Nutritional Standards and Methods of Evaluation for Food Legume Breeders

Prepared by the International Working Group on Nutritional Standards and Methods of Evaluation for Food Legume Breeders

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J.H. Hulse,* K.O. Rachie,* and L.W. Billingsley**

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Chapter 5. Background Papers

Breeding Strategy for the Nutritional Improvement of Pulses

G.C. Hawtin, K.O. Rachie, and J.M. Green

The successful development of high-yielding cereal varieties in recent years has served to emphasize the value of plant breeding in increasing world food production. Efforts are now underway, in both international and national programs, to achieve similar successes with a wider range of crops. Because of their value both nutritionally and in farming systems, the pulses are now considered to be one of the most important groups of crops requiring urgent attention. The majority of pulses grown in the developing world are unimproved local cultivars, and the potential for the genetic improvement of these species is enormous.

Nutritionally the pulses are important primarily as a source of protein, although their contribution to the carbohydrate, mineral, and vitamin fractions of the diet can often be significant. From an agricultural standpoint the pulses are valuable in the maintenance of soil fertility, primarily through their ability to fix atmospheric nitrogen. They also frequently play an important role in crop associations and rotations, in the stabilization of soils, in generating farmer incomes, and in agricultural diversification.

Breeding Objectives

It is generally accepted among breeders that the most important objective in pulse improvement is the increase and stabilization of seed yields. Often, this can be best achieved by breeding for resistance or tolerance to factors that adversely affect yield in addition to raising the potential yielding capacity of the crop. The pulses are subject to a wide range of hazards including pests, diseases, weeds, drought, waterlogging, cold, heat, salinity, and lack of available nutrients. Cultivars exhibiting resistance to these have a greater chance of achieving their maximum potential. Other agronomic characteristics may also be considered by breeders for genetic improvement, such as an increased ability to fix nitrogen in symbiotic association with suitable Rhizobium bacteria, a plant growth habit suitable for mechanized harvesting, nonshattering of pods, and a maturity period designed to optimize production in a given agricultural situation.

Since the primary use of the pulses is as a human food, nutritional quality is of concern to most breeders. Accepting that the improvement and stabilizing of seed yield and yield-related characteristics constitute the main objectives of most programs, there is considerable scope for nutritional improvement, especially through the international programs. Even in cases where the resources required to undertake positive nutritional improvement are not available, care should be taken that the nutritional level of released cultivars does not fall below an acceptable standard.

Nutritional Objectives

Nutritional factors can be broadly classified into two groups: (a) those factors, such as cooking quality and organoleptic properties that are of direct concern to the consumer and that must be at an acceptable level if a variety, however agronomically superior, is to be adopted by the farmer; (b) factors that may be desirable nutritionally, e.g., high protein quantity and quality, but that are generally of little concern to the farmer in the absence of a system of premium pricing. If varieties having superior food value are to be widely accepted by the farmer, it is generally necessary that any such improvements be accompanied by a higher or more stable yield or improved agronomic characteristics.

Of the wide range of possible nutritional factors in a breeding program, the choice of ones to concentrate on will depend on (a) their relative importance as determined by nutritionists, (b) the availability of suitable screening methods, and (c) genetic considerations.

Screening Methods

Before the positive genetic improvement of a nutritional character can be attempted, screening methods must be available that allow a large number of samples to be measured with acceptable accuracy and in a short period of time. Plant breeding is to a large extent a matter of chance, and breeding methods have been evolved to maximize the probability of obtaining desirable
gene combinations. It is now recognized by most breeders that the handling of large populations is important in this process. It may be necessary to screen as many as 10,000 individual plant progenies from F2 and F3 generations in a major pulse breeding program, and as little as 10 g of seed may be available for testing from each sample. Most breeding programs attempt to grow at least two generations per year to advance as quickly as possible. The nutritional screening of one generation may have to be undertaken in only a few weeks, before the planting of superior genotypes in the next.

In the absence of suitable mass screening methods, the breeder is limited to selecting at a later stage in the program when large quantities of seed are produced, and there are fewer entries to screen. In this case genetic advance, if any, is likely to be slow, but at least it can be ensured that desired standards are maintained.

**Genetic Considerations**

A breeding program can only be truly efficient if there is some knowledge of the genetic systems involved. Unfortunately there has been relatively little work done on the genetics of nutritional factors in the pulses and there is an urgent need for further study. In the absence of detailed genetic knowledge for a particular species, breeding strategies must be based on existing limited data, and extrapolation from the genetics of other species.

Some of the more important genetic considerations are outlined below.

**Genetic variation**

Genetic advance can only be achieved if there is genetic variation in the character concerned. Table I indicates some of the variation that has been found for protein percentage in the seed of several pulse species. Variation has also been reported in other nutritional factors, e.g., Kelly (1) reported a range in available methionine in dry beans of 0.8–3 mg/g of bean; Porter et al. (2) obtained from 2.15 to 3.16 g of sulfur–amino acids per 16 g N in dry beans; and Yohe et al. (3), in a study of 313 strains of mung beans, found a range in methionine of 5.5–17.8 mg/g of protein.

In fact, in all cases in which a large number of genotypes have been studied for a particular nutritional factor, genetic variation has been found. In some cases, however, this reported variation is comparatively small, and the opportunity for genetic advance by selecting within such variation is limited.

**Environmentally induced variation**

In addition to genetic variation, nutritional factors, in common with most plant characteristics, are subject to variation caused by the environment. The protein content of the seed, for example, may be affected by soil nitrogen levels and the addition of nitrogenous fertilizers or *Rhizobium* bacteria may greatly enhance the percentage protein. Ivanov (4) reported a range of 12.6–31.2% protein in noninoculated and inoculated chick-peas, respectively, within the same cultivar.

Other nutritional factors are also affected by the environment, e.g., Wassimi (5) reported that the soil potassium level influenced cooking quality in lentils, and Bliss (6) reported a significant effect of location on the methionine content of cowpeas.

Because it is only by selecting within genetic variation that genetic advance can be achieved, it is necessary to reduce environmental effects to a minimum. Screening nurseries must thus be planted under uniform conditions, and if possible, in an environment that allows the greatest expression of genetic differences. In a trial to study the influence of the environment on cooking quality in broad beans (1) it was found that at one location all the lines were equally good but at another location, where the average cooking quality of all the lines tested was poorer, considerable genetic variation could be identified.

**Genotype × environment interactions**

There are several reports in the literature of interactions between the genotype and the environment. Bliss (6), for example, reported significant genotype × location and genotype × location × day length interactions for the protein percentage of cowpea seeds and Sandhu et al. (7) reported significant genotype × year interactions for protein percentage and sulfur content as a percentage of the protein in the seed.

It is desirable that superior cultivars should be nutritionally stable across a range of environments. It is possible that the statistical techniques developed for the analysis of stability and wide adaptation in yield (e.g., the regression analysis of interactions proposed by Finlay and Wilkinson (8)) can usefully be adapted for the study of nutritional factors.

**Heritability**

Heritability estimates provide a measure of the proportion of the total variance in a character that is of genetic origin. Such estimates are valuable in determining the genetic advance possible through selection. Very few heritability

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1Personal communication from E.A.E. Ahmed, 1975.
estimates have been reported for nutritional factors in the pulses. Most of these are broad sense heritabilities, based on total genetic variance, rather than the more useful narrow sense heritabilities, which estimate only the additive genetic component as a proportion of the total genetic plus environmental variance.

**Major genes**

Breeding for the improvement of any character is greatly simplified if major genes can be identified. Such genes, which are simply inherited, can generally be easily transferred by breeding to a desired genetic background. In addition, they frequently have a large effect and tend to be less influenced by environmental variation. As a result, screening procedures often need be less precise when major genes are involved. If the gene has a pleiotropic effect, or is closely linked to a gene conferring an easily identified morphological characteristic, screening is further simplified by selecting on the basis of the pleiotropic or linked character.

In the pulses no major genes have been reported affecting protein quantity or quality, but this should not discourage attempts to find them. In maize, the discovery of the Opaque-2 gene, which confers a higher lysine content in the seed, has enabled breeders to develop “high-lysine” maize cultivars with comparative ease. A few major genes affecting other nutritional factors in the pulses are known. In cowpeas, for example, seeds having a rough testa are easier to dehusk and there is evidence (9) that high vitamin C content in chick-peas is associated with the simply inherited green cotyledon character. In pulses in general, genotypes having a dark seed coat are thought to be nutritionally inferior due to the presence of polyphenols. Seed coat colour is usually a simply inherited character.

**Minor genes**

The few studies to date of the inheritance of protein quantity and quality in the pulses have all indicated polygenic control of these characters, with additive genetic effects generally being the most important.

Work on peas in Hungary, referred to by Meiners and Litzenberger (10), indicated that in general the protein content of the progeny was intermediate between the parents and was inherited quantitatively. Bond (11) reported that the inheritance of high protein content in broad beans tended to be recessive, but that additive effects were also important.

In view of the existing data, breeding methods that are efficient at combining additive genes are likely to be the most effective for the improvement of protein quantity and quality. Further genetic studies are required, however, to confirm this and to explore the genetic systems involved in the inheritance of other nutritional factors.

**Linkage**

The useful effects of genetic linkages and pleiotropism have already been referred to in the section “Major genes” above. They can also have undesirable effects, however, and may need to be taken into consideration in a breeding program. A close genetic linkage between a desirable character and an undesirable one may require a large number of crosses to break. Breeders must take care when linkages or pleiotropic effects are suspected, that in breeding for an improvement in one character they are not simultaneously developing a genotype that is poor in another respect. There is some evidence, for example, that good cooking quality in lentils may be associated with poor resistance to weevils. There is also evidence to suggest that resistance to certain pests and diseases may be associated with the presence of polyphenols in the seed coat. In developing genotypes with a low polyphenol content care must be exercised that the pest or disease resistance does not fall to an unacceptable level.

**Transgressive segregation**

Breeders continually hope for transgressive

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Table 1. Reported range in protein values for selected pulse species.

<table>
<thead>
<tr>
<th>Species</th>
<th>No. of samples</th>
<th>Range in protein %</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pigeon pea (Cajanus cajan)</td>
<td>2262</td>
<td>18.4-28.8</td>
<td>ICRISAT collection</td>
</tr>
<tr>
<td>Chick-pea (Cicer arietinum)</td>
<td>2667</td>
<td>18.7-28.3</td>
<td>NEC collection&lt;sup&gt;2&lt;/sup&gt; ALAD</td>
</tr>
<tr>
<td>Lentil (Lens culinaris)</td>
<td>1688</td>
<td>23.4-36.4</td>
<td>NEL collection&lt;sup&gt;2&lt;/sup&gt; ALAD</td>
</tr>
<tr>
<td>Dry bean (Phaseolus vulgaris)</td>
<td>4524</td>
<td>17.0-35</td>
<td>Kelly (1)</td>
</tr>
<tr>
<td>Broad bean (Vicia faba)</td>
<td>511</td>
<td>22.3-37.1</td>
<td>NEB collection&lt;sup&gt;2&lt;/sup&gt; ALAD</td>
</tr>
<tr>
<td>Cowpea (Vigna unguiculata)</td>
<td>118</td>
<td>20.4-28.2</td>
<td>IITA (18)</td>
</tr>
</tbody>
</table>

<sup>1</sup>N × 6.25, dry weight basis.
<sup>2</sup>Germ plasm collections analyzed at the Grain Research Laboratory, Winnipeg, Canada, 1976.
segregation (i.e., segregants that fall outside the parental range) in their breeding nurseries. There is evidence that such segregants can be expected for nutritional characteristics, and hence the hope exists of pushing nutritional levels beyond those already identified. Bliss (6) reported finding two F_{3} families of dry beans whose means were greater than the mean of the highest parent.

Correlations
Both positive and negative correlations between protein content and seed yield have been reported in the literature. Evans (12) lists correlation coefficients from several sources and her table is reproduced here as Table 2. Bond (11) studied the relationship between yield and protein content in seven trials of field beans and found correlation coefficients ranging from –0.291 to +0.232.

In view of the conflicting evidence on the relationship of protein quantity to yield, there is hope of being able to combine both high protein and high yield in a single genotype. The trials of Leleji et al. (13) demonstrate that at least in their F_{2} and F_{3} dry bean progenies sufficient variation existed to allow the simultaneous selection of both high yield and high protein.

Other correlations that may be important from a breeder's standpoint have also been reported in the literature; for example, in beans, Rutger (14) reported a negative correlation between seed weight and protein content and Adams (15) reported significant negative correlations between the sulfur-containing amino acids and the nitrogen content of the seed.

Breeding Methods
The choice of a breeding method depends on a number of factors, such as the pollinating system of the plant and the genetics of the characters it is desired to improve.

Most of the pulses are self-pollinated and if out-crossing occurs, it is generally at a low level. Chick-peas, cowpeas, dry beans, and lentils all come in this category. A few species, however, have a much higher level of natural out-crossing, e.g., both broad beans and pigeon peas may reach 40% out-crossing under field conditions. In such cases techniques must be employed to ensure selfing or else breeding methods appropriate for the improvement of cross-pollinated crops may be adapted.

Whatever the pollinating system, a breeder's activities can generally be divided into four separate areas: (a) the identification of genetic variation; (b) hybridization; (c) selection; (d) testing and variety release.

Germ Plasm
The initial step in any breeding program is the identification of genetic variation. This is normally done by screening as much of the available germ plasm as possible for the desired characters. The IARCs all maintain inclusive collections for this purpose and germ plasm is made available from these centres to any other breeders. Efforts are currently underway by certain national programs, the IARCs and the FAO Germ Plasm Project to enlarge the existing collections in an attempt to maintain and identify the largest possible range of genes.

If the desired character is not identified within existing germ plasm, a breeder may attempt to introduce genes from related species by interspecific hybridization or to induce mutations through the use of physical or chemical mutagens. These methods are normally only employed, however, as a last resort when the search for genes already present in the species has been unsuccessful.

Once the desired character has been identified, it may be possible to arrive at a superior cultivar merely by selection. In most cases, however, it is

| Table 2. The correlation between protein and seed yield (after Evans (12)). |
|------------------|------------------|------------------|
| Crop             | Correlation      | Authority        |
|                  | coefficient (r)  |                  |
| Soybeans         | –0.33            | Johnson et al. (20) |
|                  | –0.08            |                  |
| Phaseolus beans  | –0.635           | Tandon et al. (21) |
| Phaseolus beans  | –0.23            | Rutger (14)      |
|                  | –0.36            |                  |
| Peas             | Low + ve correlation (NS)* | Furedi (22) |
| Phaseolus beans  | –0.446           | Leleji et al. (13) |

*NS, not significant.
necessary to transfer the genes to another better-adapted genetic background by a process of hybridization and selection. During this phase of the program many options are open to the breeder and only a few of the more commonly used methods will be outlined in the following sections.

**Breeding Methods to Maintain Nutritional Levels**

As indicated previously, even if a breeder does not aim to improve nutritional quality, the nutritional level should not be allowed to fall below an acceptable standard. In this case advanced lines must be screened to ensure that varieties of poor quality are not released. Table 3 shows the flow of genetic material in a conventional breeding program such as a pedigree or bulk population system. The generation in which single plant selection or nutritional screening is first carried out may vary from those indicated in the figure, though the basic scheme is common to all.

Following the identification of suitable parents, crosses are made and the F1s grown out. Selection is rarely carried out in the F1 generation, except following multiple crosses. Single plant selection may or may not be carried out in the F2, but frequently single plants are selected in the F2 generation, and the F4 is grown as progeny rows. Superior F4 rows may be bulked for testing in the F4 generation. It is at this stage that the agronomically superior lines can be screened for nutritional quality, and only those elite lines that have an acceptable nutritional standard should pass to the F6 yield trial stage. Sufficient quantities of seed are normally available following the F6 generation to begin biological evaluation.

**Breeding Methods for Nutrition Improvement**

A breeder may adopt one of several approaches to the nutritional improvement of pulses. In all cases, nutritional improvement should run concurrently with the improvement of other factors such as yield or disease resistance.

**Pedigree or bulk breeding**

In conventional breeding programs, the scheme followed for nutritional improvement follows the same general lines as that given in Table 3. The difference is that at least one of the original parents is chosen as a source of quality genes, and whenever selection is carried out in the segregating generations, sequential screening is undertaken. The top 20% of plants or bulks are selected on the basis of yield, agronomic or resistance characteristics, and the best of these are further screened and selected for nutritional quality. It is well known that the heritability of yield is very low in the pulses and sequential selection in the F2 generation should be on the basis of highly heritable resistance or agronomic characters followed by screening for nutritional factors of high heritability. Selection for yield and nutritional characteristics of low heritability should be reserved for later generations.

**Backcross breeding**

The backcross system is of particular value when it is desired to transfer genes for a particular nutritional characteristic from a donor gene source to an already elite genetic background. It is most effective for the transfer of major genes, especially if they can be recognized (e.g., in the case of genes for nutritional factors by a morphological pleiotropic effect), before or during flowering.

In conventional backcross breeding program,

<table>
<thead>
<tr>
<th>Season</th>
<th>Generation</th>
<th>Operation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Parents/ F1</td>
<td>Hybridization</td>
</tr>
<tr>
<td>2</td>
<td>F1/ F2</td>
<td>No selection</td>
</tr>
<tr>
<td>3</td>
<td>F2/ F3</td>
<td>Single plant selection and (or) bulking</td>
</tr>
<tr>
<td>4</td>
<td>F3/ F4</td>
<td>Single plant selection</td>
</tr>
<tr>
<td>5</td>
<td>F4/ F5</td>
<td>Bulking of best progeny rows</td>
</tr>
<tr>
<td>6</td>
<td>F5/ F6</td>
<td>Testing of bulks. Superior bulks screened for nutritional quality</td>
</tr>
<tr>
<td>7</td>
<td>F6/ F7</td>
<td>Further yield testing and biological evaluation</td>
</tr>
</tbody>
</table>
backcrosses are normally made between the B₁ (the generation following the backcross) and the recurrent parent. In attempting to transfer genes for nutritional quality in pulses, however, backcrosses are made between the B₂ generation and the recurrent parent, to allow selection for nutritional quality in the B₁/B₂ seed.

Table 4 gives an outline of a theoretical backcross breeding program for the transfer of genes for high protein to an agronomically elite genetic background. Only three backcrosses are shown in the table but in practice up to six or seven may be made.

**Population improvement**

Population breeding methods were originally developed for the improvement of cross-pollinated species, but their use has since extended to self-pollinated crops that have a high level of out-crossing or that are easy to pollinate by hand. The methods are particularly suited to the improvement of characters controlled by additive genes because a large number of parents can be used in the constitution of a population. In addition, because of the repeated cycles of hybridization and selection, a greater opportunity is provided for breaking up genetic linkages.

The basic scheme for population improvement in pulses is shown in Table 5, though many modifications are possible. The first step in the scheme is the setting up of the original population. This is done by crossing between the parents, either at random or in a controlled manner, for several generations to ensure a thorough mixing of the genes. Random crossing may be achieved through the use of pollinating insects in certain pulses such as pigeon peas and broad beans. The scheme is also possible if large numbers of crosses can be made by hand, either in crops that are easy to cross, or through the use of genetic male sterility. The identification of a reliable gametocide would allow the method to be used in those crops in which male sterility has not yet been discovered.

Following the constitution of the original population, the S₀ generation (tentative F₁) is grown out and single plants can be selected. The progeny of the selections are grown out in the S₁ (first selfed) generation and selection is carried out on a row basis. Superior rows in the S₁ are tested in the S₂ generation at several locations and the superior entries recombined the following generation. The cycle is then repeated and each cycle should result in an improvement of the population. At any stage superior plants can be selected and handled by normal pedigree or bulk population systems.

The method outlined above is based on S₂ testing; however, Rachie and Gardner (16) outlined several other population breeding methods that can be used in partially out-crossing species, and other methods, e.g., the diallel selective mating scheme (17), have been developed for use in self-pollinated crops. S₂ family testing requires four generations per cycle, which, in short duration crops like some of the Vigna and Phaseolus species, may be undertaken in a single year. More often 18 mo or 2 yr are required per cycle. Modifications such as S₁ family testing, half-sib family testing, and mass selection, requiring three, two, and one generations per cycle, respectively, may be adapted for pulse improvement in certain cases, though with
correspondingly reduced precision and efficiencies.

In a breeding program based on population improvement methods, the mainstream of the program should be devoted to the improvement and stabilization of yield and other agronomic characters. Separate subpopulations can be established for developing other characters such as disease resistance and nutritional factors. The selection pressure applied to the subpopulation will be for a single character only, and when sufficient advance has been made in the subpopulation, the character can be transferred to the mainstream population through an intermediate back-up population. This process is shown in Fig. 1.

**Future Trends in Nutritional Improvement**

Breeding for nutritional improvement in the pulses is still in its infancy and future research will undoubtedly enable breeders to handle their programs more effectively. At present, progress in nutritional improvement is limited by (a) the paucity of genetic knowledge, (b) the lack of suitable screening methods for many nutritional factors, and (c) the immediate need for emphasis on yield and agronomic and resistance characteristics.

The discovery of major genes for nutritional factors could revolutionize breeding for nutritional quality, especially if such genes are easily identified phenotypically. The search for male sterility in all pulses is likely to succeed and would enable many more crosses to be made. Likewise the development of gametocides would greatly simplify the hybridization process.

Techniques for crossing between species could play an important role in future pulse improvement programs and research is needed to identify closely related wild species having genes for superior nutritional quality. In a recent screening of eight lines of *Vicia narbonensis* (a species closely related to *V. faba*) one was found having over 33% protein in the seed. Some success has recently been attained in wide crossing among *Phaseolus* species in which lima beans (*P. lunatus*) were crossed with *P. pedicellatus* and *P. ritiensis*, and *P. vulgaris* was crossed with *P. ritiensis* (18). A bridge may thus be provided between *P. vulgaris* and *P. lunatus* that could result in the development of a broader range of genetic variability in both species. The initial results of crossing between lentils (*Lens culinaris*) and *L. orientalis* at ALAD also look promising.

**Table 5. Outline of a population breeding program using an S₂ testing procedure.**

<table>
<thead>
<tr>
<th>Step</th>
<th>Operation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Constitution of original population by random or controlled crossing between parents for several generations</td>
</tr>
<tr>
<td>2</td>
<td>The S₀ generation is grown out; single plants are selected for desired characters</td>
</tr>
<tr>
<td>3</td>
<td>The S₁ (first selfed) generation is grown out in progeny rows; selection is carried out on a row basis</td>
</tr>
<tr>
<td>4</td>
<td>The best rows from the S₁ generation are tested in the S₂ at several locations</td>
</tr>
<tr>
<td>5</td>
<td>The best entries in the S₂ trials are recombined by random or controlled crossing</td>
</tr>
</tbody>
</table>

Note: High protein lines have been identified at ICRISAT in derivatives of crosses between *Cajanus cajan* and *Atylosia* sp. *F₆* lines from crosses with *Atylosia scarabaeoides* and *Atylosia sericea* have given slightly over 30% protein, while within the *Cajanus* germ plasm the highest reading has been 28.8%.

Success in breeding for nutritional improvement may also be achieved through screening for physiological processes. As more becomes known about the ways in which a plant manufactures its protein, for example, so the possibility exists of screening for greater efficiency. Sprague (19) reported on a screening process to determine a plant’s capacity to reduce nitrate to nitrite, one of the steps involved in the synthesis of protein. By combining genes conferring efficiency for each step of the process, it is con-
Fig. 1. Outline of a population breeding program for the improvement of yield and protein content.

1) Superior plants from mainstream populations are combined with high protein selections to form the backup population.

2) Plants combining high yield with high protein are fed into the mainstream population.

It is conceivable that a genotype could be developed having a very good overall efficiency for producing protein.

As better screening techniques are developed, it will be possible to handle greater quantities of material with greater accuracy. The ultimate screening method will be nondestructive measurement of a single seed, as is already possible in measuring oil content by nuclear magnetic resonance.

References


In recent years, renewed attention by agricultural scientists has been given to the increased production of cereal grains and food legumes, because these basic foods can provide the basic energy and protein needs of populations living in the developing countries. To achieve increased productivity, plant breeders and other agricultural scientists are maximizing the efficiency of the plant to utilize energy, carbon dioxide, water, and soil nutrients; attention is also being given to a more efficient supply of limiting soil nutrients and to biological processes dealing with a more efficient control of plant diseases and pests.

The full meaning of productivity is not complete, however, if it stops with increased production per unit of arable land. Productivity (kilograms per hectare) must be viewed as the efficiency with which the nutrients in the food best meet the needs of the population, with minimum of waste. As expressed by the equation in Table 1, more efficient use of available arable land and of other factors in food production is concerned with production/hectare when corrected by the nutritive value and a technological value.

The basis for selection of food crops must, therefore, be based on production/hectare as the first component of productivity, modified by the nutritional quality, and finally by a technological index. The nutritional quality factor refers mainly to protein. The protein quality factor can be determined either by improvement of the nutritional composition of the food item by itself, or on the basis of the pattern of total food consumption of which the food item is commonly part. From the practical point of view the second approach appears sounder as well as easier to attain. The technological index refers to the attributes the food must have to be acceptable to both the consumer and the food processor.

Although increased production must continue to be the most important objective, nutritional considerations are also important to improve the efficiency of utilization of the food produced. Programs in this particular research area appear to have been impaired by the lack of clear objectives and recommendations to be followed by plant breeders; or in some instances, goals proposed by nutritionists are too ambitious and therefore difficult to attain.

### Table 1. Basis for selection of food crops.

| Productivity = Yield (kg/ha) × Nutritive value × Technological value |
| Nutritive value of the food itself or as component of a diet. |
| Expressed as utilizable protein or in terms of percentage of protein-calorie of total calories. |
| Technological value (includes all functional characteristics) expressed as percentage of standard. |

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