

USE OF QUANTITATIVE GENETICS IN PLANNING MULTIPLE-TRAIT BREEDING

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SUMMARY

There are several methods of multiple-trait selection which vary in effectiveness and suitability depending on program goals. Tandem selection is a method to improve several traits, one trait at a time in a specified order. Selection is ordinarily done on the most important trait first. After sufficient gain has been obtained, the second most important trait is considered and so on. Another method of multiple-trait selection is the use of independent culling levels. With this method, several traits are measured in the population and a minimum value for each trait is established. For a tree to be selected, it must be above the culling level in each trait being considered. Thus, several traits can be considered simultaneously, and individual traits can be emphasized by varying the culling levels. Both methods are relatively simple to apply, but neither accounts for effects of genetic correlations among traits.

Index selection utilizes a multiple regression equation to predict the genetic worth of the individual on the basis of economic and genetic information. It is theoretically the most efficient of the three methods of selection discussed. It gives maximum flexibility from one generation of selection to the next, both in traits to be selected and assignment of relative weights to various traits, and it permits relatively precise estimates of genetic gains. Methods of index selection have changed little in some 30 years of breeding practice. Yet surprisingly few documented examples of the use of a selection index, appeared in the literature during that period. It is probable that only in a few cases has selection been carried out solely on the basis of index values. Nevertheless, the index not only serves as a tool for selecting candidate trees but also provides increased understanding of the mechanisms of selection and the genetics of the population involved.

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Tandem Selection

Tandem selection is a method to improve several traits, one trait at a time in a specified order. Selection is done on the most important trait first. After sufficient gain has been obtained, the second most important trait is considered and so on.

The biggest disadvantage with this method is that genetic correlations cannot be considered. If the first trait selected is negatively correlated with the second, an adverse response may partially nullify gains in the first. Note that the second trait in this case may or may not be one targeted for selection at a later phase of the program. This consideration emphasizes the importance of the aggregate genotype comprised of more traits than those currently under selection (Gjedrem, 1972).

Another disadvantage is the inflexibility of tandem selection when changes in product goals call for changes in emphasis on certain traits. To choose the most important trait at any given time is not a simple task.

The advantages of tandem selection are that it is simple to apply and all effort is devoted to the most important trait, thereby maximizing gains in that trait. For example, if a stand cannot be established and carried to harvest unless disease resistance is obtained, selection for disease resistance may be considered without regard to any other traits. Until disease resistance is obtained, no other traits are important. The situation, however, is relatively rare.

Selection by Culling Levels

Another method of multiple-trait selection is the use of independent culling levels. With this method, several traits are measured in the population and a minimum value for each trait is established. For a tree to be selected, it must be above the culling level in each trait being considered. This method is relatively simple to apply and allows selection for several traits simultaneously. Individual traits can be emphasized by varying the culling levels. However, efficiencies can be poor if strong genetic correlations exist among traits. For this and other reasons accurate predictions of expected genetic gains are almost impossible. As more traits are added, it becomes progressively more difficult to find a particular tree having minimum levels for all traits. Nevertheless, the method is widely applied and often yields satisfactory gains.

Index Selection

Index selection was first proposed by Smith (1936) and Hazel (1943), and methods have changed very little in some 30 years of breeding practice. Yet surprisingly few documented examples of the use of a selection index have appeared in the literature during that period. It is probable that in only a few cases has selection been carried out solely on the basis of index values. Nevertheless, if index values were never used

specifically to make selections, the value of the index in requiring the computation of genetic and environmental parameters and their organization into an interpretable model would be sufficient to justify the effort involved. Indeed, the assigning of index values is one of the best ways of organizing and interpreting genetic information about a population, regardless of the selection method to be applied.

Index selection utilizes a multiple regression equation to predict the genetic worth of an individual on the basis of economic and genetic information. It is theoretically the most efficient of the three methods discussed. It gives maximum flexibility from one generation of selection to the next, both in traits to be selected and in assignment of relative weights to various traits, and it permits relatively precise estimates of genetic gain (Henderson, 1963). A disadvantage of the method is that it involves a complex statistical procedure. However, modern computers have greatly simplified this step. Although limited in application to a rather strictly defined population whose parameters have been estimated, the index permits generalizations of great utility in certain circumstances (Singh and Bellmann, 1972). A more formidable disadvantage is that the system requires reliable estimates of genetic and environmental parameters which can only be obtained through well-designed and properly established field experiments.

The genetic worth of a tree is defined by (1) its combining ability for traits of economic importance and (2) the relative economic weights assigned to those traits. Information on combining ability is obtained through various progeny and sib testing designs. Thus, the portion of the index equation that concerns combining ability may involve several traits as well as several sources of genetic information such as grandparents, parents, siblings, etc. The varying emphasis given to different sources of information through weighting coefficients not only maximizes the efficiency of the index but also provides information needed in planning future studies. The mathematical approach to developing this portion of the index equation is beyond the scope of this paper but is well documented in the literature (Namkoong, 1966; Burrows, 1966). The approach to economic weights should be a very general one in which broad basic values are emphasized rather than current or projected economic conditions. Since only relative weights are necessary, it may often be sufficient to consider rate of volume production versus wood quality as principal components of value.

Accounting for genetic correlations between various traits is one of the most important advantages of the index. If all traits were independent of each other, the index would simply be the sum of phenotypic values, each weighted according to its heritability and economic value. In practice, this is seldom the situation. Therefore, the index equation is derived by a procedure which minimizes the deviation of genetic worth from the index value. This minimizing assures the maximum gain possible with the given combination of traits.

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If the decision is made to derive a selection index for a particular improvement program, it will usually be necessary to design one or more experiments to produce genetic information for use in the index. Of utmost importance in this research is the choice of experimental designs and locations which adequately test a representative sample of the gene pool over a representative series of environments. Predictive value of information derived in such tests, and thus of the index itself, rests squarely on reliable experimental designs (Harris 1963). Since time and resources are always limiting, planning such experiments is an optimization process to derive the most information from the available resources. The data derived from such experiments not only provide an index as a working tool for selection, but they also provide a basis for choosing alternative selection strategies through estimates of when and in what amounts gains may be expected. The knowledge gained through the process of deriving a selection index will serve well in any type of selection system which may be applied.

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