariance

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

$h^2 = VA/VP$

h^2 is stand for the heritability, VA = additive variance and VP = phenotypic variance.

The heritability may be presented as the regression of breeding value on phenotypic value.

$h^2 = b_{AP} = VA/PA$

Covariance of cov.AP = VA

$P = A + R$

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

Correlation between breeding value and a phenotypic value, r_{AP} , is equal to the square root of the heritability.

$r_{AP} = b_{AP} \cdot \sigma_P / \sigma_A = h^2 \cdot 1/h = h$

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

On the other hand, therefore, A (predicted) = $h^2 P$ = Breeding Value.

Genetic Advance: Genetic advance may be defined as the difference between the mean genotypic value of the selected lines and genotypic value of a parental population or an original population. Predicted, genetic gain or advance under selection according to [13] as followed;

Genetic Advance (GA) = $\sigma^2_g / \sigma^2_p \times K$ or $\sigma^2_g / \sigma^2_p \times \sigma_{px} K$

Where, σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

K = Phenotypic standard deviation

σ_p = Selection differential takes into account the mean phenotypic value of the selected families.

The range of genetic advance as suggested [14] as followed;

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

Heritability and the genetic advance are important selection parameters.

Heritability along with the genetic advance is more useful in predicting the genetic gain under selection.

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

Gene action and breeding methods

1. 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: Both type of gene action, population improvement by reciprocal recurrent selection to be carried out for the trait and genotypes. In an study on maize reported that Additive and non-additive gene effects were involved in the inheritance of GY and other traits under low-N and DS conditions. However, the additive gene effect for GY was twice as large as non-additive gene effect [15]. On the other hand a comparative study depicted each strategy was compared across three levels of half-sib family mean dominance and over dominance model). Among and within half-sib selection performed better than among half-sib selection for all scenarios [16].

The System of Mating: Alteration of the genetic composition of a population may be carried out with the help, selection and mating system.

Selection: Identify and reselecting the individual which to would give better performance in a future generation prospective purpose congenial to a growing environment.

Mating System: Pollination and nature of fertilization is to produce the breeding population or develop new variety.

Classification of Matting

Random Mating

It may be defined as each female gamete is equally likely to unite with gamete, and the rate of reproduction of each genotype is equalized without artificial selection.

Consequences;

- a) Gene frequencies remain fix.
 - b) Variance for the character remains constant, and
 - c) The correlation between relatives and prepotency does not alter.
- 1.However, in breeding populations some form of selection is practiced; such as a mating system is known as random mating with the selection.
 - 2.Practically in field, random mating is influenced with time of flowering, sequence of flowering, wind direction etc.
 - 3.Due to selection in random mating, frequencies of allele increased those alleles are selected during the selection.
 - 4.Influence on variance, during selection in a random mating population affects by the number of genes control the trait and their nature of heritability.
 - 5.In random mating with small population lead to inbreeding and genetic drift increasing the homozygosity.

Genetic Assortative Matting

This is commonly known as inbreeding, when matting occurs between more closely related ancestries than in random mating [17-21].

Consequences:

- 1.Increases homozygosity and reduces heterozygosity.
- 2.Due to self-fertilization characters becomes towards fix.
- 3.Due to rapid inbreeding, breeding population become large and need selection to maintain the population for better handling.
- 4.Genetic variability increased rapidly in the population but in case of an

interbreeding ultimate variability reduces.

- 5.In selection, genetic variability reduces rapidly in a population and when a line selected genetic variability is very small or zero.
- 6.Inbreeding leads prepotency to increase.
- 7.Prepotency is the property of an individual to produce progeny, similar to each other and parent.
- 8.Normally, prepotency is affected with homozygosity, dominance, epistasis and linkage.
- 9.An individual would be most propotent, when completely homozygous for all the dominant alleles existed.
10. The genetic assertive mating is used to develop and maintenance of both partial and complete inbreeds.

Genetic Dissoortive matting

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 migrant population.
- 5.In this mating system homozygosity is reduced and heterozygosity is increased.

Phenotypic assortative matting

Mating between phenotypically more similar individuals 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 a development, an increase in homozygosity.
- 5.Dominance and non additive gene actions reduce the effect of phenotypic assortative mating.
- 6.This type of mating system is used in the isolation of extreme phenotypes.

Phenotypic dissortative matting

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

Consequences:

- 1.It is used 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 toparents.
- 6.It may be used on the maintenance of the small population variability due to inbreeding reduction.

Conclusion

The genetic composition of cross-pollinated crops give us an immense exposure to understand the genetics inside of the cross pollinated crops and genetic insights, the out-breeding and maintaining the genotypic genetic 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 follow the role of nature, naturally by means of out crossing. In general, variability is more exited in 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 with respect to the environmental response.

Application of research: Systematic Text literature development work has been carried out which to be helpful to the reader easy to conceptualization of the concept. It is the fundamental concept reviewing and development of the study or review materials.

Research Category: Cross pollination

Acknowledgement / Funding: Authors are thankful to School of Agriculture and Rural Development, IRDM Faculty Centre, Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur, Kolkata, 700103, West Bengal, India

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Research project name or number: PhD Thesis

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur, Kolkata, 700103, West Bengal, India

Cultivar / Variety / Breed name: Nil

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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