DOCUMENTATION OF THE CIMMYT WHEAT BREEDING PROGRAMS

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Preface

The CIMMYT Wheat Breeding Simulation Project (CIM 8 at CIMMYT, or UQ 123 at the UQ) is jointly supported by GRDC, the University of Queensland of Australia, and CIMMYT. The aims of this project are to:

1. Design a simulation module based on QU-GENE software to identify opportunities to further improve the efficiency of the CIMMYT wheat breeding and dissemination programs,
2. Develop a characterization of the target population of environments (TPE) in client countries (including those in Australia) that are relevant to CIMMYT wheat breeding objectives and develop procedures for its storage in ICIS, and
3. Develop a software and data exchange interface between QU-GENE and ICIS to enable the use of the genotype and environment characterization information held in ICIS for the modelling of CIMMYT and Australian wheat breeding strategies by QU-GENE.

The initial step for breeding simulation is to document the CIMMYT wheat breeding programs. Due to the similarity between the methodology used in bread wheat breeding and that used in durum wheat and triticale breeding, only the operations and activities within the CIMMYT bread wheat breeding program are expounded in this documentation in a quantitative and breeding/genetic fashion. Those within durum wheat and triticale breeding programs are only briefly introduced in this documentation. This detailed description will then be used for designing the QU-GENE simulation module for CIMMYT's wheat breeding programs.

Abbreviations and Acronyms

A: Adapted durum wheat or triticale used as parents for crossing.

AABBDD: The full hexaploid genome of bread wheat (*Triticum aestivum* L.), comprising two full sets of chromosomes, each from three distinct grass progenitors.

AL: Advanced Lines.

AS: Acid Soil environment.

ASWSN: Acid Soil Wheat Screening Nursery.

BV: El Batan Verano, the summer breeding cycle at El Batan, the CIMMYT headquarter.

BYD or BYDV: Barley Yellow Dwarf Virus or “Barley Yellow Dwarf Virus resistance”.

BW: Bread Wheat.

C: Column, an incomplete block in some experimental designs for PYT and YT in durum wheat and triticale breeding programs.

CB: Crossing Block in CIMMYT’s wheat breeding programs.

CBS: Crossing Block of Spring Wheat in CIMMYT’s Bread Wheat Program.

CBW: Crossing Block of Winter Wheat in CIMMYT’s Bread Wheat Program.

CIANO: Centro de Investigaciones Agricolas del Noroeste.

CIMMYT: International Maize and Wheat Improvement Center (Centro Internacional de Mejoramiento de Maiz y Trigo).

CISN: Candidates of International Screening Nurseries.

CISNYT: Candidates of International Screening Nurseries and Yield Trials.

CIYT: Candidates of International Yield Trials.

cM: centi-Morgan, used to represent the chromosome length, or distance between two loci.

CTD: Canopy Temperature Depression.

DR: Double Row.

DW: Durum Wheat.

EAL: Elite Advance Lines.

EDUYT: Elite Durum wheat Unreplicated Yield Trial.

EPC: Elite PC (*Parcela Chica*, “Small Plot” in Spanish).

ESWYT: Elite Spring Wheat Yield Trial.

F1: The first self-pollinated generation from the hybrid seed of two parents. F2 is the second generation, and so on.

F1T: The first self-pollinated generation from top-crossed seed.

FAWWON: FAcultative and Winter Wheat Observation Nursery.

FEFWS: Favorable Environments Facultative Wheat Screening Nursery.
FM: Female Master list with selected outstanding female parents for crossing.
GEI: Genotype by Environment Interaction.
GRDC: Grains Research and Development Corporation, Australia.
HL: High Latitude environment.
HLB: Helminthosporium Leaf Blight or "Helminthosporium Leaf Blight resistance".
HLWSN: High Latitude Wheat Screening Nursery.
HMW: High Molecular Weight (glutenin).
HR: High Rainfall environment, or Head-to-Row line (family).
HRWSN: High Rainfall Wheat Screening Nursery.
HRWYT: High Rainfall Wheat Yield Trial.
HTWYT: Heat Wheat Yield Trial.
IBWSN: International Bread Wheat Screening Nursery.
ICARDA: International Center for Agricultural Research in the Dry Area.
ICIS: International Crop Information System.
IDYN: International Durum wheat Yield Nursery.
ISNYT: International Screening Nurseries and Yield Trials.
IR: Irrigation environment.
ITSN: International Triticale Screening Nursery.
ITYN: International Triticale Yield Nursery.
IWIS: International Wheat Information System.
KB: Karnal Bunt or "Karnal Bunt resistance".
L: Long arm of the wheat chromosome.
LR: Leaf Rust or "Leaf Rust resistance".
M: Meter or Multiplication.
MA: Medium Adapted durum wheat used for crossing.
ME: Mega-environment. There are 12 MEs defined in CIMMYT's wheat breeding programs.
MISNYT: Multiplication of International Screening Nurseries and Yield Trials in Mexicali, Mexico.
MM: Male Master list with selected outstanding male parents for crossing.
MP: Moderately Plump, used to represent visual seed quality.
MODPED: Modified pedigree and bulk selection used in CIMMYT's wheat breeding program.
MR: Moderately Resistant for some biotic or abiotic resistance.
MT: Moderately Tolerant for some biotic or abiotic resistance.

MV: Mexico-Verano (= State of Mexico-summer), CIMMYT’s summer breeding cycle in Toluca, State of Mexico, Mexico.
MXI: CIMMYT’s seed multiplication cycle in Mexicali, Mexico.
NARS: National Agricultural Research Systems.
P: Plump, used to represent visual seed quality.
PC: *Parcela Chica*, “Small Plot” in Spanish, used for disease observation by inoculation.
PYT: Preliminary Yield Trial, usually without replications.
PZ: CIMMYT’s breeding nursery in Patzcuaro, Mexico.
QU-GENE: QUantitative-GENEtics, a computer simulation platform for the quantitative analysis of genetic models developed by the School of Land and Food, The University of Queensland, Brisbane, Australia.
R: Resistant, Reserved seed, or Row.
RYT: Regular Yield Trial, equivalent to YT.
S: Short arm of wheat chromosome, or Spring durum wheat or Spring wheat.
SA: Semi Arid environment.
SAWSN: Semi-Arid Wheat Screening Nursery.
SAWYT: Semi-Arid Wheat Yield Trial.
SELBLK: Selected bulk selection method used in CIMMYT’s wheat breeding program.
SC: Scab or “Scab resistance”.
SDS: Sediments content in durum wheat.
SJ: CIMMYT’s breeding nursery in Sierra de Jalisco, Mexico.
SR: Stem Rust or “Stem Rust resistance”; or Single Row.
T: Tolerant.
TE: Tropical Environment.
TKW: Thousand-Kernel Weight.
TPE: Target Population of Environments.
TR: Triple Row.
U: Unadapted durum wheat used as parents for crossing.
W: Winter durum wheat or Winter wheat used as parents for crossing.
WANA: West Asia and North Africa.
WAWSN: Warmer Area Wheat Screening Nursery.
WON-IR: Winter Wheat Observation Nursery, Irrigated.
WON-SA: Winter Wheat Observation Nursery, Semi-Arid.
WWEEYT: Winter Wheat East European Yield Trial.

Y: CIMMYT’s winter breeding cycle in the Yaqui Valley, Cd. Obregon, Sonora, Mexico.

YT: Yield Trial, usually with two to three replications.

YR: Yellow Rust (stripe rust) or “Yellow Rust resistance”.

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Documentation of the CIMMYT Wheat Breeding Programs

Introduction

The major objective of plant breeding programs is to develop new genotypes that are genetically superior to those currently available for a specific target mega-environment or a target population of environments (TPE). To achieve this objective, plant breeders employ a range of selection methods. For example at CIMMYT, pedigree selection was mostly used from the 1940s till the early 1980s; modified pedigree/bulk selection first started being used from the early 1980s onwards; and the selected bulk method is currently being used for certain populations in the Bread Wheat Breeding Program. Generally speaking, quantitative genetics theory provides much of the framework for the design and analysis of selection methods used within breeding programs. However, there are usually some assumptions in quantitative genetics in order to render some theories mathematically or statistically tractable. Some assumptions can be easily tested or satisfied by some experimental designs. Some assumptions can never be true, for example assumptions of no linkage and no genotype by environment interaction (GEI). Still other assumptions are difficult to test, for example the existence of epistasis. Computer simulation gives us the opportunity to lessen these assumptions and therefore establish more general and more valid genetic models in quantitative genetics and then use these models in plant breeding. The CIMMYT Wheat Breeding Simulation Project aims at developing computer software to simulate the CIMMYT wheat and triticale breeding programs and then find ways to further enhance breeding efficiency. These breeding programs have already been tremendously successful, but fine-tuning may still be possible.

A system analysis of the CIMMYT wheat breeding activities is the initial step for the simulation project. This documentation will provide details in a quantitative way as far as possible on the operations and activities within the CIMMYT bread wheat breeding program aiming for optimum conditions. Modifications used in the other breeding programs (bread wheat targeted for marginal areas, durum wheat, and triticale) are also described. This documentation will then be used for designing a QU-GENE application module that will simulate the operations of CIMMYT’s wheat breeding programs and provide flexibility to examine the impact of possible modifications.

Historical Background of the CIMMYT Wheat Program

The precursor of the present CIMMYT Wheat Program originated in 1944 under the sponsorship of the Rockefeller Foundation and the Office of Special Studies of the Mexican Ministry of Agriculture. In 1966, CIMMYT was established as a non-profit organization responsible to an internationally elected board of trustees. The CIMMYT breeding programs currently distribute advanced lines to more than 60 countries. Our primary clients are the national agricultural research systems (NARS) in developing countries. Germplasm distribution and utilization are dependent upon their close cooperation. The Wheat Program has attempted to address the specific problems and limitations associated with wheat production in those countries.

The development of broadly adapted, durable disease resistant, high yielding, and stable germplasm within the context of each mega-environment is the Program's primary goal. Emphasis is also given to maintenance of genetic diversity within each mega-environment to counter the effects of genetic vulnerability. To breed for wide adaptation and high yield potential, the breeding program shuttles segregating materials between alternative sites within Mexico, while pyramiding genes that carry durable resistance to various pathogens. International multi-locational testing, through the distribution of the International Screening Nurseries and Yield Trials (ISNYT) with the cooperation of the NARS, provides vital information for use in the Wheat Program's crossing and selection activities.

The impact of CIMMYT's Wheat Breeding Program has been significant (Rajaram 1999). The total spring bread wheat (*Triticum aestivum* L.) area in developing countries, excluding China, is around 63 million ha, of which 36 million ha or 58% are planted to cultivars derived from CIMMYT germplasm (Table 1). During the 1966-90 period, 1317 bread wheat cultivars were released by developing countries, of which 70% were either direct releases from CIMMYT advanced lines or had at least one CIMMYT parent (Table 1). Simultaneously, the use of dwarfing genes has continued to increase over time. Today, regardless of the type of wheat, more than 90% of all wheat cultivars released in developing countries are semi-dwarfs, which covered 70% of the total wheat area in developing countries by the end of 1990. The continuous adoption of semi-dwarf spring wheat cultivars in the post-Green Revolution period (1977-90) resulted in about 15.5 million tons of additional wheat production in 1990, of which 50% is attributed to the adoption of new Mexican semi-dwarf wheat cultivars. In 1990, an estimated 93% of the total spring wheat production in developing countries, excluding China, came from semi-dwarf spring wheats, which covered about 83% of the total spring bread wheat area in developing countries.

Table 1 Origin of spring bread wheat cultivars in developing countries excluding China

Period	CIMMYT cross	NARS cross		
		CIMMYT parents	CIMMYT ancestor	No CIMMYT
1966-90	45%	28%	3%	24%
1991-97	58%	30%	3%	9%

CIMMYT's Wheat Breeding Mega-Environments

The cornerstones of CIMMYT's breeding methodology are the use of a diverse gene pool for crossing, targeted breeding for mega-environments, shuttle breeding, selection for yield under optimum conditions, and multi-locational testing to identify superior germplasm with good disease resistance. CIMMYT's Wheat Program has, throughout its history, carefully defined its target production environment, a prerequisite for any successful breeding enterprise. In the 1940s, this characterization was restricted to Mexico. But as is well known, a global scope has been achieved. With this expansion, the need, especially among breeders, arose to define separate target environments in terms of the crop traits required. Geographical description alone had become clearly inadequate. Three overriding considerations had to be blended: (1) the profound diversification of production systems requesting our assistance; (2) the ever growing conviction of the need for wide adaptation and stability of yield performance; and (3) the realization that in specific conditions specialized traits were necessary. Over time and largely empirically, a set of so-called agro-ecological zones was developed, based on a mixture of plant, disease, and edaphic and climatic characteristics. By the late 1970s, the following 15 different agro-ecological zones had been conceived:

1. Subcontinent (India, Pakistan, Bangladesh and Nepal)
2. Eastern Asia (China, Japan and Korea)
3. Middle East (Turkey to Afganistan)
4. North Africa and Iberia
5. Nile Valley (Egypt and Sudan)
6. East Africa (including Ethiopia, Kenya, Tanzania and Madagascar)
7. Southern Africa
8. Northern Mexico
9. Central America
10. Andean region

11. Southern Cone of South America
12. Australasia
13. USA/Canada
14. Southern Europe (Italy, Yugoslavia, Bulgaria, etc.)
15. Western Europe (England, France, Germany, etc.)

CIMMYT's wheat breeding programs were organized to serve the germplasm needs of agro-ecological regions 1-11. However, the base breeding efforts utilized germplasm from all 15 regions in its hybridisation program, including regions 12-15 in the advanced world.

In the 1980s attempts to redefine these zones included socio-economic traits. Presently, the term mega-environment (ME) is being used to describe the target global domains. A mega-environment is defined as a broad, not necessarily continuous area, occurring in more than one country and, frequently, more than one continent. Biotic and abiotic stresses, cropping-system requirements, and consumer preferences are similar throughout a given mega-environment. The importance of a ME can be approximately gauged by volume of production. Germplasm generated for a particular ME is presumably useful throughout it, accommodating major stresses, but perhaps not all significant secondary stresses.

By 1992, 12 MEs involving global wheat areas had been defined. Among the 12 recognized MEs, six are for spring wheats and three each for facultative and winter wheats. Spring wheats cover almost 95 million hectares in developing countries, and facultative and winter wheats almost 25 million hectares (Table 2). CIMMYT's Wheat Program currently emphasizes 10 such MEs, i.e. ME1-ME6, ME7, ME9, ME10, and ME12, and has accordingly structured its breeding programs to address the respective germplasm needs. Representative sites for most of the spring wheat MEs, except ME6, are found in Mexico, and it is also possible to grow facultative and winter germplasm in the field at high altitude sites that have cold winters, like Toluca. So, all spring wheats are addressed from Mexico. Most winter wheat breeding is done in Turkey in collaboration with the Turkish National Program and ICARDA.

Six MEs pertaining to spring wheat are ME1 (irrigated), ME2 (high rainfall), ME3 (high rainfall and acid soils), ME4 (low rainfall), ME5 (irrigated and high temperature) and ME6 (high latitude). Three MEs assigned to facultative wheat are ME7 (irrigated), ME8 (high rainfall) and ME9 (low rainfall). Additionally, three MEs belonging to the winter wheat are ME10 (irrigated), ME11 (high rainfall) and ME12 (low rainfall) (Table 2 and Table 3).

Spring Wheat

ME1: Irrigated, low rainfall environment

ME1 represents the optimally irrigated, low rainfall areas of the world. The climate during the wheat period ranges from temperate to conditions of late heat stress. Representative areas include the Gangetic Valley (India), the Indus Valley (Pakistan), the Nile Valley (Egypt), parts of Zimbabwe, irrigated river valleys in parts of China (e.g. Chengdu), and the Yaqui Valley (Mexico). Kano (Nigeria) and Wad Medani (Sudan) are typically irrigated and hot locations. This ME encompasses 36 million hectares spread primarily over Asia and Africa between 35°S-35°N latitudes.

Breeding objectives include high yield potential, input responsiveness, lodging resistance (which includes maintenance of *Rht1* and/or *Rht2* dwarfing genes), improved industrial quality, durable resistance to the three rusts (leaf rust, stem rust and stripe rust), and mostly resistance to Karnal bunt. Some heat tolerance is needed for certain locations. Greater emphasis will be given to tolerance to saline soils. White (amber)-grained types predominate in most areas. Quality requirements are increasing.

There are four major sub-MEs:

- ME1IR: Favourable irrigated environment, only rust may be a serious problem
- ME1KB: Karnal bunt (*Tilletia indica*) is present
- ME1HT: (Late) Heat occurs during the grain-filling stage
- ME1SL: Soil/water salinity hinders growth

ME2: High rainfall environment (>500mm rainfall during the cropping cycle)

ME2 is defined by representative high rainfall locations in the West Asia and North Africa (WANA) Region, the Southern Cone and Andean Highlands of South America, Kulumsa (Ethiopia), Izmir (Turkey), and Toluca (Mexico). Total area exceeds 8 million hectares.

Stripe rust, leaf rust, *Septoria tritici*, and pre-harvest sprouting are major production constraints. *Fusarium* head blight (FHB) is becoming a more widespread and serious problem in many locations. Resistances to leaf rust, BYDV, bacteria, powdery mildew and the root disease complex must also be considered in many parts of ME2. Tolerance to soil micronutrient imbalance is becoming more important. For high yield potential, semi-dwarf stature is essential. Red grain wheat provides better sprouting tolerance than white grain wheat. Red grain type is generally preferred, with the exception of a few areas (e.g. Ethiopia). Demands for better industrial quality are increasing.

ME3: High rainfall, acid soil environment

Soils have pH<5.5, temperate environments with an average of more than 500 mm of rainfall during the cropping cycle. Disease and stress problems are similar to ME2; however, aluminium and manganese toxicities, plus phosphorus deficiency, are major constraints to production. Area is estimated at just under 2 million hectares, mostly in Brazil, Central Africa, and the Himalayas. Red grain is generally preferred, except in the Himalayas.

ME4: Low rainfall, drought environment

Less than 500 mm of water are available during the cropping cycle. Three distinct types of drought or sub-MEs have been identified based on the stage of plant development at which drought is most severe. These are:

- **ME4A**: Winter rain or Mediterranean-type drought associated with post-flowering moisture and heat stress typical of the WANA region. Stripe rust, leaf rust and stem rust, root rots, nematodes, and bunts are the key biotic constraint. Representative locations include Aleppo (Syria) and Settat (Morocco). White grain is preferred.

- **ME4B**: Winter drought or Southern Cone-type rainfall associated with pre-flowering moisture stress. Marcos Juarez (Argentina) is a representative location. Total estimated area is about 5.8 million hectares. Resistance to leaf rust, stripe rust and stem rust is also a common problem. Red seeded cultivars have preference, and high industrial quality is demanded.

- **ME4C**: Stored moisture after monsoon rains results in continuous or Subcontinent-type drought under receding moisture conditions. A representative location is Dharwar (India). Total estimated area is about 5 to 6 million hectares, and probably decreasing. Leaf rust occurs occasionally. Seed must be large, bold and amber in color.

The Bread Wheat Program attempts to combine high yield potential with drought resistance for MEs 4A and 4B. For ME4C, more specifically adapted germplasm is needed. Most breeding research for ME4A is carried out by the CIMMYT Outreach breeders based at ICARDA, Aleppo, Syria. The combination of water-use efficiency and water responsive traits plus yield potential is important in drought environments where rainfall is frequently erratic across and within years. When rains are significantly above average in certain years, the crop must respond appropriately (water responsive) with high yields.

ME5: Warmer area environment (areas 23°S-23°N, <1000 masl)

The mean minimum temperature of the coolest month in this environment is greater than 17°C. Relative humidity is high. Representative locations are Pusa (Bihar, India), Joydebpur (Bangladesh), Chiangmai (Thailand), Encarnacion (Paraguay), and Poza Rica (Mexico). The estimated area is about 7 million hectares. In these humid locations, resistance to *Helminthosporium sativum*, and leaf rust, plus tolerance to sprouting are major objectives.

ME6: High latitude environment (>45°N or S)

Wheat is spring-sown in this ME, as winters are too severe for survival. The higher latitude requires that the materials have a certain level of photoperiod sensitivity unlike that in all other spring MEs. Harbin (Heilongjiang, China) is a representative location, with pre-anthesis drought followed by rainfall during flowering and grain filling. Resistances to *Fusarium* spp., *Helminthosporium tritici-repentis*, stripe rust, leaf rust, stem rust, and tolerance to sprouting are breeding objectives in this environment. However, very dry representative locations also occur, such as the northern Kazakhstan (10 million ha) and southern Siberia wheat belt (8 million ha). The major diseases are leaf rust and root disease. In addition, drought tolerance is paramount. The total estimated area in these two distinct regions is 20 million hectares.

Facultative wheat

ME7: Favourable, irrigated, moderately cold (0-5°C coolest month) environment

Precipitation is lacking during the growing season. Breeding objectives are yield potential and resistances to stripe rust, leaf rust, and powdery mildew. A representative location is Zhengzhou (Henan, China).

ME8: High rainfall (>500 mm), moderately cold (0-5°C coolest month) environment

Major diseases are stripe rust, powdery mildew, leaf rust, and eyespot. Representative locations are Temuco (Chile) and Corvallis (Oregon).

ME9: Semi-arid, low rainfall, moderately cold (0-5°C coolest month) environment

Drought tolerance and resistance to stripe rust and bunts are requirements. Representative locations are Diyarbakir (Turkey) and Vernon (Texas).

Winter wheat

<u>ME10: Favourable, irrigated, severely cold (-10-0℃ coolest month) environment</u>

High yield potential and resistance to stripe rust, leaf rust, and powdery mildew are requirements. Beijing (China) is a representative location.

<u>ME11: High rainfall (>500 mm), severely cold (-10-0℃ coolest month) environment</u>

Major diseases are leaf rust, stripe rust, powdery mildew, and eyespot. Representative locations are Odessa (Ukraine) and Krasnodar (Russia).

<u>ME12: Semi-arid, low rainfall, severely cold (-10-0℃ coolest month) environment</u>

Drought tolerance and resistance to the bunts are needed. Ankara (Turkey) and Kansas (USA) are representative locations.

Table 2 Mega-environments used in CIMMYT Wheat Breeding Program

ME	Latitude	Moisture regime	Temperature regime	Wheat type	Sown season	Area* (m. ha (%))	Production** (million t)	Year when breeding began at CIMMYT
ME1IR	Low	Low rainfall, Irrigated	Temperate	Spring	Autumn	36 (29.7)	83	1945
ME1KB		Plus Karnal bunt						
ME1HT		Plus Heat						
ME1SL		Plus Salinity						
ME2HR	Low	High rainfall	Temperate	Spring	Autumn	10 (8.2)	25	1972
ME3AS	Low	High rainfall, Acid soil	Temperate	Spring	Autumn	1.7 (1.4)	3	1974
ME4	Low	Low rainfall	Temperate/hot	Spring	Autumn	21.6 (19.7)	20	1974
ME4A		Winter dominant				10		
ME4B		Summer dominant				5.8		
ME4C		Residual moisture				5.8		
ME5TE	Low	Irrigated/High rainfall	Hot	Spring	Autumn	7.1 (5.8)	12	
ME5A		High humidity				3.9		1981
ME5B		Low humidity				3.2		1975
ME6HL	High	Semi-arid	Temperate	Spring	Spring	20 (16.5)	20	1989
ME7IR	High	Irrigated	Cool	Facultative	Autumn	10 (8.2)	23	1986
ME8HR	High	High rainfall	Cool	Facultative	Autumn			
ME9SA	High	Semiarid	Cool	Facultative	Autumn			
ME10IR	High	Irrigated	Cold	Winter	Autumn	15 (12.4)	30	1986
ME11HR	High	High rainfall	Cold	Winter	Autumn			
ME12SA	High	Semiarid	Cold	Winter	Autumn			

IR = Irrigated environment; HR = High Rainfall; AS = Acid Soil; SA = Semi-arid; TE = Tropical Environment; HL = High Latitude; Low = Less than about 35-40 degrees; Hot = Mean temperature of the coolest month > 17.5°C; Cold =< 5.0°C; *: Braun et al (1996) and van Ginkel & Rajaram (1993); **: Rajaram et al (1997)

Table 3 Breeding traits for spring wheat MEs: ME1 to ME6

ME	Breeding traits
ME1	• Spring habit (*Vrn1*, *Vrn2*, and/or *Vrn3*) • Photoperiod insensitive (*Ppd1* and/or *Ppd2*) • Normal maturity • “Short dwarf” in stature (*Rht1* and/or *Rht2*, plus modifier genes) • High yield potential • Stable yield performance in temporal and spatial sense • Input-responsiveness and –efficiency (expressed as adaptation and yield potential, respectively) • Resistance to stem rust (*Sr2*-complex, etc.), leaf rust (*Lr34*-complex, etc.), and stripe rust • Good balance of HMW glutenins (preferably: 1 or 2*, 7+8 or 17+18, 5+10) • Some heat tolerance • Lodging tolerance • Largely white/amber grain
ME2	• Spring habit (*Vrn1*, *Vrn2*, and/or *Vrn3*) • Photoperiod insensitive (*Ppd1* and/or *Ppd2*) • Normal maturity • Semi-dwarf in stature (*Rht1* or *Rht2*, and sometimes *Rht8*, plus modifier genes) • High yield potential • Stable yield performance in temporal and spatial sense • Input-responsiveness and –efficiency • Resistance to stem rust (*Sr2*-complex, etc.), leaf rust (*Lr34*-complex, etc.), and stripe rust • Better resistance/tolerance to *Septoria tritici*, BYDV, stripe rust, *Fusarium* head scab (FHB), powdery mildew and the root disease complex • HMW glutenins (preferably: 1 or 2*, 7+8 or 17+18, 5+10) • Some heat tolerance • Lodging tolerance • Pre-harvesting sprouting tolerance • Largely red but some white grain
ME3	• Same as for ME2, plus • Tolerance to aluminium/manganese toxicity • Efficient phosphorus uptake/utilization
ME4	• Spring habit (*Vrn1*, *Vrn2*, and/or *Vrn3*) • Semi-dwarf to “tall dwarf” in stature (*Rht1* or *Rht2* with modifier genes) • Combination of input responsiveness (yield potential) and input efficiency (drought tolerance) • *Sr2* and *Lr34* complexes and common bunt resistance needed • Septoria, stripe rust, root rots and nematode resistance • Some heat tolerance • Some cold tolerance • Both white/amber and red grain
ME5	**A: Low humidity tropics:** ME1 characteristics superimposed with high temperature tolerance; targeted for countries such as Sudan and Peninsular India **B: High humidity tropics:** ME2 characteristics superimposed with high temperature tolerance and *Helminthosporium sativum* resistance; sometimes sprouting tolerance needed; targeted for such areas as Bangladesh, Eastern India and Paraguay
ME6	**A: High rainfall:** Same as for ME2, with *ppd1* or *ppd2* allele(s) for photoperiod sensitivity **B: Semiarid:** Same as for ME4, with *ppd1* or *ppd2* allele(s) for photoperiod sensitivity

CIMMYT’s wheat breeding locations in Mexico

Two major locations are used for spring wheat breeding in Mexico: Cd. Obregon and Toluca. One minor location, that at CIMMYT’s headquarters, El Batan, Texcoco, is used on occasion for testing.

Ciudad Obregon

Cd. Obregon is located at 27.5°N, 40 masl, in the State of Sonora, northwestern Mexico. It is a dry, irrigated, low-altitude site. Mean rainfall during the wheat crop cycle is about 50 mm. Irrigated yields in the region are high, in the order of 8-11 t/ha in experimental plots and 5-8 t/ha in farmers’ fields.

This is one of the two most important breeding and screening sites for the CIMMYT wheat breeding programs. About 45 ha are annually planted to Bread Wheat Program (Optimum section) breeding materials, and an additional 70 ha for the other breeding programs. Leaf rust and stem rust are major diseases, in addition to Karnal bunt. Breeding nurseries are sown from about November 10 till December 10, and harvested from about April 10 till May 10. Late plantings are sown in January and February, and harvested in May and June. Yield trials for ME1, ME4 and ME5 are planted here.

This location represents ME1 when optimally irrigated and managed. Reduced irrigation and late planting simulate aspects of ME4 and ME5, respectively. The use of supplementary lighting allows simulation of day length similar to that in northern latitudes such as in Kazakhstan, thereby allowing simulation of ME6.

Toluca

Toluca is located at 19°N, 2640 masl, west of Mexico City in the state of Mexico. Some of the land used is CIMMYT property; the rest is given in loan or rented. This temperate, high rainfall, high altitude site is the most important summer cycle location for the CIMMYT wheat breeding programs. The major part of the Wheat Program (Optimum section), including all segregating materials, is sown here during the summer, totalling about 25 ha. Yield trials for ME2 and ME3 are planted here.

It is a high rainfall environment (900 mm/annum during the growing cycle) with good disease expression, especially of stripe rust, *Septoria tritici*, and *Fusarium nivale*. Also BYDV generally establishes well. The highest yields realized in experimental plots are in the order of 7-

10 t/ha. Spring breeding materials are sown from May 10 till June 10, and harvested from October 1 till November 10. This site represents aspects of ME2 and ME3. The use of supplementary lighting allows simulation of day length similar to that in northern latitudes such as in Kazakhstan, thereby allowing simulation of ME6.

El Batan

El Batan is located at 19°N, 2249 masl. This is the administrative center of the CIMMYT Wheat Program, situated to the northeast of Mexico City in the State of Mexico. The land is CIMMYT property. Irrigation is available during periods of erratic rainfall. It may represent ME2 and/or ME4, depending on water availability and irrigation regime.

Due to land limitations (5 ha) plantings are usually restricted to the crossing block (CB), advanced lines (ALs), *Parcela Chicas* (PCs, “small plot” in Spanish), elite advanced lines (EALs), elite *Parcela Chicas* (EPCs), observation nurseries (ONs), and multiplications of selected advanced materials and special studies. Leaf rust usually develops in epidemic proportions. Stripe rust occurs at irregular frequencies. Sowing is from May 20 till June 20 and materials are harvested from October 1 till November 1.

Materials intended for final multiplication in Mexicali, before being internationally distributed in nurseries or trials, are first increased in El Batan under the strictest protection against diseases by using fungicides.

CIMMYT’s Breeding Methodology

From their very inception in the 1940s CIMMYT’s wheat breeding programs have used the pedigree method of breeding with good success. In the early 1970s, top (or three-way) crosses and double (or four-way) crosses were employed to increase the genetic variability of populations. By the late 1970s double crosses were dropped due to poor results relative to simple, top, and limited backcrosses. From the 1980s onwards all crosses onto selected F1s were either backcrosses and/or top crosses.

With the globalization of CIMMYT’s Wheat Breeding Program in the 1980s and the evolution of the concept of 12 MEs, the number of crosses made annually increased dramatically from 2,000 in the early 1970s to 10,000 in the 1980s for the Bread Wheat Program alone. The total number of segregating plus advanced populations (F2-F7) grew from 20,000 lines to 150,000 lines. Similarly, the number of entries in yield trials increased from 1,000 to 5,000 annually. The total acreage in breeding and testing expanded from 30 ha to 100 ha in the same period just for the Bread Wheat Program.

To accommodate this increase in breeding populations, the methodology of selection changed from a pedigree system to a modified pedigree-bulk selection approach. The new method allowed one experienced CIMMYT breeder to evaluate all segregating populations in a timely fashion. Simultaneously, total mechanization of planting and harvesting, and the computerization of field books have allowed a limited group of well trained and experienced support staff and technicians to carry out all responsibilities as before. These three major changes introduced into the operation have increased the ability to introgress variability by significantly increasing the number of crosses directed for specific MEs, while keeping the selection program highly efficient, and without sacrificing population size per cross. CIMMYT's modified pedigree-bulk methodology of handling segregating population allows the selection of lines in the F3-F6 generations that could be more tolerant to lodging plus adapted to growing in a community, because the seed rate is kept at a commercial level. The method also identifies lines that are vigorous, with dense, highly fertile spikes, closed canopy architecture, and consequently with higher biomass. These traits have been found correlated with high yield in many studies.

The modified pedigree/bulk selection scheme also allowed economizing the breeding program without losing genetic variability. This scheme is briefly described below.

Crossing block (CB)

The crossing blocks (CBs) are collections of elite breeding source material arranged by MEs. In order to facilitate crossing operations, each CB is sown on four or five different dates, about ten days apart. The largest CB is the crossing block of spring wheats (CBS). In the Toluca winter cycle, a crossing block of winter wheats (CBW) is also assembled and planted.

Spring crossing block (CBS)

The production of high yielding, widely adapted, stable and durable resistant spring wheat germplasm with acceptable quality is the primary consideration of the Bread Wheat Program. For this reason, the CBS is the largest and most diversified of the two types of CBs. Germplasm has been grouped according to MEs. Within each ME, the lines are sub-grouped based on their country of origin or specific character expression (e.g. disease resistance, abiotic stress tolerance, industrial quality). CBS entries include (1) major varieties released in different targeted countries, (2) elite CIMMYT and other germplasm identified from international and national testing, and (3) advanced lines exhibiting desirable expression of one specific trait or group of traits, including those made available by the Pathology, Wide Cross, and other sections within the Wheat Program (Table 4).

Genotypes from each section of the CBS carry genes specific to their defined ME. For example, ME1 genotypes carry genes or combination of genes coding for one or more of the following: high yield potential, dwarfing genes (*Rht1*, *Rht2*, and/or *Rht8*), lodging tolerance, durable resistance to the rusts or Karnal bunt, resistance to powdery mildew and aphids, tolerance to saline soils, improved industrial quality, etc. There are five CBSs arranged by MEs (Table 4). These are:

- CBME1IR for irrigated areas
- CBME2HR for high rainfall areas (containing CBME3AS)
- CBME3AS for high rainfall areas with acid soils (included in CBME2HR)
- CBME4SA for semi-arid areas
- CBME5TE for warm tropical areas
- CBME6HL for high latitude areas

Other special CBs and ONs (Observation Nurseries) are also used for crossing, totalling some additional 500-1000 entries.

Considerable genetic diversity enters the breeding system in the form of introductions from most collaborating countries. From 2000 to 4000 entries are received annually from our collaborators. In addition, the CIMMYT Pathology and Wide Cross sub-programs provide unique gene combinations for inclusion in the breeding program. Once introduced, these materials are classified according to MEs with regard to disease resistance, agronomic type, and adaptability, and then considered for crossing. About 2000 crosses/year are made onto these introductions.

Twice a year, around 25% of the parental stocks are replaced with outstanding introductions from within and outside CIMMYT.

Table 4 Constituent of entries in each crossing block in bread wheat breeding program

CB	Major released cultivars in the target ME	Elite CIMMYT germplasm from YT	Elite CIMMYT germplasm from ISNYT	Advanced lines from CIMMYT Pathology	Advanced lines from CIMMYT Wide Cross	Total
CBME1	30 (6)	380 (76)	10 (2)	30 (6)	50 (10)	500 (100)
CBME2	20 (6.7)	235 (78)	5 (2)	20 (6.7)	20 (6.7)	300 (100)
CBME3	5 (10)	32 (64)	3 (6)	5 (10)	5 (10)	50 (100)
CBME4	20 (7)	200 (67)	20 (7)	30 (10)	30 (10)	300 (100)
CBME5	5 (5)	80 (80)	5 (5)	5 (5)	5 (5)	100 (100)
CBME6	60 (60)	20 (20)	10 (10)	5 (5)	5 (5)	100 (100)

Note: The number in brackets is the percentage to the total number of entries in the CB.

Male master and female master lists for crosses

Not all entries in a CB are finally involved in crossing. Before making crosses targeted to a specific ME, the male master (MM) and female master (FM) lists are first determined within each crossing block.

The male master list represents the best entries in the crossing block (Table 5) based on field observations (agronomic type in the field from the past cycles and the current cycle) and relevant data bases (yield, adaptation, disease resistance, end-used type, and protein content etc.). These entries are used as male parents for simple crosses, but simple crosses are also made among those top parents themselves. In addition they provide the majority of males in crosses with other entries in top- and limited backcrosses (Table 6).

The female master list includes some CB and ON entries that still require specific improvements but carry certain traits of great interest. These entries will only be used as female parents for crossing to the entries from the MM list. The approximate numbers of entries in the male master and female master lists, plus the criteria for selecting them, are listed in Table 5. On average, an entry in the MM list will be crossed with 4 to 10 other entries on the MM list; however, an entry in the FM list will be crossed with 1 to 3 best entries on the MM list. And an entry in a ME-specific MM or FM list can be crossed with entries on the MM list for another ME (Table 6).

F1 and segregating populations

Crosses are always directed toward a specific ME, taking into account the relevant requirements for the respective ME. The resulting segregating populations are labelled accordingly. Mostly introduced materials are used as females in their original crosses, in order to possibly expand the genetic base of CIMMYT bread wheat cytoplasm, but also for practical/logistical reasons.

Outstanding F1 populations are top- and/or backcrossed. Top crosses are used to expand variability. Limited backcrosses are carried out to stabilize variability, as the genetic distance between parents becomes greater, and are proving very effective in expanding adaptation and performance while introgressing new genetic diversity. The female and male parents for a ME-targeted cross can be from the same crossing block or from two different crossing blocks (Table 6).

Table 5 Approximate numbers of entries, male master (MM) and female master (FM) in each crossing block and parental selection criteria for MM and FM

Targeted ME	Number of entries	Male master (MM)		Female master (FM)	
		Number of MM	Selected traits (arranged by importance) and criteria	Number of FM	Selected traits (arranged by importance) and criteria
CBME1	500	75 (15% of 500)	Photo-insensitivity = *Ppd* alleles Major commercial cultivar Adaptation High yield SR = 0 LR < 10% YR < 10% KB < 10% Lodging tolerance Grain color = White (90%) Industrial quality = 1a, 1b, or 2a Combining ability	150 (30%)	Adaptation High yield SR < 5% YR < 50% LR < 50%
CBME2	300	50 (17%)	Photo-insensitivity = *Ppd* alleles Major commercial cultivar Adaptation High yield SR = 0 YR < 10% LR < 10% ST = R (resistant) or MR (moderately resistant) SC = R or MR Lodging tolerance Industrial quality = 1a, 1b, or 2a Grain color = White (50%) Combining ability	100 (33%)	Adaptation High yield SR < 5% YR < 50% LR < 50%
CBME3	50	10 (20%)	Photo-insensitivity = *Ppd* alleles Major commercial cultivar Adaptation High yield SR = 0 YR < 10% LR < 10% ST = R or MR SC = R or MR Lodging tolerance Industrial quality = 1a, 1b, or 2a Grain color = White (50%) Combining ability Acid soil tolerance	20 (40%)	Adaptation High yield SR < 5% YR < 50% LR < 50%

CBME4	500	50 (10%)	Photo-insensitivity = *Ppd* alleles Major commercial cultivar Adaptation High yield SR = 0 YR < 10% LR < 10% ST = R or MR Common bunt resistance Grain color = White (90%) Heat tolerance (low CTD) Cold tolerance Drought tolerance Industrial quality = 1a, 1b, or 2a	200 (40%)	Adaptation High yield SR < 5% YR < 50% LR < 50%
CBME5	100	10 (10%)	Photo-insensitivity = *Ppd* alleles Major commercial cultivar Adaptation High yield SR < 50% YR < 30% LR < 10% HLB = R or MR Lodging tolerance Grain color = White (90%) Industrial quality = 1a, 1b, or 2a Combining ability	50 (50%)	Adaptation High yield SR < 5% YR < 50% LR < 50%
CBME6	200	50 (25%)	Photo-sensitivity = *ppd* alleles Maturity = L (late) Major commercial cultivar Adaptation High yield SR = 0 YR < 10% LR < 10% Common bunt resistance Grain color = White (50%)	100 (50%)	Adaptation High yield SR < 5% YR < 50% LR < 50%

Table 6 Approximate number of simple and top/back crosses for each ME, and origin of their parents

Targeted ME	Number of simple crosses	Parents for simple cross	Number of top crosses	Criteria for selecting F1 for top crossing	Parents for top/back cross
ME1IR	1000	ME1 (MM+FM)× ME1 (MM) (100%)	500 (50%*)	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% Lodging < 5% Maturity = N (normal)	F1ME1×ME1 (MM) (100%)

ME2HR	400	ME2 (MM+FM)× ME2 (MM) (>90%) ME2 (MM+FM)× ME1 (MM) (5-10%)	250 (62.5%)	Photo-insensitivity = *Ppd* alleles Height = 80-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% Lodging <= 5% ST = R or MR BYDV = R or MR SC = R or MR Maturity = N	F1ME2×ME2 (MM) (100%)
ME3AS	50	ME3 (MM+FM)× ME2 (MM) (90-95%) ME3 (MM+FM)× ME3 (MM) (5-10%)	30 (60%)	Photo-insensitivity =*Ppd* alleles Height = 80-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% Lodging <= 5% ST = R or MR BYDV = R or MR SC = R or MR	F1ME3×ME3 (MM) (90%) F1ME3×ME2 (MM) (10%)
ME4SA	500	ME4 (MM+FM)× ME4 (MM) (60%) ME4 (MM+FM)× ME1 (MM) (20%) ME4 (MM+FM)× ME2 (MM) (20%)	250 (50%)	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = R or MR Maturity = N	F1ME4×ME4 (MM) (100%)
ME5TE	50	ME5 (MM+FM)× ME1 (MM) (>90%) ME5 (MM+FM)× ME5 (MM) (1-10%)	30 (60%)	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N or E (early)	F1ME5×ME1 (MM) (80%) F1ME5×ME5 (MM) (20%)
ME6HL	200	ME6 (MM+FM)× ME1 (MM) (40%) ME6 (MM+FM)× ME2 (MM) (30%) ME6 (MM+FM)× ME4 (MM) (30%)	100 (50%)	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >=4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = R or MR SC = R or MR Maturity = L (late)	F1ME6×ME6 (MM) (100%)

MM = Male master; FM = Female master; F1ME1 = F1s targeted for ME1, and so on.

*: Number in parenthesis is the percentage of the number of top crosses to that of simple crosses.

As a rule, 4-5 spikes are emasculated for simple crosses and 7-10 for top- or backcrosses. Once a cross has been made and classified, its segregating progenies are selected in a shuttle breeding fashion between Toluca and Cd. Obregon. Certain generations may be planted under the real or simulated stresses specific to their targeted ME. However, since all elite CIMMYT advanced material is tested over a wide range of environments both in Mexico and internationally, some lines may express additional adaptation in the process and consequently enter into more than one ME selection stream.

The diagram in Figures 1, 2, 3 and 4 is a hypothetical representation of germplasm flow, starting out from parental selection and resulting in replicated yield testing (YT) and final nursery distribution. In the early 1980s, the pedigree selection method was exchanged for a combination of pedigree and bulk breeding, called the modified pedigree-bulk method, which operates as follows (also see Tables 7 to 12).

F1: A simple cross is made. About 2000-2500 simple crosses are made per cycle.

F1Top: About one third of the most outstanding F1's are top crossed to one or more third parents, or a (limited) backcross is made back to the adapted parent. Per cycle about 1000-1500 top and limited backcrosses are made. Independent of the target ME an epidemic is created of the prevalent diseases, either in Cd. Obregon or Toluca. In the first segregating generation of such crosses, only some negative selection is practiced. Seeds sampled from all remaining plants are promoted to the F2.

F2: F2 populations exist of about 750-1500 plants per cross, which are space-planted at 10-15 cm between plants. Both simple, top and (limited) backcrosses are represented. Again an epidemic is created of the prevalent diseases. The poorest F2 populations are completely discarded. Within the better F2 populations, the best plants are selected by the breeders with additional assistance of experienced research assistants, during 3-5 rounds, based on good agronomic type, appropriate height, synchronous tillering, desired spike type, large spike, good fertility, durable disease resistance, and desired maturity (Tables 7, 8, 9, 10, 11 and 12). These plants are harvested and threshed on an individual basis (Figure 4), and the seed is visually observed for grain filling characteristics, boldness, lack of diseases, yellow berry, other markings, and color. About 30-50% of the entries are thus discarded.

F3: the seed from individually selected F2 plants is planted as a double (in Toluca) or triple (in Cd. Obregon) row, 2 m in length, at a normal seeding rate (80-100 kg/ha). The advantage of this planting method is that plants can develop more or less as they would in farmers’ fields with few tillers and in close proximity to neighbouring sister plants. All materials, except those targeted for ME4, are planted under well-watered conditions. ME4 F3 lines, when in Cd. Obregon, are planted under drought stress (one pre-sown irrigation). Under all conditions, except under drought, an epidemic is created of the prevalent diseases. The best lines are selected by the breeders based on agronomic type, fertility, lodging tolerance, durable disease resistance, and expected yielding ability, plus somewhat for phenotypic uniformity. Subsequently, within the best lines 10 good spikes are harvested by breeders and experienced research assistants, and threshed in bulk. The advantage of this two-phase selection process is that the breeders can personally carry out all the between-line selection. Seed selection follows. This generates the bulked seed for the next generation.

F4, **F5,** and **F6**: The methodology detailed in the F3 is repeated, all the while alternating the generations between Toluca and Cd. Obregon. Epidemics of the prevalent diseases are created. The number of lines retained decreases considerably from F3 till F6. Selection intensity increases as the modified pedigree-bulk selection process progresses and additive gene complexes express themselves more clearly. In the full pedigree method used earlier, the number of lines increased greatly, making it increasingly difficult for breeders themselves to personally select all the desired individual plants.

In the F6, the selected 10 spikes are individually threshed. Due to the low amount of seed per entry, no seed selection is practiced.

In the case of ME4 targeted materials, the F3-F6 generations are alternated between sufficient rainfall (Toluca) and drought stress (Cd. Obregon, one pre-sowing irrigation). In this fashion, drought tolerance and performance under drought are combined with responsiveness to increased moisture availability and yield potential.

F7: The head-to-row planting allows thousands of entries to be planted in a small area. Again an epidemic is created of the prevalent diseases. The best and most uniform lines are visually selected and harvested in bulk. Seed selection follows. These entries are promoted to advanced lines (AL). Because the lines are bulked in the F7, some residual heterozygosity and heterogeneity are retained. This provides an opportunity for cooperators receiving CIMMYT’s International Nurseries and Yield Trials to carry out reselection under their own conditions, even within lines.

In Mexico, segregating generations targeted for a specific ME may occasionally be sown outside the regular Obregon/Toluca shuttle in other locations, such as El Batan and, in the past, Huamantla. In some instances, yield trials may also be conducted in the early segregating generations depending on the nature of the materials.

Advanced lines and yield trials

AL: The newly bulked Advanced Lines (AL) derived from F7's are exposed to observation for agronomic type and disease resistance. Several major industrial quality characteristics are determined (grain hardness, grain protein, SDS sedimentation values) based on Obregon seed. The bottom group (5-20%) is generally discarded based on minimum quality requirement, but entries outstanding for key traits are retained even if they have poor quality.

PYT: The best AL entries are promoted to the first-year Preliminary Yield Trials (PYTs), including checks, and planted and analysed according to specific statistical designs to eliminate the bottom end of the yield distribution. PYTs targeted for ME1, ME4 and ME5 are carried out in Cd. Obregon. This is where the targeted conditions can be simulated: ME1 by applying 5-6 irrigations; ME4 by withholding all irrigations except for one pre-sowing irrigation, thus creating very stringent drought conditions; ME5 by planting late (in January or February) resulting in considerable heat stress at the time for flowering and grain filling. Lines targeted for ME2 and ME3 are grown in PYTs in the high rainfall environment of Toluca. Thus each target environment (e.g. ME1: irrigated, ME2 and ME3: high rainfall, ME4: drought, ME5: heat) is somewhat represented or simulated during the yield trial phase.

The trials are either planted on beds (per entry: 2 beds, each 76 cm in width, in Toluca, and 80 cm in width each in Cd. Obregon, 3-4-m long with 2 rows/bed in Toluca and 3 rows/bed in Cd. Obregon), or in irrigation units called *melgas* (*melga* means "irrigation basin" in Spanish) with 30 plots/*melga*. In *melgas* every entry is sown as an 8-row plot, 3.8 m long.

PCs (for *Parcela Chica*, "small plot" in Spanish) are planted separately at the same time as the preliminary yield trials, with exactly the same entries as in the PYTs, in an area where relevant diseases are artificially inoculated. The PCs provide disease resistance data. In addition the PCs form small seed multiplication plots, where roguing can be carried out to provide clean, pure seed for subsequent cycles.

During the summer cycle in central Mexico, PCs may be sown for disease and adaptation evaluation in many different sites, including Patzcuaro, El Tigre (Sierra de Jalisco), and Oaxaca. Most of the relevant diseases are represented in these sites, though obviously other virulence and levels of aggressiveness may be present than at the target MEs on other continents.

The entries are keenly scrutinized for lodging tolerance in the large PYT plots. Based on absolute and relative yield, agronomic type, disease resistance, and additional industrial quality tests, including alveograms (based on Cd. Obregon seed), the best lines are promoted to an EAL.

EAL: When grown as Elite Advanced Lines (EAL), the materials are exposed to disease epidemics and also selected for quality traits, if in Cd. Obregon.

YT: The best EAL entries enter the second-year Yield Trials (YTs). As with the PYTs the materials are grown under representative relevant environmental conditions. Latinized alpha-lattice designs with three replications are used. The trials are spatially analysed.

EPCs (for Elite *Parcela Chica*), containing the same entries as the YTs, are planted separately in an area where diseases are artificially inoculated. As with the PCs, data and clean seed are obtained. What needs further explanation is that EPCME2 of YTME2 (MV) and EPCME3 of YTME3 (MV) are all planted at the same time as the trials in MV, also in the MXI block in BV. So in November when the entries for the new ISNYTs based on the MV yields have been decided, only those entries that will enter the new ISNYTs in the MXI block in BV are harvested and sent to MXI for large multiplication.

Following data taking of the YTs and the EPCs, seed of selected entries is fully quality tested, including baking trials. The best entries are selected as candidates for International Screening Nurseries and Yield Trials (ISNYT) for international distribution. The lines that enter into the ISNYT are those that yielded best in the relevant YTs, but also showed good resistance and performance in the EPCs which are always planted at the same time in the disease area, where artificial inoculation with very virulent races (rust) and straw (*Septoria tritici*) takes place. These lines are expected to be good for diseases since they have been screened for resistance since the F1 onwards. Industrial quality is also taken into account, but a very high-yielding line that has low industrial quality may still be included in the ISNYT, since many countries still value quantity over quality. The lines should also not lodge excessively in the YTs, plus must be very uniform. Furthermore we do not want to send just a few crosses and tens of sister lines from each cross, so that the genetic diversity can be maintained.

Space permitting, un-replicated or replicated trials may be sown in other (simulated) mega-environments to gauge the performance of materials outside their initially targeted ME. Although genotypes are developed for a designated/targeted ME based on their parents and enforced through their subsequent selection history, their performance may justify them crossing over into other MEs.

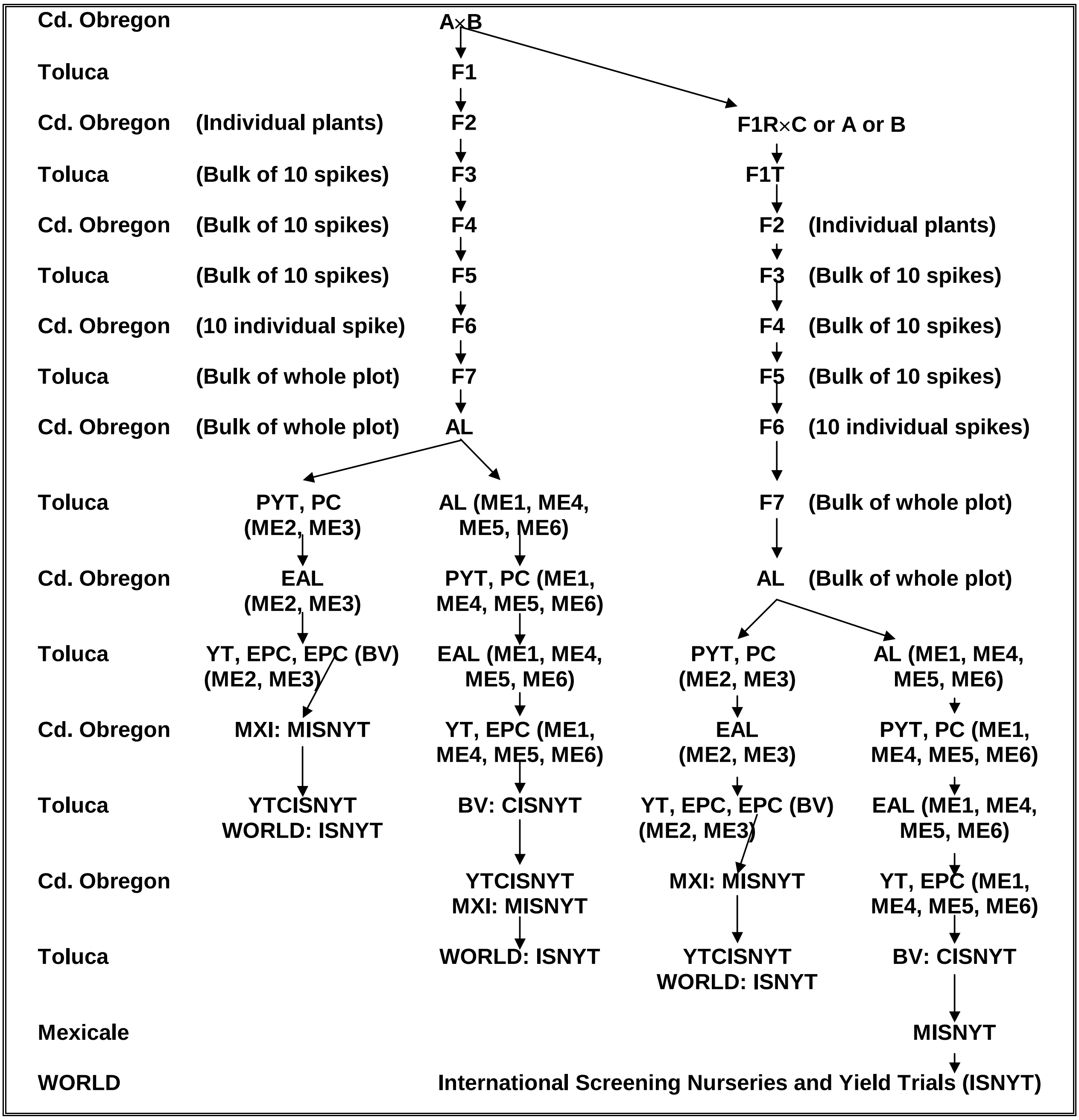


Figure 1 Diagram of germplasm flow in CIMMYT's Bread Wheat Breeding Program for the modified pedigree/bulk selection method.

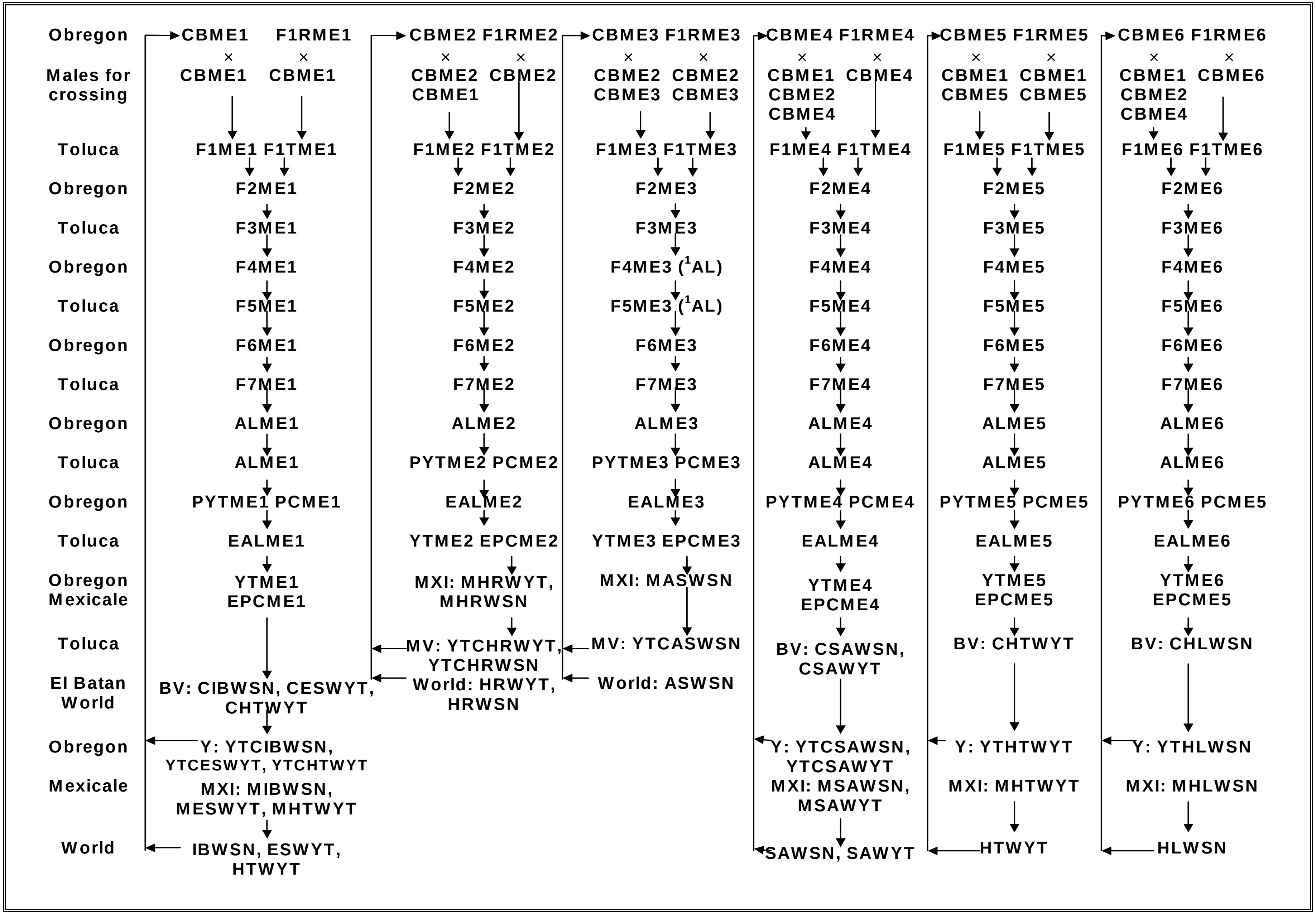


Figure 2 Germplasm flow when making crosses in Obregon (^{1}AL = Aluminium tolerance screening in laboratory)

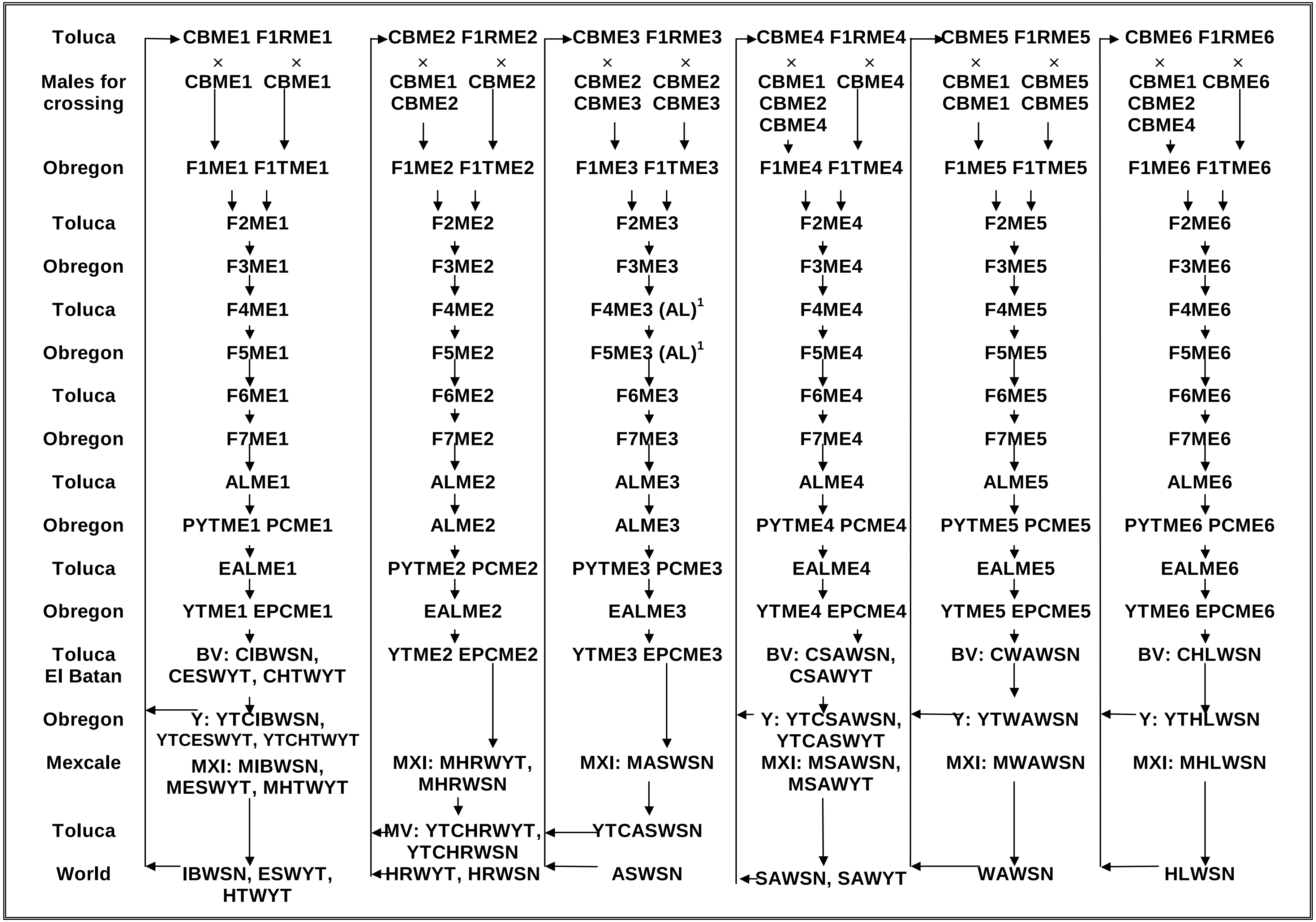
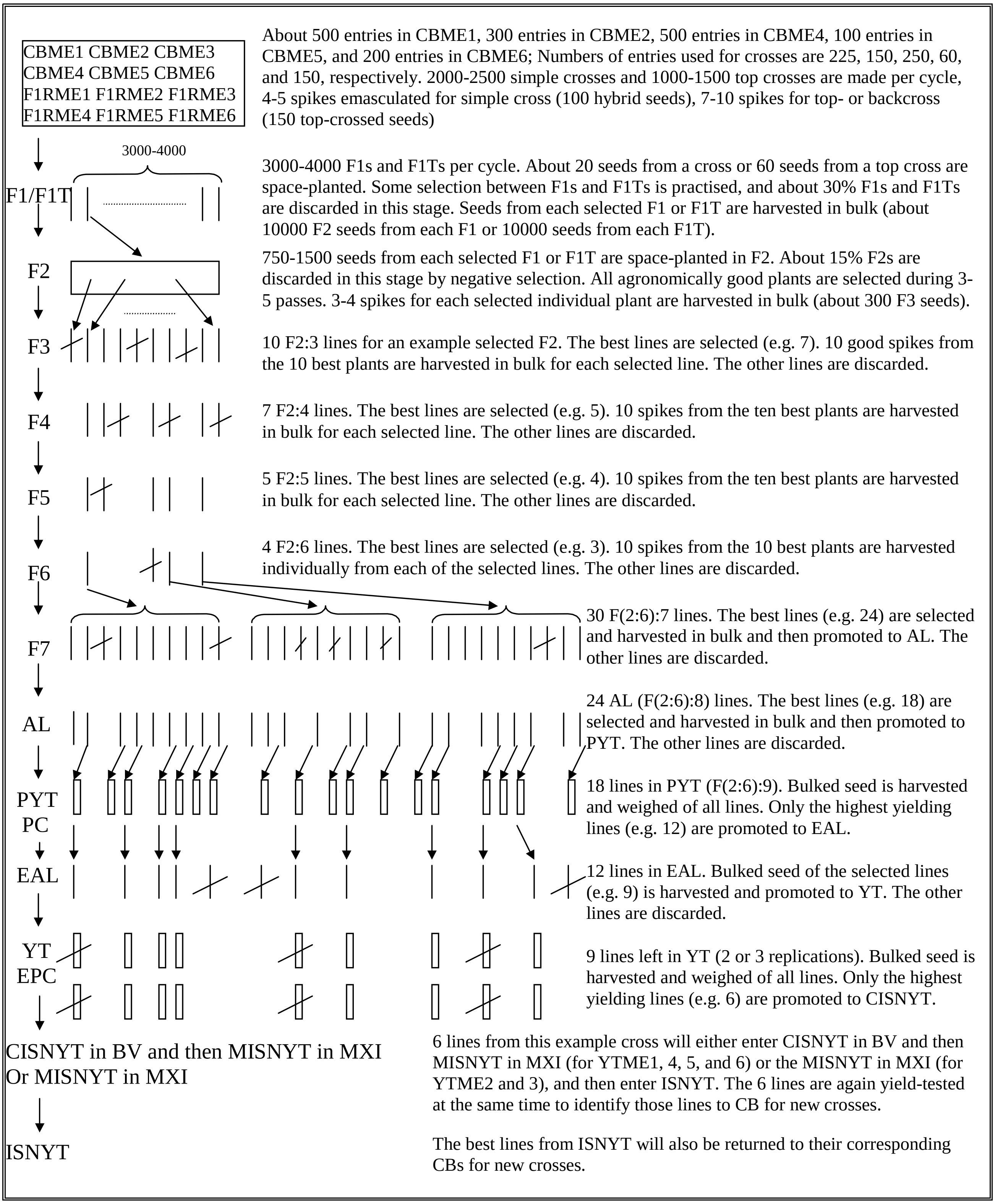


Figure 3 Germplasm flow when making crosses in Toluca ([1]AL = Aluminium tolerance screening in laboratory)



About 500 entries in CBME1, 300 entries in CBME2, 500 entries in CBME4, 100 entries in CBME5, and 200 entries in CBME6; Numbers of entries used for crosses are 225, 150, 250, 60, and 150, respectively. 2000-2500 simple crosses and 1000-1500 top crosses are made per cycle, 4-5 spikes emasculated for simple cross (100 hybrid seeds), 7-10 spikes for top- or backcross (150 top-crossed seeds)

3000-4000 F1s and F1Ts per cycle. About 20 seeds from a cross or 60 seeds from a top cross are space-planted. Some selection between F1s and F1Ts is practised, and about 30% F1s and F1Ts are discarded in this stage. Seeds from each selected F1 or F1T are harvested in bulk (about 10000 F2 seeds from each F1 or 10000 seeds from each F1T).

750-1500 seeds from each selected F1 or F1T are space-planted in F2. About 15% F2s are discarded in this stage by negative selection. All agronomically good plants are selected during 3-5 passes. 3-4 spikes for each selected individual plant are harvested in bulk (about 300 F3 seeds).

10 F2:3 lines for an example selected F2. The best lines are selected (e.g. 7). 10 good spikes from the 10 best plants are harvested in bulk for each selected line. The other lines are discarded.

7 F2:4 lines. The best lines are selected (e.g. 5). 10 spikes from the ten best plants are harvested in bulk for each selected line. The other lines are discarded.

5 F2:5 lines. The best lines are selected (e.g. 4). 10 spikes from the ten best plants are harvested in bulk for each selected line. The other lines are discarded.

4 F2:6 lines. The best lines are selected (e.g. 3). 10 spikes from the 10 best plants are harvested individually from each of the selected lines. The other lines are discarded.

30 F(2:6):7 lines. The best lines (e.g. 24) are selected and harvested in bulk and then promoted to AL. The other lines are discarded.

24 AL (F(2:6):8) lines. The best lines (e.g. 18) are selected and harvested in bulk and then promoted to PYT. The other lines are discarded.

18 lines in PYT (F(2:6):9). Bulked seed is harvested and weighed of all lines. Only the highest yielding lines (e.g. 12) are promoted to EAL.

12 lines in EAL. Bulked seed of the selected lines (e.g. 9) is harvested and promoted to YT. The other lines are discarded.

9 lines left in YT (2 or 3 replications). Bulked seed is harvested and weighed of all lines. Only the highest yielding lines (e.g. 6) are promoted to CISNYT.

6 lines from this example cross will either enter CISNYT in BV and then MISNYT in MXI (for YTME1, 4, 5, and 6) or the MISNYT in MXI (for YTME2 and 3), and then enter ISNYT. The 6 lines are again yield-tested at the same time to identify those lines to CB for new crosses.

The best lines from ISNYT will also be returned to their corresponding CBs for new crosses.

Figure 4 Flow chart of the modified pedigree/bulk selection method

Table 7 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME1

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Lodging < 5%	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N (normal) Lodging < 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N (normal) Lodging < 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N Lodging < 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	0.03-30% 5-150 best plants harvested individually
F2:3	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% Maturity = N Lodging < 5% Phenotypic uniformity >= 60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:4	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 20%	10 spikes from the 10 best plants Bulked seed

	YR < 30% Maturity = N Lodging < 5% Phenotypic uniformity >= 70%		YR < 20% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	
F2:5	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% YR < 20% Maturity = N Lodging < 5% Phenotypic uniformity >= 80%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 15% YR < 15% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:6	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% Maturity = N Lodging < 5% Phenotypic uniformity >= 90%	60-80%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Harvested individually
F(2:6):7	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Lodging < 5% Phenotypic uniformity = 100%	30-70%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm	80-90%	No	100%

	Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Grain color = White (90%)			Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
CIBWSN CESWYT CHTWYT	BV: 98% of entries will enter MXI for multiplication.			
YTCIBWSN YTCESWYT YTCHTWYT MIBWSN MESWYT MHTWYT	Y: Best lines from the YT will enter CBME1 for new crosses. MXI: 98% will be distributed to ISNYT.			
IBWSN ESWYT HTWYT	World: The top best lines will return to CBME1 for new crosses.			

Table 8 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME2

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant) BYDV = T (tolerant) or MT (moderately tolerant) SC = R or MR	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5%	50-70% Negative selection: spikes are taken from all good to

	LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging < 5%		LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging < 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	0.03-30% 5-150 best plants harvested individually
F2:3	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Phenotypic uniformity >= 60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:4	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Phenotypic uniformity >= 70%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 20% YR < 20% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:5	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	30-40%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	10 spikes from the 10 best plants Bulked seed

	SR < 5% LR < 20% YR < 20% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Phenotypic uniformity >= 80%		SR = 0% LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	
F2:6	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Phenotypic uniformity >= 90%	60-80%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Harvested individually
F(2:6):7	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 100%	30-70%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet>=4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR	30-50%	No	100% Bulked seed

	Maturity = N Lodging < 5% Yield Grain color = White (90%)			
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
MHRWSN MHRWYT	MXI: 98% will be distributed to ISNYT. The seeds for multiplication are from the EPC in BV.			
YTCHRWSN YTCHRWYT HRWSN HRWYT	Toluca: Best lines from the Toluca YT will return to CBME2 for new crosses. World: Best lines form ISNYT will return to CBME2 for new crosses.			

Table 9 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME3

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant) BYDV = T (tolerant) or MT (moderately tolerant) SC = R or MR	70%	No	100% Bulked seed

F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	0.03-30% 5-150 best plants harvested individually
F2:3	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering>5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:4	Tolerance to AL in lab test	100%	AL tolerance	5% Of 50 seeds about 6-7 are advanced
F2:5	Tolerance to AL in lab test	100%	AL tolerance	5% Of 50 seeds about 15-20 are advanced
F2:6	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5%	60-80%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0%	10 spikes from the 10 best plants Harvested individually

	LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 90%		LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	
F(2:6):7	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 95%	30-70%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet>=4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N	80-90%	No	100% Bulked seed

	Lodging <= 5% Grain color = White (90%)			
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
MASWSN	MXI: 98% of entries will enter ISNYT. The seed for multiplication is from the EPC in BV.			
YTCASWSN ASWSN	Toluca: Best lines from Toluca YT will return to CBME3 for new crosses. World: Best lines from ISNYT will return to CBME3 for new crosses.			

Table 10 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME4

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant)	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR	70%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm, *Rht1* or *Rht2* Tillering > 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR	85%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm, *Rht1* or *Rht2* Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST=R or MR ST = R or MR	0.03-30% 5-150 best plants harvested individually

			Heat tolerance Cold tolerance Grain color = White (90%)	
F2:3	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR Phenotypic uniformity>=60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 30% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:4	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR Phenotypic uniformity >= 70%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 15% YR < 20% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:5	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% YR < 20% ST = R or MR Phenotypic uniformity >= 60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 100-110cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:6	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% ST = R or MR Phenotypic uniformity >= 90%	60-80%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR<1% LR<10% YR<10% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)	10 spikes from the 10 best plants Harvested individually
F(2:6):7	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR	30-70%	No	100% Bulked seed

	Phenotypic uniformity >= 95%			
AL	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles Height = 100-120cm SR < 0% LR < 10% YR < 10% ST = R or MR Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR < 0% LR < 10% YR < 10% ST = R or MR Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
CSAWSN CSAWYT	BV: 98% of entries will enter MXI for multiplication.			
YTCSAWSN YTCSAWYT MSAWSN MSAWYT	Y: Best lines from the YT will enter CBME4 for new crosses. MXI: 98% of entries will enter ISNYT.			
SAWSN SAWYT	World: Best lines will return to CBME4 for new crosses.			

Table 11 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME5

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	70%	No	100% Bulked seed

	SR < 5% LR < 40% Lodging <= 5%			
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N (normal) Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N (normal) Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	0.03-30% 5-150 best plants harvested individually
F2:3	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% Maturity = N Lodging < 5% Phenotypic uniformity >= 60%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:4	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% Maturity = N Lodging < 5% Phenotypic uniformity >= 70%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 20% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed
F2:5	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% Maturity = N Lodging < 5% Phenotypic uniformity >= 80%	30-40%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 15% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Bulked seed

F2:6	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% Maturity = N Lodging < 5% Phenotypic uniformity >= 90%	60-80%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% YR < 10% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10 spikes from the 10 best plants Harvested individually
F(2:6):7	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% Lodging < 5% Phenotypic uniformity = 100%	30-70%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% *Helminthosporium sativum* spot blotch (HLB) = R or MR Maturity = N Lodging < 5% Heat tolerance Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% HLB = R or MR Maturity = N Lodging < 5% Heat tolerance Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% HLB = R or MR Maturity = N Lodging < 5% Heat tolerance Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% HLB = R or MR Maturity = N Lodging < 5%	40-60%	No	100% Bulked seed

	Heat tolerance Yield Grain color = White (90%) IQ = non tenacious			
CWAWSN	BV: 98% of entries will enter MXI for multiplication.			
YTCWAWSN MWAWSN	Y: Best lines from the YT will enter CBME5 for new crosses. MXI: 98% will enter ISNYT			
WAWSN	World: Best lines will return to CBME5 for new crosses.			

Table 12 Breeding traits, selection intensity, selection criteria and harvest method in each generation for modified pedigree/bulk selection for materials targeted to ME6

Generation	Among-cross (for F1 and F2) or family (for F3 and on) selection		Within-cross (for F2) or family (for F3 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant) BYDV = R SC = R or MR	70%	No	100% Bulked seed
F1T	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = R SC = R or MR	70%	Photo-sensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* or *Rht2*, and sometimes *Rht8* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = R SC = R or MR Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-sensitivity = *ppd* alleles Height = 80-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR<5% YR<40% LR <40% ST = R or MR BYDV = R SC = R or MR Lodging <= 5%	85%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = R SC = R or MR Grain color = White (50%)	2-3% 30-60 best plants harvested individually
F2:3	Photo-sensitivity = *ppd* alleles Height = 80-100cm	30-40%	Photo-sensitivity = *ppd* alleles Height = 80-100cm	10 spikes from the 10 best plants

	Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% ST = R or MR BYDV = R SC = R or MR Lodging < 5% Phenotypic uniformity >= 60%		Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	Bulked seed
F2:4	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% ST = R or MR BYDV = R SC = R or MR Lodging < 5% Phenotypic uniformity >= 70%	30-40%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 15% YR < 15% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10 spikes from the 10 best plants Bulked seed
F2:5	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% ST = R or MR BYDV = R SC = R or MR Lodging < 5% Phenotypic uniformity >= 80%	30-40%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10 spikes from the 10 best plants Bulked seed
F2:6	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% ST = R or MR BYDV = R SC = R or MR Lodging < 5% Phenotypic uniformity >= 90%	60-80%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10 spikes from the 10 best plants Harvested individually
F(2:6):7	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1%	30-70%	No	100% Bulked seed

	LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Lodging < 5% Phenotypic uniformity >= 95%			
AL	Photo-sensitivity = *ppd* alleles SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%)	50-80%	No	100% Bulked seed
PYT PC	Photo-sensitivity = *ppd* alleles SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%) IQ=1a, 1b, or 2a Yield	30-50%	No	100% Bulked seed
EAL	Photo-sensitivity = *ppd* alleles SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%)	80-90%	No	100% Bulked seed
YT EPC	Photo-sensitivity = *ppd* alleles SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = R SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (90%) IQ = 1a, 1b, or 2a Yield	40-60%	No	100% Bulked seed

CHLWSN	BV: 98% of entries will enter MXI.
YTCHLWSN MHLWSN	Y: Best lines from the YT will enter CBME6 for new crosses. MXI: 98% of entries will enter ISNYT.
HLWSN	World: Best lines will return to CBME6 for new crosses.

Alternative selection method: selected bulk

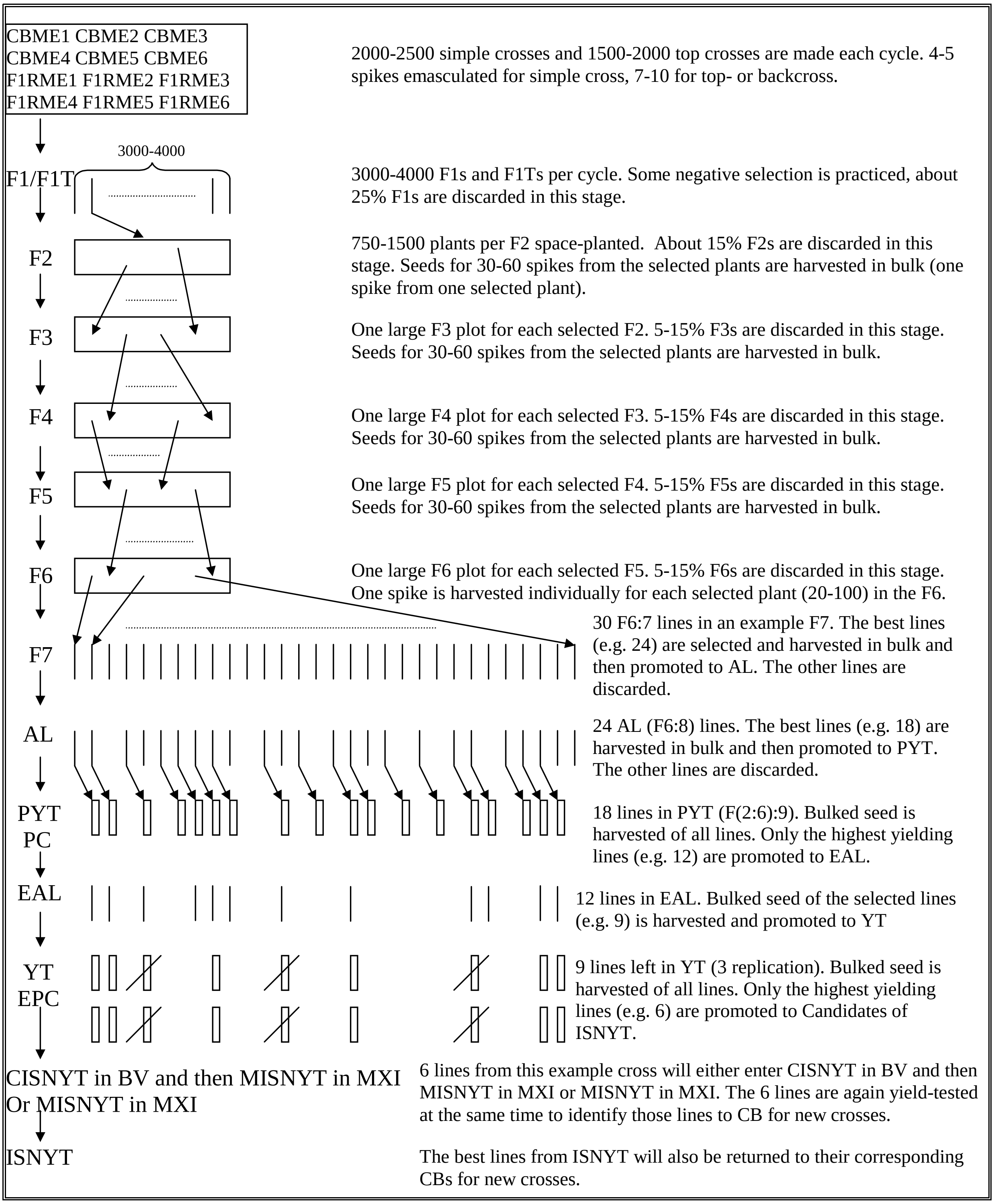
In the past 12 years, CIMMYT has experimented with another selection methodology called "selected bulk". The difference between the new method and the modified pedigree/bulk method first becomes apparent in F2 generation (Figure 4 and Figure 5). Spikes of the selected F2 plants within one cross are harvested in bulk and threshed together, resulting in one F3 seed lot per cross. If this seed successfully passes the visual seed selection, the single F2 plot will generate one large F3 plot. The immediate result then is that the number of F3 plots drops dramatically compared to the modified pedigree/bulk method. Since the mean number of plants finally promoted per cross in the F2 is about ten, the number of F3 plots drops to about 10% of what it would have been in the modified pedigree/bulk method. However, since the F3 contains seed of several distinct plants from the F2, plot size needs to be larger than just a 2-m triple row to allow the greater genetic variability to be properly sampled. Usually a plot size of two 10-m triple rows is used (Table 19). The latter plot size is about 10 times as large as the one triple 1-m or 2-m row used for the pedigree or modified pedigree/bulk methods. Thus it may seem that overall not much space is saved with less larger plots being planted. However, since fewer larger plots will require fewer alleyways, some land is saved. However, the key cost advantage lies in the fact that fewer seed lots need to be handled at harvest, threshing, visual seed discard, nursery preparation, planting and plot labelling. This constitutes significant savings in time, labour, and costs, and reduces potential sources of error in the program.

In the F3 phase certain uniformly unadapted plots are discarded. The remainder is selected by harvesting 30-60 spikes from the best plants within each blot. Since genetic variability is larger than in the modified pedigree/bulk method, we are sampling more than just the 10 spikes selected in the modified pedigree/bulk method. These spikes are treated in bulk, and will generate one F4 plot, if not discarded during the visual seed discard. Likewise, the F4 to F6 stages are executed.

Finally, in the F6 the best 20-100 spikes are individually selected, harvested, threshed, prepared for planting and planted as F7 head rows in one 1-m triple row plots. The number of spikes selected is again larger than in the F6 of the modified pedigree/bulk method. For the same reason as stated above, a greater genetic variability is contained in the F6 because the initially selected F2 plants were bulked. Hence this genetic variability should be sampled.

Selected F7s are bulk harvested and enter ALs, as in the modified pedigree/bulk method. In case the F7s are still segregating somewhat, individual spikes are again selected and F8 head rows are grown. These F8s are the bulk harvested and then enter advanced lines (ALs).

This selected bulk method of breeding has been applied somewhat more widely since the early to mid 1990s. In a few years, larger numbers of lines emanating from this method can be compared to those obtained using the modified pedigree/bulk method. The selected traits, selection intensity for each segregating generations for materials targeted to ME1 to ME6 are expounded in Table 13 to 18, respectively.



2000-2500 simple crosses and 1500-2000 top crosses are made each cycle. 4-5 spikes emasculated for simple cross, 7-10 for top- or backcross.

3000-4000 F1s and F1Ts per cycle. Some negative selection is practiced, about 25% F1s are discarded in this stage.

750-1500 plants per F2 space-planted. About 15% F2s are discarded in this stage. Seeds for 30-60 spikes from the selected plants are harvested in bulk (one spike from one selected plant).

One large F3 plot for each selected F2. 5-15% F3s are discarded in this stage. Seeds for 30-60 spikes from the selected plants are harvested in bulk.

One large F4 plot for each selected F3. 5-15% F4s are discarded in this stage. Seeds for 30-60 spikes from the selected plants are harvested in bulk.

One large F5 plot for each selected F4. 5-15% F5s are discarded in this stage. Seeds for 30-60 spikes from the selected plants are harvested in bulk.

One large F6 plot for each selected F5. 5-15% F6s are discarded in this stage. One spike is harvested individually for each selected plant (20-100) in the F6.

30 F6:7 lines in an example F7. The best lines (e.g. 24) are selected and harvested in bulk and then promoted to AL. The other lines are discarded.

24 AL (F6:8) lines. The best lines (e.g. 18) are harvested in bulk and then promoted to PYT. The other lines are discarded.

18 lines in PYT (F(2:6):9). Bulked seed is harvested of all lines. Only the highest yielding lines (e.g. 12) are promoted to EAL.

12 lines in EAL. Bulked seed of the selected lines (e.g. 9) is harvested and promoted to YT

9 lines left in YT (3 replication). Bulked seed is harvested of all lines. Only the highest yielding lines (e.g. 6) are promoted to Candidates of ISNYT.

6 lines from this example cross will either enter CISNYT in BV and then MISNYT in MXI or MISNYT in MXI. The 6 lines are again yield-tested at the same time to identify those lines to CB for new crosses.

The best lines from ISNYT will also be returned to their corresponding CBs for new crosses.

Figure 5 Flow chart of the selected bulk method

Table 13 Breeding traits, selection intensity, selection criterion, and harvest method in each generation for selected bulk strategy for materials targeted to ME1

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Lodging <= 5%	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N (normal) Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N (normal) Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering >= 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% Maturity = N Lodging <= 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% Maturity = N Lodging <= 5% Seed quality =P or MP Grain color = White (90%)	5-10% 30-60 spikes from the best plants Bulked seed
F4	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0%	10-20% 30-60 spikes from best plants Bulked seed

	LR < 30% YR < 30% Maturity = N Lodging < 5%		LR < 20% YR < 20% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	
F5	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% YR < 20% Maturity = N Lodging < 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 15% YR < 15% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10-20% 30-60 spikes from the best plants Bulked seed
F6	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% Maturity = N Lodging < 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-insensitivityv = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Phenotypic uniformity >= 95%	30%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	100% Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are harvested individually.
F6:8	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Phenotypic uniformity >= 100%	50%	No	100% Bulked seed
AL (F6:9)	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10%	50-80%	No	100% Bulked seed

	YR < 10% Maturity = N Lodging < 5% Grain color = White (90%)			
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% Maturity = N Lodging < 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
CIBWSN CESWYT CHTWYT	BV: 98% of entries will enter MXI for multiplication.			
YTCIBWSN YTCESWYT YTCHTWYT MIBWSN MESWYT MHTWYT	Y: Best lines from the YT will enter CBME1 for new crosses. MXI: 98% of entries will enter ISNYT.			
IBWSN ESWYT HTWYT	World: Best lines will return to CBME1 for new crosses.			

Table 14 Breeding traits, selection intensity, selection criteria and harvest method in each generation for selected bulk strategy for materials targeted to ME2

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5%	70%	No	100% Bulked seed

	LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant) BYDV = T (tolerant) or MT (moderately tolerant) SC = R or MR			
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N (normal) Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = white (90%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 60%	90%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	5-10% 30-60 spikes from the best plants Bulked seed
F4	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30%	90%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 20%	10-20% 30-60 spikes from best plants Bulked seed

	YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 70%		YR < 20% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	
F5	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% YR < 20% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 80%	90%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-20% 30-60 spikes from the best plants Bulked seed
F6	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 90%	90%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity = 100%	30%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging<=5% Seed quality = P or MP Grain color = white (90%)	100% Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are harvested individually.
F6:8	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10%	50%	No	100% Bulked seed

	YR <10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity = 100%			
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
MHRWSN MHRWYT	MXI: 98% of entries will enter ISNYT. The seed for multiplication is from the EPC in BV.			

YTCHRWSN YTCHRWYT HRWSN HRWYT	Toluca: Best lines form Toluca YT will return to CBME2 for new crosses. World: Best lines form ISNYT will return to CBME2 for new crosses.

Table 15 Breeding traits, selection intensity, selection criteria and harvest method in each generation for selected bulk strategy for materials targeted to ME3

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant) BYDV = T (tolerant) or MT (moderately tolerant) SC = R or MR	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, Rht1 and/or Rht2 Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering>5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-insensitivity = *Ppd* alleles	90%	Photo-insensitivity = *Ppd* alleles	5-10%

	Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 60%		Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	30-60 spikes from the best plants Bulked seed
F4	Tolerance to AL in lab test	100%	AL tolerance	5% Of 50 seeds about 6-7 are advanced
F5	Tolerance to AL in lab test	100%	AL tolerance	5% Of 50 seeds about 15-20 are advanced
F6	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% YR < 15% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity >= 90%	90%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering>5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Phenotypic uniformity =100%	30%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR<10% YR<10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = white (90%)	100% Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are harvested individually.
F6:8	Photo-insensitivity = *Ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10%	50%	No	100% Bulked seed

	ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5%			
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging < 5% Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed
MASWSN	MXI: 98%. The seed is from the EPC in BV.			
YTCASWSN ASWSN	Toluca: Best lines form the Toluca YT will return to CBME2 for new crosses. World: Best lines form ISNYT will return to CBME2 for new crosses.			

Table 16 Breeding traits, selection intensity, selection criteria and harvest method in each generation for selected bulk strategy for materials targeted to ME4

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 100-120cm SR < 5% LR < 40% YR < 40% ST = R (resistant) or MR (medium resistant)	Selection intensity	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR	70%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm, *Rht1* or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)+Red (10%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR	90%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm, *Rht1* or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR<5% LR<40% YR<40% ST = R or MR Heat tolerance Cold tolerance Grain color =White (90%)+Red (10%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 3% LR < 30% YR < 50% ST = R or MR	90%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 3% LR < 30% YR < 30% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)+Red (10%)	5-10% 30-60 spikes from the best plants Bulked seed
F4	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 2% LR < 20% YR < 20% ST = R or MR	90%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 15% YR < 15% ST = R or MR Heat tolerance	10-20% 30-60 spikes from best plants Bulked seed

			Cold tolerance Grain color = White (90%)+Red (10%)	
F5	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR	30%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)+Red (10%)	10-20% 30-60 spikes from the best plants Bulked seed
F6	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR	90%	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Heat tolerance Cold tolerance Grain color = White (90%)+Red (10%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%) Phenotypic uniformity >= 90%	90%	No	100% Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are harvested individually.
F6:8	Photo-insensitivity = *Ppd* alleles Height = 100-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%) Phenotypic uniformity >= 95%	90%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%)	90%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20)	50%	No	100% Bulked seed

	Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%) Yield			
EAL	Photo-insensitivity = *Ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%)	50%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR Grain color = White (90%) Yield	80%	No	100% Bulked seed
CSAWSN CSAWYT	BV: 98% of entries will enter MXI.			
YTCSAWSN YTCSAWYT MSAWSN MSAWYT	Y: Best lines from the YT will enter CBME4 for new crosses. MXI: 98% of entries will enter ISNYT.			
SAWSN SAWYT	World: Best lines will return to CBME4 for new crosses.			

Table 17 Breeding traits, selection intensity, selection criteria and harvest method in each generation for selected bulk strategy for materials targeted to ME5

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Lodging <= 5%	70%	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N (normal)	70%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N (normal)	50-70% Negative selection: spikes are taken from all good to acceptable plants

	Lodging <= 5%		Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (90%)	
F2	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering > 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% Maturity = N Lodging <= 5%	85%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm, *Rht1* and/or *Rht2* Tillering > 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% Maturity = N Lodging <= 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 30% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	5-10% 30-60 spikes from the best plants Bulked seed
F4	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 30% Maturity = N Lodging <= 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 20% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-20% 30-60 spikes from best plants Bulked seed
F5	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 20% Maturity = N Lodging <= 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 15% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-20% 30-60 spikes from the best plants Bulked seed
F6	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 15% Maturity = N Lodging <= 5%	90%	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% Maturity = N Lodging <= 5% Seed quality = P or MP Grain color = White (90%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-insensitivity = *Ppd* alleles	30%	Photo-insensitivity = *Ppd* alleles	100%

	Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% Maturity = N Lodging <= 5% Phenotypic uniformity >= 95%		Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% Maturity = N Lodging < 5% Seed quality = P or MP Grain color = White (90%)	Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are harvested individually.
F6:8	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR <10% Maturity = N Lodging <= 5% Phenotypic uniformity = 100%	50%	No	100% Bulked seed
AL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% *Helminthosporium sativum* spot blotch (HLB) = R or MR Maturity = N Lodging <= 5% Grain color = White (90%)	50-80%	No	100% Bulked seed
PYT PC	Photo-insensitivity = *Ppd* alleles SR = 0% LR < 10% Maturity = N Lodging <= 5% Heat tolerance Yield Grain color = White (90%)	30-50%	No	100% Bulked seed
EAL	Photo-insensitivity = *Ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike > 20) Fertility (grains/spikelet >= 4) SR = 0% LR < 10% HLB = R or MR Maturity = N Lodging <= 5% Grain color = White (90%)	80-90%	No	100% Bulked seed
YT EPC	Photo-insensitivity = *Ppd* alleles SR = 0% LR<10% Maturity = N Lodging <= 5% Heat tolerance Yield Grain color = White (90%) IQ = non tenacious	40-60%	No	100% Bulked seed

CWAWSN	BV: 98% of entries will enter MXI.
YTCWAWSN MWAWSN	Y: Best lines from the YT will enter CBME5 for new crosses. MXI: 98% of entries will enter ISNYT.
WAWSN	World: Best lines will return to CBME5 for new crosses.

Table 18 Breeding traits, selection intensity, selection criteria and harvest method in each generation for selected bulk strategy for materials targeted to ME6

Generation	Among-cross (for F1 to F6) or family (for F7 and on) selection		Within-cross (for F2 to F6) or family (for F7 and on) selection	
	Selected traits (arranged by the selection sequence) and criteria	Selection intensity	Selected traits (arranged by the selection sequence) and criteria	Intensity and harvest method
F1	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T (tolerant) or MT (moderately tolerant) SC = R or MR	Selection intensity	No	100% Bulked seed
F1T	Photo-insensitivity = *Ppd* alleles Height = 60-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%	70%	Photo-insensitivity = *Ppd* alleles Height = 90-100cm, *Rht1* and/or *Rht2* Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Maturity = N Lodging <= 5% Seed quality = P (plump) or MP (medium plump) Grain color = White (50%)	50-70% Negative selection: spikes are taken from all good to acceptable plants
F2	Photo-sensitivity = *ppd* alleles Height = 60-120cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% YR < 40% LR < 40% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%	90%	Photo-sensitivity = *ppd* alleles Height = 90-110, *Rht1* or *Rht2* or *Rht8* Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 5% LR < 40% YR < 40% ST = R or MR BYDV = T or MT SC = R or MR Grain color = White (50%)	2-3% 30-60 spikes from the best plants Bulked seed
F3	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	90%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	5-10% 30-60 spikes from the best plants

	SR < 4% YR < 30% LR <30% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%		SR < 1% LR < 30% YR < 30% ST = R or MR BYDV = T or MT SC=R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	Bulked seed
F4	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 3% YR < 20% LR < 20% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%	90%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 15% YR < 15% ST=R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10-20% 30-60 spikes from best plants Bulked seed
F5	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 2% YR < 10% LR < 10% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%	90%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10-20% 30-60 spikes from the best plants Bulked seed
F6	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% YR < 10% LR < 10% ST = R or MR BYDV = T or MT SC = R or MR Lodging <= 5%	90%	Photo-sensitivity = *ppd* alleles Height = 80-100cm Tillering >= 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST=R or MR BYDV = T or MT SC=R or MR Maturity = E or ME Seed quality = P or MP Grain color = White (50%)	10-50% 20-100 spikes from the best plants Harvested individually
F6:7	Photo-sensitivity = *ppd* alleles Height = 90-110cm Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR	90%	No	100% Bulked seed Note: If the population still segregates somewhat, 3-5 spikes are

	BYDV = T or MT SC = R or MR Lodging <= 5% Phenotypic uniformity >= 90%			harvested individually.
F6:8	Photo-sensitivity = *ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC=R or MR Lodging <= 5% Phenotypic uniformity >= 95%	90%	No	100% Bulked seed
AL	Photo-sensitivity = *ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%)	90%	No	100% Bulked seed
PYT PC	Photo-sensitivity = *ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%) Yield	50%	No	100% Bulked seed
EAL	Photo-sensitivity = *ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4) SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%)	50%	No	100% Bulked seed
YT EPC	Photo-sensitivity = *ppd* alleles Tillering > 5 Spike size (spikelets/spike >= 20) Fertility (grains/spikelet >= 4)	80%	No	100% Bulked seed

	SR < 1% LR < 10% YR < 10% ST = R or MR BYDV = T or MT SC = R or MR Maturity = E or ME Lodging < 5% Grain color = White (50%) Yield			
CHLWSN	BV: 98% of entries will enter MXI.			
YTCHLWSN MHLWSN	Y: Best lines from the YT will enter CBME6 for new crosses. MXI: 98% of entries will enter ISNYT.			
HLWSN	World: Best lines will return to CBME6 for new crosses.			

Table 19 gives the population size, sown-grain weight (g) and plot size for each generation planted in CIMMYT’s bread wheat breeding program.

Table 19 Population size, sown-grain weight (g) and plot size for each generation planted in Toluca and Obregon for modified pedigree/bulk and selected bulk methods

Generation	**Modified pedigree/bulk (MPED)**		**Selected bulk (SBLK)**	
	Obregon cycle	**Toluca cycle**	**Obregon cycle**	**Toluca cycle**
CB	400, 15, 2DR/2M	400, 15, 2DR/2M	400, 15, 2DR/2M	400, 15, 2DR/2M
F1	20, *, 1DR/1M	20, *, 1DR/1M	20, *, 1DR/1M	20, *, 1DR/1M
F1T	60, *, 1DR/2M	60, *, 1DR/2M	60, *, 1DR/2M	60, *, 1DR/2M
F2	1000, 40, 4DR/10M or 1500, 60, 6DR/10M	1000, 40, 4DR/10M or 1500, 60, 6DR/10M	1000, 40, 4DR/10M or 1500, 60, 6DR/10M	1000, 40, 4DR/10M or 1500, 60, 6DR/10M
F3	70, 3, 1TR/1M	70, 3, 1DR/1M	500, 20, 2DR/10M	500, 20, 2DR/10M
F4	70, 3, 1TR/1M	70, 3, 1DR/1M	625, 25, 2DR/10M	625, 25, 2DR/10M
F5	70, 3, 1TR/1M	70, 3, 1DR/1M	625, 25, 2DR/10M	625, 25, 2DR/10M
F6	140, 7, 1TR/2M	140, 7, 1DR/2M	750, 30, 2DR/10M	750, 30, 2DR/10M
F7	70, 3, 1TR/1M	70, 3, 1DR/1M	70, 3, 1TR/1M	70, 3, 1DR/1M
AL	70, 3, 1TR/1M	70, 3, 1DR/1M	70, 3, 1TR/1M	70, 3, 1DR/1M
PYT PC	1200, 45, 2TR/4M 70, 3, 1DR/1M	1200, 45, 2DR/4M 70, 3, 1DR/1M	1200, 45, 2TR/4M 70, 3, 1DR/1M	1200, 45, 2DR/4M 70, 3, 1DR/1M
EAL	70, 3, 1TR/1M	70, 3, 1DR/1M	70, 3, 1TR/1M	70, 3, 1DR/1M
YT EPC	1200 plants/plot, 45, 2TR/4M, latinized Alpha-design, 2 or 3 replications 70, 3, 1DR/1M	900 plants/plot, 35, 2DR/3M, latinized Alpha-design, 2 or 3 replications 70, 3, 1DR/1M	1200 plants/plot, 45, 2TR/4M, latinized Alpha-design, 2 or 3 replications 70, 3, 1DR/1M	900 plants/plot, 35, 2DR/3M, latinized Alpha-design, 2 or 3 replications 70, 3, 1DR/1M
CISNYT	**El Batan cycle**			
	Population size	Sown-grain weight	Plot size	
	70	3	1DR/1M	
MISNYT	**Mexicali cycle** (No replications)			
	Population size	Sown-grain weight (g)	Plot size	

MIBWSN	560	24	2DR/4M
MESWYT	5600	240	8DR/10M
MHTWYT	4200	180	6DR/10M
MHRWSN	560	24	2DR/4M
MHRWYT	4200	180	6DR/10M
MASWSN	560	24	2DR/4M
MSAWSN	560	24	2DR/4M
MSAWYT	4200	180	6DR/10M
MWAWSN	420	18	2DR/3M
MHLWSN	420	18	2DR/3M

ISNYT	**World**						
	No. locations	No. entries	Expeimental design	No. replicates	Plot size	Sown-grain weight (g)	Population size per plot
IBWSN	180	300-450	Spatial analysis	1	Flexible	7	Flexible
ESWYT	235	50	Alpha-design	2		75	
HTWYT	160	50	Alpha-design	2		75	
HRWSN	80	250-400	Spatial analysis	1		7	
HRWYT	140	50	Alpha-design	2		75	
ASWSN	40	100-150	Spatial analysis	1		7	
SAWSN	120	250-350	Spatial analysis	1		7	
SAWYT	150	50	Alpha-design	2		75	
WAWSN	50	200	Spatial analysis	1		7	
HLWSN	50	200	Spatial analysis	1		7	

Notes: DR = Double Row; TR = Triple Row; M = Meter; For F1/F1T and F2 generations, seeds are space-planted with 12-13 individual seeds in a single row one meter long (1SR/1M). Due to early generation natural selection pressure, only about 10 healthy seeds per meter actually emerge and develop into plants. For other generations, seeds are planted in a commercial rate. A seed rate of about 100 kg/ha translates into about 70 individual seeds being planted in a 1DR/1M or 1TR/1M, assuming a TKW of about 40 grams. We also suppose one spike will have about 20-25 spikelets with 3-4 seeds per spikelet, thus bearing approximately 60-100 seeds.

Multilocation testing

After the final yield trials the elite breeding lines enter the multilocation process. The final objective after all is for the lines to be sent to our collaborators outside Mexico. During this process very clean seed must be produced. This is achieved in two phases.

During the first multiplication phase the selected lines are increased in El Batan as Candidate International Nurseries, Yield Trials and Segregating Populations, where special care is taken to produce clean seed. The entries are treated with fungicides during their development. Entries in CISNYTs for ME1, ME4, ME5 and ME6 are those selected from YTME1, YTME4, YTME5 and YTME6 in the Yaqui valley, respectively. Entries in CISNYTs for ME2 and ME3 are the same as in EPCME2 and EPCME3 in the MV cycle, respectively. Those entries which will enter ISNYTs are decided in November based on the yields in the MV cycle.

During the second multiplication phase (MISNYT) the lines are grown out in Mexicali, in northwestern Mexico, an irrigated, high yielding and Karnal bunt free location. At the same time the entries are again yield-tested in Cd. Obregon, or Toluca, depending on their targeted environment. The latter is done to identify more precisely key outstanding lines for direct introduction into the crossing blocks and special promotion with NARSs.

Finally, adapted materials are distributed internationally as International Screening Nurseries, International Yield Trials and Segregating Population by the International Nursery section within the Wheat Program. The seed from MISNYT was cleaned and treated with a mixture of Terrazan and Vitavax before shipment. Based on these observations, International Screening Nurseries directed towards specific MEs are prepared and distributed to our cooperators around the world. Thus materials are exposed to various stresses in up to 150 different locations around the globe, spanning all true MEs. Almost all entries in the MISNYT enter ISNYT. There is a minor discard if seed from the MISNYT is somehow mixed (for grain color, type, and appearance etc.) or otherwise poor (very shrivelled).

The population size, sown-grain weight and plot size for each breeding nursery can be found in Table 19. Table 20 presents the germplasm flow after YT for ME1, ME4, ME5 and ME6, and after EAL for ME2 and ME3.

International Screening Nurseries and Yield Trials (ISNYT)

The International Screening Nurseries serve as a vehicle for the dissemination of improved and genetically diverse bread wheat germplasm. The materials can be used in national wheat crossing programs, or tested for direct release to farmers. The International Yield Trials serve both a germplasm distribution function and a research tool. CIMMYT produces the following types of International Screening Nurseries and International Yield Trials to furnish the needs for different MEs.

Spring wheats

ME1: International Bread Wheat Screening Nursery (IBWSN): Distributed to 180 locations; contains 300-450 entries.

Elite Selection Wheat Yield Trial (ESWYT): Distributed to 235 locations; contains 50 entries.

Heat Wheat Yield Trial (HTWYT): Distributed to 160 locations; contains 50 entries.

ME2: High Rainfall Wheat Screening Nursery (HRWSN): Distributed to 80 locations; contains 250-400 entries.

High Rainfall Wheat Yield Trial (HRWYT): Distributed to 140 locations; contains 50 entries.

ME3: Acid Soil Wheat Screening Nursery (ASWSN): Distributed to 40 locations; contains 100-150 entries.

ME4: Semi-arid Wheat Screening Nursery (SAWSN): Distributed to 120 locations; contains 250-350 entries. Also, similar germplasm is distributed from ICARDA, Aleppo, Syria.

Semi-arid wheat yield trial (SAWYT): Distributed to 150 locations; contains 50 entries.

ME5: Warmer Areas Wheat Screening Nursery (WAWSN): Distributed at 50 locations; contains 200 entries.

ME6: High Latitude Wheat Screening Nursery (HLWSN): Distributed to 50 locations in Kazakhstan, Russia and Heilongjiang (China); contains 200 entries.

Facultative and winter wheats

One screening nursery is distributed from Mexico:

ME7, ME8, ME11 and ME12: Favorable Environments Facultative Wheat Screening Nursery (FEFWS): Targeted towards the Southern Cone of Latin America and China.

Several international screening nurseries and international yield trials are distributed from the joint CIMMYT winter and facultative breeding program Turkey to cooperators in ME7 to ME12:

(1). **Facultative and Winter Wheat Observation Nursery (FAWWON)**
(2). **Winter Wheat East European Yield Trial (WWEERYT)**
(3). **Elite Yield Trial Irrigated**
(4). **Elite Yield Semi-Arid**
(5). **Winter Wheat Observation Nursery Irrigated** (**WON-IR)**
(6). **Winter Wheat Observation Nursery Semi-Arid** (**WON-SA)**
(7). **Winter Durum Observation Nursery**

More details about ISNYT can be found in Table 20 and Table 21.

Table 20 Germplasm flow after YT

Germplasm flow	YTME1 (Y)	EALME2 (Y)	EALME3 (Y)	YTME4 (Y)	YTME5 (Y)	YTME6 (Y)
MV: YT BV: Small increase	CIBWSN CESWYT CHTWYT	MV: YTME2 EPCME2 (CHRWSN, CHRWYT)	MV: YTME3 EPCME3 (CASWSN)	CSAWSN CSAWYT	CWAWSN	CHLWSN
MXI: Large multiplication	MIBWSN MESWYT MHTWYT	MHRWSN MHRWYT	MASWSN	MSAWSN MSAWYT	MWAWSN	MHLWSN
World: ISNYT	IBWSN ESWYT HTWYT	HRWSN HRWYT	ASWSN	SAWSN SAWYT	WAWSN	HLWSN

Table 21 Entry constituent in ISNYT

YT	YTME1	YTME2	YTME3	YTME4	YTME5	YTME6	Total
Number of entries in YT	2000	2000	300	800	600	300	
IBWSN	300-450						300-450
ESWYT	50						50
HTWYT	50 from YTME1HT						50
HRWSN		250-400					250-400
HRWYT		50					50
ASWSN			100				100
SAWSN				250			250
SAWYT				50			50
WAWSN					200		200
HLWSN						200	200

Number of entries per generation from CIMMYT historical breeding data

The numbers of entries in different breeding generations vary from cycle to cycle. Some idea will need to be obtained of ranges and means of population sizes. Table 22 summarized these numbers from cycle Y96-97 to cycle MV-00.

Table 22 Number of entries in each block from Y96-97 to MV-00

Block	**Y96-97**	**MV-97**	**Y97-98**	**MV-98**	**Y98-99**	**MV-99**	**Y99-00**	**MV-00**
CBME1IR	398	345	313	259	259	259	259	217
CBME2HR	225	210	268	196	196	240	240	186
CBME3AS								
CBME4SA	135	118	102	105	105	206	206	
CBME5TE	59	51	57	61	70	94	94	72
CBME6HL	26	25	35	55	55	68	68	
F1ME1	1313	1093	757	569	48	353	414	900
F1ME2	568	834	645	112	33	326	670	700
F1ME3	21	260	69	72		19		27

F1ME4	692	801	429	452	20	338	353	
F1ME5	349	601	182	491	22	13	158	137
F1ME6	124	142	94	248	19	126		
F1TME1	886	458	822	515	49	321	40	320
F1TME2	305	106	314	329	85	158	37	281
F1TME3		11	38	129	6	17		11
F1TME4	78	171	471	347	52	201	12	
F1TME5	122	150	145	268	27	283	34	40
F1TME6	37	25	147	28	30	113		
F2ME1	827	1141	1047	290	444	290	348	322
F2ME2	312	474	537	225	44	238	279	412
F2ME3		11	148	41	23	53	18	
F2ME4	130	439	703	288	439	483	365	
F2ME5	104	179	579	100	184	251	108	97
F2ME6	64	93	96	175	8	59	134	
F3ME1	600	6830	8475	3733	287	443	163	173
F3ME2	311	3335	3378	2106	297	44	156	232
F3ME3			10	538	38	23		10
F3ME4		1574	5120	3555	301	479	347	
F3ME5	69	1216	2564	4023	99	178	194	30
F3ME6	34	546	1463	733	1459	8		
F4ME1	463	253	2143	2224	920	185	335	47
F4ME2	77	185	1221	748	202	301	41	124
F4ME3				3		38	19	25
F4ME4	374	259	688	1481	882	229		
F4ME5	52	58	447	513	329	75	115	156
F4ME6	20	28	454	317	108	605		
F5ME1	67	2254	209	561	407	560	121	
F5ME2	7	977	146	319	159	50	152	38
F5ME3	105			53			13	9
F5ME4	30	59	203	350	513	618		
F5ME5	5	223	58	67	86	141	45	94
F5ME6	16	340	28	170	90	33		
F6ME1	247	700	893	180	75	622	84	156
F6ME2	268	120	431	138	39	218	17	127
F6ME3	359				301	9	9	11
F6ME4	60	40	133	152	116	259		
F6ME5		50	70	52	16	231	93	44
F6ME6	138	222	181	25	51	44		
F7ME1	2280	2000	3450	7465	174	360	9230	6924
F7ME2	1260	1860	650	3864	96	240	2355	160
F7ME3	1970	1250	700			4910	2218	326
F7ME4	410	910	650	1765	151	630	2224	
F7ME5		890	220	320	51	70	1908	1429
F7ME6			1240	300	25	900		
ALME1	3125	1094		1017	1877	1398		2451
ALME2	1236	568	174	720			560	471
ALME3		457	127	609			1531	555
ALME4	1353	887		894	2482	377	32	
ALME5				28		80		325
ALME6	201			418	650	128		
PYTME1	994		1840		750		1560	

PYTME2		232		660		360		1150
PYTME3		159		660		480		560
PYTME4	533		1154		680			
PYTME5	480		250		100		360	
PYTME6	6	110						
EALME1	137	419		787		349		
EALME2	361		164	164	451		144	
EALME3	4		109	109	357		64	
EALME4		272		379		182		
EALME5				81	41	70		
EALME6			80	80	65			
YTME1	1048		890		2190			
YTME2		2360	90	790		1090		2960
YTME3				190		390		
YTME4	360		790		790			
YTME5	948		290		90			
YTME6								
	Y96-97	**MV-97, BV-97**	**Y97-98**	**MV-98, BV-98**	**Y98-99**	**MV-99, BV-99**	**Y99-00**	**MV-00, BV-00**
CIBWSN		211, 211		474, 474		513, 513		698, 698
CESWYT		72, 72		46, 46		50, 50		213, 213
CHTWYT				87, 87	87	51	51	107, 151
CHRWSN								
CHRWYT								
CASWSN							124	
CSAWSN		155, 155		194, 194		351, 351		*, 240
CSAWYT		58, *		49, 49		48, 48		*, 49
CWAWSN				35, 35	35	47, *	47	
CHLWSN						413, 413		*, 338
	MXI96-97		**MXI97-98**		**MXI98-99**		**MXI99-00**	
MIBWSN	268		139		402		445	
MESWYT	64		67		46		50	
MHTWYT	36		76		58		45	
MHRWSN	305		261		215		274	
MHRWYT	33		50		47		49	
MASWSN					32		124	
MSAWSN	185		103		191			
MSAWYT	70		38		49			
MWAWSN			72		81			
MHLWSN								

Note: In MV-98, instructions were given by management to cease all labor support to the production of crosses, due to budgetary reasons. Hence the totals of subsequently emanating generations from that year are very low. * and blank: missing data.

Simulated mega-environments utilized in shuttle breeding

As stated before, ME1, ME4, ME5 and ME6 can be simulated in Cd. Obregon environment by optimum irrigation, reduced irrigation, late planting and supplementary lighting, respectively. ME2 and ME6 can be simulated in Toluca environment by high rainfall and supplementary lighting. ME3 can be simulated to an extent in Patzcuaro. All the crosses and segregating generations are arranged according to and targeted to these six MEs. The materials targeted for different MEs are grown in their respective simulated MEs in the shuttle breeding process on several occasions but not every cycle. For example all generations are grown in Toluca which is an ME2-type location, no matter whether they are targeted towards ME2 or not. The simulated MEs under which respectively targeted generations are grown are presented in Table 23 and Table 24 for crosses made in Obregon and Toluca, respectively. The flow of breeding nurseries is shown in Table 25.

Table 23 Simulated MEs in Mexico where generations emanating from crosses made in Obregon are grown

Cycle	Generation	Shuttling site	Targeted environments					
			ME1	ME2	ME3	ME4	ME5	ME6
Y0	CB (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV1	F1 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y2	F2 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV3	F3 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y4	F4 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME4	ME1	ME6
MV5	F5 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y6	F6 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV7	F7 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y8	AL (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV9	AL (ME1, 4, 5, 6)	Toluca (ME2, ME6)	ME2			ME2	ME2	ME2/6
	PYT (ME2, 3)	Toluca (ME2, ME6)		ME2	ME2			
PZ9	PC (ME2)	Patzcuaro (ME2/3)		ME2/3	ME2/3			
SJ9	PC (ME3)	Sierra de Jalisco (ME2/3)		ME2/3	ME2/3			
Y10	PYT (ME1, 4, 5, 6)	Obregon (ME1, ME4, ME5, ME6)	ME1			ME4.1	ME5	ME1/4
	EAL (ME2, 3)	Obregon (ME1, ME4, ME5, ME6)		ME1	ME1			
MV11	EAL (ME1, 4, 5, 6)	Toluca (ME2, ME6)	ME2			ME2	ME2	ME2/6
	YT (ME2, 3)	Toluca (ME2, ME6)		ME2	ME2			
PZ11	EPC (ME2)	Patzcuaro (ME2/3)		ME2/3	ME2/3			
SJ11	EPC (ME3)	Sierra de Jalisco (ME2/3)		ME2/3	ME2/3			
BV11	EPC (ME2, 3)	El Batan (ME2/4)	ME2/4			ME2/4	ME2/4	ME2/4
Y12	YT (ME1, 4, 5, 6)	Obregon (ME1, ME4, ME5, ME6)	ME1			ME4	ME5	ME1/4
	EPC (ME1, 4, 5, 6)	Obregon (ME1, ME4, ME5, ME6)	ME1			ME4	ME5	ME1/4
BV13	CISNYT (ME1, 4, 5, 6)	El Batan (ME2/4)	ME2/4			ME2/4	ME2/4	ME2/4
MXI14	MISNYT (all MEs)	Mexicali (ME1IR)	ME1	ME1	ME1	ME1	ME1	ME1
ISNYT		World (all MEs)	ME1	ME2	ME3	ME4	ME5	ME6

Notes: ME1.4 for PYT targeted for ME4 means that PYT is conducted under both the drought condition (ME4, only one pre-sown irrigation) for actual yielding and the reduced irrigation condition (one more irrigation during flowering than the trial under ME4) for input responding.

Table 24 Simulated MEs in Mexico where generations emanating from crosses made in Toluca are grown

Cycle	Generation	Shuttling site	Targeted environments					
			ME1	ME2	ME3	ME4	ME5	ME6
MV0	CB (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y1	F1 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV2	F2 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y3	F3 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME4	ME1	ME6
MV4	F4 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y5	F5 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME4	ME1	ME6
MV6	F6 (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y7	F7 (ME1-6)	Obregon (ME1, ME4, ME5, ME6)	ME1	ME1	ME1	ME1	ME1	ME6
MV8	AL (ME1-6)	Toluca (ME2, ME6)	ME2	ME2	ME2	ME2	ME2	ME2/6
Y9	PYT (ME1, 4, 5, 6)	Obregon (ME1, ME4, ME5, ME6)	ME1			ME4.1	ME5	ME1/4
	AL (ME2, 3)	Obregon (ME1, ME4, ME5, ME6)		ME1	ME1			
M10	EAL (ME1, 4, 5, 6)	Toluca (ME2, ME6)	ME2			ME2	ME2	ME2/6
	PYT (ME2, 3)	Toluca (ME2, ME6)		ME2	ME2			
PZ10	PC (ME3)	Patzcuaro (ME2/3)		ME2/3	ME2/3			
M10	PC (ME3)	Sierra de Jalisco (ME2/3)		ME2/3	ME2/3			
Y11	YT (ME1, 4, 5, 6)	Obregon (ME1, ME4, ME5, ME6)	ME1			ME4	ME5	ME1/4
	EAL (ME2, 3)	Obregon (ME1, ME4, ME5, ME6)		ME1	ME1			
MV12	YT (ME2, 3)	Toluca (ME2, ME6)		ME1	ME1			
PZ12	EPC (ME2)	Patzcuaro (ME2/3)		ME2/3	ME2/3			
SJ12	EPC (ME3)	Sierra de Jalisco (ME2/3)		ME2/3	ME2/3			
BV12	EPC (ME2, 3)	El Batan (ME2/4)		ME2/4	ME2/4			
MXI13	CISNYT (all MEs)	Mexicali (ME1IR)	ME1	ME1	ME1	ME1	ME1	ME1
ISNYT		World (all MEs)	ME1	ME2	ME3	ME4	ME5	ME6

Notes: ME1.4 for PYT targeted for ME4 means that PYT is conducted under both the drought condition (ME4, only one pre-sown irrigation) for actual yielding and the reduced irrigation condition (one more irrigation during flowering than the trial under ME4) for input responding.

Table 25 Breeding nurseries after the Obregon or Toluca cycle

Shuttling site	Target	Obregon (current cycle)														BV
	ME	CB	F1	F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT (ME1, 4, 5, 6)	EAL (ME2, 3)	YT (ME1, 4, 5, 6)	CISNYT
Toluca (next cycle)	ME1	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		BV: CIBWSN, CESWYT, CHTWYT	MXI: MISNYT
	ME2	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		
	ME3	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		
	ME4	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		BV: CSAWSN, CSAWYT	
	ME5	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		BV: CHTWYT, CWAWSN, CESWYT, CIBWSN	
	ME6	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		BV: CHLWSN	
		Toluca (current cycle)														MXI
Cd. Obregon (next cycle)		CB	F1	F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT (ME2, 3)	EAL (ME1, 4, 5, 6)	YT (EPC: BV) (ME2, 3)	MISNYT
	ME1	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		World: ISNYT
	ME2	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		MXI: MHRWYT, MHRWSN	
	ME3	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	AL	EAL		MXI: MASWSN, MHRWYT, MHRWSN	
	ME4	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		
	ME5	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		
	ME6	F1	F2/F1R	F1T	F2	F3	F4	F5	F6	F7	AL	PYT/PC		YT/EPC		

Durum Wheat and Triticale Breeding Programs at CIMMYT

Introduction

Durum wheat (*Triticum turgidum* L. var. *durum*), a major stable food crop of the Mediterranean Basin, is cultivated on approximately 17 million hectares worldwide. About 60% of this area is located in developing countries. Durum wheat production is concentrated in the WANA (West Asia and North Africa) region, Mediterranean Europe, Ethiopia, the Asian subcontinent, and the America's -- in Argentina, Chile, the Andean region, Mexico, the USA, and Canada. World durum wheat productivity is low (1.7 t/ha), particularly in developing countries (1.2 t/ha), and reflects semi-arid, marginal and low input growing conditions. However, as a result of the transformation of the tall traditional durum wheat into modern, short-statured, high yielding materials with enhanced adaptation and risk efficiency, the genetic yield potential of durum wheat is high (in fact, in high production areas durum wheat grain yields frequently surpass those of hexaploid wheat).

Triticale (*X Triticosecale* Wittmack) is resulting from a cross between wheat (*Triticum* spp. L.) and rye (*Secale cereale* L.). While the main food crops of the world were all domesticated at least 3000 years ago, triticale, the first successful "man-made" cereal grain, was first deliberately produced in Scotland in 1876. However, the first fertile triticale was produced in 1888 by Rimpau in Germany. The discovery of colchicine's affect in chromosome doubling in the late 1930s, and the development of embryo culture and embryo rescue techniques in the 1940s were milestones in the development of triticale. According a recent estimate from the 4th International Triticale Symposium in Canada in 1998, triticale is cultivated on approximately 2.9 million ha in more than 30 countries. The largest triticale producing countries are Poland, Germany, Russia, USA, France and Brazil. About 80% of the area is under winter triticales and 20% under spring types. The CIMMYT triticale program is the major source of spring triticale germplasm for many national programs. Under marginal land conditions, where abiotic stresses related to climatic (drought, extreme temperatures, etc) and soil (extreme pH levels, salinity, trace elements deficiency or toxicity, etc) conditions are the limiting factors for grain production, triticale has consistently showed its comparative advantages over existing cultivated cereal crops.

CIMMYT’s durum wheat improvement program was established in late 1960s. Its major goals were to incorporate dwarfing genes, photoperiod insensitivity, enhanced spike fertility, and better disease resistance, and thus high yielding, widely adapted, disease resistant germplasm with good end-use quality characteristics could be supplied to developing countries. To achieve these objectives, the spring durum program directs its breeding efforts towards three main mega-environments: ME1, ME2 and ME4. The methodology used in durum wheat and triticale breeding is similar to that in bread wheat breeding. So only the major differences compared to bread wheat breeding are reported in this section for durum wheat breeding and triticale breeding programs.

CIMMYT's Triticale Improvement Program started in 1964 under the leadership of Dr. Borlaug. The first major breakthrough came with a triticale plant resulting from a natural outcross between an introduced Canadian triticale and an unknown Mexican semidwarf bread wheat (*Triticum aestivum* L.). It was widely used as parent to transfer fertility to many progenies in triticale programs around the world. The selected line, named "Armadillo", made a major contribution to triticale improvement worldwide.

The major diseases and insect pests in durum wheat are different in different mega-environments. Table 26 gives the distribution of them in ME1, ME2 and ME4. Rusts are the major diseases in ME1. Aside from rusts, powdery mildew, septoria blotch, tan spot and head scab can all be problems for durum wheat production in ME2. Stripe rust and bunts are the major diseases in ME4. Moreover, sawfly and Hessian fly are also problems in ME4.

Table 26 Distribution of diseases and insect pests on durum wheat by ME

Disease/Insect	ME1: Irrigated	ME2: High rainfall	ME4: Semi-arid
Stem rust	X	X	
Leaf rust	X	X	
Stripe rust	X	X	X
Powdery mildew		X	
Septoria blotch		X	
Tan spot		X	
Head scab		X	
Bunts			X
Sawfly			X
Hessian fly			X

Germplasm flow in durum wheat and triticale breeding

Unlike the situation in the bread wheat breeding program, there is only one CB in the durum wheat breeding program, consisting of 200 to 300 entries. Some entries perform well in only one or two MEs (data from PYT, YT and/or IDYN, EDUYT, observations, reports from outreach and NARS etc.), however some entries may perform well in all the three MEs (this can be viewed as wide adaptation). Some entries may have very good quality, while some entries may have very good resistances to diseases and pests. While making simple crosses, the following traits are considered in sequence for the selection of parents: yield (high), adaptation (wide), pigment content (high), SDS-sedimentation (high) and protein content (%) (high), biotic and abiotic stress resistance, and agronomic components.

The two parents for a simple cross should overcome each other's disadvantages. For top crossing, only those F1Rs with very good agronomic scores (graded from 1 to 9, only 6 or more is accepted, and the score data are from both the past cycle and the current cycle) are selected. Once the F1R has been selected, the most suitable one entry in the CB, which will overcome the remaining disadvantages and reinforce some traits in the F1, will be selected to be the male parent for the top cross. Generally speaking, only one top cross is made for each selected F1R.

Considering both the short-term and long-term breeding objectives, 5 different kinds of crosses are made each cycle in the durum breeding program, which include (Bread Wheat)×(Durum Wheat) (BW×DW), (Winter durum)×(Spring durum) (W×S), (Unadapted durum)×(Adapted durum) (U×A), (Medium Adapted durum)×(Adapted durum) (MA×A), and (Adapted durum)×(Adapted durum) (A×A) (Table 27). The genetic distance between the two parents of a simple cross will determine whether the simple cross will be backcrossed, or top-crossed, or directly promoted to F2. The genetic distance between two adapted parents is the closest among all crosses. A×A crosses consist of about 60% of the total simple crosses made in a cycle. However, less than 10% of A×A crosses will be top or backcross-crossed; the others will be promoted to F2 directly. 20% of the total simple crosses are MA×A crosses. 30-60% such crosses will directly be promoted to F2; the others will be top-crossed and then promoted to F2. For U×A crosses, if the unadapted parents are landraces, more than 90% of them will be backrossed; if the unadapted parents are wild relatives, all crosses will be backcrossed. For W×S crosses, 80% of them will be backcrossed. For BW×DW crosses, all of them must be backcrossed because of sterility. This will make it possible to select 60-100 good individual plants from each F2 in the field.

Table 27 Crossing type in Durum Breeding Program

Crossing type	Percentage	Top or backcrossing
BW×DW	5%	100% F1s backcrossed
W×S	5%	80% F2 backcrossed
U×A	10%	More than 90% F1s backcrossed
MA×A	20%	40-70% F1s top crossed
A×A	60%	Less than 10% F1s top crossed

The selection method used in durum wheat breeding is mainly the modified pedigree/bulk. In each breeding cycle, there are about 600 simple crosses and 600 top crosses (including a few limited backcrosses), totalling 1200 crosses. Both F1 and F1T are harvested in bulk (Figure 6). The simple cross-derived F2 is planted in a large plot (4-6 DR/11M). F1T is planted in a relatively small, 2-row, 2-3-m plot, bulk harvested, and in the following generation (F2) planted in a 4-6 DR/11-m plot. There are about 1000 to 1200 individual plants in each F2, regardless of whether the F2 is from a simple cross or from a top cross. If the F2 is grown in Obregon (ME1), the pedigree selection will be used, i.e., the best plants from each selected F2 generation are harvested individually and planted as a (plant) head-to-row family in F3 generation. From F3 to F5, bulk selection is applied. If the F2 is grown in Toluca (ME2), bulk selection will be used in F2, and pedigree selection will be applied in F3 generation. In the F4 and F5, bulk selection is applied. This is purely due to economic considerations, such as labor costs at harvest (drying required) in Toluca and land limitations. Pedigree selection will be applied in F6 again, and the bulk method will be applied in all subsequent generations. The first yield trial (PYT) starts from F6 (in exceptional situations in F5) generation. There are three options for the germplasm flow starting from the F6 generation (Figure 6).

- **Option 1:** The seeds from the bulk of a F2:6 plot (PYT in Obregon) are planted in El Batan for promotion to the F2:7 and at the same time planted in Toluca for observation in ME2. For the next cycle in Obregon, the seeds from the selected individual in the F2:7 in El Batan are planted as a head-to-row F(2:7):8 family, and the seeds from the bulk of a F2:6 plot two cycles before in Obregon again are planted for the second yield trial under ME1 and ME4. The number of ME4 yield trials depends on the available land. In exceptional cases, if there is not enough land, the YT will only be grown under ME1. The seeds from the bulk of the whole F(2:7):8 plot will be planted in El Batan for promotion to F(2:7):9 and yield tested at Toluca under ME2. And then the seeds from the bulk of a F(2:7):9 plot will again be yield tested in Obregon under ME1 and/or ME4 according to previous results on adaptation, and at the same time multiplied in Mexicali for ISNYT.
- **Option 2:** The seeds from the selected individual in F2:6 are planted in a head-to-row family in El Batan for promotion to the F(2:6):7. At the same time, the seeds from the bulk of the F2:6 plot are planted in Toluca for observation in ME2. For the next cycle in Obregon, the seeds from a F(2:6):7 head-to-row family are planted for the third yield test under ME1 and if land is available under ME4. As a modification, F2:6 bulks can be yield tested under ME4. Seeds from the bulk of the F(2:6):8 plot will be planted in El Batan for promotion to the F(2:6):9 and in Toluca in yield trials under ME2. Then the

seeds from the bulk of the F(2:6):9 plot in El Batan will again be yield tested in Obregon for ME1 and/or ME4 according to previous results on adaptation, and at the same time multiplied in Mexicali for ISNYT.

- **Option 3:** Seeds from the selected individual in F2:6 are planted in a head-to-row F(2:6):7 family in El Batan. At the same time, seeds from the bulk of the whole F2:6 plot are planted in Toluca for observation under ME2. For the next cycle, seeds from the F(2:6):7 head-to-row family are advanced to F(2:6):8 family in Obregon, and seeds from the bulk of the F2:6 plot two cycles before are again planted for the second yield trial under ME1 and ME4. Seeds from the bulk of the whole F(2:6):8 plot will be planted in El Batan for promotion to F(2:6):9 and in Toluca in yield trials under ME2. Then seeds from the bulk of the F(2:6):9 plot will again be yield tested in Obregon under ME1 and/or ME4, according to previous results on adaptation, and at the same time multiplied in Mexicali for ISNYT.

After the fourth yield test in Obregon, the best materials will go to the first Obregon Elite Trial under ME1 with four replications. Then the best materials from the Elite Trial will go to the second Obregon Elite Trial under ME1 and the first CIANO Trial with five planting dates and 2 and 3 row beds in each planting date. The best materials will go to the third Obregon Elite Trial and the second CIANO trial. Some lines may be released as commercial varieties in the end.

All seeds from the Obregon yield trial and Obregon Elite Trial will be quality tested in the laboratory for pigment, sediments, and protein content. Only those entries with acceptable quality will enter the next cycle. The method described above ensures that all seeds for YT come from the Obregon breeding cycle. Seeds from Obregon have less disease and better quality.

The germplasm flow (Figure 7) in triticale breeding is very similar to that in durum wheat breeding program. In each breeding cycle, both simple crosses and top crosses are made. The F1s used for top crosses are from F1 reserved seeds two cycles ago. F2s (which can be from F1 or F1T) are space planted. If the F2 is grown in Obregon (ME1), the pedigree selection will be used, i.e., the best plants from each selected F2 generation are harvested individually and planted as a (plant) head-to-row family in the F3 generation. From F3 to F4, bulk selection is applied. Only some negative selection is applied, and seeds from the whole plot are harvested in bulk. If the F2 is grown in Toluca (ME2), bulk selection will be used in F2, and pedigree selection will be applied in F3 generation. In the F4 and F5, bulk selection is applied. Pedigree selection will be applied in F5 or F6 again in the Toluca cycle, and the bulk selection method will be applied in all subsequent generations. For the second pedigree selection in F5 or F6, only one spike from each individual selected plant is harvested and planted as a head-to-row (HR) line in F6 or F7 as F6HR or H7HR (Figure 7). The first yield trial (PYT) starts from F(3:6):8 or F(2:5):7 in the Obregon cycle under reduced irrigation (one pre-sowing irrigation and one pre-flowering irrigation) (Figure 2). At the same time as PYT, the entries in PYT_F8 (or PYT_F7) are also planted as PC_F8 (or (PC_F7) for observation. The seeds from PC_F8 (or PC_F7) will be planted in Toluca as F9OBS_2 (or F8OBS_2), and in the next cycle are planted in Obregon for RYT under both ME1 (full irrigation) and ME4 (one pre-sowing irrigation only) conditions. The entries in PC_2007 are the same as those in RYT_PC2007. PCs will provide seeds for next RYT in Toluca, and so on. After two regular yield trials in Obregon under both ME1 (full irrigation, about four times) and ME4 (one pre-sowing irrigation only) conditions and two regular yield trials in Toluca under ME2 condition, the best lines will be multiplied in Mexicali and then distributed to ITSN and ITYN. Those lines are again yield tested in Obregon and Toluca to find the best lines for new crosses.

There are two international yield trials and one international screening nursery for durum wheat, and one international yield trial and one international screening nursery for triticale. They are:

Elite Durum Wheat Unreplicated Yield Trial (EDUYT): 128 entries distributed to 70-80 locations (112 entries plus 16 check plots, 2 to 4 different checks).

International Durum Wheat Yield Nursery (IDYN): 50 entries distributed to 90-100 locations, two replications.

International Durum Wheat Screening Nursery (IDSN): 270-290 entries distributed to 90-100 locations.

International Triticale Yield Nursery (ITYN):

International Triticale Screening Nursery (ITSN):

There are three common checks: Mexicali 75, Yavaros 79, and Altar 84, plus local checks in EDUYT, IDYN and IDSN.

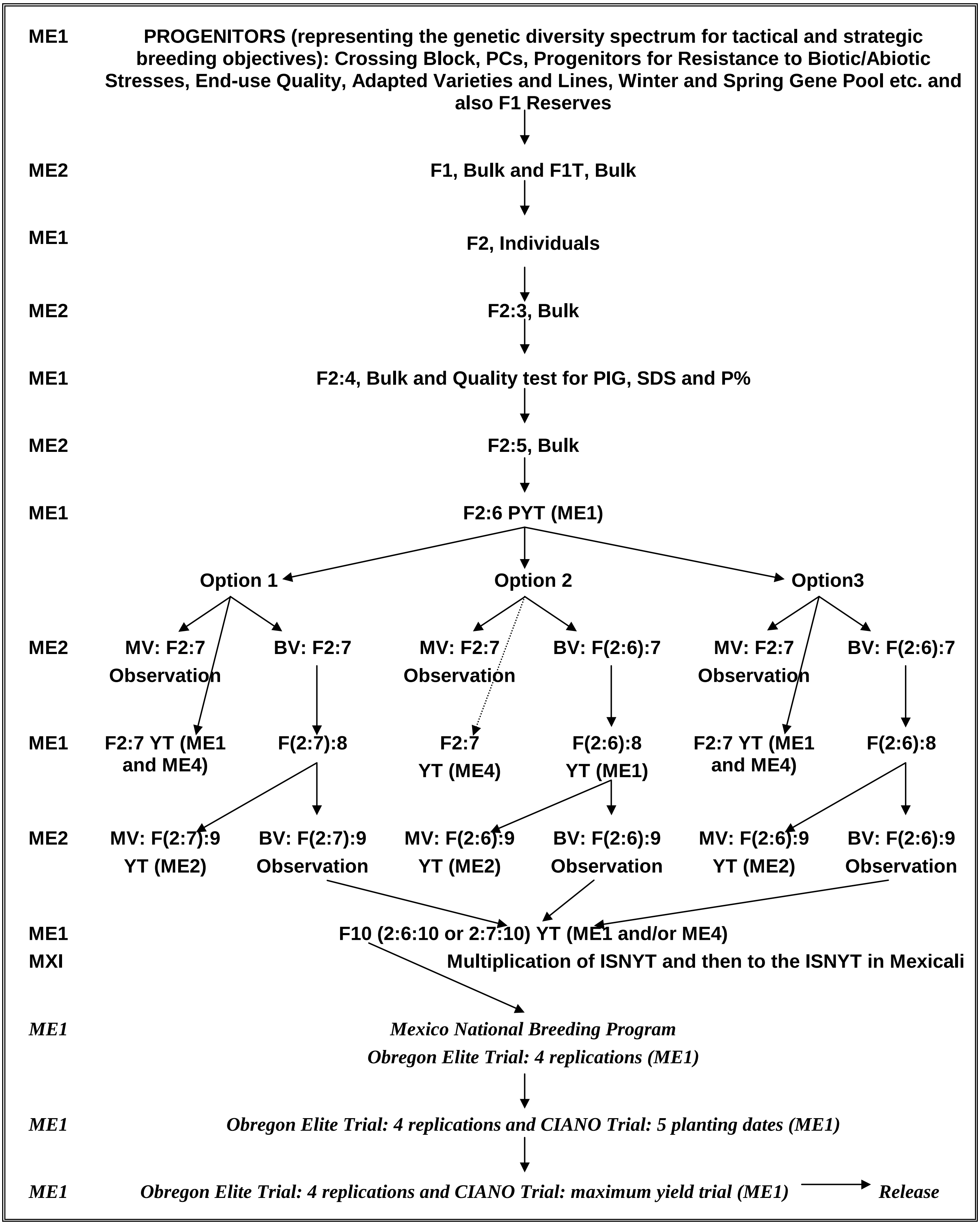
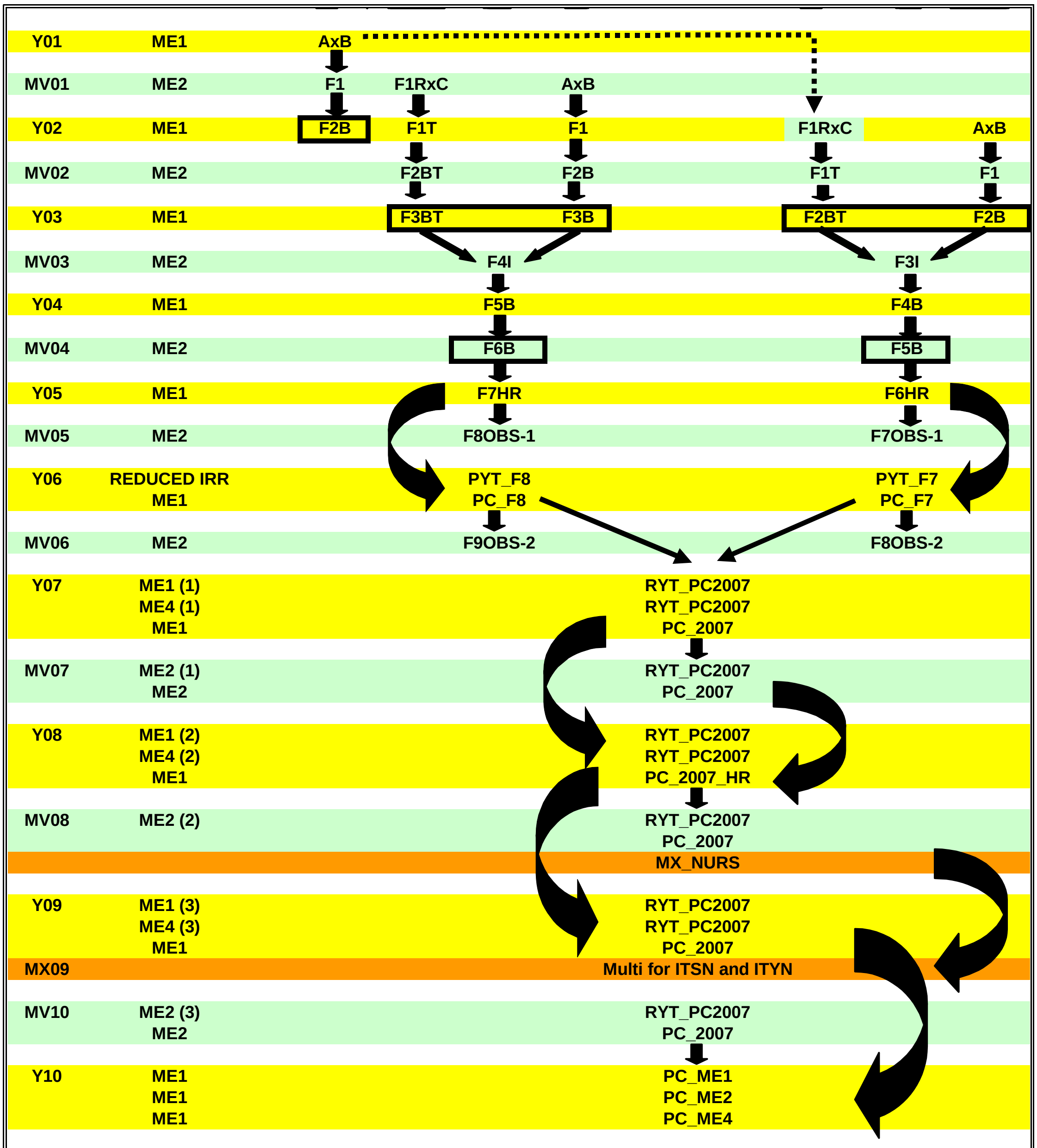


Figure 6 Germplasm flow in the durum wheat breeding program

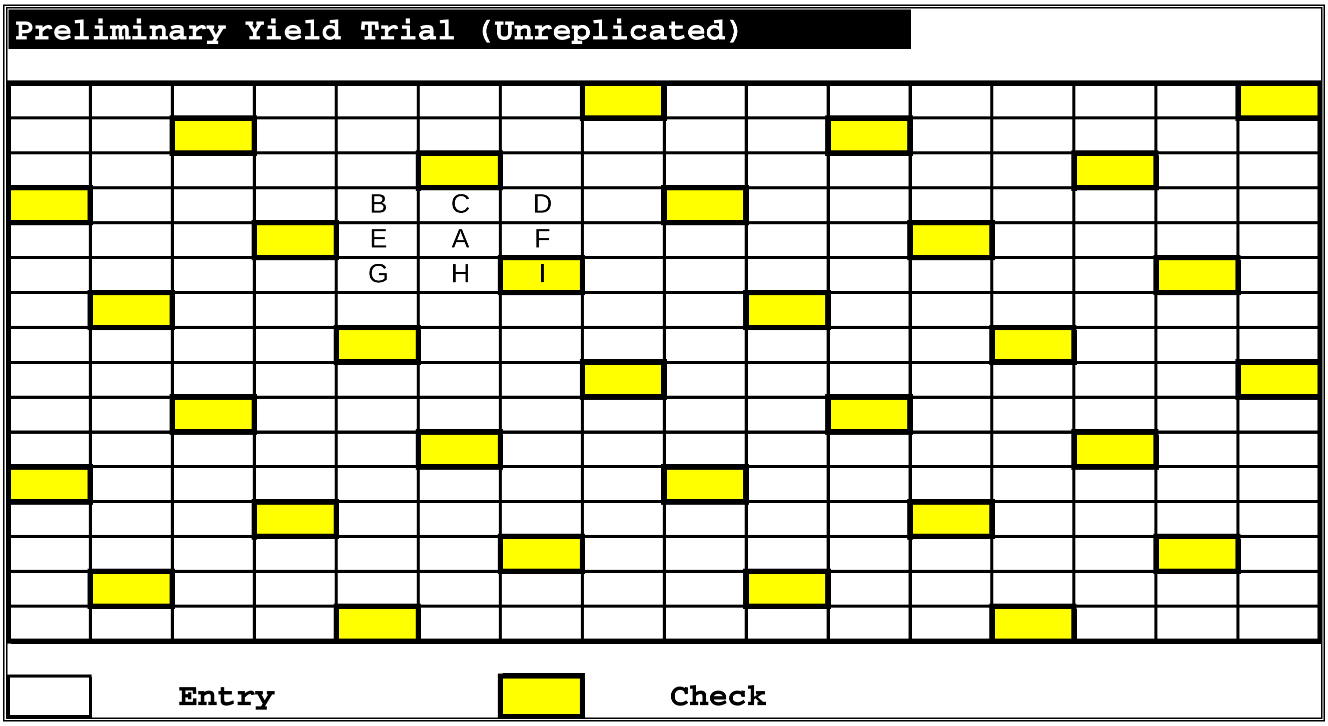


Notes: F1R: F1 reserved seeds; F1T: F1 top cross; F2B or F2BT: F2 from F1 or F1T bulked seeds; F3I or F4I: F3 or F4 family from an individual F2 or F3 plant; F6HR or F7HR: Head-to-row lines in F6 or F7 derived from one spike in F5 or F6.

Figure 7 Germplasm flow in the triticale breeding program

Experimental designs in PYT and YT

Figure 8 shows the experimental design used for PYT in the durum wheat breeding program. It is a 16×16 lattice, so 256 entries can be contained in this design. Of those entries, 32 are checks, evenly distributed in columns and rows, i.e., each column or row has two and only two check entries. The relative value of an entry (e.g. A in Figure 8) is calculated as its absolute value divided by the average of the eight entries (B, C, D, E, F, G, H, and I in Figure 8) surrounding it and itself (A in Figure 8).



Preliminary Yield Trial (Unreplicated)

							🟨								🟨
		🟨								🟨					
					🟨								🟨		
🟨				B	C	D		🟨							
			🟨	E	A	F					🟨				
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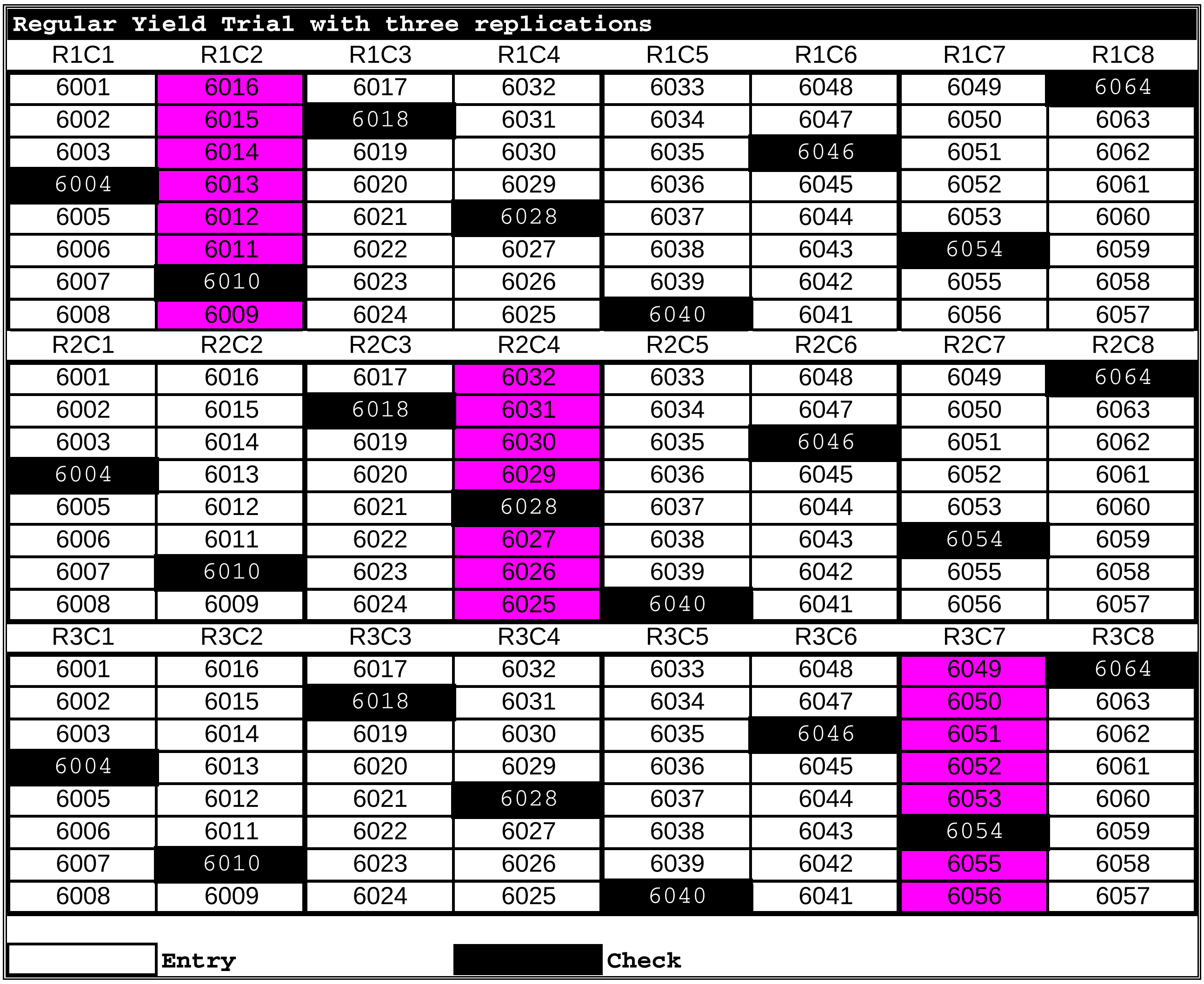
☐ **Entry** 🟨 **Check**

Figure 8 Experimental design of PYT with 256 entries and no replication in the durum wheat breeding program

Figure 9 shows the experimental design used for YT with three replications in the durum wheat breeding program. Each replication is an 8×8 lattice, so 64 entries can be contained in this design. There are 8 check entries in each replication, which are evenly distributed in columns and rows, i.e., each column or row has one and only one check entries. There are two steps of randomization in this design. One is randomization of columns, and the other one is randomization of entries in a column, except the check entry. So, in Figure 9, the second column in the first replication (R1C2) will randomly become the fourth column in the second replication (R2C4), and the seventh column in the third replication (R3C7). The entries in R1C2, R2C4 and R3C7 are the same, but the sequence of entries is different except the check entry. The check remains at a constant position.



Regular Yield Trial with three replications

R1C1	R1C2	R1C3	R1C4	R1C5	R1C6	R1C7	R1C8
6001	6016	6017	6032	6033	6048	6049	6064
6002	6015	6018	6031	6034	6047	6050	6063
6003	6014	6019	6030	6035	6046	6051	6062
6004	6013	6020	6029	6036	6045	6052	6061
6005	6012	6021	6028	6037	6044	6053	6060
6006	6011	6022	6027	6038	6043	6054	6059
6007	6010	6023	6026	6039	6042	6055	6058
6008	6009	6024	6025	6040	6041	6056	6057
R2C1	R2C2	R2C3	R2C4	R2C5	R2C6	R2C7	R2C8
6001	6016	6017	6032	6033	6048	6049	6064
6002	6015	6018	6031	6034	6047	6050	6063
6003	6014	6019	6030	6035	6046	6051	6062
6004	6013	6020	6029	6036	6045	6052	6061
6005	6012	6021	6028	6037	6044	6053	6060
6006	6011	6022	6027	6038	6043	6054	6059
6007	6010	6023	6026	6039	6042	6055	6058
6008	6009	6024	6025	6040	6041	6056	6057
R3C1	R3C2	R3C3	R3C4	R3C5	R3C6	R3C7	R3C8
6001	6016	6017	6032	6033	6048	6049	6064
6002	6015	6018	6031	6034	6047	6050	6063
6003	6014	6019	6030	6035	6046	6051	6062
6004	6013	6020	6029	6036	6045	6052	6061
6005	6012	6021	6028	6037	6044	6053	6060
6006	6011	6022	6027	6038	6043	6054	6059
6007	6010	6023	6026	6039	6042	6055	6058
6008	6009	6024	6025	6040	6041	6056	6057

☐ **Entry** ■ **Check**

Figure 9 Experimental design of YT with 64 entries and three replications in the durum wheat breeding program

Realization of the CIMMYT Wheat Breeding Simulation Module

Important breeding traits considered in simulation

Common wheat, *Triticum aestivum* (2*n*=6*x*=42), is an allo-hexaploid comprising three distinct genomic components, namely A, B, and D with the genomic structure AABBDD. However, because of pairing control, wheat behaves cytologically as a diploid, and recombination only occurs between homologous chromosomes. Consequently, alleles on homoeologous chromosomes (homoeoalleles) segregate independently of one another. The effects of polyploidy are thus not on gene segregation, but on gene expression, where the presence of alleles on one chromosome can affect the phenotypic expression of segregation at a corresponding homoeoallelic locus. In genetic experiments this manifests itself as epistatic disturbances of segregation ratios for major genes and the expression of epistatic components of variation for quantitative characters. Numerous characters show the effects of such homoeoallelic variation—for example, major genes controlling vernalization requirement, photoperiodic response, dwarfing, and a wide range of quantitative characters such as height, yield, and yield components—although the effects do vary between different crosses.

Disease resistance

Table 32 lists genes for resistance to diseases such as stem rust, leaf rust, stripe rust, powdery mildew, BYDV, FHS, *Septoria tritici* leaf blotch, and Karnal bunt, and their locations on the chromosome arm. Other diseases that should also be considered in the simulation project are *Pyrenophora tritici-repentis* tan spot and *Helminthosporium* spot blotch, among others.

- *Stem rust*: Stem rust resistance has been stable after 40 years of utilization of genes derived from variety Hope. Losses due to stem rust have been negligible since the late 1960s. The resistance is based on the gene complex *Sr2*, which actually consists of *Sr2* plus 4-5 minor genes pyramided into three to four gene combinations. *Sr2* alone behaves as a slow rusting gene. Since there has been no major stem rust epidemic in areas where CIMMYT germplasm is grown, the resistance seems to be durable (Rajaram 1999).
- *Leaf rust*: Leaf rust resistance has been stabilized by using genes derived from many sources, in particular the Brazilian cultivar Frontana. No major epidemic has been observed in almost 20 years. Four partial resistance genes, including *Lr34*, give a slow rusting response and have been the reason for the containment of leaf rust epidemics in the developing world during the last 15 years. About 60% of CIMMYT germplasm carries one to four of partial resistance genes. *Lr34* is linked to *Yr18* as well as to a morphological marker (leaf tip necrosis) that makes the gene particularly attractive for breeders (Singh 1922).
- *Stripe rust (yellow rust)*: Slow rusting genes for stripe rust like *Yr18* have been identified; However, their interaction is less additive than for leaf rust and stem rust. More basic research is needed to understand the status of durable resistance in high yielding germplasm.
- *Septoria tritici*: Initially all semidwarf cultivars developed for irrigated conditions were susceptible. Today more than eight resistant genes have been identified in CIMMYT germplasm, and two to three genes in combination provide acceptable resistance.
- *Karnal bunt*: More than five genes have been identified, and most of them are partially dominant. Genes providing resistance to Karnal bunt have been incorporated into high yielding lines.

- *Powdery mildew*: CIMMYT germplasm is considered vulnerable to this disease. The disease is absent in Mexico and the responsibility to incorporate resistance genes has been delegated to CIMMYT's regional breeders in South America.

Abiotic stress resistance

Stress resistances should include resistance or tolerance to heat, drought, acid soils, and cold, etc.

Agronomic and grain traits (Table 33)

1. Height

   Rht1 (4AS), *Rht2* (4DS), *Rht3* (4AS), *Rht10* (4DS), *Rht4* (recessive, reduce plant height by about 45%), *Rht5* (partially dominant, *Rht5Rht5* reduces plant height by 50%), *Rht7* (recessive, 2A, reduces plant height by 24%), *Rht8* (2D), *Rht9* (7BS).

2. Awnedness

   Hd (dominant, 4BS), *B1* (dominant, 5AL), *B2* (dominant, 6BL). Awnedness can be inhibited by these three dominant alleles. *Hd* causes the hooded awn phenotype, while *B1* and *B2* cause awnless or tipped awned phenotype. A bearded or fully awned phenotype occurs with genotype *hd b1 b2*.

3. Grain color

   R1 (dominant, 3D), *R2* (dominant, 3A), *R3* (dominant, 3B), additive. White grain is obtained when recessive alleles *r1*, *r2* and *r3* are present together. Although alleles R1, R2 and R3 are capable of conferring red grain phenotype, they work in an additive manner; therefore, a variety with all three alleles will have very dark red grain, compared to a variety with only one of the alleles (Table 28).

4. Maturity
5. Lodging
6. Number of tillers
7. Spike size (represented by the number of spikelets per spike)
8. Fertility (represented by the number of grains per spikelet)
9. Grain storage proteins (LMW)
10. Yield components and yield

Adaptive characters

1. Vernalization (lack of a vernalization requirement is dominant to sensitivity)

   Vrn1 (dominant, 5AL), *Vrn2* (dominant), *Vrn3* (dominant, 5DL), *Vrn4* (dominant, 5BL), *Vrn5* (dominant, 7BS). Pugsley (1973) indicated that the winter wheats possibly possess all vernalization alleles, and that differences among cultivars with respect to vernalization requirement are possibly due to multiple recessive alleles.

2. Photoperiod sensitivity (photoinsensitivity is dominant)

Ppd1 (dominant, 2D), *Ppd2* (dominant, 2BS), *Ppd3* (dominant, 2A)

Industrial quality

Four traits are considered for industrial quality (or end-use type) classification in bread wheat breeding. They are grain hardness, grain color, gluten type, and protein content (Table 28). There are two types of grain hardness (H: hard; S: soft), two types of grain color (W: white; R: red), five types of gluten type (S: strong; MS: medium-strong; T: tenacious; W: weak; WT: weak-tenacious), and two types of protein content (H: high, protein content greater than 12.5%; L: low, protein content between 11.5% and 12.5%). The end-use types 1a, 1b, 2a, 2b are good for bread making. Classification of gluten type is based on sediment, mixing property, alveogaph, and loaf volume, etc.

Table 28 Classification of industrial end-use type of bread wheat

Hardness	Grain color	Gluten type	Protein content	End-use type
H (*haha*)	W (*r1r1r2r2r3r3*)	S	H/L	1a/1b
H (*haha*)	W (*r1r1r2r2r3r3*)	MS	H/L	2a/2b
H (*haha*)	W (*r1r1r2r2r3r3*)	W	H/L	3a/3b
H (*haha*)	R (Any other)	S	H/L	1a/1b
H (*haha*)	R (Any other)	MS	H/L	2a/2b
H (*haha*)	R (Any other)	W	H/L	3a/3b
S (*HaHa*)	W (*r1r1r2r2r3r3*)	S	Either H or L	Unacceptable
S (*HaHa*)	W (*r1r1r2r2r3r3*)	MS	Either H or L	4a
S (*HaHa*)	W (*r1r1r2r2r3r3*)	W	Either H or L	4b
S (*HaHa*)	R (Any other)	S	Either H or L	Unacceptable
S (*HaHa*)	R (Any other)	MS	Either H or L	4a
S (*HaHa*)	R (Any other)	W	Either H or L	4b
Either H or S	Either W or R	T or WT	Either H or L	Unacceptable

Notes: Under hardness, H = hard; S = soft; under grain color, any other = Any other gene combinations except *r1r1r2r2r3r3*.

Gene Linkage Map of Wheat

Gene Number and Location

The underlying basis for simulation has to be a genetic model. The genes and their location on the chromosomes constitute the first component of a genetic model. Here we only consider loci with two or more alternative alleles. Tables 29 and 30 list some known genes and their locations on the chromosome. Due to their limited numbers, known and located genes do not cover the whole wheat genome. Table 31 presents the length in centi-Morgan (cM) of each wheat chromosome and chromosome arm from two molecular linkage maps (Nelson et al, 1998; Gale et al, 1995). We will use these chromosome length data in our simulation module.

Not much information is available about the yield and yield component genes in wheat, which is not surprising, given that yield and yield components are the most complicated breeding traits. Genes controlling these traits are very difficult to locate precisely. For simulation work it is preferable if we know the number of yield genes and their locations on the chromosome. For this purpose, we will make educated guesses of the number of yield genes and temporarily assign these genes on the linkage map in Table 30. Then we will use historical CIMMYT data to test this estimated gene number.

Gene Effect

Another component of a genetic model is the gene effect, which includes intragenic interaction (additive and dominance effects), intergenic interaction (epistasis), and their expression in different mega-environments (genotype x environment interactions).

Table 29 Symbols in the wheat gene linkage map

Symbol	Implication	Symbol	Implication
Acph	Acid phosphatase	*Lg*	Liguleless
Adh	Alcohol dehydrogenase	*Lpx*	Lipoxygenase
Amp	Aminopeptidase	*Lr*	Reaction to *Puccinia recondita*
Amy	Amylase	*Ltp*	Low temperature pairing
B	Inhibitor of awns	*Ms*	Male sterility
Bg	Black glume color	*Ne*	Hybrid necrosis
Bs	Inhibitor of basal sterility in speltoids	*Pbc*	Pseudo-black chaff
Bt	Reaction to *Tilletia* spp.	*Pc*	Purple culm
C	Club spike chlorosis	*Pde*	Phosphodiesterase
Ch	Hybrid chlorosis	*Ph*	Pairing homoeologous
Cn	Chlorina	*Pln*	Sterol esterification
Co	Corroded	*Pm*	Reaction to *Eryisyphe graminis*
Cre	Reaction to *Heterodera avenae*	*Ppd*	Response to photoperiod
Crr	Reaction to *Cochliobolus sativus*	*Pro*	Protein in seeds
D	Grass clump dwarfness	*Pur*	Lipopurothionin
Ep	Endopeptidase	*Q*	Spelt factor
Est	Esterase	*R*	Red grain color
Gai	Gibberellic acid insensitivity	*Ra*	Red auricles
Gli	Gliadin	*Rc*	Red coleoptiles
Glu	Glutenin	*Rf*	Restorer for cytoplasmic male sterility
Got	Glutamate oxaloacetate transaminase	*Rg*	Red glume color
Gpi	Glucose phosphate isomerase	*Rht*	Reduced height
H	Reaction to *Mayetiola destructor*	*S*	Sphaerococcum factor
Ha	Grain hardness	*Skdh*	Shikimate dehydrogenase

Hd	Hooded (awns)	*Sr*	Reaction to *Puccinia graminis*
Hg	Hairy glume	*Tg*	Tenacious glumes
Hk	Hexokinase	*Tri*	Triosephosphate isomerase
Hl	Hairy leaf	*V*	Virescent
Hn	Hairy node	*Vrn*	Response to vernalization
Hp	Hairy peduncle	*W*	Waxiness
Ki	Pollen killer	*Yr*	Response to *Puccinia striiformis*
Kr	Crossability with rye		

Table 30 Gene linkage map of wheat

Chro. Arm	**Locus**	**Position (cM)**	**Chro. Arm**	**Locus**	**Position (cM)**	**Chro. Arm**	**Locus**	**Position (cM)**
1AS	*Gli-A1*	-59.4	1BS	*Rg1*	-49	1DS	*Lr21*	-40
1AS	*Glu-A3*	-59.4	1BS	*Gli-B1*	-49	1DS	*Rg2*	-38
1AS	*Hg*	-52.4	1BS	*Glu-B3*	-46.4	1DS	*Gli-1*	-35.6
1AS	*Pm3a*	-52.4	1BS	*Yr9^A^*	-41.9	1DS	*Glu-D3*	-33.6
(Break)			1BS	*Lr26^A^*	-41.9	1DS	*`Sr21'*	-27
1AS	*Gli-A3*	-17.6	1BS	*Sr31^A^*	-41.9	1DS	*Sr33*	-27
1AS	*Tri-A1*	-10.2	1BS	*Pm8^A^*	-41.9	1DS	*Gpi-D1*	-22.4
1A	*Centromere*	0	1BS	*rf3*	-26.8	1DS	*Tri-D1*	-13.4
1AL	*Glu-A1*	14.9	1BS	*Gpi-B1*	-24.2	1DS	*Hk-D1*	-2.7
			1BS	*Gli-B3*	-20.1	1D	*Centromere*	0
			1BS	*Yr15*	-12.7	1DL	*Sr18*	2.6
			1BS	*Nor-B1*	-8.6	1DL	*Glu-D1*	18.7
			1BS	*Per-B1*	-5.6			
			1BS	*Hk-1*	-2.6			
			1B	*Centromere*	0			
			1BL	*Sr14*	0.8			
			1BL	*Lr33*	4.4			
			1BL	*Glu-B1*	15.5			
2AS	*Lr17*	-49.1	2BS	*W1*	-58.8	2DS	*Lr22*	-61.8
2AS	*Lr38*	-49.1	2BS	*Lr16*	-54.5	2DS	*Tg*	-61.8
2AS	*Yr17*	-49.1	2BS	*Sr23*	-54.5	2DS	*W2*	-61.8
2AS	*Sr38*	-49.1	(Break)			(Break)		
(Break)			2BS	*Sr36*	-3.9	2DS	*Lr15*	-27.9
2A	*Centromere*	0	2BS	*Ne2*	-3.9	2DS	*Lr2a*	-27.9
2AL	*Sr21*	4.7	2BS	*Sr19*	-3.9	2DS	*Sr6*	-27.9
(Break)			2BS	*Lr23*	-3.9	2DS	*C*	-0.4
2AL	*Pm4*	59	2BS	*Lr13*	-3.9	2D	*Centromere*	0
			2B	*Centromere*	0	(Break)		
			2BL	*Sr9*	15	2DL	*D1*	52.4
			2BL	*Yr7*	15			
			2BL	*Yr5*	15			
			2BL	*Dfq1*	28.4			
			2BL	*Sr28*	39.6			
			2BL	*D2*	48			
			2BL	*Sr16*	64.4			
3A	*Centromere*	0	3BS	*Lr27*	-40.3	3DS	*Lr32*	-26.4
3AL	*Sr35*	40	3BS	*Sr2*	-40.3	3D	*Centromere*	0
3AL	*R2*	40	3BS	*v1*	-1.9	3DL	*Got-D3^A^*	5.9
			3B	*Centromere*	0	3DL	*Lr24^A^*	26
			3BL	*Est-B5*	93.4	3DL	*Sr24^A^*	26
						3DL	*Ch2*	43.5
						3DL	*R1*	56.4

Table 30 Gene linkage map of wheat (continued)

4AL	*Lr28*	-66.9	4BS	*ms1*	-68.6	4DS	*ms2*	-32.2
4AL	*Sr7*	-66.9	(Break)			4DS	*Adh-D1*	-25.4
(Break)			4BS	*Adh-B1*	-39.2	4DS	*Rht2*	-10.5
4AL	*Lr30*	-1.9	4BS	*Rht1*	-21	4DS	*Gai2*	-10.5
4A	*Centromere*	0	4BS	*Gai1*	-21	4DS	*Rht10*	-10.5
4AS	*Hd*	8.8	4BS	*Gai3*	-21	4D	*Centromere*	0
			4BS	*Lr25^A^*	-1.6	(Break)		
			4BS	*Pm7^A^*	-1.6	4DL	*beta-Amy-D1*	28
			4B	*Centromere*	0			
			4BL	*Hp^A^*	35.7			
			(Break)					
			4BL	*beta-Amy-B1*	48.1			
5AS	*ms3*	-3.5	5B	*Centromere*	0	5DS	*Pm2*	-20.3
5A	*Centromere*	0	5BS	*Ne1*	10.2	(Break)		
(Break)			5BS	*Crr*	44.1	5DS	*Nor-D3*	-3.9
5AL	*Vrn1*	9.4	5BS	*Ph1*	44.1	5D	*Centromere*	0
5AL	*Kr2*	12.5	5BS	*Kr1*	44.1	5DL	*Lr1*	39.5
5AL	*Q*	18.3	5BS	*Lr18*	44.1	(Break)		
5AL	*Hn*	47.8				5DL	*Vrn3*	46.5
5AL	*B1*	58				5DL	*Sr30*	51.7
5AL	*beta-Amy-A1*	63.2						
6AS	*Sr8*	-57	6BS	*Lr36*	-45.7	6DS	*Sr5*	-59.4
6AS	*Gli-A2*	-34.1	(Break)			(Break)		
6A	*Centromere*	0	6BS	*Gli-B2*	-19.4	6DS	*Gli-D2*	-37.6
6AL	*alpha-Amy-A1*	5.8	6BS	*Nor-B2*	-7.6	6D	*Centromere*	0
(Break)			6B	*Centromere*	0	6DL	*alpha-Amy-D1*	12.3
6AL	*Sr26^A^*	20.5	6BL	*Lr9^A^*	2.6	6DL	*Got-D2*	29.8
6AL	*Sr13*	55.3	6BL	*B2*	7.1	6DL	*H13*	46.4
			6BL	*alpha-Amy1*	9.5	(Break)		
			6BL	*alpha-Amy-B1*	16.6	6DL	*Sr29*	65.4
			6BL	*Sr11*	55.3			
			6BL	*Lr3*	55.3			
7AS	*Per-A4*	-61	7BS	*Vrn5*	-43	7DS	*Rc3*	-18.5
7AS	*Amp-A3*	-19	7BS	*LrMod*	-30.8	7D	*Centromere*	0
7A	*Centromere*	0	7BS	*Pc*	-19	7DL	*alpha-Amy-D2*	9.9
7AL	*Sr22*	29.4	7B	*Centromere*	0	7DL	*Lr19^A^*	24.5
7AL	*cn-A1*	40.7	7BL	*alpha-Amy-B2*	6.7	7DL	*Sr25^A^*	24.5
7AL	*Pm1*	63.8	7BL	*Pm5*	56.9	7DL	*cn-D1*	49.2
7AL	*Lr20*	63.8	7BL	*Sr17*	56.9	7DL	*LrVPM*	52.5
7AL	*Sr15*	63.8	7BL	*Lr14a*	68.9	7DL	*Ep-D1*	67.7
			7BL	*Ep-B1*	68.9	7DL	*Pch1*	67.7

Source: G.E. Hart, M.D. Gale and R.A. McIntosh. 1993. In: S.J. O'brien, Ed. Genetic Maps: Locus Maps of Complex Genomes. Cold Spring Harbor Laboratory Press.

Superscript ^A^ indicates that the gene mapped is from an alien source, for which the map location is that of the wheat-alien chromosome break-point

Table 31 Length (cM) of wheat chromosome and arm

Chromosome	Nelson 1998				Gale 1995			
	Short arm	Centromere	Long arm	Length	Short arm	Centromere	Long arm	Length
1A	0	55.7-57.2	164.1	**164.1**	-44.5	0	79.9	**124.4**
1B	0	36.4	136	**136**	-44.8	0	79.9	**124.7**
1D	0	32.1-70.4	152.1	**152.1**	-45.4	0	79.9	**125.3**
2A	0	122.2-131.7	186.3	**186.3**	-63.3	0	63.3	**126.6**
2B	0	70.8-76.2	185.8	**185.8**	-56.8	0	63.3	**120.1**
2D	0	124.5-132.4	196.2	**196.2**	-63.3	0	63.3	**126.6**
3A	0	56.5-63.4	231.1	**231.1**	-51.6	0	100.8	**152.4**
3B	0	71.3-93.1	260.7	**260.7**	-51.6	0	100.8	**152.4**
3D	0	77.5-82.6	171.3	**171.3**	-51.6	0	100.8	**152.4**
4A	0	20.7-24.7	144.7	**144.7**	-19.5	0	117.3	**136.8**
4B	0	11.6-19.8	57.5	**57.5**	-45.5	0	56.6	**102.1**
4D	0	50.9-54.7	121.8	**121.8**	-45.5	0	56.6	**102.1**
5A	0	0-16.3	143	**143**	-32.1	0	124.7	**126.8**
5B	0	26.9-31.9	138.6	**138.6**	-32.1	0	123.9	**156**
5D	0	9.4-14.9	191.4	**191.4**	-32.1	0	123.9	**156**
6A	-88.5	0	88.5	**177**	-59.3	0	47.1	**106.4**
6B	-53.5	0	78	**131.5**	-57.5	0	47.1	**104.6**
6D	-83.5	0	108.5	**192**	-65.7	0	47.1	**112.8**
7A	0	119.5-125.5	235.7	**235.7**	-81.5	0	101.5	**183**
7B	0	38.1-38.7	106.1	**106.1**	-20.7	0	101.5	**122.2**
7D	0	78.8-88.8	150	**150**	-82.8	0	101.9	**184.7**

Gale MD, Atkinson MD, Chinoy CN, Harcourt RL, Jia J, Li QY and Devos KM. 1995. Genetic Maps of Hexaploid Wheat. Proceedings of the 8th International Wheat Genetics Symposium, China Agricultural Scientech Press, Beijing, China (Li ZS & Xin ZY eds.). pp. 29-40.

Nelson C, 1998. Wheat Groups 1 - 7 chromosomes, mapped in Synthetic W7984 x Opata85. From Allen Van Deynze. Last update Apr 1998

Table 32 Some resistance genes, their chromosome locations and gene frequencies in CIMMYT germplasm

SR			LR			YR, Bunt, Karnal bunt			PM, BYDV, ST and FHS		
Gene	Location	Frequency (CBME1/2/4)	Gene	Location	Frequency (CBME1/2/4)	Gene	Location	Frequency (CBME1/2/4)	Gene	Location	Frequency (CBME1/2/4)
Sr2	3BS, -40.3cM	0.6/0.6/0.6	*Lr1*	1B, 5DL	0.2/0.2/0.2	*Yr1*	2AL	0.2/0.2/0.2	*Pm1*	7AL	0.2/0.2/0.2
Sr5	6DS	0.2/0.2/0.2	*Lr2a*	1B, 2DS	0.2/0.2/0.2	*Yr2*	7B	0.2/0.2/0.2	*Pm2*	5DS	0.2/0.2/0.2
Sr6	2D	0.2/0.2/0.2	*Lr2b*	2D	0.2/0.2/0.2	*Yr3*	1B	0.2/0.2/0.2	*Pm3a*	1AS, -52.4cM	0.2/0.2/0.2
Sr7a	4BL, -66.9cM	0.2/0.2/0.2	*Lr2c*	2D	0.2/0.2/0.2	*Yr4a*	6B	0.2/0.2/0.2	*Pm3b*	1AS	0.2/0.2/0.2
Sr7b	4BL	0.2/0.2/0.2	*Lr3*	6BL	0.2/0.2/0.2	*Yr4b*	6B	0.2/0.2/0.2	*Pm3c*	1AS	0.2/0.2/0.2
Sr8a	6A-alpha	0.2/0.2/0.2	*Lr3ka*	6BL	0.2/0.2/0.2	*Yr5*	2BL	0.2/0.2/0.2	*Pm4a*	2AL, 59cM	0.2/0.2/0.2
Sr8b	2BL	0.2/0.2/0.2	*Lr3bg*	6BL	0.2/0.2/0.2	*Yr6*	7BS	0.2/0.2/0.2	*Pm4b*	2AL	0.2/0.2/0.2
Sr9a	2BL	0.2/0.2/0.2	*Lr9*	6BL	0.2/0.2/0.2	*Yr7*	2BL	0.2/0.2/0.2	*Pm5*	7BL (recessive)*	0.2/0.2/0.2
Sr9b	2BL	0.2/0.2/0.2	*Lr10*	1AS	0.2/0.2/0.2	*Yr8*	2D	0.2/0.2/0.2	*Pm6*	2B	0.2/0.2/0.2
Sr9d	2BL	0.2/0.2/0.2	*Lr11*	2A	0.2/0.2/0.2	*Yr9*	1BS, -41.9cM	0.2/0.2/0.2	*Pm7*	4BL	0.2/0.2/0.2
Sr9e	2BL	0.2/0.2/0.2	*Lr12*	4B	0.2/0.2/0.2	*Yr10*	1BS	0.2/0.2/0.2	*Pm8*	1BS, -41.9cM	0.2/0.2/0.2
Sr9f	2BL	0.2/0.2/0.2	*Lr13*	2BS	0.3/0.3/0.3	*Yr15*	1BS	0.2/0.2/0.2	*Pm9*	7AL	0.2/0.2/0.2
Sr9g	2BL	0.2/0.2/0.2	*Lr14a*	7BL	0.2/0.2/0.2	*Yr16*	2D	0.2/0.2/0.2	*Pm10*	1D	0.2/0.2/0.2
Sr10	2B	0.2/0.2/0.2	*Lr14b*	7BL	0.2/0.2/0.2	*Yr17*	2AS	0.2/0.2/0.2	*Pm11*	6BS	0.2/0.2/0.2
Sr11	6BL	0.2/0.2/0.2	*Lr15*	2DS	0.2/0.2/0.2	*Yr18*	7D	0.6/0.6/0.6	*Pm12*	6B	0.2/0.2/0.2
Sr12	3BS	0.2/0.2/0.2	*Lr16*	4B, 2BS	0.2/0.2/0.2	*Yr19*	5B	0.2/0.2/0.2	*Pm13*	3B	0.2/0.2/0.2
Sr13	6AL	0.2/0.2/0.2	*Lr17*	2AS	0.2/0.2/0.2	*Yr20*	6D	0.2/0.2/0.2	*Pm14*	6B	0.2/0.2/0.2
Sr14	1BL, 0.8cM	0.2/0.2/0.2	*Lr18*	5BL	0.2/0.2/0.2	*Yr21*	1B	0.2/0.2/0.2	*Pm15*	7DS	0.2/0.2/0.2
Sr15	7AL	0.2/0.2/0.2	*Lr19*	7DL	0.2/0.2/0.2	*Yr22*	4D	0.2/0.2/0.2	*Pm16*	4A	0.2/0.2/0.2
Sr16	2BL	0.2/0.2/0.2	*Lr20*	7AL	0.2/0.2/0.2	*Yr23*	6D	0.2/0.2/0.2	*Pm17*	1AS	0.2/0.2/0.2
Sr17	7BL (recessive)	0.2/0.2/0.2	*Lr21*	1DL	0.2/0.2/0.2	*Yr24*	1BS	0.2/0.2/0.2	*Pm19*	7D	0.2/0.2/0.2
Sr18	1DL, 2.6cM	0.2/0.2/0.2	*Lr22a*	2DS	0.2/0.2/0.2	*Yr25*	1D	0.2/0.2/0.2	*Pm20*	6BL	0.2/0.2/0.2
Sr19	2BS	0.2/0.2/0.2	*Lr23*	2BS	0.2/0.2/0.2	*Yr26*	6AS	0.2/0.2/0.2	*Pm21*	6AS	0.2/0.2/0.2
Sr20	2BL	0.2/0.2/0.2	*Lr24*	3D	0.2/0.2/0.2	*Yr27*	2BS	0.2/0.2/0.2	*Pm22*	1D	0.2/0.2/0.2
Sr21	2AL, 4.7cM	0.2/0.2/0.2	*Lr25*	4BS	0.2/0.2/0.2	*Yr28*	4DS	0.2/0.2/0.2	*Pm23*	5A	0.2/0.2/0.2
Sr22	7AL	0.2/0.2/0.2	*Lr26*	1BL-1RS	0.2/0.2/0.2	*Yr modifiers*	3BS 3DS 5DS	See Table 29	*Pm24*	6D	0.2/0.2/0.2
Sr23	4B	0.2/0.2/0.2	*Lr27*	4BS	0.2/0.2/0.2						
Sr24	3DL, 26cM	0.2/0.2/0.2	*Lr28*	4AL	0.2/0.2/0.2	Bunt, dwarf smut, stinking smut			BYDV		
Sr25	7DL	0.2/0.2/0.2	*Lr29*	7DS	0.2/0.2/0.2	*Bt1*		0.2/0.2/0.2	*Bdv1*	7DS	0.6/0.6/0.6
Sr26	6AL	0.2/0.2/0.2	*Lr30*	4AL	0.2/0.2/0.2	*Bt2*		0.2/0.2/0.2	*Bdv2*	7DL	0/0.01/0
Sr27	3A	0.2/0.2/0.2	*Lr31*	4BL	0.2/0.2/0.2	*Bt3*		0.2/0.2/0.2			
Sr28	2BL	0.2/0.2/0.2	*Lr32*	3D	0.2/0.2/0.2	*Bt4*	1B	0.2/0.2/0.2	*Septoria tritici* blotch		
Sr29	6DL	0.2/0.2/0.2	*Lr33*	1BL	0.2/0.2/0.2	*Bt5*	1B	0.2/0.2/0.2	*Stb1*		0.2/0.2/0.2
Sr30	5DL	0.2/0.2/0.2	*Lr34*	7DS	0.6/0.6/0.6	*Bt6*	1B	0.2/0.2/0.2	*Stb2*		0.2/0.2/0.2
Sr31	1BL, -41.9cM	0.2/0.2/0.2	*Lr35*	2B	0.2/0.2/0.2	*Bt7*	2D	0.2/0.2/0.2	*Stb3*		0.2/0.2/0.2
Sr32	2A, 2B, 2D	0.2/0.2/0.2	*Lr36*	6BS	0.2/0.2/0.2	*Bt8*		0.2/0.2/0.2	*Stb4*		0.2/0.2/0.2

Sr33	1DL, -27cM	0.2/0.2/0.2	*Lr37*	2AS	0.2/0.2/0.2	*Bt9*		0.2/0.2/0.2			
Sr34	2A, 2D	0.2/0.2/0.2	*Lr38*		0.2/0.2/0.2	*Bt10*		0.2/0.2/0.2	*Fusarium* head scab		
Sr35	3AL, 40cM	0.2/0.2/0.2	*Lr39*		0.2/0.2/0.2				*Fhs1*		0.2/0.2/0.2
Sr36	2BS	0.2/0.2/0.2	*Lr40*		0.2/0.2/0.2	Karnal bunt resistance			*Fhs2*		0.2/0.2/0.2
Sr37	4BL	0.2/0.2/0.2	*Lr41*	1D	0.2/0.2/0.2	*Kb1*		0.2/0.2/0.2			
Sr38	2AS	0.2/0.2/0.2	*Lr42*	1D	0.2/0.2/0.2	*Kb2*		0.2/0.2/0.2			
Sr39	2B	0.2/0.2/0.2	*Lr43*	7DS	0.2/0.2/0.2	*Kb3*		0.2/0.2/0.2			
Sr40	2BS	0.2/0.2/0.2	*Lr44*	1B	0.2/0.2/0.2	*Kb4*		0.2/0.2/0.2			
Sr41	4D	0.2/0.2/0.2	*Lr45*	2A	0.2/0.2/0.2	*Kb5*	Recessive*	0.2/0.2/0.2			
Sr42	6DS	0.2/0.2/0.2	*Lr46*	1B	0.2/0.2/0.2	*Kb6*	Recessive*	0.2/0.2/0.2			
Sr43	7DL	0.2/0.2/0.2									

* The resistance gene is dominant or partially dominant, except if specified.

Table 33 Genetic control of breeding traits for simulation

Breeding trait	Gene for trait	Chromosome location	Gene frequency			Genetic mode	Heritability*	$\sigma^2_{g\times e}/\sigma^2_g$	Phenotypic measurement
			CBME1	CBME2	CBME4				
Photo-insensitivity	*Ppd1*	2DL	0.8	0.8	0.8	Insensitivity is dominant	100%	0	Number of *Ppd* alleles, flowering, maturity
	Ppd2	2BS	0.8	0.8	0.8				
	Ppd3	2AL	0	0	0				
Vernalization	*Vrn1*	5AL, 9.4cM	0.8	0.8	0.8	No vernalization requirement is dominant.	100%	0	Number of *Vrn* alleles, stem extension, flowering
	Vrn2	5BS	0.8	0.8	0.8				
	Vrn3	5DL, 46.5cM	0.8	0.8	0.8				
Stem rust resistance	*See Table 25 for major genes*					Resistance is partially dominant	60-70%	Small	% (average coefficient of infection, ACI), infection type
	SR minor genes	15 loci	0.2	0.2	0.2	Additive, 5-50% reduction in SR			
Leaf rust resistance	*See Table 25 for major genes*					Resistance is partially dominant	60-70%	Small	% (average coefficient of infection, ACI), infection type
	LR minor genes	15 loci	0.2	0.2	0.2	Additive, 5-50% reduction in LR			
Yellow rust resistance	*See Table 25 for major genes*					Resistance is partially dominant	60-70%	Small	% (average coefficient of infection, ACI), infection type
	YR minor genes	15 loci	0.2	0.2	0.2	Additive, 5-50% reduction in YR			

Powdery mildew resistance	*See Table 25 for major genes* *PW modifiers*	 5 loci	 0.2	 0.2	 0.2	Resistance is partially dominant Additive	80%	Small	%
BYDV tolerance BYDV resistance	*Bdv1* *BYDV modifiers* *Bdv2*	7DS 5 loci 7DL	0.3 0.2 0	0.6 0.2 0.01	0.1 0.2 0	Resistance is partially dominant	60%	Small	Symptom & plant vigor, grades 1 to 9. x<=4 for tolerance.
Septoria tritici blotch resistance	*See table 25 for major genes* *ST modifiers*	 15 loci	 0.2	 0.2	 0.2	Resistance is dominant Additive	60%	Small	Double-digit scale
Bunts and Karnal bunt resistance	*See table 25 for major genes*					Resistance is dominant	80%	Small	%
Fusarium head scab (FHS) resistance	*See table 25 for major genes* *FHS modifiers*	 10 loci	 0.2	 0.2	 0.2	Nonspecific genes, quantitatively inherited.	50%	Small	%
Heat tolerance	*HT Modifiers*	About 10 loci	0.2	0.2	0.2	Additive	40%	Medium	
Cold tolerance	*CT Modifiers*	About 10 loci	0.2	0.2	0.2	Additive	40%	Medium	
Plant height	*Rht1* *Rht2* *Rht3* *Rht10* *Modifiers*	4BS, -21cM 4DS, -10.5cM 4AS 4DS, -10.5cM 5 loci	0.8 0.8 0 0 0.2	0.7 0.7 0 0 0.2	0.7 0.7 0 0 0.2	Reduced height is dominant Additive	60%	Small	cm
Grain color	*R1* *R2* *R3*	3DL, 56.4cM 3AL, 40cM 3B	0.1 0.1 0.1	0.9 0.9 0.9	0.5 0.5 0.5	Red is dominant	100%	0	Number of *R* alleles
Maturity		*About 5 loci*	0.5	0.5	0.5	Additive	60%	Small	Days from planting to maturity
Lodging		*About 10 loci*	0.5	0.5	0.5	Additive	60%	Medium	%
Number of tillers		*About 10 loci*	0.5	0.5	0.5	Additive	70%	Small	Integer
Synchronous tillering		*About 5 loci*						Small	
Green leaf duration (“stay-green”)		*About 10 loci*						Small	
Number of spikelets per spike		*About 5 loci*	0.5	0.5	0.5	Additive	70%	Medium	Integer
Number of grains per spikelet		*About 5 loci*	0.5	0.5	0.5	Additive	70%	Medium	Integer
Grain weight		*(About 10 loci)*	0.5	0.5	0.5			Medium	

IQ	Hardness (Puroindolines)	*Ha* *Pina-D1* *Pinb-D1*	5DS 5DS 5DS	0.5 0.5 0.5	0.5 0.5 0.5	0.5 0.5 0.5	*HaHa*: soft; *haha*: hard	100%	0	End-use type: 1a, 1b, 2a, 2b, 3a, 3b, 4a, 4b, and unacceptable
	HMW-glutenins LMW-glutenins Gliadins	*Glu-1* *Glu-3* *Gli-1* *Gli-2* *Gli-3*	1AL, 1BL, 1DL 1AS, 1BS, 1DS 1AS, 1BS, 1DS 6AS, 6BS, 6DS 1AS, 1BS	0.5 0.5 0.5 0.5 0.5	0.5 0.5 0.5 0.5 0.5	0.5 0.5 0.5 0.5 0.5		80%	Small	
	Protein content	*Pro1* *Pro2*	5DL 5DS	0.5 0.5	0.5 0.5	0.5 0.5		30%	Medium	
	Enzymes	*Alpha-amy-1* *Alpha-amy-2*	6AL, 6BL, 6DL 7AL, 7BL, 7DL	0.5 0.5	0.5 0.5	0.5 0.5		100%	0	
	Starch (amylose/amylopectin) GBSS	*Wx-A1* *Wx-B1* *Wx-D1*	7AS 4AL 7DS	0.5 0.5 0.5	0.5 0.5 0.5	0.5 0.5 0.5		100%	0	
Phenotypic uniformity								100%	0	Genetic diversity
Yield			*50 loci*	0.5	0.5	0.5	Additive and epistatic effects	20%	Large, 1.5 to 2.0	Real number

Notes:
1. The heritability value is based on individual plants; Heritability 100 means there is no environmental effect on the phenotype.
2. The gene frequencies of modification genes (modifiers) are all set to be 0.2, and the intra-genic action for modifier is additive.
3. There are about 5 rust genes conferring resistance to all rusts; Three to five rust modifiers combining together will have the acceptable resistance in breeding.

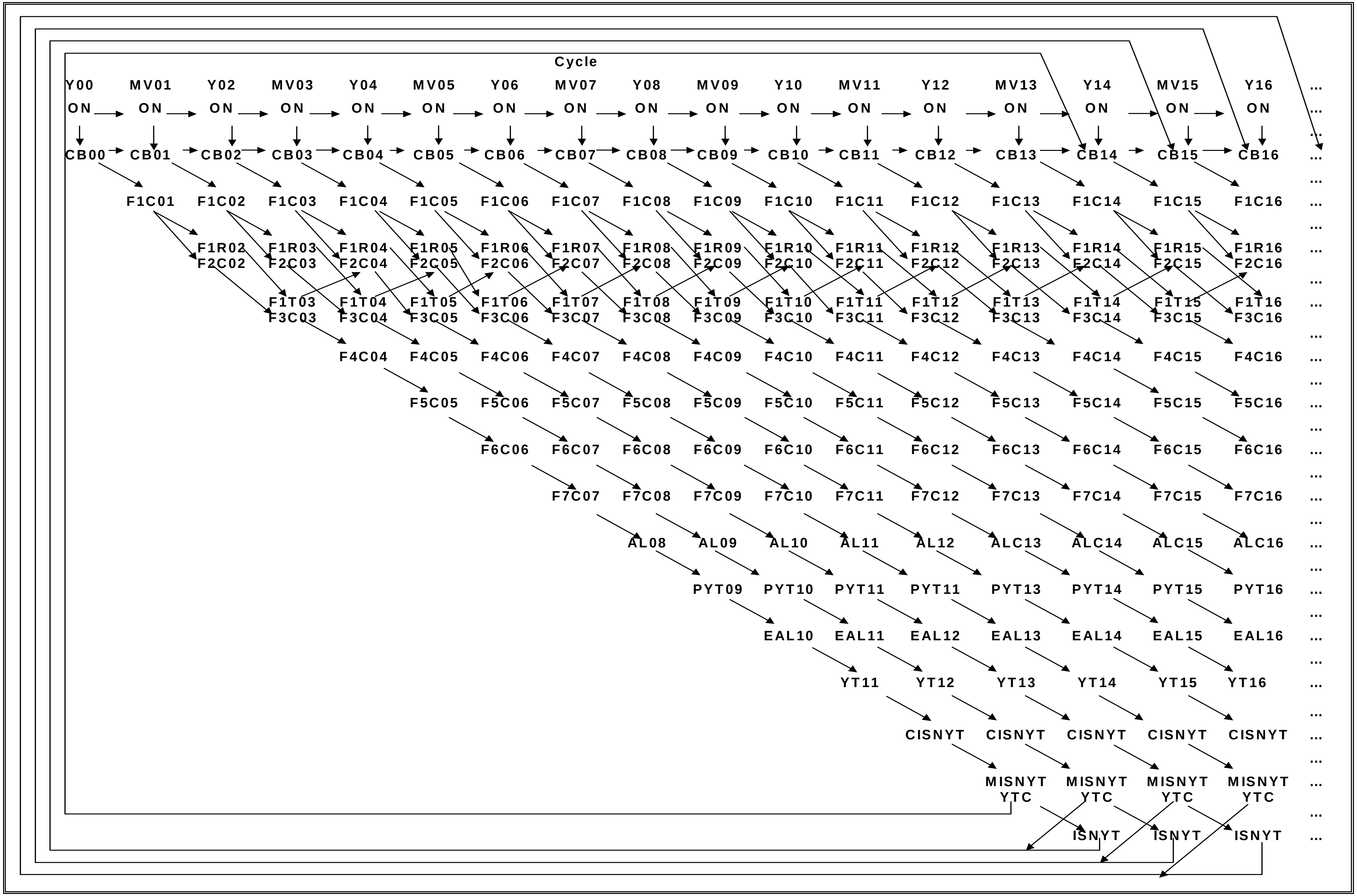


Figure 10 Schematic representation of the CIMMYT wheat breeding simulation

Scheme of the Simulation Module

Test of genetic models, especially for yield

1. Genetic model: The most frequently used genetic model in classical quantitative genetics is the additive and dominance model, with each gene having a similar small effect to phenotype, without linkage, without epistasis, without GEI.
2. Number of genes for yield: Genetic gains from historical data will give an idea of actual number of genes involved in yield. A small number of genes will result in a fast genetic gain, while a large number of genes will result in a slow genetic gain.
3. Linkage: gene linkage map and marker linkage map.
4. Genotype by environment interaction (GEI): Some genes contribute to yield in all MEs, some genes contribute to yield only under favorable MEs but not under unfavorable MEs. Likewise it is possible that some genes contribute to yield under unfavorable MEs but not under favorable MEs. This question can be studied by using CIMMYT's multilocational trials.
5. Epistasis: intergenic interaction, difficult to test but can be accommodated in simulation program.

Ways of comparing selection methods

Selection strategies can be compared from the following aspects.

1. Genetic advance or gain
2. Increase in the frequency of the favourable allele
3. Probability of selecting the best genotype
4. Mean and variance of the final selected population
5. Genetic diversity of the final selected population
6. Number of lines above predetermined check or best parent

Some questions to be answered by simulation in CIMMYT wheat breeding program

A lot of questions in breeding can be studied by simulation as well as by the field experiments. Here are only some examples.

1. Comparison of pedigree selection, modified pedigree/bulk, and selected bulk used in CIMMYT's wheat breeding programs (Table 34).
2. Comparison of simple, top, back, and double crosses in regard to (1) introducing genes from the donor parent and (2) retention of genes from the adapted parent.
3. Balance between the number of crosses and population size of the segregating populations (Table 34).

4. Suitable selection intensity for each generation: high selection intensity in early generations or in late generations (Table 34)?
5. The correlation between parents and their offspring: Can F1 hybrids predict advanced lines?
6. Effectiveness of different selection sites and their order/sequence in shuttle breeding (Table 34).
7. Ways to better accommodate genotype by environment interaction and epistasis.
8. The effective distance between the marker and the objective gene, and the generation when to apply marker assisted selection (MAS).
9. Comparison of breeding/selection/evaluation methodologies to develop germplasm with wide and/or specific adaptation expressing stable yields.
10. Utilization of international yield trial data to direct crossing and targeting of germplasm.
11. Why are CIMMYT's wheat breeding programs so successful?

Table 34 A hypothetical simulation experiment: Comparison of modified pedigree/bulk and selected bulk in plant breeding

		Modified pedigree/bulk					Selected bulk				
Growing ME	Generation	Number of crosses or families	Number of plants in a plot	Among cross or family selection	Within family selection	Total number of plants	Number of crosses or families	Number of plants in a plot	Among cross or family selection	Within family selection	Total number of plants
ME1	F1	100	50	0.8	1	5000	100	50	0.8	1	5000
ME2	F2	80	1500	0.9	0.02	120000	80	1500	0.9	0.02	120000
ME1	F3	2160	50	0.4	0.1	108000	72	2000	0.9	0.1	144000
ME2	F4	864	300	0.5	0.2	259200	65	1500	0.9	0.2	97200
ME1	F5	432	300	0.5	0.2	129600	58	600	0.9	0.2	34992
ME2	F6	216	200	0.55	0.2	43200	52	200	0.9	0.5	10498
ME1	F7	4752	50	0.8	1	237600	4724	50	0.8	1	236196
ME2	AL	3802	25	0.7	1	95040	3779	25	0.7	1	94478
ME1	PYT	2661	300	0.7	1	798336	2645	300	0.7	1	793619
					Total	1795976				Total	1535983

<u>Schematic representation of the simulation module</u>

Figure 10 is a schematic representation of the CIMMYT wheat breeding simulation module. In this case we assume that the wheat breeding program started from the crossing blocks having been planted in Cd. Obregon.

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