

ROLE OF QUANTITATIVE GENETICS IN THE IMPROVEMENT OF CROP YIELDS BY CONTROLLED BREEDING

By

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Plant breeding is the art and the science of changing and improving the heredity of plants. Plant breeding was first practiced when man learned to select the better plants; thus selection became the earliest method of plant breeding.

Although hybridization was practiced before the time of Mendel, its significance was not clearly understood until Mendel's findings were rediscovered in 1900 and laid the basis for understanding of the mechanism of heredity. As knowledge of genetics and allied plant sciences increased, plant breeding became less of an art and more of a science. Modern plant breeding is based on a thorough understanding and use of genetic principles.

The science of genetics was first founded on the inheritance of qualitative characters such as flower colour and seed coat which showed a discontinuous variation. Mendel disregarded the continuous variation observed in his experimental populations. Qualitative characters are simply inherited, mostly by single genes. With respect to these characters, the phenotypes can be classified into a smaller number of easily recognized, qualitative groups. But many of the characters or traits of agronomic importance, e.g. yield and growth etc., with which the breeder works are not inherited in this simple manner. If a genetically heterogeneous population is studied with respect to, for example, yielding ability, one could observe that individuals would differ in yielding ability by rather minute amounts and would range rather uniformly from high to low in yielding ability. If the measurement of yielding ability is accurate enough, there won't be two individuals with the same measurement. In such a population variation is said to be continuous with individuals having the average expression most common. Characters of this nature which show a continuous range of variability from one extreme to the other are referred to as quantitative or metrical characters because such characters could be measured by same scale e.g. kg, cm etc. Their inheritance is dependent upon many genes, each of which contributes in an additive manner to the final effect. The individual effect of a gene is small when compared to the total effect of the genes controlling the trait. Quantitative characters are influenced by environmental factors making the distribution curve smooth. Simultaneous segregation of many genes with small and similar effects, and the superimposition of variation arising from non-genetic causes translate the intrinsically discontinuous variation caused by genetic segregation into the continuous variation seen in quantitative characters.

Types of traits described above, qualitative characters inherited by 2 genes and quantitative characters inherited by many genes are just two extremes. In nature there are many intermediary types, thus transission from one extreme to the other is gradual.

Since phenotypes in respect to a quantitative character cannot be classed into distinct groups, simple classical Mendelian techniques that were used to study qualitative traits cannot be employed to study the inheritance of quantitative characters. Still the Mendel's laws provided the basis of the analysis of continuous variation while the biometrical approach showed the way in which to handle continuous variation. It was the fusion of these two approaches, genetical and biometrical, that contributed to the greater understanding of the variation observed in quantitative characters. The branch of genetics that deals with quantitative traits is called quantitative genetics or biometrical genetics. The importance of this branch of genetics need hardly be stressed as most of the characters, of economic value such as yield and growth are quantitative characters exhibiting continuous variation.

Variation in a quantitative character of a plant population are of two kinds: a) Variation due to environment b) Variation due to hereditary or genetic differences. Heritable variation in plants originates from three main processes a) gene segregation and recombination after hybridization b) mutation and c) polyploidy.

Most plant breeding programmes directed to improve yield utilize the heritable variation that originates due to gene segregation and recombination following hybridization and hence will be considered here, in details. Though artificially induced mutations and polyploidy have been used in improving yields their use is rather limited and restricted to a few crop species.

Results of Johanssen's (1903) experiments clearly showed that selection for environmental variation has no effect and if selection to be a success genetic variation must be present in the breeding population. In other words the selection can act effectively only on genetic variation. Thus in any controlled breeding programme to improve quantitative characters such as yield genetic or heritable differences must be present in the original population. If absent genetic differences must be generated before the selection is practiced. In all most all cultivated crops this is done by artificial crossing or hybridization of carefully selected parents at the beginning of the breeding programme. As a result of this hybridization, segregation and recombination of parental genes occur in subsequent generations. East (1916) in his classical experiments demonstrated that, segregation and recombination of parental genes following hybridization can generate new heritable variation upon which artificial selection can successfully be practiced.

The selection procedure of the segregating-generations following hybridization depends, to a great extent, on the relative magnitude of the three constituent components of genetic variation. The three components of genetic variation to which the quantitative geneticist has focussed his attention and in which the plant breeder is most interested are defined as follows:

1. Additive genetic variance arising from the additive effects of the genes summed over the segregating loci.
2. Dominance variance due to the allelic interaction (interaction of alleles at the same locus) of segregating genes.
3. Epistatic variation resulting from interaction between non-allelic genes.

In addition to these, it is necessary to separate genotype-environment interaction component as this can bias the other components.

The knowledge of the relative magnitudes of genetic components of variation and environmental variation is essential in determining and refining the breeding methodology for any quantitative trait such as yield. The principal sources of estimates of genetic components of variation have been a) unrelated families and b) full and half-sib progenies developed according to mating designs. The statistical analyses, parameters estimated and their genetic interpretation have been useful to the breeders in determining breeding methods.

The magnitude of additive genetic variance relative to other genetic and environmental variation gives valuable information which can help the breeder in choosing the most effective breeding procedure.

A usual measure is the heritability. Heritability in layman terms, can be described as a "measure of the relative importance of heredity and environment". For the term to be meaningful for the plant breeder, it is necessary to specify the basis on which it is calculated. The heritability in the "broad" sense is the ratio of the total genotypic variance to the total phenotypic variance and provides a measure of the overall importance of hereditary determination of a trait. Heritability in the "narrow" sense, is the ratio of "additive genetic variance" to the total phenotypic variance and measures the portion of the total variation which can be

utilized, by the breeder, for improvement of a given population with respect to that trait by mass selection. The degree of heritability can be influenced by developments that have occurred in the origin of the material. A character in a population which has been under intense selection would be expected to have a lower heritability than the same character in a population where additive genetic variance has not been reduced by selection pressure when both populations are evaluated under identical environmental conditions. Also, the heritability of a character such as yield may be relatively high when measured in early segregating generations of a population created by crossing widely divergent parents. From the estimates of heritability plant breeders have been able to take decision as to 1) whether the trait under selection pressure will respond or not, 2) predict progress from various degrees of selection schemes. By using additive genetic variance in combination with other genetic and non-genetic variance components it is possible to compute the expected progress, the breeder can make by employing various selection schemes such as mass selection, half-sib family selection, full-sib family selection and reciprocal recurrent selection. Such evaluation will certainly help the plant breeder to make decision as to what selection scheme will give best results, thus making the breeding programme more precise.

The dominance component of genetic variation sometime can play a very important role in determining the breeding technique. It is in relation to dominance that we have to explain the complex topic heterosis. Heterosis may be defined as the superiority of F_1 hybrid over its better parent.

Heterosis can occur due to two causes:

1. Super dominance or over dominance at some or all loci *i.e.* dominance component for those loci exceeds the additive genetic components of the same loci and
2. The dispersion of increasing genes more or less equally between the two parents. When two such parents are crossed the F_1 receives all the increasing (yield) alleles from both parents so that F_1 is superior to both parents.

If over dominance is the cause of heterosis then the plant breeder has no alternative but to produce hybrid seeds every season for planting, if he is to utilize the hybrid vigour. This is an expensive exercise as special techniques and more time and land have to be used in producing hybrid seeds. In the case of crops which can be vegetatively propagated, F_1 can be multiplied by vegetative propagation, for example by cloning, without losing the hybrid vigour. Vegetative propagation is much less expensive and easy when compared to those of producing hybrid seeds every year.

If the cause of heterosis is not the overdominance, then the plant breeder can produce, by selecting (using conventional breeding methods) the segregating generations obtained by selfing heterotic F_1 , an inbred line as good as F_1 hybrid, if not better.

The experimental evidence so far does not support very much the over dominance theory, even in corn where hybrid seeds are being produced and widely used for planting. But there remains the possibility that a relatively small proportion of over dominant loci could exist in populations that have been experimented with. It is further possible that such loci, even in low frequency if they exist, could have significant role in breeding programmes if such loci being accumulated in corn inbred lines produced by using a type of selection procedures that favoured the selection of inbred lines having more over-dominant genes. Thus while the possibility of important over dominant loci in population of corn has not been eliminated, a strong case has been built against the overdominance theory in quantitative genetic studies of corn.

The distinction of the two causes of heretosis has very great practical and economic importance; as breeding methods that are required to exploit the heterosis caused by over-dominance is quite expensive and complicated. Fortunately, there are mating designs by which the plant breeder can now distinguish between the two causes of heterosis.

Epistasis or non-allelic interaction remains a most complex problem and on which it is extremely difficult to obtain reliable experimental results. It is assumed that epistasis is a major factor in the explanation of heterosis exhibited in some crop plants. To utilize the epistatic variation one has to combine specific parents in the crossing programme. Once combined certain types of epistatic effects in (heterozygous loci interacting with other heterozygous loci) can have their full effect only in the hybrid. In subsequent segregating generations their effects become less and less. Therefore to utilize such epistatic effects, the plant breeder has to either produce the hybrid seed every year or resort to vegetative propagation as in the case of crops showing overdominance.

A major role of quantitative genetics in plant breeding is the use of estimated genetic components of variance to predict genetic improvement in selection programmes. This was emphasized earlier as the prime concern with additive genetic variance and applies in varying degrees with dominance and epistatic variance. Since these components enter into the equation which predicts the progress to selection, use of genetic components for predictive purposes depends to a large extent on the bias imposed on them by the interaction between the genotype and the environments. The bias in the estimates of genetic parameters can lead the plant breeder to take erroneous decisions with regard to his selection procedures. The subject of genotype-environmental interactions has been an issue of major concern to the plant breeder. Research on this important aspect has made it possible to detect, separate and quantify the genotype-environmental interactions component from the rest of the genetic components.

Analytical methods are also available to quantify and describe the stability of varieties when grown under different environmental conditions. This provides necessary assessment techniques to the plant breeder to select stable varieties with respect to important traits such as yield.

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