

Maize Research-for-Development Scenario: Challenges and Opportunities for Asia

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Introduction

Maize is the key crop for food and feed security and income generation for millions of smallholder farmers in sub-Saharan Africa (SSA), Asia and Latin America. It is a major source of calories in the diets of nearly 230 million inhabitants of developing countries – 81 million in sub-Saharan Africa, 141 million in South Asia, and 8 million in Latin America. Annual per capita maize consumption averages 36, 10, and 23 kilograms (kg), respectively, in these regions, but this masks significant variation and per capita food consumption of maize. In Mesoamerica, annual maize consumption exceeds 80 kg per capita in Guatemala, Honduras, and El Salvador, rising to 125 kg in Mexico (Shiferaw et al. 2011).

Maize accounts for almost half of calories and protein consumed in eastern and southern Africa (ESA) and one-fifth of the calories and protein consumed in West Africa. Maize consumption levels exceed 130 kg per capita per year in Lesotho, Malawi, and Zambia. The highest amounts of maize consumed are found in southern Africa, at 85 kg/capita/year, as compared to 27 kg/capita/year in East Africa and 25 kg/capita/year in West and Central Africa (Shiferaw et al. 2011). In South and Southeast Asia, where direct maize consumption on an annual average, is estimated to be only 6 and 16 kg per capita, respectively, there are several areas (especially in the highlands and tribal regions) where maize is consumed directly at much higher rates (Babu et al. 2013a).

Impressive growth of maize in Asia

Notably, eight major maize-producing countries – China, India, Indonesia, Nepal, Pakistan, Philippines, Thailand, and Vietnam – taken together, produce 98 percent of Asia's maize and 28 percent of global maize. In most of these countries, maize is predominantly grown under rainfed conditions by smallholder, resource-poor farmers. Despite constraints, including over-dependence on rainfall, frequent droughts, yield losses due to pre- and post-harvest pathogens and insect-pests, weeds, poor agronomic management, lack of access to quality seed, etc., several Asian countries have registered impressive growth rate in terms of maize area, production and productivity over the past decade. Countries like China, India and Indonesia recorded growth rates in maize production from 5 to 6 percent per year.

Maize is now the crop with the largest- cultivated area in China, totaling nearly 33.5 million hectares (ha) (Hu and Zimmer, 2013); globally, China's maize acreage and production are second only to the United States (U.S.). Maize yields have registered impressive increases in China, from 4.5 t/ha to 5.75 t/ha (+0.9 percent per annum). The corn belt of China, stretches from the northeast to the southwest of the country, spans 11 provinces (Heilongjiang, Jilin, Hebei, Henan, Shandong, Inner Mongolia, Liaoning, Shanxi, Yunnan, Sichuan and Shaanxi) and accounts for 81 percent of area under maize and nearly 83 percent of total maize produced (Hu and Zimmer, 2013).

India is the second-most important maize growing country in Asia, and now ranks as the world's sixth-largest producer and the fifth-largest consumer of maize. Indian maize production rose from 11.15 million tons in 2002-03 to 22.5 million tons in 2012-3. The growing poultry industry is the biggest driver of maize in the country, consuming nearly 13-14 million tons of maize, or over half of country's maize production.

Indonesia is the third-major maize growing country in Asia, and produced nearly 9 million metric tons of maize in 2013. This production is, however, well-short of demand, especially from the feed industry. Thus, Indonesia is one of the largest importers of maize, with 2013-2014 import figures reaching almost 3.1 million tons. The country, however, offers enormous opportunities for increasing maize production and utilization in the coming decades.

Thailand has successfully evolved from a strong public-sector led maize research and development (R&D) program into a hub of private-sector investment, especially for seed production and supply to several countries in Asia, especially in Southeast Asia (Napasintuwong, 2014). In 2012, maize seed exports from Thailand to Southeast Asia and other destinations accounted for 42 percent of Thailand's total seed exports and were valued at approximately US\$120 million. In addition, Thailand dominates the global baby corn trade with both fresh- and canned-products, and contributing more than 1 billion Thai Baht to the country's economy.

Maize growth in Bangladesh is a major success story, driven by the rapid expansion of the poultry industry during the past 15 years. Although the total area under

maize is just around 2 million hectares, with the introduction and widespread adoption of maize hybrids, coupled with favorable environmental conditions, an average yield of almost 6.5-7 t/ha is currently achieved in Bangladesh, which is the highest-productivity realized in Asia (Miah et al., 2013).

Meeting the rapidly growing demand for maize

Despite this impressive growth, maize production and productivity must be significantly improved if Asia is to successfully meet the rapidly growing demand for maize. Maize demand is projected to increase 87 percent by 2020 based on demand in 1995 (IFPRI, 2003). An array of factors contributing to this sharp increase in maize demand, include the increase in per capita income, changing diets, and a rapidly growing poultry sector (Shiferaw et al., 2011). For example, India's maize demand has been forecast to grow by 36 percent in the next four years touching 30 million tons in 2017, and demand is expected to double within the next nine years to touch about 44 million tons by 2022. Fuelled by the demand from the poultry and industrial sectors, India's hybrid maize seed sector could more than double to 200,000 tons a year (from 90,000 tons now) in the next two years (Kesireddy 2014).

As Asia's economies and agribusiness, food and feed processing industries continue to grow, the demand for use of maize as food, feed, fodder and for industrial purposes will increase significantly. The industrial use of maize has already seen big increases in China, Japan and Thailand. Indonesia, China and Vietnam are already large-importers of maize. The key question under debate is: can Asia sustainably meet its rapidly-growing demand for maize only through area expansion? The answer has to be "no", given the unsustainable nature of increasing maize production by expanding area at the cost of ecosystem health and biodiversity.

Climate change compounds the challenge of improving maize productivity in Asia

Drought is recognized as the most important constraint across the rainfed lowland and upland environments, covering about 70 percent of the maize production area in Asia. This situation is likely to be exacerbated in the coming decades due to climate change, often leading to inadequate and/or uneven incidence of rainfall during the cropping season alongside temperature changes (IPCC, 2007; ADB, 2009). Alleviating the effects of drought alone could increase average maize yields by 35 percent across Asia-7 (excluding China), and by 28 percent in Southwest China (Gerpacio and Pingali, 2007).

Countries in the greater Himalayas region—Bangladesh, Bhutan, northern India, and Nepal—are facing increased frequency and magnitude of extreme weather events, resulting in flooding, landslides, devastation of agricultural crops, and negative impacts on ecological health. The coastal areas of Bangladesh, India, the Maldives, and Sri Lanka are at high-risk for projected sea level rise that may cause displacement of human settlements, saltwater intrusion, loss of agricultural land and wetlands, and a negative impact on tourism and fisheries (Ahmad and Suphachalasai, 2014).

Maize is particularly vulnerable to reproductive stage-heat-stress. Climate projections also suggest that elevated temperatures, especially in the drought-prone areas of Sub-Saharan Africa and rainfed areas in South Asia, are likely to result in significant crop yield losses (Cairns et al. 2013a). High-temperature-stress and drought are expected to increase in northern China (Piao et al., 2010) as well as in many tropical maize growing areas, especially in South and Southeast Asia. Spring maize is an important option for intensifying and diversifying cropping systems in South Asia. However, it is prone to severe-heat-stress during flowering/early grain filling stages, particularly in the upper and middle regions of the Indo-Gangetic plains. These highlight the importance of developing improved maize varieties with tolerance to both drought- and high-temperature-stress (Cairns et al. 2013a,b).

The changing climate not only affects the frequency of abiotic stresses, but also biotic stresses on crop plants. Maize in Asia is already affected by an array of diseases and insect-pests; these include the downy mildews, post-flowering stalk rots (PFSR), Gray leaf spot (GLS), Banded leaf and sheath blight (BLSB), Turicum leaf blight (TLB), ear rots, stem borers and weevils, and high-incidence of mycotoxins in some countries. Rising-temperatures and variations in humidity could potentially affect the diversity and responsiveness of pathogens and insect-pests, and could lead to new and perhaps unpredictable epidemiologies. For example, GLS is now becoming an important disease globally, with high-incidences reported in Nepal, China, Bhutan, Colombia, Mexico, Brazil and several countries in Africa.

The use of higher spatial resolution modelling is essential for the identification of high-priority geographic areas for development and deployment of improved germplasm suited to the future climates. Temperature thresholds for current cereal varieties and the interaction of heat stress with other components of climate change (especially drought and biotic stresses) must also be considered. The application of biophysical and economic models in maize improvement, decision support and foresight

requires the implementation of harmonized procedures for data acquisition, incorporating diverse and actual datasets (cultivar-specific data, climatic data, soil data, important macro- and micro- nutrients, pests/pathogens data, crop management practices, and socio-economic data) in a meaningful way for reliable predictions and practical utility (Prasanna et al. 2013a).

Maize lethal necrosis (MLN) has emerged as a serious threat

The outbreak and rapid spread of a new disease in eastern Africa emerged as a significant challenge to smallholder maize farmers in the region and concerns among institutions engaged in maize research and development. In 2011, outbreak of a serious disease was reported on maize in the Bomet County in Kenya, with crop losses estimated to be 70 to 100 percent. The disease was diagnosed in 2012 as Maize lethal necrosis (MLN), commonly known in the U.S., as corn lethal necrosis (CLN) was first identified in the U.S. in 1976 (Niblett and Claflin 1978). The disease is caused by the double infection of maize plants with MCMV and any of the cereal viruses in the family, Potyviridae, such as *Sugarcane mosaic virus* (SCMV), *Maize dwarf mosaic virus* (MDMV), or *Wheat streak mosaic virus* (WSMV). A single infection of MCMV or SCMV typically produce mild chlorotic symptoms. However, mixed infection of these viruses results in a synergistic reaction with lethal symptoms causing serious damage to plant and/or kills the infected plants in a span of two to three weeks. MLN in eastern Africa was found to be due to co-infection of maize with MCMV and SCMV (Wangai et al. 2012; Adams et al. 2013).

In areas where the MLN disease was very serious, farmers in eastern Africa experienced extensive or complete crop loss. The infected plants are frequently barren; the ears formed are small, deformed and set little or no seeds, drastically reducing the yield (Figure 1).



Figure 1. Typical symptoms of MLN often leading to early stage necrosis or death or barren plants or poor seed set.

Within the first year of its report, the disease spread to 55 districts in Kenya across the Rift Valley, Nyanza, Western, Central and Eastern provinces. Over 77,000 ha of maize were estimated to be affected in 2012, translating into an estimated loss of 1.4 million bags, each of 90 kg, worth about US\$ 52 million. Since 2012, MLN was reported in Tanzania, Uganda, Rwanda, and very recently in the eastern region of Democratic Republic of the Congo and Ethiopia. There are also un-confirmed reports of the disease occurrence in South Sudan. The negative impact of MLN on the entire maize sector and value chain, is shouldered by the small and medium seed enterprises. For example, in the years after MLN, seed-demand reportedly decreased in the MLN-affected regions in Kenya by approximately 30 percent. Various factors including a favorable environment for insect-vectors, maize mono-cropping, and the aggressive nature the viral strains (especially MCMV), contributed to the severity of incidence in eastern Africa.

A network of national research organizations in eastern Africa, and international agricultural research centers such as CIMMYT, are intensively tackling the MLN challenge through various strategies. In September 2013, a centralized MLN Screening Facility was established jointly by CIMMYT and Kenya Agricultural and Livestock Research Organization (KALRO) at Naivasha in Kenya, through a project funded by the Bill & Melinda Gates Foundation and the Syngenta Foundation for Sustainable Agriculture. During 2012 to 2014, CIMMYT evaluated (under MLN artificial inoculation) a large array of germplasm (nearly

25,000 entries) including inbred lines, breeding populations and pre-commercial hybrids. These efforts led to the identification and validation of promising MLN tolerant germplasm, including inbred lines and pre-commercial hybrids. Some MLN tolerant hybrids are also now in the pipeline for fast-tracked release in eastern Africa.

Efforts are also underway for the validation and deployment of genomic regions conferring resistance to MLN through molecular marker-assisted breeding. In addition to strengthening the maize seed sector through seed multiplication activities will include the exchange of MLN tolerant maize lines and pre-commercial hybrids, capacity building and awareness generation among partner institutions in sub-Saharan Africa on the effective diagnosis and management of MLN.

It is, however, of serious concern that despite intensive efforts by various institutions to raise awareness about the possibility of seed transmission of MLN-causing viruses, the disease has spread rapidly to several countries in eastern Africa, including Ethiopia more recently. It must be noted that the MLN-causing viruses could not only spread through the insect-vectors, but MCMV could be transmitted through seed at a frequency much higher than reported earlier (Jensen et al. 1991). It is imperative that seed companies that provide cross-border supply also implement necessary quarantine procedures, to curtail the spread of the disease to other regions. Asia also needs to be cautious of the MLN-causing viruses, especially MCMV, which has already been reported in a few countries, especially in Thailand and southern China. SCMV has been prevalent in Asia for several decades. Equally important is to initiate strong-breeding efforts to introgress MLN resistance (using validated trait donors) in the product pipelines.

Developing and deploying climate resilient maize varieties

CIMMYT has been implementing several projects, especially in Sub-Saharan Africa (SSA) and Asia for developing and deploying climate resilient varieties. Under the Drought Tolerant Maize for Africa (DTMA) project, jointly implemented by CIMMYT and the International Institute of Tropical Agriculture (IITA), in close collaboration with the National Agriculture Research Service (NARS) and private sector institutions in 13 countries in SSA, nearly 160 drought-tolerant maize varieties have been released during the period 2007 to 2013, with close to 60 percent of them being hybrids. These varieties perform as-well-as or better-than the commercial varieties currently available on the market under optimum (no water-deficit-stress) conditions and out-

perform the best commercial checks by at least 25-30 percent under drought stress and low-input conditions. DTMA has also facilitated production and delivery of about 30,000 tons of DT maize seed in 2013 through partnerships with about 90 seed companies, benefiting an estimated 2 million African households.

The Water Efficient Maize for Africa (WEMA) Project is another important public-private partnership, that is intensively engaged in developing and deploying drought-tolerant and insect-resistant white maize varieties in five-target countries in SSA (Kenya, Tanzania, Uganda, Mozambique, and South Africa), through a combination of conventional breeding, marker-assisted breeding and transgenic breeding.

CIMMYT's Global Maize Program is undertaking intensive efforts to develop maize germplasm with high temperature tolerance as well as with tolerance to combined drought and heat stresses, especially in the tropical genetic backgrounds of Asia and SSA. Initial experiments by the CIMMYT-Asia team to identify heat-stress-tolerant tropical maize lines among the elite, drought-tolerant maize germplasm developed in Mexico, Asia and Africa revealed: (a) high vulnerability of most of the tropical maize germplasm, including commercial cultivars in South Asia, to reproductive stage heat stress; and (b) poor correlation between drought and heat tolerance, indicating that physiological mechanisms that contribute to heat stress tolerance in maize may be different from those that contribute to drought tolerance (Cairns et al. 2012, 2013b). CIMMYT currently implements two major research projects, supported by USAID under the Feed-the-Future initiative, for developing and deploying heat-resilient maize for SSA. The Heat Tolerant Maize for Asia (HTMA) Project, launched in 2012, brings together public- and private- institutions based in South Asia (Bangladesh, India, Nepal and Pakistan), as well as Purdue University, for accelerated development and deployment of heat-stress-resilient maize germplasm.

For developing climate-resilient maize germplasm, breeding programs need to incorporate packages of traits more efficiently. In southern Africa and South Asia, maize farmers are likely to require varieties with tolerance to drought-stress at elevated temperatures. Similarly, tolerance to both drought- and waterlogging- is becoming increasingly important for some areas in South and Southeast Asia, and may be required by farmers in small areas in SSA (Cairns et al. 2013a). For developing such varieties, breeding programs may need to be re-oriented for simultaneous selection under various combinations of stresses. This would warrant development of managed stress screening sites and standardized protocols for specific

combinations of stresses predicted in the target environment.

Affordability and timely access to quality seed of stress resilient maize varieties. A common constraint for small and medium enterprise (SME) seed companies in the rapid scale-up of new varieties is parental line maintenance and foundation (basic) seed production. CIMMYT has been providing appropriate technical support for these activities, at least in the initial phases of variety commercialization, on a case-by-case basis in SSA, Latin America and Asia. The basis for determining this support is from the “seed road maps” that are developed with partner institutions for effective scale-up, promotion and delivery of improved varieties to the smallholders in the target geographies.

Another recent CIMMYT initiative involves establishing the International Maize Improvement Consortium (IMIC) in Asia and in Latin America, in partnership with nearly 80 SME seed companies. The underlying principles of this partnership is to implement client-determined research and a more focused, demand-driven approach for product development, while drawing synergies through a collaborative testing network for targeted impacts.

Developing and releasing climate resilient varieties only, is not adequate to shelter communities from climate vulnerability. Innovative approaches as well as partnerships are required to deploy stress-resilient varieties for the benefit of the smallholders in the climate vulnerable regions. CIMMYT experiences strongly indicate that in addition to strengthening the seed sector (especially the SME seed companies), appropriate government policies and the adoption of progressive seed laws and regulations, are vital for

improving smallholder farmers’ access to improved seed and for over-coming key bottlenecks affecting maize seed value chain, particularly in the area of policy, credit availability, seed production, germplasm and marketing. A proactive approach that combines promising technological, institutional and policy solutions can help vulnerable communities manage risks if they are implemented by institutions operating at different levels (community, sub-national, and national) with the capacity to manage climate variability and extremes (Shiferaw et al. 2014). Geographic information systems (GIS) could also play an integral role in targeting breeding programs by predicting regions of vulnerability, targeting germplasm movement and identifying future climates for agricultural production environments (Cairns et al. 2013a).

Enhancing genetic gains and breeding efficiency

The ability to develop, in a cost-effective and time-efficient manner, elite maize hybrids with high-yield potential and necessary adaptive traits (abiotic and biotic stress resilience) will be critical for the improved productivity and diversification of cropping systems. While conventional breeding has been successful in developing an array of elite maize hybrids, rapid advances in breeding tools and techniques, especially doubled haploidy (DH), high-throughput phenotyping for traits of interest, mechanization of breeding operations (to the extent possible), molecular marker-assisted breeding, and decision support tools/systems (Figure 2) offer excellent opportunities for improving genetic gains and enhancing breeding efficiency. A few of these important components will be discussed.

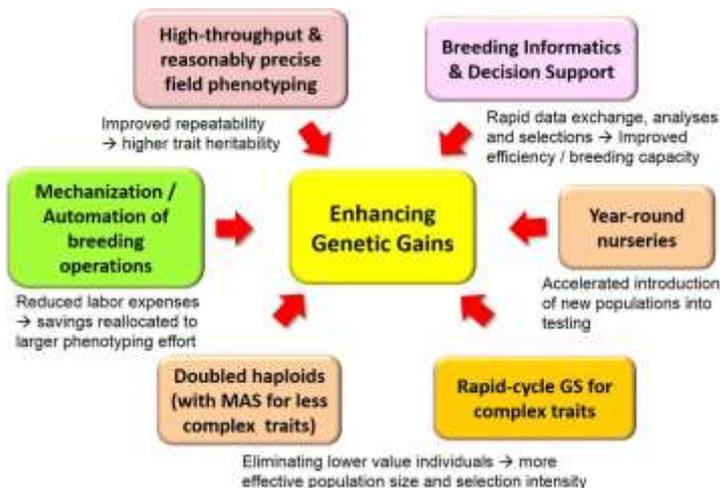


Figure 2. Components for enhancing genetic gains in maize.

Doubled haploid (DH) technology in maize breeding

Greater access to low-cost hybrid seed and more rapid development of improved hybrids are vital for achieving increased maize productivity and enhance income opportunities to maize growers, while meeting the demands of food, feed and nutrition security. Development of stable and productive inbred lines to produce hybrid seed is the cornerstone of successful and affordable hybrid maize technology. The DH technology is now a powerful tool to accelerate development, identification and use of elite breeding lines. DH not only significantly reduces the time and resources required for generating homozygous lines, but also enhances “forward breeding” (Geiger and Gordillo, 2009; Prasanna et al. 2012).

The *in vivo* haploid induction using temperate haploid inducers (genetic stocks with high-haploid induction capacity) has been adapted by an array of commercial maize breeding programs in Europe, North America, and more recently in Asia (especially China), but the lack of tropically adapted haploid inducer lines impeded the application of DH technology in the tropical maize breeding programs (Prigge et al. 2012). Tropically-adapted haploid inducers with a haploid induction rate (HIR) of up to 10 percent have been recently developed through collaboration between CIMMYT and the University of Hohenheim (Prigge et al. 2011; Prasanna et al. 2012). These tropicalized haploid inducers have already been shared with a large number of interested institutions in Africa, Latin America and Asia, for research or commercial use under specific terms and conditions. The availability of tropicalized haploid inducers is expected to significantly enhance the efficiency of DH line production, increasing seed set and rates of induction, and reducing the cost of inducer line maintenance and seed production. CIMMYT is also in the process of further optimizing the DH protocol, and developing second-generation haploid inducer lines adapted to specific tropical environments, especially sub-Saharan Africa, Asia and Latin America, to further widen the application of DH technology in maize breeding programs.

While DH technology is the primary mode of deriving new inbred lines by several large, private sector, breeding programs, NARS and SMEs seed companies in several Asian countries, have so far not derived benefits out of maize DH technology for various reasons. CIMMYT, in partnership with Kenya Agricultural and Livestock Research Organization (KALRO) has also established a centralized maize DH facility at Kiboko (Kenya) for strengthening maize breeding programs, including those of national agricultural research systems (NARS) and small and medium enterprise (SME) seed companies in sub-Saharan Africa. A similar facility is being planned for Asia, in partnership with Asian institutions.

High-throughput and reasonably precise phenotyping

Field-based phenotyping still remains a major bottleneck for future breeding progress. Phenotyping capacity of several institutions in Asia is lagging far behind the capacity to generate genomic information. Phenotyping capacity is constrained in many countries, limiting our ability to breed better cultivars with higher grain yield and stress resilience (Prasanna et al. 2013b; Araus and Cairns, 2014). Field-based phenotyping of appropriately selected traits, using low cost, easy-to-handle tools, is now possible, and should become an integral and key component in the maize breeding programs. There is also a distinct need for the public and private institutions to come together and establish “phenotyping networks” for comprehensive and efficient characterization of genetic resources and breeding materials for important target traits.

Molecular breeding strategies, such as genome-wide association studies (GWAS), marker-assisted recurrent selection (MARS) and genome-wide selection (GS) are being implemented by several institutions worldwide. However, genotypic predictions for both MARS and GS based strategies depend heavily on a single phenotyping cycle, thus increasing the need for reliable phenotyping methodologies (Cobb et al. 2013).

Combining advances in aeronautics and high-performance computing is paving the way in the development of field-based phenotyping platforms (White et al. 2012); such platforms could range from ground- to aerial-based. Recently, under the MAIZE CGIAR Research Program, the Crop Breeding Institute (Zimbabwe), University of Barcelona (Spain), AirElectronics (Spain), Consejo Superior de Investigaciones Científicas (Spain), and CIMMYT, developed a UAV (unmanned aerial vehicle), called “Skywalker”. The “Skywalker” is able to carry a payload of up to 1 kg and can carry several sensors including thermal, multispectral and digital cameras. This UAV is currently being used to identify genotypic variability in plant water status under drought- stress and biomass production and senescence under drought-, heat- and low-N-stresses (Cairns et al. 2012b) at CIMMYT-Harare, with promising results.

Beyond such technological advances, there is also an immense need for measuring and reducing the effects of field variability, and thereby increasing the genetic signal-to-noise ratio to detect real differences between genotypes. CIMMYT is intensively working to characterize field variability at the key phenotyping sites worldwide and improving field-based phenotyping through various approaches, such as monitoring soil moisture using neutron probes/Time-

Domain Reflectometer (TDR), non-destructive estimation of biomass (using NDVI or Normalized Differential Vegetation Index), and analysing canopy behavior using Infrared thermography, and functional aspects of roots using Rhizotronics etc. (Prasanna et al. 2013b).

Genomics-assisted breeding

Molecular marker-assisted or genomics-assisted breeding is the way forward in effectively meeting the greater challenge of developing cultivars with combinations of relevant adaptive traits, including biotic and abiotic stress tolerance, and nutritional quality. With the rapid reduction in genotyping costs, new genomic selection technologies have become available that allow the maize breeding cycle to be greatly reduced, facilitating inclusion of information on genetic effects for multiple stresses in selection decisions.

High-density genotyping using platforms such as genotyping-by-sequencing (GBS) is now an integral part of CIMMYT's maize molecular breeding strategies. GWAS is being implemented by CIMMYT-GMP for identification of genomic regions associated with an array of important traits, especially abiotic stress tolerance and disease resistance, coupled with validation of the significant genomic leads in an array of tropical/subtropical bi-parental populations (Prasanna et al. 2014). Marker-assisted recurrent selection (MARS) and genome-wide selection (GS) are being implemented by CIMMYT and partners through several projects in the tropics, especially for improvement of complex traits. A recent comparative study of pedigree selection, MARS and GS undertaken across 8-to-10 bi-parental populations demonstrated the superior performance of hybrids derived from Cycle 3 of both MARS and GS schemes over pedigree selection in most populations compared with the Cycle 0. The overall gain per year for MARS and GS under managed drought and well-watered environments was 2-to-3-fold higher than the gain achieved via pedigree selection (Beyene et al. 2014).

CIMMYT is also employing joint GWAS and linkage mapping approaches for identifying breeder-ready markers for resistance to major diseases affecting tropical maize like Turcicum leaf blight (TLB), Grey leaf spot (GLS), Maize lethal necrosis (MLN), common rust, ear rots, and corn stunt complex. A recent example is the Maize streak virus (MSV), a major disease that affects maize productivity in several countries in SSA. CIMMYT Maize Program has fine-mapped and identified SNP markers for a major QTL for MSV resistance (*msv1*) and validated these markers on a set of DH lines that have been phenotyped for responses to MSV in different locations in sub-Saharan Africa (Sudha Nair et al., manuscript in preparation). Forward breeding and

MABC are ongoing using a three-marker haplotype for *msv1* selection. Simultaneous with the marker discovery and validation, strategies for incorporating validated markers in breeding pipelines, through both conventional and DH based breeding schemes, are also being developed and implemented (Prasanna et al. 2014).

Breeding informatics and decision support tools

A careful balance of many diverse elements is required to design and implement an appropriate decision support system that provides an optimal combination of time, cost and genetic gain (Xu et al. 2012). Such a system would need to include: (a) managing and analysing large amounts of genotype, pedigree, phenotype and environment data; (b) selecting desirable recombinants through an optimum combination (in time and space) of phenotypic and genotypic information; and (c) developing breeding systems that minimize population sizes, number of generations and overall costs while maximizing genetic gain for traditional- and novel- target traits (Prasanna et al. 2014).

Effective management of product- and trait- pipelines in breeding programs requires effective management of pedigree, phenotypic and genotypic databases, accurate forecasting of genotyping and phenotyping services, as well as optimized decision making tools/system. Standardized software tools for forecasting, project management, and conventional and molecular breeding data review can streamline the process from initial discovery to final deployment of products through coordinated workflows.

Nutritionally enriched maize

Maize is the predominant staple food in regions such as sub-Saharan Africa and Latin America where vitamin A deficiency abounds. While carotenoids are absent in white maize kernels, yellow maize is known to accumulate carotenoids in the endosperm, and is thus a good target for bio-fortification efforts. Most yellow maize grown and consumed throughout the world, however, has only 2 µg/g or less of provitamin A carotenoids (Babu et al. 2013).

HarvestPlus, a multi-institutional program on agriculture for improved nutrition and health, leads a global effort to develop and deliver bio-fortified staple food crops with one or more of the three most-limiting nutrients in the diets of the poor: vitamin A, zinc, and iron (Brown 1991; Bouis and Welch 2010). Under the HarvestPlus- maize program, where the primary target is improving provitamin A (proA) concentration in the endosperm, considerable progress has been achieved till date at CIMMYT and IITA on developing provitamin A-enriched maize germplasm, in active collaboration with several institutions/Universities

worldwide. CIMMYT maize program also validated the effects of three-key polymorphisms (*LcyE*-5'TE, *LcyE*-3'Indel and *CrtRB1*-3'TE) in several diverse tropical genetic backgrounds, and developed PCR-based assays for detecting the favorable alleles (Babu et al. 2013). *CrtRB1*-3'TE had an impressive two to ten-fold effect on enhancing β -carotene and total proA content, irrespective of the genotypic constitution at *LcyE*. CIMMYT studies clearly demonstrated that MAS using markers diagnostic of specific functional polymorphisms can significantly and efficiently increase proA carotenoid concentration in maize germplasm. These molecular markers also offer an efficient means of tracking the favorable alleles in backcross or pedigree breeding programs, and are now adopted by several institutions, especially in China and India.

One of the key target countries for deployment of high proA maize under the HarvestPlus-maize program is Zambia, where the average per capita consumption of maize is more than 130 kg per year (356 g per day), and the vitamin A deficiency is as high as 54 percent in children under five and 13 percent in women aged 15-49 (WHO, 2009). The first-generation proA-enriched hybrids developed by CIMMYT have about 6 to 9 $\mu\text{g/g}$ of proA; three of such hybrids have been released in September, 2012 in Zambia, after National Performance Trials (NPTs) (2010 to 2011). Several institutions in China and India are on the path toward developing and deploying proA-enriched maize hybrids using marker-assisted breeding.

Quality Protein Maize (QPM), one of the major success stories in biofortification, has been highlighted in several publications over the years (e.g., Vasal 2000; Prasanna et al. 2001; Babu and Prasanna 2014). Many important lessons could be learned from the long experience of institutions such as CIMMYT in developing and disseminating nutritionally enriched maize germplasm, especially QPM. These include the need for: (a) assurance of competitive agronomic performance of the nutritionally enhanced germplasm (vis-à-vis normal maize); (b) high throughput, low-cost and easily accessible phenotyping/screening tools; (c) generation of adequate awareness among the stakeholders (including farmers and consumers) on the strengths and constraints (if any) of nutritionally-enriched germplasm; (d) effective seed production systems; and (e) strong partnership with national partners, health and agricultural ministries for complementing the technologies with proper policy support and institutional innovations.

“Seeds of Discovery” (SeeD) – a novel initiative

Maize has enormous genetic diversity that offers incredible opportunities for genetic enhancement. There is no lack of favorable alleles in the global

maize germplasm that contribute to higher yield, abiotic stress tolerance, disease resistance or nutritional quality improvement. However, these desirable alleles are often scattered over a wide array of landraces or populations. Our ability to broaden the genetic base of maize and to breed climate-resilient and high-yielding cultivars adaptable to diverse agroecologies where maize is grown will undoubtedly depend on the efficient and rapid discovery and introgression of novel/favorable alleles and haplotypes (Prasanna 2012).

A well-characterized and well-evaluated germplasm collection would have greater chances of contributing to the development of novel and improved varieties, and consequently, greater realization of benefits for the resource-poor farmers. The CIMMYT gene bank holds ~27,000 maize entries, of which ~24,000 are landraces/OPVs collected from diverse regions in Latin America, Africa and Asia and held in trust for several decades to date (Ortiz et al. 2010; Prasanna 2012). Simultaneous with the wider adoption of high-throughput molecular tools, there is a distinct need to establish global phenotyping networks for comprehensive and efficient characterization of genetic resources and breeding materials for an array of target traits, particularly for biotic- and abiotic-stress tolerance and nutritional quality. This would significantly accelerate genomics-assisted breeding, diversification of the genetic base of elite breeding materials, creation of novel varieties and countering the effects of global climate changes.

“*Seeds of Discovery*” (*SeeD*) is a novel project, funded by the Mexican Government, which aims to discover the extent of allelic variation in the genetic resources of maize and wheat, through high-density genotyping/re-sequencing, multi-location phenotyping for prioritized traits, and novel bioinformatics tools for discovery and use of favorable alleles and haplotypes associated with important traits (Peter Wenzl and Kevin Pixley, personal communication).

GM maize in Asia

The global area under transgenic or genetic modified (GM) crop cultivation has increased more than 100-fold from 1.7 million in 1996 to over 175 million in 2013. GM maize was grown on 57.4 million hectares (m ha) out of 179 m ha globally (32 percent of the total) in 2013. This area is primarily in the USA, Argentina, Canada, South Africa, Uruguay, Egypt, the Philippines and South America.

Several institutions in Asia are undertaking research on transgenic traits in maize. However, the Philippines is the only Asian country currently under commercial cultivation of GM maize. Herbicide-resistant and insect-protected GM maize is planted in about 800,000 hectares, which is 32 percent of the total

maize area (2.5 mha) in the country. Vietnam is the only other country in Asia with an ambitious plan to cultivate GM maize, as the country already imports large volumes of maize (nearly 1.34 million tons) and soybeans (approx.. 897,000 tons) to meet the domestic demands. The Ministry of Agriculture and Rural Development of Vietnam approved in August 2014, the use of GM maize to produce food for humans and feed for livestock. The Ministry of Natural Resources and Environment issued the biosafety certification to MON 89034 of Dekalb-Vietnam Co. Ltd., a subsidiary of Monsanto. Such an approval, if GM maize is approved by the two Ministries, indicates support for GM crops by central authorities in Vietnam.

Conclusions

Breeding programs in the majority of the NARS and SME seed companies in developing countries, including in Asia, have limited capacity for undertaking precision phenotyping, particularly under repeatable- and representative-levels of abiotic stresses in the field. Intensive efforts are therefore required to build the capacity of the Asian institutions to characterize and control field site variation (for improving repeatability), adopt appropriate experimental designs, select the “right” traits for phenotyping, proper integration, analysis and application of heterogeneous datasets, as well as to generate better awareness of technological advances with regard to phenotyping.

Intensive multi-institutional efforts are required to identify and utilize climate-resilient tropical/subtropical maize germplasm in product development pipelines. This warrants (a) carefully undertaken field-based phenotyping at several relevant sites as well as under technically demanding managed-stress screens; (b) better understanding of the genetic architecture of traits such as heat-stress-tolerance as well as tolerance to combined drought- and heat- stresses; (c) utilization of modern breeding tools/strategies, including genome-wide association studies, genomic selection, and doubled haploid (DH) technology for the rapid development of improved products; (d) identification of hot spots of climate vulnerability for germplasm deployment; and (e) multi-institutional efforts, especially public-private alliances, to ensure that the products (climate resilient-varieties) effectively reach the climate change-vulnerable farming communities.

Genetics and breeding alone cannot solve the complex challenge of enhancing maize productivity at the smallholder farm level, especially in the face of depleting/degrading natural resources and changing climates. There is a distinct need to effectively complement improved maize cultivars using suitable

conservation agriculture practices as well as institutional and policy innovations that support maize growth and development. This includes understanding the smallholder farmers’ budget constraints and access to quality seed and effective measures to help them overcome constraints for the scaled adoption of high-yielding, stress resilient and nutritionally enriched maize varieties, and partnerships and policies to significantly enhance maize production and utilization.

References

- Adams IP, Miano DW, Kinyua ZM et al. (2013) Use of next-generation sequencing for the identification and characterization of *Maize chlorotic mottle virus* and *Sugarcane mosaic virus* causing maize lethal necrosis in Kenya. *Plant Pathology* 62: 741-749.
- ADB (2009) Food security under threat from climate change. <http://reliefweb.int/report/>.
- Ahmed M, Suphachalasai S (2014) Assessing the costs of climate change and adaptation in South Asia. Mandaluyong City, Philippines: Asian Development Bank.
- Araus JL, Cairns J (2014) Field high-throughput phenotyping—the new crop breeding frontier. *Trends Plant Sci.* 19: 52–61.
- Babu R, Palacios N, Prasanna BM (2013a) Biofortified maize – a genetic avenue for nutritional security. In: *Translational Genomics for Crop Breeding: Abiotic Stress, Yield, and Quality*, First Edition. (eds. RK Varshney, R Tuberosa). John Wiley & Sons, pp. 161-176.
- Babu R, Palacios NP, Gao S et al. (2013b) Validation of the effects of molecular marker polymorphisms in *LcyE* and *CrtRBI* on provitamin A concentrations for 26 tropical maize populations. *Theor Appl Genet* 126:389–399.
- Babu R, Prasanna BM (2014) Molecular breeding for Quality Protein Maize (QPM). In: *Advances in Genomics of Plant Genetic Resources* (eds. R Tuberosa, RK Varshney). Springer, pp. 489-505.
- Beyene Y, Semagn K, Crossa J, et al. (2014) Genetic gains in grain yield through genomic selection in eight biparental maize populations evaluated under managed drought stress environments in sub-Saharan Africa. *Crop Science* [In Press].
- Cairns JE, Sonder K, Zaidi PH, et al. (2012). Maize production in a changing climate: impacts, adaptation and mitigation strategies. *Advances in Agronomy* 114: 1-58.
- Cairns JE, Hellin J, Sonder K et al. (2013a) Adapting maize to climate change in sub-Saharan Africa. *Food Sec* 5:345-360.
- Cairns JE, Crossa J, Zaidi PH et al. (2013b) Identification of drought, heat and combined drought and heat tolerant donors in maize. *Crop Sci* 53:1335-1346.
- Cobb JN, DeClerck G, Greenberg A, Clark R, McCouch S (2013) Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement. *Theor. Appl. Genet.* 126: 867-887.

- Kesireddy RR (2014) Hybrid maize seed market set to double in two years. *The Economic Times*, India, 9 April 2014.
- Kumar R, Srinivas K, Sivaramane N (2013). Assessment of the maize situation, outlook and investment opportunities in India. Country Report – Regional Assessment Asia (MAIZE-CRP), National Academy of Agricultural Research Management, Hyderabad, India.
- Napasintuwong, O (2014) Seed Industry in Thailand: Market Structure, Regulations, Policies and Prospect. Paper presented at the 18th International Consortium on Applied Bioeconomy Research: Bioeconomy and Development, June 18-20, Nairobi, Kenya.
- Niblett CL, Claffin LE (1978) Corn lethal necrosis – a new virus disease of corn in Kansas. *Plant Disease Reporter* 62: 15–19.
- Geiger HH, Gordillo GA (2009) Doubled haploids in hybrid maize breeding. *Maydica* 54:485–499.
- Gerpacio RV, Pingali PL (2007) Tropical and Subtropical Maize in Asia: Production Systems, Constraints, and Research Priorities, CIMMYT, Mexico D.F.
- IPCC (2007) Fourth Assessment Report: Synthesis, published online 17 November 2007. http://www.ipcc.ch/pdf/assessment-report/ar4/syr/ar4_syr.pdf.
- Jensen SG et al. (1991) Seed transmission of maize chlorotic mottle virus. *Plant Disease* 75: 497–498.
- Ortiz R, Taba S, Tovar VHC et al. (2010) Conserving and enhancing maize genetic resources as global public goods – a perspective from CIMMYT. *Crop Sci* 50:13-28.
- Piao SL, Ciais P, Huang Y et al. (2010) The impacts of climate change on water resources and agriculture in China. *Nature* 467: 43–51.
- Prasanna BM (2012) Diversity in global maize germplasm and novel initiatives for characterization and utilization. *J Biosci* 37:843–855.
- Prasanna BM, Vasal SK, Kassahun B, Singh NN (2001) Quality Protein Maize. *Current Science* 81: 1308–1319.
- Prasanna BM, Chaikam V, Mahuku G (2012) Doubled haploid technology in maize breeding: theory and practice. Mexico D.F.: CIMMYT, 50 pages.
- Prasanna BM, Cairns J, Xu Y (2013a) Genomic tools and strategies for breeding climate resilient cereals. In: *Genomics and Breeding for Climate Resilient Crops. Vol. I. Concepts and Strategies* (ed. C Kole), Springer–Heidelberg, New York, pp. 213-239.
- Prasanna BM, Araus JL, Crossa J et al. (2013b) High-throughput and precision phenotyping in cereal breeding programs. In: Gupta PK, Varshney RK (eds) *Cereal Genomics-II*, Springer, Dordrecht, Netherlands, pp 341–374.
- Prasanna BM, Babu R, Nair S, et al. (2014) Molecular marker-assisted breeding for tropical maize improvement. In: *Genetics, Genomics and Breeding of Maize* (eds. M Bohn, J Lai, R Wusirika), Science Publishers/CRC Press, Boca Raton, USA, pp. 89-118.
- Prigge V, Sanchez C, Dhillon BS et al. (2011) Doubled haploids in tropical maize: I. Effects of inducers and source germplasm on *in vivo* haploid induction rates. *Crop Sci* 51: 1498–1506
- Prigge V, Xu X, Li L, et al. (2012) New insights into the genetics of *in vivo* induction of maternal haploids, the backbone of doubled haploid technology in maize. *Genetics* 190:781–793.
- Shiferaw B, Prasanna B, Hellin J, Banziger M (2011) Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. *Food Security* 3: 307–327.
- Shiferaw B, Tesfaye K, Kassie M, Abate T, Prasanna BM, Menkir A (2014) Managing vulnerability to drought and enhancing livelihood resilience in sub-Saharan Africa: technological, institutional and policy options. *Weather and Climate Extremes* [<http://dx.doi.org/10.1016/j.wace.2014.04.004>].
- Vasal SK (2000) The quality protein maize story. *Food Nutr. Bull.* 21:445-450.
- Wangai A et al. (2012) First report of Maize chlorotic mottle virus and Maize lethal necrosis in Kenya. *Plant Disease* 96: 1582.
- WHO (2009) Global prevalence of vitamin A deficiency in populations at risk 1995-2005. In: WHO Global Database on vitamin A deficiency, Geneva: World Health Organization, pp. 1–55.
- Xu Y, Xie CX, Wan J et al. (2012) Marker-assisted selection: strategies and examples from cereals. In: Gupta PK, Varshney RK (eds) *Cereal Genomics-II*. Springer, Dordrecht, Netherlands, pp 375–411.