

**Maize Crop Vulnerability Statement
Recommendations**
12 December 2016

Summary of key points (1 p. maximum) Maize (*Zea mays* L.) is the most important crop in the United States and one of the top three cereals in world calorie production. The United States is the world's leading exporter of maize. Because of the importance of the crop to the United States economy and the world food supply, it is essential that maize germplasm be protected, maintained, and enhanced. In this report, present germplasm activities are reviewed, status of vulnerability of the maize crop is examined, and germplasm needs are discussed.

Recommendations of the maize crop germplasm committee

1. Pathogens are under constant selection pressure to evolve greater virulence. Organisms that are currently non-pathogenic may evolve virulence. USDA-ARS must take the lead in developing monitoring systems to evaluate the development of new threats and systematic screening of maize accessions for resistance to pests and diseases deemed significant threats to US agriculture. International collaborations must be initiated to screen for resistance to diseases not yet found in the US.
2. The genetic health of the maize crop is a matter of National security. Thus, it is imperative that there is publicly available knowledge of the genetic diversity of the standing US maize crop. The genetic diversity of the standing US maize crop should be evaluated using DNA based tools. The maize crop germplasm committee recommends that such an evaluation take place as soon as possible.
3. Regeneration of currently held accessions must be expanded. Categorization must also be expanded. An estimated additional \$1,000,000 per year is needed for *Zea* genetic resources in the North Central Regional Plant Introduction Station budget.
4. Many landraces, populations, and wild relatives are at risk in situ. Most maize collections throughout the world have extremely limited budgets and these collections are at risk. NPGS must make every effort to obtain samples of these populations at risk. The system should continue acquiring public germplasm, including older inbreds, from programs that are being closed.
5. Expand the effort on enhancement of germplasm. As one step, increase funding of the GEM project from the present level to \$2.5 million per year. This project will help speed incorporation of tropical germplasm into elite U.S. material and disease resistance evaluation efforts.

1. Introduction to the crop (3 pp. maximum)

1.1 Biological features: Maize (*Zea mays mays*), is a robust, annual, C4 grass and one of the most important cereal grains in the world. It is monoecious and is naturally highly cross pollinated. Maize pollen is relatively heavy and crossing between individuals separated by more than 30m is generally low, <1% (Goggi et al. 2006; Ireland et al. 2006). However cross pollination can occur over much greater distances. Maize is grown for grain on approximately 177 million ha worldwide, with the majority being used for animal feed and the remainder consumed directly by humans or used for industrial purposes (Oklahoma State University, 2014). Specialized types of maize are grown for specialty starches, forage, popcorn, snack foods, baby ear maize, and vegetable maize. All types of maize are properly classified as *Zea mays* ssp. *mays*. (Tracy, 1993).

Maize was domesticated in central Mexico 7,000 to 10,000 years ago from the wild annual grass, teosinte (Galinat, 1988, Doebley lab citation). The annual Mexican teosintes have been classified into two subspecies (Illitis and Doebley, 1980), *Z. mays* ssp. *mexicana* and *Z. mays* ssp. *parviglumis*. The perennial teosintes are *Z. diploperennis* and *Z. perennis*. Other members of the genus include *Z. luxurians*, *Z. nicaraguensis* and three new species recently described by Sanchez et al. (2011). Recently (Silva et al., 2015) populations of *Z. luxurians* has been reported in southern Brazil. *Z. mays* ssp. *parviglumis* has been established as the direct ancestor of maize, which was likely domesticated multiple times (van Heerwaarden et al., 2011)). The main reproductive difference between the teosintes and maize is the morphology of the pistillate inflorescence (Galinat, 1988). *Zea* and the genus *Tripsacum* are the American members of the tribe *Maydeae*. The genus *Tripsacum* includes 16 species. The various *Tripsacum* species are perennial and highly variable in their morphology and adaptation. It is possible to make crosses between maize and some *Tripsacum* species usually using tools such as embryo rescue (ref?). There is some evidence that maize and *Tripsacum* have intermated in nature.

All *Zea* has 10 pairs of chromosomes (2n=20) with the exception of *Zea perennis* which is tetraploid. Some stocks have supernumerary (B) chromosomes. Triploids, tetraploids, pentaploids, and hexaploids have been produced artificially but are not used in any types of commercial maize. Aneuploid series, trisomes, and monosomes, have also been generated and used in cytogenetic studies. Certain cytogenetic stocks, such as translocations, are maintained and distributed by the Maize Genetics Stock Center (NPGS) in Urbana, Illinois.

1.2 Ecogeographical distribution Maize is a highly diverse and widely adapted species. It is grown from latitude 58° N to 40° S, from sea level to 3800 m above sea level, and from arid to very humid areas. Over 300 races of maize have been described (Hallauer, 1987; Goodman and Brown, 1988). Racial classifications generally predate molecular tools and are based mainly on morphology but data on regional adaptation, chromosome morphology, and DNA based methods have also been utilized.

1.3 Plant breeding and its products

1.3.a History: The original races found in what is now the continental United States were a small sample of worldwide maize diversity. The productive U.S. 'Corn Belt Dents' (CBD) were derived in the 19th century from crosses between the races 'Southern Dent' (SD) and 'Northern Flint' (NF). Modern CBD has a greater proportion of alleles from SD than NF. Because of the highly productive conditions in the area designated as the U.S. Corn Belt, intense on farm breeding efforts took place on CBD during the 19th early 20th centuries. Productive landrace varieties (open-pollinated varieties) were developed by seedsmen and farmers throughout the region. The open-pollinated varieties were used before the advent of hybrids and provided the basic germplasm for U.S. hybrid breeding programs.

After Shull (Shull, 1909) suggested the pure line hybrid concept, breeding efforts focused on testing the concept to provide a practical method for developing lines for use in hybrids. A key step in applying Shull's ideas to CBD maize was Jones' (?) innovation of double cross hybrids. By the 1930s, double-cross hybrids (Jones, ref?) were available for farmer use. Hybrids were rapidly accepted and by 1950 most of the U.S. Corn Belt was planted to hybrid maize. Inbred lines developed for use in the original hybrids were derived from the open-pollinated varieties.

Breeding methods to exploit the pure line-hybrid concept of maize breeding reduced the interest in the original landrace varieties. Pedigree selection among progeny of crosses of elite lines was emphasized. The long-term potential value of the landraces was not appreciated, and some were lost or inadequately sampled for storage in germplasm banks. Development of successive generations of recycled inbred lines resulted in continuing increases in yield and general performance of hybrids. Results of testing hybrids introduced during the various decades under a variety of plant density regimes indicate that over time, yield increases were due to increased tolerance to progressively higher plant densities and stress tolerance and reduced anthesis-silking interval, with essentially no per plant yield gain (Duvick, 2005).

Genetic variability within maize breeding programs was extensively discussed after the southern corn leaf blight epidemic in 1970. The southern corn leaf blight epidemic was caused by *Helminthosporium maydis* (*Y. Nisik & C. Miyake*) Shoemaker (also known as *Bipolaris maydis*, (*Y. Nisik & C. Miyake*)), Race T, which infected plants with Texas male sterile cytoplasm (Tcms). In 1970 as much as 90% of the hybrid seed available to farmers was produced with aid of Tcms. In 1970, weather favorable for disease development, a susceptible host, and a virulent pathogen were all present, and *H. maydis* Race T spread rapidly from the southeastern U.S. to the central Corn Belt. The severity and wide range of this disease in 1970 generated wide-spread concern about the genetic vulnerability of the U.S. maize crop. Although the *H. maydis* Race T epidemic was due to cytoplasmic uniformity, concern was also expressed about the possibility of excessive nuclear uniformity. (Duvick, 1972).

The 1970 *H. maydis* Race T epidemic focused attention on the genetic vulnerability of major U.S. crop species, including maize (NRC, 1972). Based on surveys of the most widely used public lines used to make commercial hybrids, it seemed that the genetic base of the U.S. maize crop was becoming more restricted over time (NRC, 1972 p. 97-118, Zuber and Darrah, 1980). B37 (26%) and B14 and its derivatives (19%), for example, were frequently included in the parentage of commercial hybrids during the 1960s (Sprague, 1971). Subsequently, B73 was one parent of 16% of the hybrid seed produced for use in 1980 (Darrah and Zuber, 1986). These data were only for lines developed by publicly supported breeding programs and did not include either recovered or new lines developed by privately supported breeding programs.

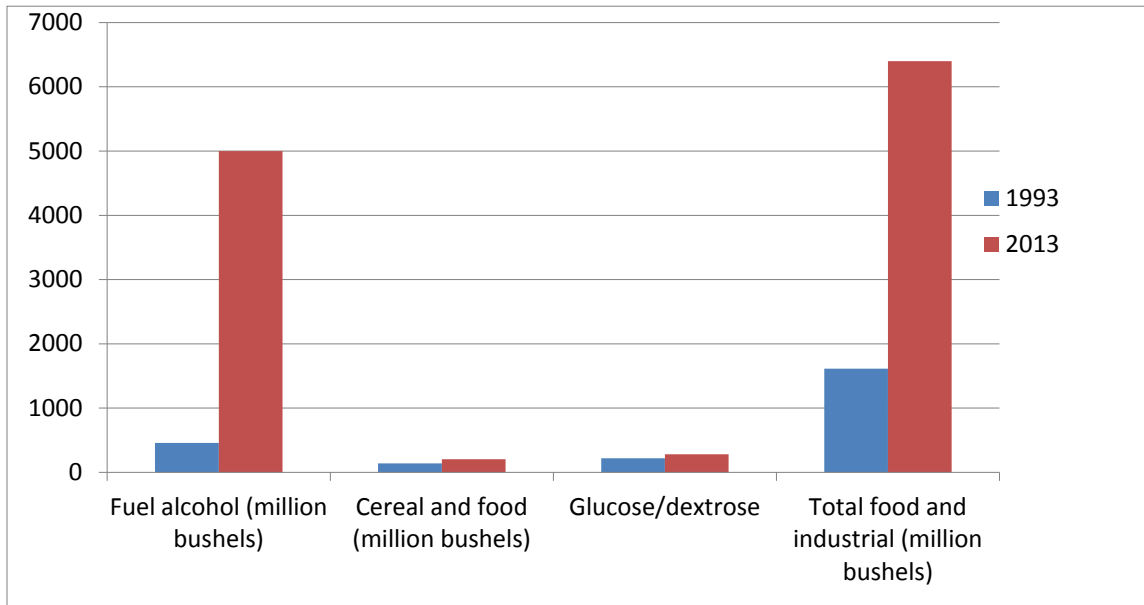
Most commercial firms have a complete product line of hybrids available to meet the customers' needs, but if a particular hybrid is superior to others, the customer will demand the best and not the second best. This can result in genetic uniformity in some areas. However, the genetic variability among hybrids increases as the production area expands because of the need to emphasize greater drought tolerance, specific pest resistance, or hybrids with different maturities in the different areas of the U.S. Corn Belt. The pedigrees among hybrids change in both the east-to-west and north-to-south directions in the United States, due to needs for adaptation to different environments. Hence, there is an automatically enforced degree of genetic diversity among hybrids between regions, within regions, and also in time (as old hybrids are replaced by new ones every few years) (Duvick, 1975, Duvick, 1984). However, no current

publically available information is available on the amount of diversity due to the geographical imperative and no historical baseline has been established.

Over the past 20 years, consolidation among elements of the seed industry has resulted in fewer companies that provide maize genetics for the US maize production areas. Competition and profit margins dictate that production costs play a major role in selection of parents and hybrid products to meet diverse customer needs. This can drive a reduction in genetic diversity offered to growers. Conversely, consolidation between companies located in geographies that span temperate and tropical climates has provided increased access to diverse sources of genetics and the opportunity to leverage such diversity in novel ways.

1.3.b Current (2014) In 2015, breeding of new CBD inbreds and hybrids is a resource and technology intensive endeavor. Doubled haploids, high throughput phenotyping, and DNA marker based tools, such as genomic selection, all mainly designed to accelerate the rate of gain and decrease cycle time, are widely used. These tools may also have the potential to accelerate the loss of diversity. Another characteristic of modern US field maize breeding programs is the near universal reliance on so-called traits. In current parlance, these are transgenes, the majority of which either confer insect resistance or resistance to widely used herbicides. These types of traits are used on 80-90% of the USA field maize production acreage. Another indicator of the narrowing of the genetic variation of the standing crop is the declining number of seed companies and universities developing improved inbreds

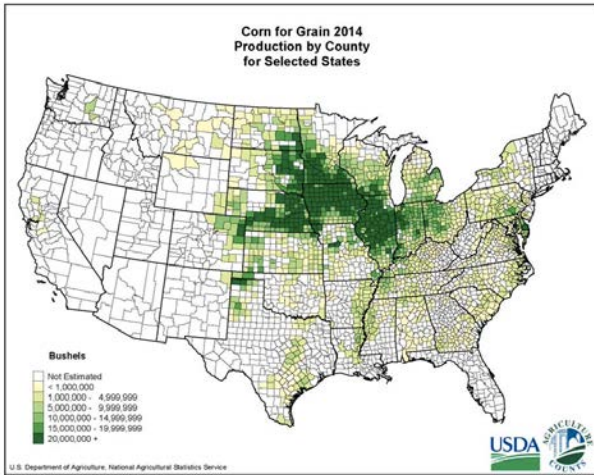
1.4 Primary crop products and their value (farmgate) Maize is an important component of the national economy and a major contributor in the export trade of agricultural products. In 2013/14, approximately 1.5 billion bushels of maize were exported. In addition to the export market, refiners process maize into products such as sweeteners, starch, alcohol, oil, and feed ingredients. Even though US exports have decreased by approximately half a billion bushels since 1994, other uses of maize have increased since 1994. Food and industrial uses have increased by nearly 300%. The largest increases were in fuel alcohol (992%), cereal and food (45%), and glucose/dextrose (28%) (National Corn Growers Association, 2014). Of the 13.9 billion bushels produced in the 2013-14 growing year, approximately 6.4 billion bushels (46%) were used for food and industrial uses and approximately 1.5 billion bushels were exported (National Corn Growers Association, 2014). Most of the rest was used for livestock feed (43%).



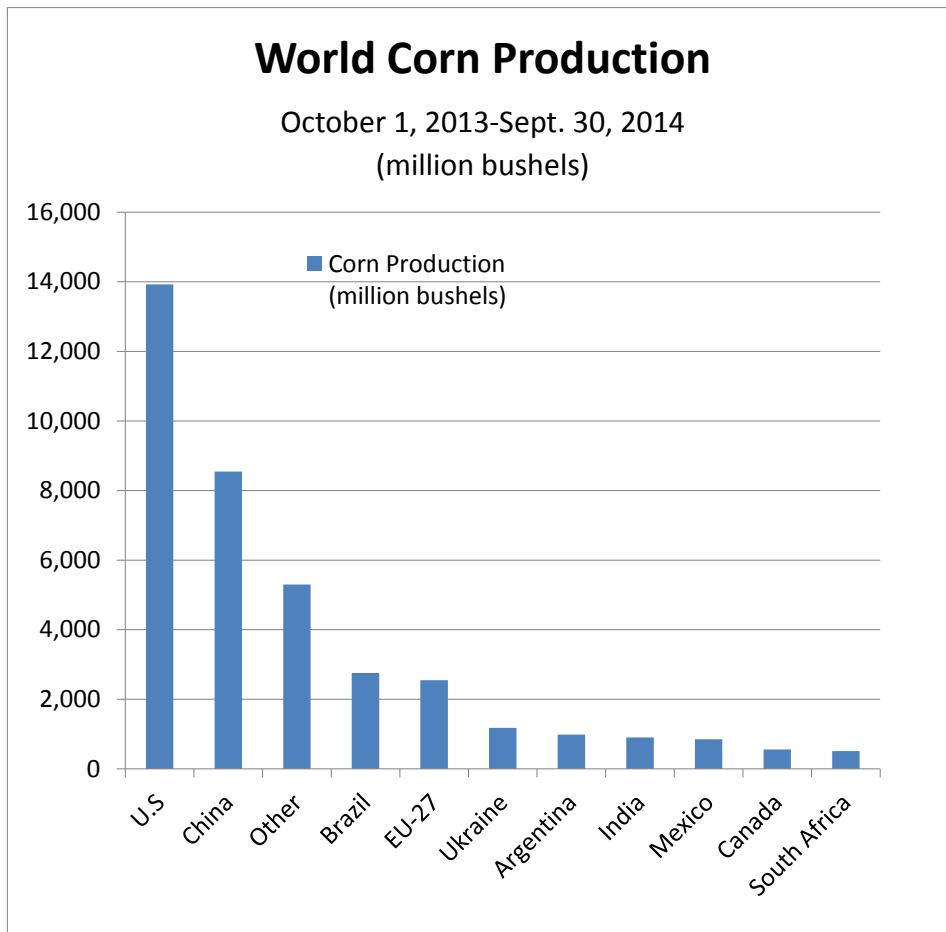
1.5 Domestic and international crop production Total U.S. maize production in the last 20 years has increased by 58% with an increase in acreage of only 30%. This was accomplished by almost doubling (1.58 times) maize yields during that time. This means an increase in yield from an average of 100.7 bu/a in 1993 to 158.8 bu/a in 2013 (National Corn Growers Association, 2014). These increases in yields were the result of a combination of plant breeding and improvements in management practices, each accounting for about 50% of the increase (Chavas, et al., 2014). Favorable climate in recent decades likely contributed as well. If these yield improvements are to continue, the germplasm base of maize must be maintained and expanded to support breeding efforts devoted to meeting new production challenges.

The United States is the leading exporter of maize in the world. Given the anticipated increased demand for maize in the Peoples Republic of China and other countries, the demand for maize in the export market will continue to increase. The continued increase in demand for maize sweeteners and fuel alcohol will also maintain strong demand. The increasing Latin American demographic in the U. S. is driving the market for corn-based foods (USDA, 2014). Given the increased need for control of soil erosion, which likely will require increased use of rotations and forage crops, the acreage planted to maize in the U.S. is unlikely to increase by large amounts in the future. Thus, if the increased demand for maize is to be met by U.S. farmers, yields on a per acre basis must continue to increase. Given the national concern about water quality, increases in nitrogen fertilizer rates are unlikely. This means more efficient exploitation of the germplasm available to breeders and the increased use of more diverse germplasm are essential.

1.5.1. U.S. (regional geography) Ranking of states



1.5.2 International ranking countries



Source: ncga.com, World of Corn, 2014

2. Urgency and extent of crop vulnerabilities and threats to food security (4 pp. maximum)

2.1. History: Dynamic breeding programs continually develop new lines and hybrids that are superior to those currently used. A few elite lines may be used extensively. Breeders continually seek new alleles or new genetic arrangements to increase stability of performance, including resistance to anticipated pests. But, the number of programs that release commercially used inbreds continues to contract. No more than a handful of public programs still develop commercially competitive inbreds and their material is not widely used. The commercial sector consists of two very large breeding programs, three or four smaller programs, and perhaps 20 independent companies that may have one or two breeders and rely heavily on inbreds and hybrids from foundation seed companies.

Commercial breeding efforts have historically concentrated on adapted elite germplasm. Goodman (1985) estimated foreign (exotic) germplasm currently accounted for less than 1% of the U.S. maize germplasm base and only about 4% of the total U.S. maize acreage. He suggested that the percentage of exotic germplasm in U.S. maize hybrids would increase very little during the next 50 years, and this prediction seems to be holding. Concern over the slow progress in introducing exotic germplasm into the U.S. hybrid maize base has prompted initiation of a program especially designed to introgress exotic germplasm into elite U.S. germplasm pools. The program, called GEM (Germplasm Enhancement of Maize) is carried out by a consortium of public breeders and seed companies (Salhuana et al., 1993/1994).

Adequate and useful genetic variation is of concern to all involved with maize germplasm, breeding, and production. The issues of genetic vulnerability have been discussed and inventories made of the materials used and available. Because of the nature of maize germplasm, breeding methods used, cultivars available for production, and the level of research activity conducted in maize, genetic variation may be available to respond to the risk of a widespread catastrophe. Access to such genetic variation is complex and governed by international, national, and regional legal constraints.

2.2 Genetic uniformity in the “standing crop” and varietal life spans Since the 1980s there have been no public estimates of genetic diversity of the standing crop. There have been studies on diversity within Corn Belt breeding germplasm, but it is unclear how those numbers translate into diversity of the standing crop. The average lifespan of a CBD hybrid is now only 5-7 years. However, some hybrids may persist 15-20 years. The lifespan of a typical commercial CBD inbred is not widely known. Lifespan

of a hybrid or its parent is dependent on stable performance in its environment over time, and the availability of new genetics offering improvement. Development of new lines that meet specific trait needs is more challenging if favorable alleles are rare, heritability is low, and/or if the environment does not consistently facilitate identification of phenotypes. Use of genomic tools to identify and select genetic variation associated with a phenotype that is difficult to evaluate can be very beneficial in a breeding program, and can accelerate progress.

The widely used tools of modern maize breeding may also accelerate the loss of diversity. Given that the typical practice of crossing elite by elite lines to develop new inbreds generally narrows the germplasm base, accelerating cycle time would be expected to accelerate the loss of alleles, without introduction of novel diversity. Likewise, while genomic selection programs can be implemented with the goal of increasing diversity, most current programs emphasize closed populations based on the most elite material so that diversity will be further narrowed.

It is clear that the ability to successfully produce high numbers of doubled haploids differs among germplasm sources. Thus it appears that there are genes that increase success. If this is the case, exclusive reliance on the doubled haploid method would inevitably narrow the genetic base for those chromosome segments linked to genes that increase the rate of doubled haploid production. The widespread deployment of the same transgenes also increases a form of genetic uniformity with respect to the type of risk tolerance conferred by the construct. It is likely, especially in locations where cropping seasons overlap and pest population turnover is high, that a widely deployed gene could lead to a situation similar to what Tcms did in the early 1970s, resulting in a vulnerability that could have widespread impacts.

There is urgent need for an evaluation of the genetic diversity of the standing US maize crop using DNA based tools. There's a general sense that genetic diversity of the standing crop has declined. Some dispute this, but there is no data to settle the question. The question is more than academic as maize is the most important crop in the US. Since the 1980s there have been no public estimates of genetic diversity of the standing crop. Surveys of the kind conducted by Darrah and Zuber (1986), Duvick (1981a, 1981b, 1984, Goodman (1985, 1998) and Smith et al (1988), to establish the amount and sources of diversity and the pace of changes in diversity in U.S. maize hybrids and breeding pools would also be useful. An approach which utilizes genomic tools and marker technologies to assess the nature and extent of diversity grown across US maize production regions is needed. Use of markers associated with gene blocks responsible for abiotic or biotic stress responses would be very valuable, as well as for general agronomic performance. Resistance to such a study seems primarily due to

concern over the many contexts and agendas for which such information could be used or abused, and the level of scientific rigor that would be employed in analysis and interpretation.

2.3 Threats of genetic erosion in situ

Across tropical maize production areas, local landrace populations are rapidly being displaced by commercial hybrids, and the knowledge base for their use is disappearing as well. Guatemalan maize populations are once example of desirable germplasm to access. However, this is not an appropriate time, politically, to collect in Guatemala. Adequate samples of 100-150 teosinte accessions from Mexico and Guatemala are lacking. Many of these have been collected by the national program (INIFAP) in Mexico but are not readily available to U.S. users, and their viability status is unknown. The NPGS should offer to back up these teosinte holdings. More recent Mexican teosinte collections made by Ross-Ibarra, Ellis, and Taba are backed up by the NPGS. Although the NPGS *Zea* collection includes relatively comprehensive holdings of maize land races from North America, and from certain Latin American countries (e.g., Mexico, Peru), land races from the following regions should be acquired: Bolivia, Brazil, Ecuador, Venezuela, Costa Rica, Guatemala, and Panama, certain Caribbean locations (e.g., Coastal Tropical Flint from Dominica), and the Amazon lowlands. Furthermore, accessions designated as "typical" representatives of Latin American land races in the maize racial bulletins should be acquired. The NCRPIS has these, but most have not been regenerated, and larger samples are needed.

The NPGS collection includes representative holdings of the maize of Europe and mid-latitude Asia. Certain ecogeographical regions in Asia and Africa are poorly represented in the NPGS collection, including the Himalayan foothills, the Philippines, former Portuguese colonies/enclaves in Africa (e.g., Mozambique), India (e.g., Goa), and Southeast Asia (e.g., Macao). As quarantine regulations allow, NPGS will try to acquire these land races via CIMMYT, other germplasm banks (e.g., the SADCC bank in Lusaka, Zambia), or by field collection. The depth and breadth of these future acquisitions will take into account the holdings at CIMMYT, and the activities of its maize germplasm bank and of other banks. But there is much that the CIMMYT bank doesn't hold, even from Mexico. Many of the national banks in Latin America are underfunded, many of which have lower budgets now than when they were established in the 1950s, and the viability of their holdings may be questionable.

The fates of the 25,000 or so accessions increased at ICA in Colombia, INIFAP in Mexico, and PCIM in Peru (with several millions of dollars from USDA-ARS) during 1984-1999? Is unclear. Initially, these increases were sent to the PI Station in Ames, with a

sample kept in cold storage at the participating bank. After 1991, samples were sent to both CIMMYT and Ft. Collins, with a sample retained at the originating bank. The status of these accessions needs to be made clear. This regeneration project was separate from the concurrent LAMP project (Latin American Maize project) for which samples are generally available (Salhuana, Sevilla, and Eberhart, 1997).

Clearly, there is much demand from both the breeding and genetics communities for foreign, elite (especially tropical) materials (inbreds and hybrids), but there has been little effort to collect and maintain these, even when they have been readily available.

In response to the user community's expressed needs, NPGS will acquire the following, more elite germplasm for distribution: 1) additional inbred lines from discontinued U.S. public maize breeding programs, especially historically-important U.S. "southern breeders' lines." The U.S. inbred lines are among the most frequently requested accessions in the NPGS collection, 2) selected tropical inbred lines from CIMMYT and the University of Hawaii program, and selected tropical hybrids (public and private), especially derived from Caribbean germplasm, and 3) selected U.S. popcorn and sweet maize germplasm.

The *Zea* curator will continue to assign P.I. numbers to LAMP and other Latin American accessions entering the NLGRP, while concurrently scanning the NSSL/NLGRP and CIMMYT inventories for germplasm needed for the NPGS collection. Bit by bit, sub-samples of *Zea* accessions held at the NLGRP but not at the NCRPIS will be secured; concurrently, the unduplicated accessions at the NCRPIS will be backed-up at NSSL.

Additional monies are required for 1) clerical assistance to inventory and process newly acquired accessions; ii) additional plantings in quarantine nurseries; iii) importing and exchanging germplasm. In addition, there has been a need for a short day, cool temperature, frost-free environment for regenerating many of the high elevation maize collections since the 1960s. This need was highlighted by the 1991 NAS-NRC report on the U.S. National Plant Germplasm System. Collaborations with international entities may be necessary to provide access to such an environment, and should be facilitated.

2.4 Current and emerging biotic, abiotic, production, dietary, and accessibility threats and needs

2.4.1 Biotic (diseases, insects)

2.4.2. Abiotic (environmental extremes, climate change)

- As long as there is genetic variability and these changes happen at a pace that matches breeding, loss can be mitigated. Diversity in elite adapted germplasm from around the world can meet these challenges. A more difficult problem is breeding for more variable conditions and more severe weather events.
 - Climate extremes enable pathogens and pests to establish in new regions, where varieties in use may not have the necessary resistance.
 - Water-limiting conditions occur sporadically in production areas, but are increasing in frequency and intensity.

2.4.3. Production/demand (inability to meet market and population growth demands)

2.4.4. Dietary (inability to meet key nutritional requirements)

2.4.5. Accessibility (inability to gain access to needed plant genetic resources because of phytosanitary/quarantine issues, inadequate budgets, management capacities or legal and bureaucratic restrictions)

3. Status of plant genetic resources in the NPGS available for reducing genetic vulnerabilities (5 pp. maximum)

3.1 Germplasm collections and in situ reserves

3.1.1 North Central Regional Plant Introduction Station Holdings, Acquisitions, Maintenance, and Regeneration

3.1.2 The Maize Genetics Stock Center Holdings, Acquisitions, Maintenance, and Regeneration

3.2 Associated information

3.2.1 Genebank and/or crop-specific web site(s)

The North Central Regional Plant Introduction Station's repository homepage:

http://www.ars.usda.gov/main/site_main.htm?modecode=50-30-10-00

The Maize Genetic Stocks Center's homepage:

<http://maizecoop.cropsci.uiuc.edu/>

3.2.2 Passport information

Passport information details accession provenance, and is essential to document the origins of plant genetic resources. The National Plant Germplasm System utilizes the FAO/BIOVERSITY Multi-Crop Passport Descriptors (MCPD V.2), developed to facilitate germplasm passport information exchange. Details about the descriptor lists can be found at <http://www.bioversityinternational.org/e-library/publications/detail/faobioversity-multi-crop-passport-descriptors-v2-mcpd-v2/>. A document describing how GRIN-Global handles these descriptors can be found at http://www.ars-grin.gov/npgs/gringlobal/docs/gg_multi_crop_passport_descriptors_MCPD.pdf. Appendix Table xx lists these descriptors.

3.2.3 Genotypic characterization data

Section 3.2.3 Updated 12/12/16

Genotypic characterization of maize lines has come a very long way in the past 10 years. Previously, scant, low-resolution isozyme and SSR were all that were available for a small number of lines. MaizeGDB (<http://www.maizegdb.org>) and the Maize Genetics Cooperation Stock Center (<http://maizecoop.cropsci.uiuc.edu/>) are the primary, long-term entry points to a wealth of high resolution genotypic information on thousands of lines. The vast majority of genotypic information for maize was generated by either whole genome sequencing, or Genotyping By Sequencing (GBS, Elshire et al 2011 PMID 21573248). The GBS approach to genotyping pairs infrequent restriction enzyme cutting with Next Generation Sequencing to deliver high-resolution genotyping at a very low cost. MaizeGDB provides access to a large collection of raw genotyping data as well as analysis tools at www.maizegdb.org/diversity which allow maize researchers to leverage maize diversity. A large collection of ~2500 maize inbreds known as the Ames diversity panel was genotyped by GBS for 680,000 SNP loci (Romay et al PMID 23759205). Data from the Ames diversity panel was used to develop the TYPsimselector tool (<http://www.maizegdb.org/TYPsimSelector>) which calculates the degree of relatedness between lines in the panel. At the individual locus level, the SNP diversity viewer tool (<http://www.maizegdb.org/snpdiversity>), has been developed by MaizeGDB to allow researchers to view SNPs at a locus for a collection of lines to potentially connect causal SNPs to phenotypes. Taken together, these two tools, as well as others at <http://www.maizegdb.org/diversity> allow maize breeders to evaluate and select germplasm for its potential usefulness to their breeding programs.

3.2.4 Phenotypic evaluation data

Phenotypic descriptor information presented in GRIN-Global is categorized as chemical (oil, protein, starch); disease and insect resistance response; growth (plant height, vigor), plant, ear, and kernel morphological traits, phenology (flowering and maturity data); production (heterotic group, 1000 kernel weight); taxonomic (primary and secondary race); digital images of ears and kernels; and core subset composition.

Phenotypic data is collected by the maize curatorial staff as it is grown for regeneration. Much information is lacking as it is not feasible to evaluate germplasm for disease or insect resistance, for example, or stress response. Comprehensive evaluations for response to economically important disease and insect threats are needed; such evaluations need to be conducted under conditions appropriate for the adaptation of the germplasm and the pathogen or insect. Digital image information is very useful to researchers looking for specific ear or kernel traits. Additional resources are needed to process and load a backlog of images that have been captured.

3.3 Plant genetic resource research associated with the NPGS

3.3.1 Goals and emphases

3.3.2 Significant accomplishments

3.4 Curatorial, managerial and research capacities and tools

3.4.1 Staffing

3.4.2 Facilities and equipment

The genebank maintains seed samples of the active collection in 4 C, 25% RH storage. Original seed samples are stored in a -18 C walk-in freezer. The station serves multiple crop curation projects and has a wide array of equipment to support summer field seed increases and growouts, seed drying, and storage. Seed processing equipment appropriate for ensuring purity of the samples includes shellers, aspirators for seed cleaning, and seed treaters. Greenhouse space is limited, and generally used to increase teosinte accessions or for critical increases of those accessions with very limited seed amounts.

The digital imaging laboratory is equipped with scanners, computers, and specialized software. Barcoded tags and ears and kernels are scanned; the software captures images with embedded metadata and transfers them to a file server for later processing. The maize curation lab is designed to support workflows to capture other information associated with an accession prior to shelling and storage.

Germinators are used for viability testing prior to storing seed increases, and at periodic intervals. Priorities for determining which accessions need to have seed increases are determined by 1) availability, or seed supply, and 2) germination rates.

3.5 Fiscal and operational resources

4. Other genetic resource capacities (germplasm collections, in situ reserves, specialized genetic/genomic stocks, associated information, research and managerial capacities and tools, and industry/technical specialists/organizations) (2 pp. maximum)

5. Prospects and future developments (2 pp. maximum)

It is of critical importance to continue to acquire unique germplasm from public research programs in order to provide genetic diversity to meet current and future challenges. As funding for public breeding and research programs that develop germplasm has declined and scientists retired, germplasm has suffered a variety of fates other than becoming publicly available. The value of these genetic resources may be dismissed and they may be thoughtlessly disposed of, or the institutions holding them may be either uncertain of their value or greatly over-estimate it, and attempt to sell or exclusively license germplasm that was developed using public resources.

It is of critical importance to continue to acquire unique germplasm from international sources. This is increasingly challenging due to the impact of the ITPGRFA, and more recently, the Nagoya Protocol. The Standard Material Transfer Agreement (SMTA) associated with the treaty is the only type of SMTA restriction that the NPGS will allow to be associated with the maize collection. Because of the terms of the SMTA, many private and public sector institutions cannot utilize germplasm that is associated with the SMTA, therefore utilization is limited.

Phytosanitary restrictions also make acquisition and exchange of plant genetic resources challenging, while demand for them continues to escalate.

Sufficient funding to ensure genebank operations and genetic resource availability are needed, along with training of the next generation of scientist devoted to understanding the value of and maintaining precious germplasm resources.

6.

7. **Appendices (number and lengths at the CGC's discretion)**