

cimmyt's maize germplasm management, improvement, and utilization program

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INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER

(CIMMYT)

summary

This paper discusses alternatives for improving the maize plant. While maize hybrids dominate in the developed world, open-pollinated varieties mostly are grown in the developing countries. The importance of population improvement in maize has been emphasized. Population improvement procedures not only improve the population for developing superior varieties but also increase the chances of extracting superior lines that will result in better hybrid combinations. The accomplishments in the development of population improvement methods in maize are discussed. Some of the important population improvement schemes, such as mass selection, modified ear-to-row selection, and several recurrent selection schemes, are briefly discussed. In addition, mating design-1 and some family selection schemes such as full-sib, half-sib, and S₁ have been mentioned.

CIMMYT's maize improvement program, including the research activities of the Advanced Unit, Back-Up Unit, Quality Protein, and Special Projects, is discussed. The structure and function of these units are presented. The Back-Up Unit handles the germplasm bank and the gene pools. A total of 29 gene pools are being improved continuously by the half-sib selection procedure. The handling of gene pools is discussed along with information on population size, selection in male and female rows before and after flowering, among- and within-family selection intensity, stresses to diseases and insects, adaptation, and introgression of new germplasm in the pools.

The various operations in the Advanced Unit are described both with normal and quality protein maize (QPM) populations. The full-sib system of family improvement is used in each population. Various stages in population improvement, such as progeny regeneration, progeny evaluation, and within-family improvement during the intervening cycles, are discussed. In addition to population improvement, site-specific and across-site experimental varieties are developed using approximately 10 top-performing families. The experimental varieties are evaluated in experimental variety trials (EVTs). The top performing EVs are designated as elites for further testing in elite experimental variety trials (ELVTs).

The breeding effort concentrating on special attributes such as earliness and resistance to downy mildew, stunt, and streak is described. Breeding for resistance to fall armyworm, borers, and earworm also is being practiced in the gene pools and populations. The technique utilizing larvae instead of egg masses has been presented and the field execution of insect resistance work is briefly described.

The problems encountered in QPM and the breeding strategy used in the accumulation and exploitation of genetic modifiers are discussed. The germplasm development effort and the breeding methodology used in breeding QPM has been presented. The salient features of the conversion process are given. The objective of QPM pools and their formation and handling have been discussed. The experimental evidence showing progress in pools and the performance of QPM materials in the international tests has been presented.

CIMMYT'S MAIZE GERMPLASM MANAGEMENT, IMPROVEMENT, AND UTILIZATION PROGRAM*

S.K. Vasal, A. Ortega C., and S. Pandey**

Importance of Population Improvement

The maize plant lends itself to genetic improvement both by inbreeding and cross-breeding procedures. These procedures provide alternatives to maize breeders for the development of maize types that will fall into two broad categories: (1) hybrid forms, which include single crosses, three-way crosses, double crosses, double top-crosses, and varietal hybrids, and (2) open-pollinated populations, in the form of local or improved varieties, which belong to particular races, broadbased composites, synthetics, and advanced generation varietal crosses.

Development and improvement of these materials, however, involve different breeding approaches. For example, in many developed countries of the world, where the hybrid seed industry is well developed, hybrids cover a large part of the total maize acreage. Consequently, the major research effort in these countries is geared towards the development of hybrid maize. Relatively less effort is devoted to population improvement.

The situation in most developing countries, however, is quite different. A hybrid seed industry either does not exist or does not do an adequate job of seed production and distribution. Also, cooperation between the private and the public sectors may be lacking; they often compete, rather than complement each other's effort.

Difficulties in seed production and distribution have prevented many countries from initiating time-consuming and expensive hybrid maize breeding programs. Thus, improvement schemes designed to improve populations and develop open-pollinated varieties seem to be a logical approach for many developing countries at the moment. With open-pollinated varieties, seed distribution can come about sooner—greatly facilitated by seed movement among the farmers themselves. The national programs with appropriate infrastructure can move toward a hybrid maize program.

Population improvement in maize need not be separated from hybrid maize development; improvements made in maize populations through various inter- and intrapopulation schemes can be profitably exploited in deriving new superior lines. As the genetic base of the material is continually improved, the opportunities to extract new and better lines become greater with each cycle of improvement. Therefore, population improvement programs are necessary if hybrid development is to maintain consistent gains over the long term. This, however, does not argue that better hybrids have not been developed in the past. On the

* "Population Improvement and Varietal Development in CIMMYT's Maize Program," an earlier version of this paper, was presented at the XVth Meeting of the Caribbean Food Crops Society, Paramaribo, Surinam, November 13-18, 1978

** Scientists, CIMMYT Maize Program

contrary, there has been remarkable progress, even without the use of classical population improvement schemes (Duvik, 1977). It is reported that much of the gain in the presently grown hybrids has been obtained from the improvement of established inbred lines through the pedigree method of inbred improvement, and that the gains from recurrent selection schemes in some synthetics from Iowa have been similar. Several other methods of inbred improvement also have been used, and these are reviewed in a paper by Bauman (1977).

Irrespective of objectives, population improvement in maize can play two important roles. Improvements made in populations through intrapopulation schemes (1) enhance the value of the population for direct and immediate use, and (2) increase their usefulness in developing new lines as potential parents of hybrids. There is sufficient data available to substantiate the idea that population improvement increases the expected performance of hybrids to a greater degree than repeated sampling of the same base population in the classical inbreeding and hybridization approach. Many breeders are aware of this; hopefully, there will be an increased realization that a balanced maize improvement program should place emphasis on the development and improvement of maize populations or source germ-plasm, in addition to development and improvement of inbred lines.

Maize Population Improvement Methods

The development and improvement of maize populations have generated considerable interest over the last two decades. Although earlier attempts to improve maize materials through mass selection had little success, there has been considerable progress in recent years. The failure to realize significant progress from earlier mass selection studies can perhaps be attributed to insufficient genetic control and inadequate field plot techniques.

An interest in quantitative genetics developed in the 1940s and voluminous data have been accumulated since then. Much of this renewed interest in improving populations stems from quantitative genetic studies in maize. Several empirical studies have indicated that there is a great amount of additive genetic variance for grain yield and other traits in heterozygous maize populations. Such findings indicate the effectiveness of various forms of intrapopulation breeding schemes in improving the performance of maize populations. The developments in quantitative genetics also have helped maize breeders to understand the types of gene action involved in the expression of different maize characters that are under polygenic control. This type of information is of considerable importance to the breeder when making a choice among alternative breeding schemes.

The quantitative geneticist also has helped the breeder in predicting genetic gains from various types of selection schemes. Several studies have been conducted using different selection schemes, and good agreement generally has been found between predicted and realized gains. The results of those studies have been reviewed by Gardner (1976) and Eberhart (1976).

Only a cursory review can be given of developments in population improvement methods. One of the simplest and oldest methods is mass selection. It exploits additive gene effects and epistatic interactions involving only additive genetic effects. Several researchers have used this method successfully (Johnson, 1963; Gardner, 1961, 1973, 1976). Mass selection can be effective for those characters that are highly heritable and can be identified before flowering, such as plant height, flowering, and susceptibility to northern corn leaf blight, thrips, and fall armyworm. The effectiveness of mass selection in changing ear number (Paterniani, 1978) and leaf angle (Ariyanayagam et al. 1974) also has been reported.

Stratified mass selection proposed by Gardner (1961) is an improvement over simple mass selection.

The modified ear-to-row selection scheme suggested by Lonnquist (1964) has been used quite widely and effectively in many programs (Webel and Lonnquist, 1967; Paterniani, 1967). This scheme involves selection among rows based on yield trial data, followed by selection within selected rows in the crossing block. It permits completion of one cycle of selection per year.

A modification of this scheme, using two seasons instead of one, also has been suggested. In the first season, only half-sib progenies are yield evaluated. In the second season, selected half sibs are recombined using remnant seed in a crossing block. For male rows, only the bulk of selected half-sib families is used. The prediction equation for estimating gains for this modified scheme has been given by Compton and Comstock (1976). Two generations per cycle are required to complete this scheme and may result in genetic gains of about one and one-half times more than the one generation per cycle scheme. An obvious advantage of this scheme involves the planting of fewer rows in the recombination block, allowing larger samples of each family to be grown. This results in an increase in the within-row selection intensity. The gains from within-family selection can thus be increased.

Several recurrent selection schemes have been suggested as a result of quantitative genetic studies. These include recurrent selection for general combining ability (Jenkins, 1940), recurrent selection for specific combining ability (Hull, 1945), and reciprocal recurrent selection for both general and specific combining ability (Comstock et al. 1949). These recurrent selection schemes differ in the type of tester and the ultimate use of the developed material. The critical differences in the schemes are based on the nature of gene action involved in the populations under selection. These schemes are similar in that they have successive cycles of selection and use only the selected portion of the population for recombination. When the only aim is to improve populations, the use of these schemes may not be highly efficient. It is probable that many of the yield increases that have been reported with these methods are primarily results of additive effects (Sprague, 1967). If this is so, it is more appropriate to exploit additive genetic effects through phenotypic recurrent selection or through various forms of family selection schemes without the use of the tester.

Various types of mating designs have been suggested by Comstock and Robinson (1952); three of their suggested genetic designs are useful in estimating additive dominance, and average degree of dominance effects. Design I is particularly effective for maize and has been used quite frequently, not only to work out genetic variances but also to identify best families for recombination and improvement in a practical maize breeding program. Also, the data can be used more efficiently in selection, taking advantage of information on both half sibs and full sibs.

Several family selection schemes have become quite popular in recent years, including full-sib, half-sib, and S_1 selection schemes. A combination of S_1 and half-sib systems also can be used for improvement of some traits, but cannot be recommended as a general breeding method.

CIMMYT's Maize Improvement Program with Gene Pools and Populations

CIMMYT's maize improvement program is a multi-stage process with a continuous, systematic flow of germplasm (Ortega et al. 1980; Paliwal and Sprague, 1981). CIMMYT

strongly believes in the interdisciplinary approach, where scientists from various disciplines can work together. The maize pyramid (Figure 1) illustrates the management of the germplasm flow at different stages of maize improvement, from initial research until it reaches the hands of the farmers. CIMMYT's maize improvement program, for management and reporting purposes, is comprised of two main stages called the Back-Up and Advanced Units. Quality protein versions of most materials have been and continue to be developed through a side-car approach as a parallel integral part of the process. Special Projects Unit has the responsibility of exploring and testing new research hypotheses, and the resulting useful information and products are incorporated in the main research activities of the program.

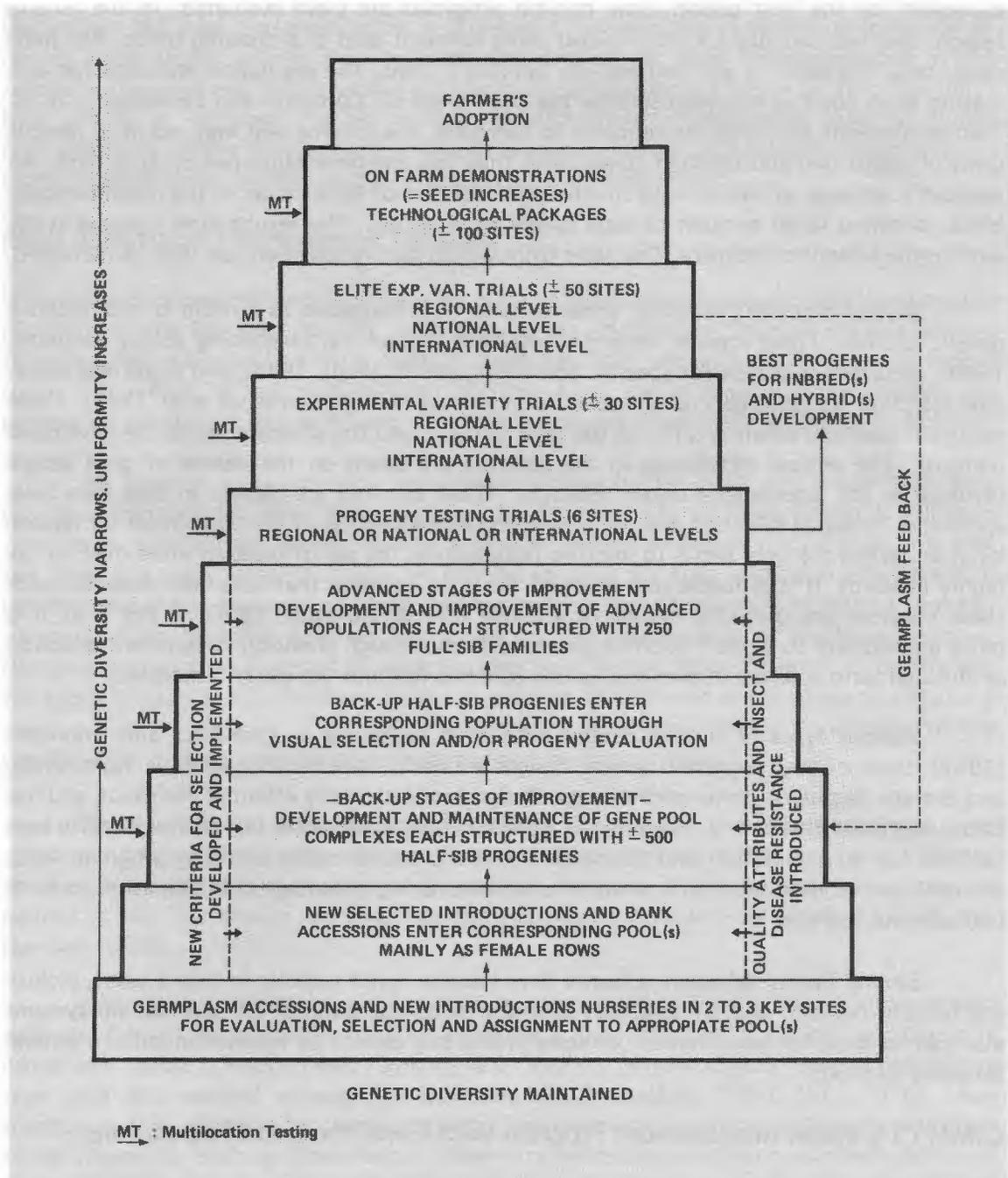


Figure 1. Stages in maize germplasm management and improvement

The Back-Up Unit serves as a support unit to provide superior genotypes or families to the Advanced Unit on a continuous basis (Figure 1) so that improvements in Advanced Unit materials can be obtained from cycle to cycle. In this way, reduction of genetic variability in Advanced Unit materials can be minimized. A similar approach was suggested by Harrison (1967), who recommended the use of back-up pools with only mild selection intensity to support the population undergoing improvement at a high selection intensity.

back-up unit

The Back-Up Unit handles the maize germplasm bank, new introductions, and 29 gene pools that have specified climatic adaptation, maturity, grain color, and texture.

The maize germplasm bank now has over 13,000 accessions representing 46 countries. It is a service unit, for resident and collaborating scientists, which maintains and catalogs the germplasm collection and renews stock as needed. Periodically, approximately 300 collections are evaluated systematically at two or more locations with appropriate pools as checks. The best performers are grouped according to their adaptation, maturity, grain color, and texture. In the following season, the selected bank collections are incorporated into the appropriate pools as female rows only. Observations can be made for the combining ability of the pools x collections and, if needed, this can be carried to F₂. Based on the performance of topcrosses, the families from these crosses are later merged with the main body of the pool.

CIMMYT requests and receives seed samples of maize materials from various programs around the world. These are grown in observation nurseries at one or more locations. The promising entries are identified and then systematically incorporated into the appropriate gene pools.

Gene pools are mass reservoirs of genes and have a broad genetic constitution. They are formed by genetic mixing of several diverse varieties, variety crosses, and hybrids with similar climatic adaptation, maturity, grain color, and texture.

CIMMYT gene pools meet the climatic requirements of tropical highland, tropical lowland, and subtropical zones. The pools within each climatic adaptation are further classified on the basis of maturity (early, intermediate, and late), grain color (white and yellow), and grain texture (flint, dent, and floury). Of the 29 gene pools, 9 are meant for tropical highland, 12 for tropical lowland, and 8 for subtropical zones. In addition, 4 new pools have been developed for temperate maize-growing areas (Table 1).

Handling and Improvement of the Gene Pools

Each gene pool is handled separately in isolation in a half-sib recombination system similar to a modified ear-to-row crossing block (Figure 2). Several modifications to the commonly used half-sib system are used, however, depending on the priorities and objectives that have been set for each pool. Two cycles of recombination and selection are completed each year in all the pools except the late highland gene pools.

The population size of each pool is kept fairly large; families within each pool range in number from 400-500. Each family has 16 plants in a 5-meter row, providing a total number of 6,400 to 8,000 female plants. Another 3,200-4,000 plants are males in the pollinator rows. In total, there is an effective population of 9,600 to 12,000 plants within each pool.

Table 1. Maize gene pools and corresponding populations in CIMMYT's maize improvement scheme

Pool No.	Pool Name	Pop. No.	Population Name
1	Highland Early White Floury	1	Blanco Harinoso Precoz
2	Highland Late White Floury	—	—
3	Highland Early Yellow Floury	2	Amarillo Harinoso Precoz
4	Highland Late Yellow Floury	3	Chillos Varios
5	Highland Early White Morocho	—	—
6	Highland Early Yellow Morocho	—	—
7	Highland Late White Morocho	—	—
8	Highland Late Yellow Morocho	—	—
9	Highland Late White Dent	—	—
15	Tropical Early White Flint	30	Blanco Cristalino-2
16	Tropical Early White Dent	—	—
17	Tropical Early Yellow Flint	31	Amarillo Cristalino-2
18	Tropical Early Yellow Dent	35	Antigua Republica Dominicana
19	Tropical Intermediate White Flint	23	Blanco Cristalino-1
20	Tropical Intermediate White Dent	49	Blanco Dentado
21	Tropical Intermediate Yellow Flint	26	Mezcla Amarilla
22	Tropical Intermediate Yellow Dent	24	Antigua Veracruz 181
23	Tropical Late White Flint	25	Blanco Cristalino-3
		32	ETO Blanco
24	Tropical Late White Dent	21	Tuxpeño 1
		22	Mezcla Tropical Blanca
		29	Tuxpeño Caribe
		43	La Posta
25	Tropical Late Yellow Flint	27	Amarillo Cristalino-1
26	Tropical Late Yellow Dent	28	Amarillo Dentado
		36	Cogollero
27	Subtropical Early White Flint	—	—
28	Subtropical Early White Dent	—	—
29	Subtropical Early Yellow Flint	46	Templado Amarillo Cristalino
30	Subtropical Early Yellow Dent	48	Compuesto de Hungría
31	Subtropical Intermediate White Flint	34	Blanco Subtropical
32	Subtropical Intermediate White Dent	44	AED Tuxpeño
		42	ETO Illinois
		47	Templado Blanco Dentado
33	Subtropical Intermediate Yellow Flint	33	Amarillo Subtropical
34	Subtropical Intermediate Yellow Dent	45	Amarillo del Bajío
—	Northern Temperate Range Gene Pool	—	—
—	Southern Temperate Range Gene Pool	—	—
—	Intermediate Temperate Range Gene Pool	—	—
—	CIMMYT German Gene Pool	—	—
—	White Flint QPM* Pool	40	White QPM
—	White Dent QPM Pool	—	—
—	Yellow Flint QPM Pool	39	Yellow QPM
—	Yellow Dent QPM Pool	—	—
—	Temperate Tropical QPM (Flint)	41	Templado Amarillo QPM
—	Temperate Tropical QPM (Dent)	—	—

* Quality protein maize

The ratio of females to males in the pools is kept at 2:1 in the recombination block. Male and female rows are planted at the same time and, if necessary, the male row planting dates can be staggered to permit thorough mixing within the pool. In some pools

Depending on their use in various locations, the pools are subjected to different stress pressures. These include sugarcane borer (*Diatraea saccharalis*), Pools 19 and 21; Southwestern corn borer (*D. grandiosella*), Pool 32; fall armyworm (*Spodoptera frugiperda*), Pools 24 and 26; corn earworm (*Heliothis zea*), Pools 1 and 3; ear rots, Pools 1, 2, 3, 4, 5, 6, and 7 with *Fusarium roseum*; Pools 20, 25, 29, 33, and 34 with *F. moniliforme*; stalk rots, Pools 15, 16, 17, 18, 22, 23, and 30 with *F. moniliforme*.

In addition to serving as pollinator for the female rows, the male rows of each pool are used for improving resistance to both ear and stalk rots. This is done by selecting 500 agronomically desirable plants around flowering time. The selected plants are artificially inoculated with stalk and ear rots. In ear rots, the spore concentration is five times greater than the one used in the normal inoculation. The ears saved at harvest are included in the same pool to further upgrade the level of ear and stalk rot resistance.

Mild selection is applied within each pool to prevent depletion of attributes or genes necessary for further advancement at a later stage. Lower selection intensity also provides better chances and opportunities for recombination among linked genes that with higher selection intensity would probably be discarded much earlier. Among-family selection pressure is about 50 to 60 percent and within-family selection in selected families is about 6 to 18 percent.

At harvest, the selected ears are classified as male (pollen source for the following cycle) and female ears. The male ears are selected from the promising families and plants. Approximately 70 percent of the selected ears fall in this group. Then, in the following cycle, all selected ears (both male and female) enter as separate female families in the half-sib crossing block. The male rows are planted with a balanced male composite made up only of selected male ears.

Promising accessions from the bank or the introduction nursery can be added as female rows in the pool. The families from the cross can be planted again as female rows and then rejected or integrated into the main pool body, depending on their performance. New additions permit continuous broadening and improvement of the pool.

Improvements or changes in each pool from cycle to cycle can be effectively monitored by planting two or more rows of each cycle of selection, with or without replications, at the end of each pool. While gene pools are being improved for stress traits, all possible care is taken to maintain genetic diversity within each pool. This would require that families or plants that are not suitable for stress traits, but otherwise show promising agronomic traits, be saved and used in the next cycle of recombination.

Bulks from various pools also are sent to CIMMYT staff members stationed in various regions. Ears saved from each location are brought back to Mexico to be included in the pools. Thus, the potential influences of other environments are introduced into the pools. This helps to further improve their adaptation.

Corresponding Advanced Unit populations are planted periodically as check entries within each pool to identify superior families for further evaluation and incorporation in the Advanced Unit populations. To obtain a quality protein version of a pool, a bulk of stable hard endosperm QPM families can be planted as female rows in the pool, with back crosses made every three or four cycles.

In summation, gene pools are recombined, improved continuously, and broadened regularly with the addition of new introductions from the national programs and with superior matching entries from the maize germplasm bank. The progress made in different pools for important agronomic traits is given in Table 2. The latest cycles are significantly higher yielding, earlier, and shorter in plant height.

Table 2. Progress made in selected pools for some important characters

Pool No.	Name	Cycles	Yield kg/ha	Days to 50% silking	Ear Ht. (cm)
Pool 15	Tropical Early White Flint	C ₀	2787	85	98
		C ₄	2917	83	81
		LSD (.05)	304	1.5	9.4
Pool 21	Tropical Intermediate Yellow Flint	C ₁	3890	73	118
		C ₈	4429	70	105
		LSD (.05)	230	0.1	3.7
Pool 24	Tropical Late White Dent	C ₁	4208	78	101
		C ₈	4519	76	92
		LSD (.05)	235	0.7	3.8
Pool 27	Subtropical Early White Flint	C ₁	4144	82	100
		C ₉	4086	78	80
		LSD (.05)	392	1.4	7.3
Pool 34	Subtropical Intermediate Yellow Dent	C ₁	4224	70	112
		C ₉	5700	67	95
		LSD (.05)	316	0.6	4.4

advanced unit

The Advanced Unit deals with normal maize and quality protein maize populations. Presently the unit is handling 27 populations, three of which carry the opaque-2 gene (Table 3). These populations are divided into two groups: group 1 consists of 13 populations, group 2 has 14 populations. Each population is sent out for International Progeny Testing Trials (IPTTs) every other year. The group 1 populations are tested in even years and group 2 populations in odd years. All populations are handled directly from CIMMYT, except Population 43 (La Posta), in cooperation with IITA, Nigeria, for streak virus resistance; Populations 22 (Mezcla Tropical Blanca), 28 (Amarillo Dentado), and 31 (Amarillo Cristalino-2), with the Thai National Maize Program, for downy mildew resistance; and Population 48 (Compuesto de Hungría), with the Turkish National Maize Program, for stalk rot resistance. These populations have been improved for yield, plant height, maturity, diseases, and other traits over two to three cycles using international progeny testing.

Before a given material is considered for the international testing program, several criteria are examined. First, populations are evaluated in variety tests in different countries;

Table 3. Advanced populations, traits emphasized in their improvement, and the corresponding pools

Pop. No.	Population Name	Group	Cycle of Selection	Emphasis on Trait(s)	Corresponding Pool
21	Tuxpeño 1	2	4	Fall armyworm resistance	24
22	Mezcla Tropical Blanca	1	4	Downy mildew resistance	24
23	Blanco Cristalino-1	1	4	Sugarcane borer resistance	19
24	Antigua Veracruz 181	1	4	Fall armyworm resistance	22
25	Blanco Cristalino-3	2	4	White flint kernel	23
26	Mezcla Amarilla	2	4	Ear rot resistance	21
27	Amarillo Cristalino-1	1	4	Sugarcane borer resistance	25
28*	Amarillo Dentado	2	4	Downy mildew resistance	26
29	Tuxpeño Caribe	2	4	Reduced plant height	24
30	Blanco Cristalino-2	2	1	White flint kernel	15
31*	Amarillo Cristalino-2	2	1	Downy mildew resistance	17
32	ETO Blanco	1	3	Ear rot resistance	23
33	Amarillo Subtropical	1	1	Ear rot resistance	33
34	Blanco Subtropical	2	4	Reduced plant height	31
35	Antigua Republica Dominicana	1	3	Standability	18
36	Cogollero	2	4	Reduced plant height	26
39	Yellow QPM	2	1	Ear rot resistance	25 QPM
40	White QPM	2	4	Ear rot resistance	23 QPM
41	Templado Amarillo QPM	2	2	Ear rot resistance	33 QPM
42	ETO Illinois	2	3	White dent kernel	32
43**	La Posta	1	4	Streak virus resistance	24
44	AED Tuxpeño	1	3	Resistance to foliar diseases	32
45	Amarillo Bajío	1	1	Ear rot resistance	34
46	Templado Amarillo Cristalino	2	0	Ear rot resistance	29
47	Templado Blanco Dentado	1	1	Southwestern corn borer	32
48***	Compuesto de Hungría	1	3	Stalk rot resistance	30
49	Blanco Dentado	2	0	Husk cover	20

* Being improved in cooperation with Thai National Corn and Sorghum Program

** Being improved in cooperation with International Institute of Tropical Agriculture (IITA)

*** Being improved in cooperation with Turkish National Maize Program

then, depending on their performance, they are sent to locations having the most potential for that material. In some cases, previous experience is used in the decision-making process, depending upon the type of germplasm involved and the genetic constitution of the population. For many populations, it is possible to make fairly accurate predictions about the areas or regions of their adaptation.

The full-sib family selection scheme is used for improvement of Advanced Unit populations. In each population, 250 reciprocal full sibs are developed and evaluated in international progeny tests both in the northern and southern hemispheres. Approximately 80-100 full-sib families are selected on the basis of across location data for the next improvement cycle. Since the retrieval of data takes about one year, one cycle of selection is completed in two years. The intervening period between the two cycles is utilized to improve the population for the most deficient trait.

Improvement of Advanced Unit Populations

The full-sib family selection method involves the following steps (Figures 3 and 4):

- (1) **Progeny Regeneration:** 250 full sibs are developed from each population through reciprocal plant-to-plant crosses among families. This provides sufficient seed for use in progeny evaluation, initiating the next cycle of improvement, and development of experimental varieties. In quality protein populations, only those pairs are saved in which both members are well modified with respect to endosperm hardness.
- (2) **International Progeny Testing Trials:** A total of 250 full sibs plus six checks are tested at six different sites, preferably in different countries, using a 16 x 16 simple lattice with two replications.
- (3) **Within-Family Improvement:** All 250 families are planted in the following season. Within-family selection is made for the deficient characteristics. Should data be available from sufficient locations before pollination, a preliminary selection can be made to save about 50 percent of the families. In such cases, within-family selection is restricted to the selected families.

Sibs or plant-to-plant sibs are made within each family to maintain the identity of the family. Within-family sibs are usually made for characteristics that can be observed before or at flowering time. For other characteristics, where the trait expression can be judged best at harvest time, either sibs or reciprocal plant-to-plant crosses are made within each family. In quality protein maize populations, when the aim is selection of better modifiers, reciprocal plant-to-plant crosses are made within each family. At harvest, an average of three sibs or three sibs is selected from each family.

- (4) **Family Improvement and Recombination:** The sibs or sibs from each family are planted in the next season. A full record is kept of all sub-families originating from each parental family. Before pollination, data usually arrive from various locations and it is possible to identify superior families on the basis of across-location data.

Selection for the same traits is again made, both among and within sub-families of a given parental family. The better individuals within the set of selected sub-families of each parental family are marked and bulk-pollinated in a hand-pollinated half-sib fashion. An average of two or three half-sib ears are selected from the progeny of each original parental full-sib family that has been selected according to across-location performance.

The selected half-sib ears are planted on an ear-to-row basis. A record is kept of all half sibs originating from the parental full-sib families. Reciprocal plant-to-plant crosses are made among half-sib families originating from different parental full-sib families. At harvest, 250 full-sib pairs are saved to continue the next cycle of selection.

A selection intensity of 30-35 percent is used in each population. As the program has evolved, the germplasm in the Advanced Unit populations has improved through selection, by partial replacement through incorporation of outstanding half-sib

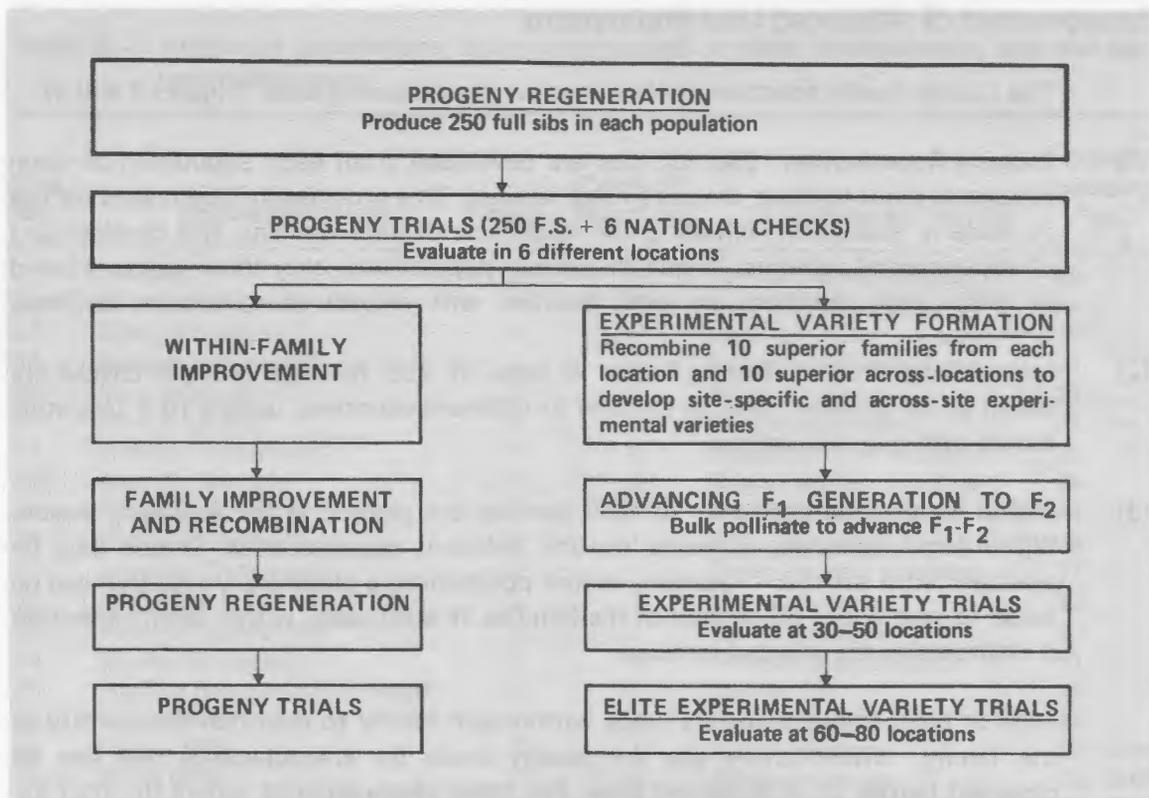


Figure 3. Steps in population improvement and experimental variety development and evaluation

STEP	SEASON	GERMPLASM IMPROVEMENT				
1	A	<u>PROGENY REGENERATION NURSERY</u> Plant \pm 300 half sibs to generate 250 F.S. families for IPTT				
		<u>PROGENY TRIALS (250 F.S. + 6 NATIONAL CHECKS)</u> <table border="1" style="margin: auto; text-align: center;"> <tr> <td>Loc. 1</td> <td>Loc. 2</td> <td>Loc. 3</td> <td>Loc. 4</td> <td>Loc. 5</td> <td>Loc. 6</td> </tr> </table>	Loc. 1	Loc. 2	Loc. 3	Loc. 4
Loc. 1	Loc. 2	Loc. 3	Loc. 4	Loc. 5	Loc. 6	
3	A	<u>WITHIN-FAMILY IMPROVEMENT</u> 1. Make selfs or within-family sibs in 100 across-site selected F.S. families 2. Save 3 sibs or selfs from each selected family				
4	B	<u>FAMILY IMPROVEMENT AND RECOMBINATION</u> 1. Plant 240-300 sub-families from \pm 80-100 selected F.S. families 2. Select one best sub-family from each selected F.S. family 3. Select best plants from each selected sub-family and bulk pollinate 4. Save \pm 300 H.S. ears				
1	A	<u>PROGENY REGENERATION NURSERY</u> Plant \pm 300 H.S. to generate 250 F.S. families for next cycle of improvement				

Figure 4. Population improvement scheme breeding sequence

families, and/or by complete substitution of the population. New populations are created by using the 200-300 best half-sib families from the gene pools. The incorporation process normally includes (1) development of full sibs, (2) evaluation in IPTT along with the families of the population, and (3) selection of superior families for final incorporation into the respective population(s).

Table 4 shows the selection gains in seven populations for three important agronomic attributes. The gains per cycle vary from 0.75 percent to 4.05 percent with an average gain of 2.60 percent. All populations registered height reduction with an average gain of 2.5 cms per cycle. The average maturity was lowered by approximately half a day.

Table 4. Gains from selection in seven advanced populations (across 3 locations data—1979)

Population	Grain yield in kg/ha		°/oGain per cycle/year	Plant height in cm.		Gain per cycle/year	Days to 50°/o silking		Gain per cycle/year
	C ₀	C ₂		C ₀	C ₂		C ₀	C ₂	
Tuxpeño 1	5200	5429	2.20	202	198	-2.0	63.2	63.5	+0.2
Mix.1.Col.Gpo.1 ETO	5172	5422	2.40	209	204	-2.5	63.7	62.7	-0.5
Mezcla Amarilla	4724	5017	3.10	199	197	-1.0	61.8	60.8	-0.5
Amarillo Dentado	5015	5311	2.95	234	228	-3.0	64.8	64.1	-0.4
Tuxpeño Caribe	5423	5718	2.70	214	210	-2.0	63.8	63.8	-0.0
ETO Blanco	4378	4442	0.75	211	203	-4.0	63.9	63.4	-0.3
Ant.Rep.Dom.	4651	5029	4.05	185	181	-2.0	58.5	57.8	-0.4
\bar{X}	4938	5195	2.60	208	203	-2.5	62.8	62.3	-0.3

Development of Experimental Varieties (EV)

A selection intensity of four percent is used in the development of experimental varieties. The varieties are developed on the basis of site-specific and across-site progeny test data. Thus, each population has a potential of producing seven experimental varieties (six site-specific and one across-site). Since the superior fraction of each population is sampled to form the experimental variety, it is expected that these varieties will show considerably higher performance as compared to the population mean, and have increased potential for immediate use and exploitation. In the formation of experimental varieties, the approximately ten superior high-yielding families with relatively uniform agronomic attributes are recombined so that the variety will be uniform in appearance.

In the formation of experimental varieties, diallel matings are made among the selected families. Uniformity among families and plants should be emphasized in recombination at this stage. At harvest the ears from each family, resulting from crosses with the other families, are saved and shelled as a bulk. A pre-calculated quantity is taken from each family bulk to make the F₁ bulk. This is advanced next season to form a random mating variety to reduce the heterotic effects and to provide seed increase for experimental variety trials (EVTs) and elite experimental variety trials (ELVTs).

The experimental varieties are named so that cooperators from different national programs who conduct the progeny tests will receive full recognition. Variety names are derived from the name of the station where the progeny test was conducted, followed by

two digits indicating the year of test. The last two figures show the population number (e.g. Tocuemen 7428).

Experimental Variety Trials (EVTs)

As noted, the site-specific and across-site experimental varieties are developed on the basis of progeny trial data. The experimental varieties so formed from different populations are grouped into experimental variety trials 11 through 17. EVT 15 is reserved for experimental varieties derived from Advanced Unit QPM populations. Each EVT is tested internationally in 30 to 40 locations. Table 5 shows the superiority of experimental varieties over their parental population.

Table 5. Performance of experimental varieties and their parental population

Experimental variety	Parental population	Grain yield kg/ha		Experimental variety yield as percent of parent population
		Exp. variety	Parental population	
Gemiza 7421	Tuxpeño 1	4456	3965	112.4
Poza Rica 7429	Tuxpeño Caribe-2	4235	4683	110.5
Across 7443	La Posta	4865	4184	116.2
Sids 7444	AED Tuxpeño	4166	3370	123.6
Delhi 7439	Yellow QPM	4272	3410	125.2
Cuyuta 7441	Composite K.H.E.02	4363	3685	118.3
San Andres 7440	White QPM	4274	3863	110.6

Elite Experimental Variety Trials (ELVTs)

The superior experimental varieties across locations are evaluated in the elite experimental variety trials. These elite experimental variety trials carry trial numbers from 18 through 20. ELVT 18 is reserved for tropical lowland, ELVT 19 for QPM, and ELVT 20 for subtropical materials. These ELVTs are sent to more than 50 locations around the world.

Off-Station Trials and Farmer Adoption

Promising elite experimental varieties can be tested in off-station trials by the national programs. After verification on larger plots, the variety then can be made available to the farmer. There must be a simultaneous seed increase of superior varieties so that enough seed is available at the time of the release.

breeding for some special attributes

The following describes the ongoing program for maize improvement for special characteristics. These include (1) breeding for earliness, (2) breeding for resistance to downy mildew, stunt, and streak virus, (3) breeding for insect resistance, and (4) breeding for quality protein maize.

Breeding for Earliness

Early maize varieties are needed in many parts of the world to fit more readily into the cropping pattern or to make full use of the growing season because of a particular

rainfall pattern. In general, very early materials are susceptible to foliar diseases and have low yield potential, even under reasonably high plant population densities. Over the past four years, CIMMYT has placed major emphasis on developing earlier genotypes for tropical, sub-tropical, and highland areas. Four approaches are being used to develop early materials:

- (1) Recurrent selection for earliness in a mid- to full-season maize population.
- (2) Crossing early types with mid- to full-season materials, followed by recombination and selection for earliness along with other desirable agronomic characteristics.
- (3) Intercrossing among early types, followed by recombination and selection for yield and resistance to foliar diseases without sacrificing earliness.
- (4) Intercrossing early tropical maize with US Corn Belt maize with the objective of combining yield, earliness, and resistance to foliar diseases.

In approach 1, about 400-500 families are being handled in an early composite using a half-sib selection program. Early plants are marked in the families and when 60 to 70 percent of the plants have silked, tassels are removed from the male rows to eliminate the later maturing fraction of the population. The material then is harvested relatively early to aid in visual separation of the drier ears. Only the best relatively drier ears from superior early plants are selected for continuation in the next cycle.

The same approach is being used in some pools, except that the experimental material has been derived from the crosses of early composites with full- to mid-season Advanced Unit maize populations. Findings from approaches 1 and 2 indicate that it is possible to produce materials half-to-one-day earlier each cycle, while maintaining about the same yield level. The last two approaches also have been tried, but results have not been encouraging.

Breeding for Resistance to Stunt, Streak, and Downy Mildew

Three maize diseases have become increasingly important in recent years. These pose potential danger to many maize-growing areas of the world: stunt in Central America and Mexico, streak virus in Africa, and downy mildew, mainly in Asia, although it also has been reported in Central and South America and Africa. In 1974 a collaborative research project was initiated between CIMMYT and six national programs to develop maize germplasm resistant to these diseases. Initially three genetically broadbased agronomically superior maize populations were chosen for this work. They had different grain colors and textures and could be grown satisfactorily in many parts of the world.

In improving genetic resistance to these diseases, a shuttle breeding approach was followed. The collaborating countries were Thailand and the Philippines for downy mildew, El Salvador and Nicaragua for corn stunt, and Tanzania and Zaire for streak virus. Alternate cycles of selection were carried out in 'hot-spot' areas of the collaborating countries to select agronomically desirable disease-resistant plants. The resistant selections then were recombined and further selected for agronomic characters in the following season in Mexico.

By 1980, four cycles of selection had been completed in each population and it was becoming apparent that an adequate level of field resistance had been attained for corn stunt and downy mildew diseases. A systematic population improvement program was intro-

duced at this point. Full sibs were developed from downy mildew and corn stunt resistant populations and the progeny trials were sent for evaluation to countries where these diseases had a good chance of expression under natural conditions. Based on the test data, stunt and downy mildew resistant experimental varieties were developed in Mexico. These experimental varieties have been tested in special downy mildew and corn stunt trials and used by various national programs.

With the relocation of the Asian regional program to Thailand, and establishment of the West African regional program at IITA, Nigeria, the responsibility for the development of resistance to downy mildew and streak virus was shifted to these programs, respectively. The work on downy mildew now involves three Advanced Unit populations—Mezcla Tropical Blanca (Pop. 22), Amarillo Dentado (Pop. 28), and Amarillo Cristalino-2 (Pop. 31). The distribution of international nurseries and further improvement of these populations is carried out in cooperation with the Thai National Maize Program with major emphasis on downy mildew resistance. Similarly, the work on developing resistance to streak virus is now carried out in collaboration with IITA, Nigeria in population La Posta (Pop. 43).

Breeding for Insect Resistance

Breeding insect resistant materials requires mass rearing and artificial infestation facilities. To meet this need, an insect-rearing facility was developed at CIMMYT in 1974. Four insect species currently are being reared: fall armyworm, sugarcane borer, Southwestern corn borer, and corn earworm. Techniques for insect rearing and larva production and collection have been improved, and sufficient numbers can be produced to artificially infest several back-up pools and advanced maize populations with larvae.

The artificial infestation technique needs special mention as it is a remarkable improvement over what entomologists have used in the past (Ortega et al. 1980). The new technique uses newly hatched larvae, instead of egg masses, mixed with ground corn cobs. This mixture is applied in the whorls with the help of a larval dispenser (bazooka) in the case of fall armyworm and borers, and on fresh silks, for earworms. The technique has considerably speeded up the insect resistance work at CIMMYT and has many advantages: active larvae begin to feed immediately and are less exposed to predators; speed and uniformity of infestation are enhanced; timeliness of infestation can be better regulated, and plants escaping infestation are reduced considerably.

For improving the level of resistance in Pools 24 and 26, eight plants in each family (female rows) are infested at the three to four extended leaf stage, depositing in the whorl two precalibrated discharges of about 20 first instar fall armyworm larvae. Three discharges of about 10 first instar larvae of the sugarcane borer in Pools 19 and 21 and of Southwestern corn borer in Pool 32 are applied when the plants reach the six to eight extended leaf stage. Split application of larvae reduces the variation in the number of larvae that each plant receives. The remaining eight plants of each family (female rows) are protected with granular insecticides. The relative yield differences between protected and infested portions together with leaf feeding ratings are used to identify families that possess both antibiosis and tolerance.

In Pools 24 and 26, all plants in the pollinator rows (male rows) are infested at seedling stage (16 hills, two plants each). At thinning, the most damaged plant in each hill is removed. At flowering, about 30 percent of the more damaged plants are detasseled before pollen shed. In Pools 19, 21, and 32, infestations of all plants in the pollinator rows are

done after thinning, and 30 percent of the most damaged plants are detasseled before pollen shed.

The highland pools (1 and 3) are infested with corn earworm when a full silk brush is present. About ten first instar larvae are discharged twice on the silks. Damage is estimated by measuring the larval penetration in centimeters at harvest time.

All breeding nurseries are established with insecticide-fungicide coated seed. This seed treatment ceases to be effective by the time the plantlets are to be artificially infested. When necessary (because of weather conditions or availability of insect material for artificial infestation), additional insecticide protection may be provided to prevent natural insect infestation.

When the availability of insect larvae permits, two to three infestations may be done to maintain the pressure up to the preflowering stage and select the plants that have the least amount of damage to first and second insect generations.

To determine plant reaction to larval leaf feeding in maize pools and populations, a rating scale of 1 (no damage) to 5, or 1 to 9 (severe damage), is used. Preference is for the 1 to 9 scale, where 1-3 includes the resistant types, 4-6 the intermediate, and 7-9 the susceptible ones. Two to four ratings may be conducted before flowering to finally select the least damaged families and plants.

In addition to the maize pools indicated above, Populations 21 (Tuxpeño 1) and 24 (Antigua Veracruz 181) are being improved for resistance to fall armyworm; Populations 23 (Blanco Cristalino-1) and 27 (Amarillo Cristalino-1) for resistance to sugarcane borer; and 47 (Templado Blanco Dentado) for resistance to Southwestern corn borer. Two cycles of S₂ recurrent selection in Tuxpeño 1 have generated a synthetic with an intermediate level of resistance.

In these populations, 8-16 plants in each family are infested in replicated or unreplicated nurseries and evaluated and selected as described for the pools.

Breeding for Quality Protein Maize

In developing quality protein maize (QPM), the opaque-2 gene has been used most extensively. Unfortunately most QPM materials have problems of reduced grain yield, unacceptable soft, chalky endosperm, slower drying following physiological maturity of the grain, and more vulnerability to ear rots and stored grain pests. These problems are fairly complex in nature and have acted as the major hurdle in the promotion and acceptance of QPM materials by the farmers. In order to develop commercially acceptable QPM materials with improved nutritional and biological value, it is extremely important that the major research thrust be placed on solving the above-mentioned problems. Though various research ideas and breeding approaches were explored and tried in order to remedy problems confronting QPM materials, the breeding strategy based on the accumulation and exploitation of genetic modifiers of the opaque-2 locus was found the most appropriate alternative (see Vasal et al. 1979, 1980; Paliwal and Sprague, 1981). Before this approach could be used effectively, however, there was a need to develop the donor stocks carrying the opaque-2 gene with modified endosperm. Though variation did exist in soft opaque-2 materials for kernel modification, a selection process had to be independently initiated in several genetic backgrounds. The partial modified types developed through the selection process were

intermated to permit pyramiding of these modifying genes. This then produced an altered phenotype almost indistinguishable from the normal endosperm. During the selection process, the protein quality was continuously monitored through laboratory analysis to maintain it at a desirable level.

The development of suitable donor stocks with completely normal kernel phenotype was a genetic breakthrough which inspired new hopes and optimism and laid the foundation for the current QPM breeding effort. In 1974, a complete switch-over was made to the breeding strategy involving the use of genetic modifiers. Concerted research efforts were initiated at this time to develop a wide array of QPM germplasm using normal maize populations and gene pools available in the advanced and back-up stages of the maize program. Two main breeding approaches were used in developing QPM germplasm: development of QPM versions of normal maize genotypes through the conversion process, and development of hard endosperm QPM gene pools. Both approaches are discussed below.

● Development of QPM versions

To develop QPM versions with modified kernel appearance, the normal maize genotypes are crossed with one or more appropriate QPM donor stocks with vitreous endosperm. Since the incorporation process involves the introduction of the opaque-2 gene and also the favorable genetic modifiers from the donor stocks, the conventional backcross program cannot be used effectively to handle both the simple and complex genetic systems involved in the conversion program. It is important that, following each backcross, the frequency of genetic modifiers be raised adequately before actually making the ensuing backcross. A combination of backcross and recurrent selection breeding approaches has been designed to develop acceptable types of QPM materials and to capitalize on the improvements made in the recurrent parent. The breeding scheme used in the conversion process (Figure 5) has the following unique features:

1. An improved version of the recurrent parent is used in each backcross. Thus the improvements made in the recurrent parent are passed on to the QPM version.
2. The procedure is fairly flexible. The degree of kernel modification plays an important role in determining the timing of the next backcross. It is often necessary to advance the QPM segregates to F₃ or even F₄ to sufficiently increase the frequency of genetic modifiers before the backcrosses are made.
3. The scheme is so designed that a portion of the QPM version can be handled generation after generation in a homozygous opaque-2 genetic background. This permits continuous accumulation of favorable genetic modifiers through the recurrent selection process. Also, this portion is continuously monitored for protein quality.
4. Following each backcross, the accumulated modifiers as well as the protein quality are maintained.
5. Systematic and more rigorous selection is exercised against such characters as presence of open spaces between kernel rows on the ear, dull modifiers, popped kernels, and slower drying, both at family and individual plant levels.
6. Selection for stable modifiers over environments is practiced. The advanced QPM families are screened for stability of modifiers at different locations in the same season, followed by recombination of the most stable ones in the next season.

7. The products of the conversion process can be used easily at any stage, either as a whole population or as a recombined bulk of superior families.

At CIMMYT, the hard endosperm QPM versions of advanced populations and back-up gene pools have been developed using the aforementioned scheme. The performance of QPM versions as against their normal counterparts is given in Table 6. The kernel phenotype of these QPM versions has approached normal appearance. Plant height and ear height are similar to that of normal counterparts. The ear rot incidence has been reduced substantially, however, some QPM materials still show somewhat higher incidence. Major emphasis over the next few years will be given to the merging of genetically similar types to develop advanced QPM populations and the appropriate QPM gene pools.

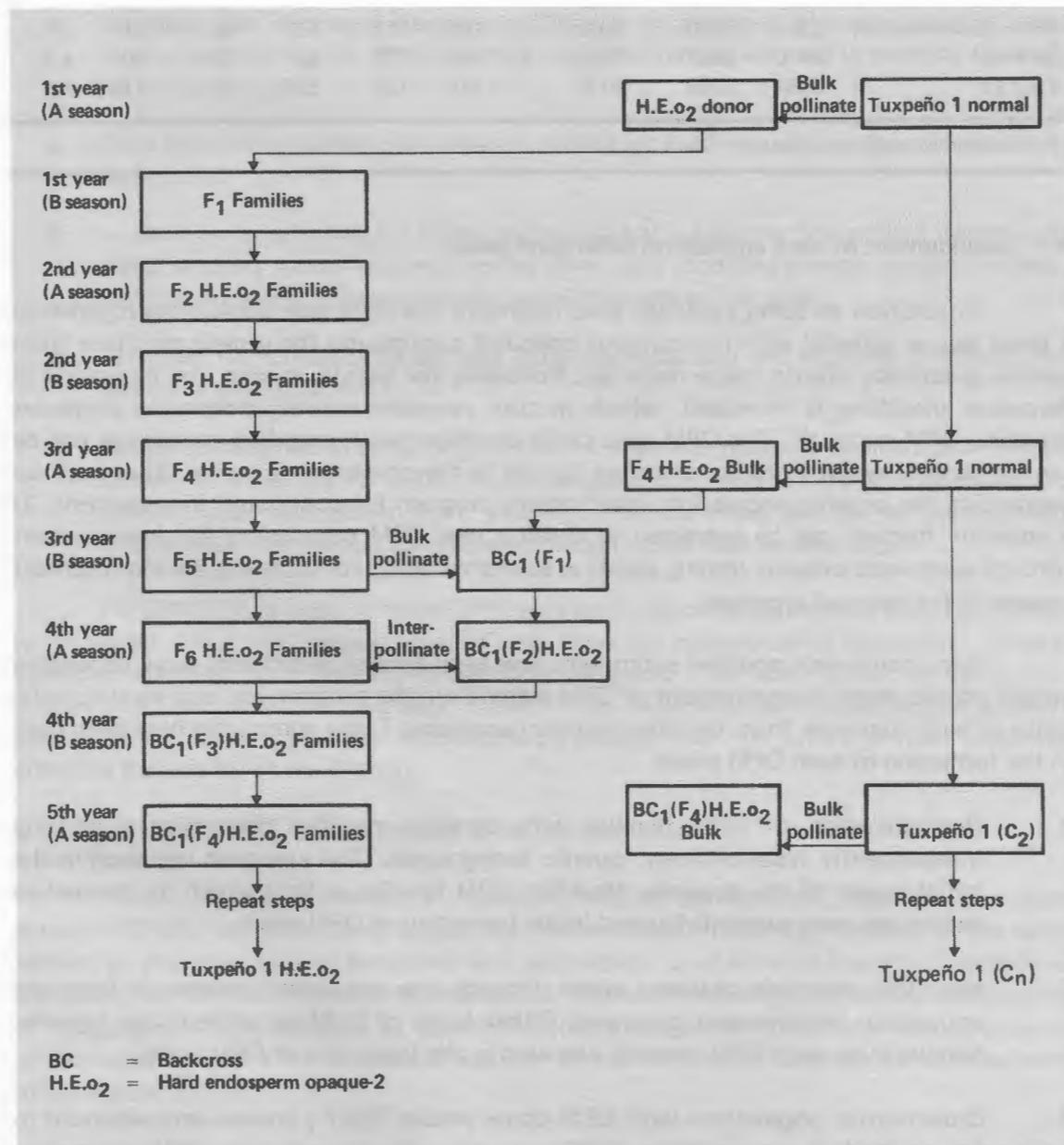


Figure 5. Backcrossing cum recurrent selection scheme for hard endosperm opaque-2 version of normal population undergoing improvement

Table 6. Comparison of normal materials and their QPM versions for yield and other agronomic traits

Material	Yield kg/ha*			Ear height (cm)		Days to 50% silking		Ear rots (%)	
	Normal	QPM	QPM as % of normal	Normal	QPM	Normal	QPM	Normal	QPM
Tuxpeño 1	6187	6152	99.4	111	110	61	60	2.2	5.4
Mezcla Tropical Blanca	6598	5593	84.8	119	111	61	59	3.3	4.2
Blanco Cristalino-1	6377	5538	86.8	113	114	58	58	2.9	3.4
Mix.1 Col.Gpo.1 ETO	6117	5681	92.9	107	105	60	58	2.9	4.5
Mezcla Amarilla	5431	5237	96.4	103	106	58	58	2.9	5.7
Amarillo Dentado	5351	5230	97.7	125	110	61	57	2.5	3.2
Tuxpeño Caribe	6393	5903	92.3	117	115	61	58	2.5	4.2
Ant.Rep.Dominicana	5351	5080	94.9	100	112	56	57	2.3	3.7
La Posta	6470	5903	91.2	131	122	62	59	3.1	4.0
Pool 23	6184	5659	91.5	115	120	59	57	4.0	4.0

* Pooled over years and locations

● **Development of hard endosperm QPM gene pools**

In addition to being excellent gene reservoirs, the QPM gene pools bring together in a given source material with homozygous opaque-2 background the genetic modifiers from several genetically diverse maize materials. Following the genetic mixing, the frequency of favorable modifiers is increased, which in turn remedies several undesirable attributes affecting QPM materials. The QPM gene pools developed with modified endosperm can be used in several ways: 1) as donor stocks for use in the conversion program, 2) as back-up support to the ongoing population improvement program for continuous improvement, 3) a superior fraction can be extracted to develop new QPM populations for improvement through systematic progeny testing, and 4) as source materials for initiating the improvement process in the national programs.

Gene pools with modified endosperm have been formed in different ways, depending largely on the stage of development of QPM materials in the program and also on the availability of such materials from the other national programs. Three approaches have been used in the formation of such QPM pools:

1. Recombination of QPM families with partially modified phenotype originating independently from different genetic backgrounds. This approach was used in the initial stages of the program. Modified QPM families or lines which by themselves had no use were successfully used in the formation of QPM pools.
2. Use QPM materials obtained either through the conversion process or from the population improvement programs. Either bulks of QPM materials or the superior families from each QPM material was used in the formation of QPM pools.
3. Cross normal populations with QPM donor stocks. The F₁ crosses were advanced to F₂ in a half-sib crossing block. QPM segregates with better kernel modification were selected from the segregating F₂ generation. The selected QPM segregates were then used for further genetic mixing in the following cycles.

During the process of genetic mixing, the major emphasis is placed on accumulating favorable alleles for altering and improving the kernel phenotype at every possible stage in the selection process without sacrificing protein quality.

Although the management and improvement of QPM pools is similar to that of normal gene pools, their handling requires special emphasis on the following points:

- Isolation of QPM pools from normal materials is essential.
- Quality protein and kernel modification are so important in the development of QPM gene pools that these two traits play an overriding role in the selection of the families. The selected ears from each cycle are subjected to laboratory analyses and the families are selected on the basis of protein content and quality.
- Selection for improved kernel modification is practiced at every possible step, both at ear and kernel level, and only modified kernels are used in planting the half-sib crossing block.
- Only selected ears with good protein quality are used to make up the balanced male composite.
- In addition to selecting for better agronomic traits, selection is practiced against such traits as open spaces between kernel rows, dull modified kernels, popped kernels, and slower drying following physiological maturity of the grain.
- Selection for resistance to ear rots, both under natural and artificial conditions, receives major emphasis.
- Partial contamination of QPM gene pools by normal pollen is done to facilitate selection of modifiers for better kernel weight and density. White gene pools can be contaminated with pollen from yellow normal materials, and for yellow materials it is necessary to develop colored seed markers to exhibit xenia effect.

At CIMMYT, a total of seven QPM gene pools are being maintained and continuously improved. Four are tropical lowland and three are subtropical in adaptation. Several cycles of selection have been completed in these pools. The latest cycles are earlier and shorter and have better modified ears (Table 7). The mean endosperm modification score of kernels in different cycles has improved progressively over the cycles without adversely affecting the quality of the protein.

- **Improvement of QPM populations in the Advanced Unit**

Three QPM Populations, 39 (Yellow QPM), 40 (White QPM), and 41 (Templado Amarillo QPM), are undergoing population improvement. These are handled in the same fashion as any other normal Advanced Unit population. In addition to important agronomic attributes, the QPM populations receive special emphasis for such characters as modification of kernel phenotype, stability of genetic modifiers, resistance to ear rots, maintenance of protein quality, and other direct and indirect criteria which can facilitate the improvement of QPM populations.

Table 8 gives the performance of some of the EVs derived from QPM populations. In several countries, QPM materials are giving yields comparable to or better than normal materials.

Table 7. Comparison of original and latest cycle of selection in two quality protein maize gene pools

Material	Cycle	Yield	Days to flower	Plant height (cm)	Ear height (cm)	% Ear rot	Endosperm modification*
Tropical Yellow Flint QPM Pool	C ₀	2827	56	208	111	10	3.2
	C ₉	3834	55	203	108	5	2.3
Temperate Tropical QPM Pool (Dent)	C ₀	4132	60	210	123	2	3.0
	C ₁₀	4340	57	187	105	3	2.2

* Rated on a scale of 1-5; 1-completely vitreous, 5-completely soft

Table 8. Performance of quality protein maize (QPM) in selected countries (EVT 15A, 1980)

Country-Location	Best check	Yield (ton/ha)	Best QPM	% Yield of best check
1. Bolivia-Iboperenda	Mez. Trop. Blanca	7.7	Ferke, 7940	99
2. Brazil-Sete Lagoas	CMS-05	6.9	Ferke, 7940/1	113
3. Ecuador-Pichilingue	Pichilingue-504	5.6	Poza Rica 7940	107
4. Venezuela-Durigua	Local Check	3.1	Across 7740	127
5. Panama-Tocumen	Tocumen 7428	4.2	Poza Rica 7940	112
6. Panama-Chiriqui	Tocumen 7428	4.8	Guanacaste 7940	111
7. Mexico-Poza Rica	Poza Rica 7643	5.7	Guanacaste 7940	98
8. Mexico-Obregon	H-510	7.1	Ferke 7940	96
9. Ghana-Kwadaso	Opaque-2 Comp.	3.7	Poza Rica 7940	111
10. Mali-Sotuba	IRAT 85	3.9	Guanacaste 7940	127
11. Mozambique-Nampula	SR 52	3.8	Across 7839	95
12. Zaire-Kaniama	Kasai I	6.9	Obregon 7940	101
13. Bangladesh-Jessore	J ₁	9.3	Guanacaste 7940	108
14. India-Varanasi	E.H. 400175	4.2	Guanacaste 7940	103
15. Nepal-Rampur	White Flint HEO ₂	8.0	Poza Rica 7940	110

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