**Selection in Cross Pollinated Crops**

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**ABSTRACT**

The group of plant species whose typical method of seed production involves a high level of cross-pollination has distinctive reproductive traits and population structure. Male sterility, self-incompatibility, monoecy, defective blooms, etc. are obstacles that make a plant dependent on outside pollen for seed setting. These plants get a mixture of pollens from various plants, each with a unique genetic makeup, resulting in a cross-pollinated population. These populations exhibit high levels of heterozygosity and heterogeneity as well as a significant amount of genetic free and potential variabilities, all of which are kept in check by free gene flow within the population.

**Keywords:** Crosses-pollination, free variability, heterozygosity, heterogeneity and potential variability,

1. **INTRODUCTION**

In a population of randomly mated individuals, selection has the potential to: (1) alter gene and genotype frequencies (2) emergence of new genotypes as a result of the altered gene frequencies, (3) induce a change in mean in the level of selection, and (4) somewhat alter population variance. The following list of factors influences the magnitudes of these effects: (1) the number of genes governing the character, (2) dominance level, (3) kind of gene action, and, to a considerable extent, (4) heritability of the concerned characteristic.

1. **Types of Selection Responses**

The results of numerous studies on the impact of selection in populations with random mating have been published. The following groups of observable reactions to selection are possible: There are five different types of responses: rapid gain followed by slow response; continued slow response for a long period; slow response for a short period; little or no response; and rapid gain plateau rapid gain response.

1. **RAPID GAIN FOLLOWED BY SLOW RESPONSE**

In some instances, selection results in some generations of rapid gain, followed by some generations of moderate gain. This kind of reaction is typical for traits like plant height, disease resistance, flowering days, etc., where selection has the following effects; 1. A mean change in the chosen direction. 2. The emergence of novel genotypes or gene pairings as a result of altered gene frequencies. 3. A decrease in variability, as seen by variance. Many genes with small impacts and few genes with substantial effects are thought to control these traits. An elevation in the frequency of favorable alleles of genes with significant effects can be seen during the time of rapid gain. This gain would be substantial at intermediate gene frequencies and would diminish over time as the population's proportion of the desired alleles increased. The slow gain, which comes after the quick gain, is caused by (1) a slow rise in the frequency of large genes as they take over, and (2) a slight rise in the frequency of minor genes. As a result, the slow gain lasts a very long time.

1. **SLOW RESPONSE FOR A LONG PERIOD**

The selection of Bur's White, an open-pollinated variety of maize, for its high oil, high and low protein contents, serves as an appropriate illustration of this kind of response. Here, we'll take into account the conclusions about high oil content selection. The oil content of the Burr White population at its inception ranged from 3.7 to 6.0 percent, with a mean of 4.7 percent. Under selection, the mean oil content grew consistently and slowly over 76 generations, eventually reaching a value of 19.0 percent. In the second generation under selection, plants with more than 6percent oil content were noticed, and by the tenth generation, every plant in the selected population had more than 6percent oil. This suggests the emergence of novel genotypes, not present in the original population As indicated by the following, the variability in the selected population after 50 generations of selection was comparable to that in the original population: (1) Variances across generations were comparable; (2) Suspension of selection led to a slight decrease in oil content; (3) Selection for low oil content in the Selected population was successful. Reverse selection started in high oil and low oil populations in generation 48. As a consequence, the mean oil levels of the reverse high oil and reverse low oil populations are comparable to those of the original Burr's White variety in generation 90. Similar outcomes were found for high oil and low protein concentrations, for which significant genetic diversity was still present even after 76 generations of selection. Additionally, selection response has persisted for up to 90 generations (Dudley and Lambert, 1992). Following is a summary of the impacts of selection for oil and protein contents. (1) A gradual shift in the mean in the chosen direction. (2) The emergence of novel gene combinations following a number of generations of selection. (3) The persistence of variability even after a protracted period of selection.

The majority of the time, many genes, each of which has a tiny and cumulative influence, control quantitative traits. Such a scenario would result in a tiny selection coefficient (q) for each gene, which would slow down the process of selection. Due to the trait's heritability being less than 100%, the progress would be further impeded. Genes would therefore rarely be fixed, and even after multiple generations of selection, there would still be a great deal of diversity. Additionally, changing one quantitative variable typically affects other unrelated characters. Correlated response to selection is the term used to describe this. For instance, in Burr's White maize, selection for high and low oil and high and low protein concentrations led to differences in maturity, plant height, tiller number, cob size, grain characteristics, and yield. For every 1.0 percentage point increase in protein due to selection, starch increased by approximately 1.0 percentage points. Similar to how starch changed in response to oil selection, it changed by 1.3–1.6 percentage points for every 1.0 percentage point change in oil.

1. **SLOW RESPONSE FOR A SHORT PERIOD**

A plateau is reached after multiple generations of slow growth for some traits due to selection. An illustration of such a response is the choice of Burr's White maize, which has a low oil content. Oil content gradually declined over the course of 25 generations of selection, reaching a low of 1.0% in the selected Burr's White population. Continued selection from 4.68% for an additional 25 generations had no effect on further lowering the oil percentage. Comparable to the last instance, selection had similar impacts on the population. The oil content decreased from 1.0% to 0.5% when the selection for low oil was kept going past the 50th generation, although the reaction was once more delayed and extended. Since abdominal chaetae quantity in Drosophila appears to have a similar response pattern to low oil, the genetic basis for the mechanisms at play should also be identical. It should be noted that most of the characters might fit this description. However, the explanation provided below is still valid for the first 50 responses in the selection. It has been noted that in the majority of ongoing plant breeding scenarios, the selection would not last more than a dozen or so generations.

There is a good chance that many genes affect the oil content. As a result, selection is anticipated to result in gradual improvements over numerous generations, with little to no impact on variability. In reality, as shown by variance estimates and the success of selection for high oil, there was still a significant amount of variability for low oil content even after 25 generations of selection. However, physiological restrictions imposed by a linked response to selection limited the progress under selection. Reduced embryo size is a side effect of selection for low oil content, and reduced embryo size is expected to have a negative impact on seed viability. The embryo would need to be a certain size to live, below which it would not. This would stop the drop in oil content until the genes controlling oil content and embryo size are no longer linked. This viewpoint is generally supported by experimental data.

1. **LACKOF RESPONSE TO SELECTION**

Some characters' selection results in little to no gain. Selection for yield in maize is one example of this kind of reaction in practise. In general, a great deal of selection for yield trials have failed to increase yield. For instance, in one experiment, the yield of the selected population was 53.3 bushels (one bushel = 36.35 litres) per acre after seven generations of selection, as opposed to 53.6 bushels for the unselected variety. Numerous studies have demonstrated that open-pollinated maize varieties have significant genetic variability for yield, much of which is additive, and should react to selection. As a result, the low heritability of this characteristic, which would restrict the progress under selection, is most likely to blame for the inability of yield to respond to selection. The fact that breeding strategies using repeatable yield trials, such as recurrent selection, actually increase yield, supports this hypothesis.

1. **RAPID GAIN-PLATEAU-RAPID GAIN RESPONSE**

For some characters, selection reveals a period of quick growth, followed by a plateau, and then another period of quick growth. For instance, Mather and Harrison's selection for a greater number of abdominal bristles in the fruit fly Drosophila melanogaster resulted in a quick gain over a period of 20 generations. But selection had to be stopped to maintain the selected population as the reproduction rate i.e. fertility had decreased sharply. Fertility returned after a few generations, but the number of bristles was significantly fewer than it had been in the population before selection was interrupted. In this new population, selection for bristle number was quite successful, but there was no decline in fertility this time around. After a few generations, bristle number climbed to a new stable level, and further selection was unsuccessful. Additionally, when selection was halted, the number of bristles did not decrease. The bristle number again shown a rapid response to selection and reached still another plateau after 50 generations at this plateau.

The following were the primary aspects of this experiment: (1) Under selection, the number of bristles rapidly increased; (2) As a result of the increased bristle number, fertility decreased. When selection was suspended, there were the following effects: (3) an increase in fertility and a decrease in bristle number; (4) a rapid gain under selection without a decrease in fertility when selection was resumed in the new population; (5) reaching a stable bristle number at which point further selection was ineffective; and (6) another rapid gain under selection resulting in yet another plateau after several generations.It is commonly accepted that individuals who are close to the population mean for various quantitative features are the best adapted or most fit in natural populations. In other words, extreme phenotypes are detrimental to a person due to natural selection. Therefore, a population must satisfy the two opposing requirements listed below: (1) it must become phenotypically uniform for immediate adaptation, i.e., the individuals must be close to the population mean for the quantitative characters; and (2) it must maintain genetic diversity to satisfy the needs of long-term evolution. If only a tiny amount of the genetic variability existing in the populations is free, or expressed, and the majority is hidden as potential variability, the populations may be able to achieve these opposing needs.

1. **FREE AND POTENTIAL VARIABILITY**

The degree and kind of genetic variability present in a population affect the efficacy of selection. Segregation and recombination, as well as mutation, can contribute to genetic variability. A population's level and kind of genetic variability is largely determined by its mode of reproduction. Genetic variability can be broadly divided into two categories: free and potential genetic variability.

1. **Free Genetic Variability**

Free variability is the genetic variation that is accessible to selection. Extreme phenotypes in a population, such as the phenotypes of the two homozygotes AA and aa in the case of a single gene with two alleles A and a, serve as a representation of it. However, only the two extreme homozygotes (AA BB and aa BB) in the case of two (or even more) genes lead in free variability.



1. **Potential Genetic Variability**

Potential variability, which is represented by the phenotypes clustering around the population mean, is not available for selection to operate on. These phenotypes can have heterozygous or homozygous genotypes, and the variability that is stored in them is released as free variability in the sexual progeny. Potential variability may be either (a) heterozygotic or (b) homozygotic.

1. **Heterozygotic Potential Variability.**

This variability is stored in hetrozygotes, such as Aa, Bb, and others, which are phenotypically homogenous and produce extremes which are remarkably close to the population mean, store this variability. And because of segregation and recombination, they would give rise to extreme phenotypes in the following generation. Thus, heterozygotes act as reservoirs for the variability that is segregated and then slowly released as free variability through recombination and segregation.

1. **Homozygotic Potential Variability**.

Homozygotes act as reservoirs of variability when there are two or more genes involved. For instance, it may be expected that the phenotypes of homozygotes AA bb and aa BB will cluster around the population mean. As a result, these genotypes would be uniform in phenotype and protected from natural selection. After hybridization, they would, however, create the extreme phenotypes AA BB and aa BB, i.e., AA bb x aa BB, followed by recombination and segregation in the F1. Therefore, in order to release homozygotic variability, it must first undergo hybridization to become heterozygotic variability, as results, it is converted into free variability more slowly than heterozygotic variability.

 Free variability, heterozygotic potential variability, and homozygotic potential variability coexist in a dynamic equilibrium in random mating populations. While free and homozygotic potential variabilities are produced through segregation and recombination in the heterozygotes (Figure 1), heterozygotic potential variability is continually generated by mating among homozygotes. In the instance of two genes controlling a polygenic trait, only 1/8th of the total variability is in the free state, with the remaining 7/8th being potential variability (Figure 2). Similar to this, the ratio of free variability to heterozygotic potential variability and homozygotic potential variability will be 1: n :(n-1) if n genes are involved. These predictions are based on the additive effects of genes. If full dominance in the positive direction were assumed so that the phenotype of AA is identical to that of Aa, and that of BB is identical to that of Bb, the proportion of free variability increases drastically from 1/8th to 10/16th, and the bulk (4/5th) of free variability is, in fact, potential heterozygotic variability, which cannot be fixed by selection until it becomes 'true' free variability. As a result, In general, dominance slows down the rate of response to selection, hence reducing the dominance impact. The dominance gene produces a skewed distribution of traits and also promotes a shift in the population mean toward dominance.



1. **LINKAGE'S IMPACT ON POTENTIAL VARIABILITY**

Multiple genes controlling a single character may be found on the same chromosome in the case of polygenic characters. If these genes were linked during the repulsion phase, that is, if positive alleles of some genes were associated with negative alleles of other genes, it would be advantageous for the population For example, out of the four schemes of arrangement for four genes, A, B, C and D, scheme number 4 would be the most desirable. This is because in this design, three crossovers at specific points would be necessary for the entire release of variability (marked by x). It is possible to predict that such intricate and sophisticated gene combinations for storing variability would emerge in wild populations. By doing so, they would be able to satisfy the competing needs of short-term fitness and long-term evolutionary goals.

It is hypothesized that the relationship between plus and minus genes impacting a quantitative characteristic is similar to that in the 4 scheme above. These genes would be connected to one another and possibly scattered among the genes for other quantitative features. In the case of bristle number in Drosophila, the first rapid gain under selection was likely caused by the selection for groups of related genes rather than for individual genes. The above-mentioned gene architecture provides a simple explanation for how the accompanying decrease in fertility constitutes a connected response to selection. Selection for one character would have an impact on other characters since the genes governing different quantitative traits would be linked together. The presence of crossing overs among the connected genes may reduce the impacts of such a coordinated response to selection. Crossovers would have happened to create new gene combinations when selection was suspended. As a result, selection for bristle number did not reduce fertility in the new population. The selection for new gene combinations brought about by linked genes recombining would be the cause of the second quick increase. This selection would be caused by the potential variability being released.

In order to convert hidden variability into free variability, connected genes' rate of recombination is crucial. The amount of free variability in the case of two genes coupled in repulsion phase is just 2r, but the amount of potential homozygous variability is 2(1-r). Recombination's many characteristics are under genetic control, and this regulation is typically polygenic. In populations of plants used for breeding, breeders constantly select for recombinants. As a result, it is reasonable to assume that the chosen lines will exhibit a higher rate of recombination than the original population. The available evidence frequently lends support to this opinion. As an example, strains of the fern Lolium perenne that have undergone extensive breeding have higher chiasma frequencies than strains that have not.

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