Project Number:	NC-007
Project Title:	Conservation, Management, Enhancement and Utilization of Plant Genetic Resources
Period Covered:	10/2019 through 09/2020
Date of this Report:	December 16, 2020
Annual Meeting Dates:	June 29-30, 2020 (virtual)
Participants:	https://www.nimss.org/projects/view/participant_list/18364
Minutes:	https://www.nimss.org/seas/minutes/51591

Accomplishments and Impacts:

Plant Introduction Research Unit and the North Central Regional Plant Introduction Station (NCRPIS):

Obj 1: Development and utilization of diverse plant genetic resource (PGR) collections (germplasm) are essential, valuable sources of genetic diversity for use in scientific research, education, and crop improvement programs in the U.S. and internationally. The NCRPIS is a key element of the National Plant Germplasm System (NPGS), specializing in heterozygous, heterogenous, outcrossing crops and their wild relatives of maize, vegetables, oilseeds, woody and herbaceous ornamentals, and a wide variety of crops such as amaranth, perilla, quinoa and more. For the past 72 years, the crop collections important to the North Central Region (NCR) have been supported through the partnerships with Hatch Multi-State Project NC-007, the USDA-Agricultural Research Service, the State Agricultural Experiment Stations of the NCR, and Iowa State University (ISU). These resources are used to improve crop production genetics and technologies to address challenges related to climate instability, changing abiotic and biotic stress pressures, a to enhance the health and nutrition of society, and demands for bioenergy resources.

Curatorial personnel acquire, maintain and conserve, phenotypically evaluate, genetically characterize, document, and distribute plant genetic resources and associated information. Collection development is a complex process, and depends on access to resources controlled by state, national, international, and both public and private entities. Identification of gaps in PGR collection representation is necessary in order to develop acquisition priorities, and gaps are addressed via exploration and/or exchange with other collections.

Obj 2, 4, 5: Germplasm Acquisition, Maintenance and Distribution: The August derecho severely damaged nursery plantings and is responsible for the need to replace the roof of the large 4C cold storage building. Temporary repairs were made to ensure preservation conditions and roof replacement has been contracted by Iowa State University.

North Central Regional Plant Introduction Station (NCRPIS) collection currently holds are 54,202 accessions compared to 54,774 in FY2019). The reduced number reflects the inactivation of the inviable 1200 maize accession Galinat collection; this collection dated to the 1950-1960. Ames genebank personnel were allowed to fulfill germplasm requests during the pandemic with appropriate safety practices. Distribution demand was reduced due to challenges associated with

the pandemic and were approximately 70% of those in the FY2019 period. From 2015-2019 more than 3,000 orders were received from researchers of the 12 Land Grant institutions of the NCR, who have received nearly 138,000 seed distributions, 30,222 from the NCRPIS.

Collection availability overall is 79% compared to 76% in 2019 More than 1,840 seed health tests were performed to comply with phytosanitary import requirements associated with international maize and sunflower seed requests. All Cucurbita seedlings were ELISA tested prior to transplanting to the field to ensure that they were free of squash mosaic virus. Field and greenhouse inspections were conducted to ensure that all plantings were free of diseases, and samples were cultured of those specimens with observable symptoms. Approximately 6,287 accessions were tested for viability as part of routine maintenance activities to ensure the quality of the collections; about 38% of the entire collection is in need of periodic viability testing. The viability team has adopted a smaller sample/rep, multiple rep testing strategy to rapidly id seed lots that potentially have low viability and require more testing; this has greatly increased our testing capacity. Backup seed lots were sent of 1,564 accessions to the National Laboratory for Genetic Resource Preservation (NLGRP) in Ft. Collins, CO, achieving 82% back up. More than 2,000 accessions were sent to the Global Seed Vault in Svalbard, Norway for backup as well.

Approximately 1,070 accessions were grown for seed increase in Ames across all taxa, including perennials that will be maintained until seed increase goals are achieved, about a 20% reduction in 2019 plantings due to pandemic-related labor concerns. Tropical maize increases were again sent to a commercial nursery provider in Mexico due to lack of temperate adaptation in fall of 2019 and 2020, based on past excellent quality seed return, and 25 highland tropical maize accessions with older, low viability seed were sent to CIMMYT for a second contract increase at their high altitude Tolucca site.

Obj 3: Evaluation and Characterization: Observations for about 8,370 accessions and 2,860 images were loaded to the GRIN-Global database. Evaluation of the *Brassica rapa* collection for winter/spring type determination has progressed, and the information obtained facilitates regeneration management decisions and practices. Optical seed sorters continue to be used to improve seed lots of maize prior to planting, and also by ISU campus researchers for sorghum, millet, and soybeans.

Obj 4: Software Development: Our development staff released multiple enhancements to various wizards used by genebank personnel to manage workflows and seamlessly integrate information in GRIN-Global, and new Curator Tool versions. These products support management of associated information, curatorial workflows, and public access to information associated with germplasm that facilitates their use. The Curator Tool and Order Wizard enhancements must be coordinated with changes made to the public GRIN-Global website's functionality.

Obj 5: Tours were cancelled due to the pandemic. Professional findings were presented at scientific and virtually post-January to educators and other stakeholders. Our curators outreach activities were directed to classrooms and interested public groups, such as the Iowa Bee Keepers and 4-H clubs. No public field day was held in 2020.

Accomplishments & Impacts– State Reports:

Illinois (Sacks)

Sacks lab: Miscanthus is of interest as a bioenergy crop; Universilty of Illinois research has focused on overwintering trials in environments which can provide a range of exposures to cold conditions and elucidating the genetic structure of populations of *Miscanthus sacchariflorus* and *Miscanthus sinensis*. Previous population structure studies provided insight on distinct genetic clusters from three regions of Japan, the Koreas, and multiple areas of China. Seed of 163 accessions of *M. sacchiflorus* collected in 2012 in Eastern Russia have been increased abd a oirtuib will be shared with the NPGS. They provide a wider spectrum of genetic resources in combination with Southern and Central Japanese sources. Multi-environment testing with these and sources from various regions of China and indicates that Southern Japanese germplasm sources tended to be less cold tolerant than Central Japanese sources and were higher yielding.

Riggins lab: Phytochemical diversity among the USDA amaranth collection offers insights on plant stress response, enhanced nutrition, and genetic improvement. Amaranth betalain pigments offer sources of natural food colorants, and amaranth studies offer insights for management of herbicide-resistant weeds.

Indiana (Hoagland)

The **Hoagland lab** supports the goals of a NIFA-OREI program aimed at addressing the critical needs of organic farmers by developing novel colored carrots with improved disease and nematode resistance, weed competitiveness and nutritional quality and flavor. The lab is working to improve understanding of how soil quality can influence genotype performance and selection; identify relationships between carrot genotypes and beneficial microbes with long-term goal of introducing selection for beneficial plant-microbial relationships into breeding programs. Results indicate that endophytes, microbes that spend at least part of their lifecycle living inside plants and may be seed-transmitted, can suppress *Alternaria dauci* and improve carrot productivity.
Beneficial activity varies among carrot genotypes. Soil health has the greatest effect on fungal community structure; a resistant genotype was most responsible to differences in soil health.

Carrots are known as 'nitrogen scavenging crops; results of experiments indicate that carrot genotypes differ in their potential to stimulate microbially0mediated decomposition of organic material in soil to obtain nitrogen, and this is correlated with shifts in soil microbiomes.

Iowa (Lübberstedt)

Lübberstedt lab: Doubled haploid (DH) lines are completely homozygous, excellent genetic research resources, and commonly used in commercial breeding programs. Producing DH lines is a complicated process. A simplified alternative for producing DH lines was explored, which focuses on spontaneous haploid genome doubling (SHGD). Research focuses on determining genomic regions for segregation distortion in the haploid doubling process, which is indicative of SHGD. SHGD advantages include increased pollen production and more kernels/ear produced on the haploid plant that is undergoing the doubling process to produce DH lines. Genetic variation exists for female donor inducibility, and for genome doubling of haploids. Male haploid fertility and seed set are key traits contributing to spontaneous genome doubling. Of 102 expired PVP lines screened, only five had high spontaneous doubling rates, and only three greater than 50%; female fertility is not an issue. Use of a mapping population enabled identification of three QTL related to SHGD. RNA-Seq was conducted to identify putative candidate genes, and a transcript identified

with the qshgd1 region, chromosome 5. This has implications for a simplified alternative for doubled haploid production, use of direct seeding of haploids to spontaneously generate doubled haploid lines rather than through artificial doubling procedures. In previous studies, no yield penalty was observed in the presence of the major SHGD QTL Testcross results indicate that SHGD genes will not affect the selection of higher performing lines, and that DH lines with SHGD genes are similar in performance to DH lines produced by artificial genome doubling (using colchicine) and to lines produced traditionally using single seed descent methods.

A funded USDA OREI program supports use of doubled haploid (DH) technology in organic maize breeding. Key for using DH technology in organic maize breeding is the ability to double haploid genomes based on a genetic mechanism rather than artificial genome doubling based on toxic chemicals such as colchicine. The major QTL for spontaneous haploid genome doubling (SHGD) will be incorporated in different genetic backgrounds including sweet corn. First results look promising: success rates for obtaining DH lines from BS39 were higher using SHGD compared to artificial colchicine treatment-based DH line development.

The **Yu lab** exploited the power of genomic prediction for eight maize traits related to the shoot apical meristem. Their findings suggest that double selection considering both prediction and reliability can be implemented in choosing selection candidates for phenotyping when exploring new diversity is desired. In this case, individuals with less extreme predicted values and moderate reliability values can be considered. This study expanded upon previous work, the turbocharging gene banks via genomic prediction from the macrophenotypes into the microphenotypic space.

Kansas (Stamm)
Kansas State University has contributed to the advancement of the NPGS through utilization of germplasm stored within the system and placement of germplasm within the system for future exploitation. Specifically, the germplasm stored at the NCRPIS in Ames, IA is a critical resource for breeding canola-quality winter cultivars for the environments of the southern Great Plains.
Weather, drought, and depressed commodity prices have slowed industry investment, but expectations are high for the region. Producers want to grow canola if profitable. Winter canola acres have decreased from nearly 330,000 in 2013/2014 to about 25,000 acres in 2019/2020. Kansas had record highest precipitation averages in May 2019 in Kansas in the past 125 years. Recent winter canola variety releases have unique performance attributes including incorporation of herbicide resistance to Roundup Ready and/or sulfonylurea residual tolerance. KS4719 offers improved winter hardiness and reduced incidence of crown and root rot. KSU is the sole developer of TruFlex™ Roundup Ready winter canola hybrid parent lines, which involved conversion of male sterile lines. Seed sales of cultivars with KSU genetics have impacted nearly 40,000 winter canola acres in each of the past four years.

New cultivars continue to have a significant impact on the expansion of the southern Great Plains canola industry. Roughly 50 percent of the winter canola acres are planted to cultivars with a Kansas State University genetic component. Kansas State released winter canola cultivars are licensed to regional and national seed companies and royalties generated support further research and development. Producers continue to employ these cultivars on their farms, improving the overall sustainability and profitability of their cropping systems through crop rotation and diversification.

Hybrid parent line development now utilizes the OGURA system licensed from INRA-France, with cytoplasmic male sterility and restorer genes developed from radish; yield trials and combining ability studies are in progress.

Sorghum germplasm has been collected from across the globe for use in crop improvement research. Specifically, up to 800 genotypes were screened to identify herbicide-tolerant traits. Four genotypes exhibiting natural tolerance to carotenoid biosynthesis-inhibitors were identified and are being characterized to understand the mechanism of tolerance. The results from this research identified genotypes with the agronomically important traits (i.e., herbicide tolerance) for use in sorghum improvement by introgression of the trait into elite backgrounds. Availability of herbicide-tolerant technology is valuable for weed management, which is a challenging constraint in grain sorghum production throughout the U.S.

Michigan (Iezzoni)

Soybean plant introductions from the USDA collection (500) were screened to identify sources of resistance to *Pythium irregulare* and *Phytophthora sansomeana* which cause soy seedling diseases, seed rot or seedling rot, and to Sclerotinia stem rot. Resistance sources to these pathogens were identified and are being used as breeding parents to develop resistant varieties. The program continues to use aphid and soybean cyst nematode resistance genes that have been transferred to elite germplasm from USDA germplasm.

Multi-disciplinary cucurbit research (watermelon, melon, cucumber, and squash), partially supported by the USDA-NIFA-SCRI CuCap Project, utilizes germplasm resources for disease resistance improvement. QTLs for disease resistance and markers have been developed and breeding programs for several important diseases that threaten production were advanced by project participants. These include Fusarium wilt, gummy stem blight, powdery mildew, fruit rot caused by Phytophthora, virus diseases, and downy mildew. Plant introductions in the core collection exhibited variation for resistance response to P. capsica.

Species related to cultivated potato are being used to create diploid self-compatible hybrids (*S. chacoense*), for bacterial wilt resistance (*S. commersonii*), and for a multi-species recurrent selection population to select for self-compatibility.

Maize germplasm from a variety of sources supports phenotype-to-genotype and crop modeling studied of cell, leaf, plant, and canopy-level traits, and for tar spot disease resistance screening. Data capture for plant and canopy morphology and composition traits is drone-based. Public germplasm resources are being screened and developed for tar spot resistance, as part of the Great Lakes Tar Spot Initiative, a multi-state USDA-funded project.

Quantitative trait loci were identified for important plant and flower traits in petunia using a high-density linkage map and an interspecific recombinant inbred population derived from *Petunia integrifolia* and *P. axillaris*.

A USDA-NIFA supported program has supported work to identify markers for high salinity tolerance in octoploid strawberry. A wild source of salinity tolerance collected from a lighthouse island in California was used to develop a genetic mapping population. About 9% of the mapping population individuals exhibit high salinity tolerance. Two putative genomic regions have been identified that are associated with this trait.

The molecular mechanisms underlying dormancy release and the induction of flowering in woody plants are poorly understood and complex. Early crop losses of many fruit crops are a result of freeze damage, subsequent to dormancy breaking and opening of flower buds, and to insufficient chilling required to induce flowering. Two major loci have been shown to control bloom time in all Prunus crops studied, determining how much chilling is needed to break dormancy (chromosome 1) and heat and chilling requirements (chromosome 4). Breeding has utilized sour cherry genetic resources from Russia (Tamaris) and Hungary (Ujfeherto) to develop new varieties with later bloom times, reducing risk of crop loss to freeze damage. .

Plants of a valuable highbush blueberry mutant, Mu-legacy, show dwarfing, earlier flower bud formation in one to two-year-old plants, and can flower under non-chilling conditions for an extended period of time. Research found that uncreased expression of a response regulator gene (VcRR2) promotes a homolog of VcGA1; increased expressed of these function in cytokinin responses and gibberellin synthesis, resulting in reduced plant height and enhanced flower bud formation in Mu-legacy plants. Differentially expressed transcripts of 17 genes of five groups of hormones were identified in non-chilled flower buds of mutant and non-mutant plants, of which 22 were chilling responsive. VcRR2 has an important role in induction of hormones that promote flowering in woody plants.

Missouri (Flint-Garcia)

Maize: The **Flint-Garcia lab** (USDA-ARS in Columbia MO) continues to investigate teosinte (*Zea mays* ssp *parviglumis*) and maize landraces as a source of novel and useful alleles to improve maize for a number of agronomic traits. Previous research germplasm resources include the 'Teosinte NILs' population, which consists of 880 near-isogenic lines of the backcross four generation, all of which have approximately 4% of their genome segments derived from the teosinte parent, and the Nested Association Mapping (NAM) recombinant inbred lines. In addition, they have created a new resource called the Zea Synthetic which contains the 27 maize inbred lines (25 NAM founders + B73+Mo17) and 11 *Zea parviglumis* accessions (the same as the Teosinte NILs), such that the expected parentage of this population is 38% B73, 2% each other maize inbred, and 12% teosinte. This population has been random mated 7 times prior to depositing at NCRPIS (Ames 32909). Approximately 2000 doubled haploid lines were derived from the Zea Synthetic and will be deposited with the Maize Genetics Stock Center in winter 2019-20.

A collaborative breeding project for food corn quality traits evaluated landraces per se and as population hybrids for a large number of traits. Landraces can be viewed as similar to heirloom varieties and provide genes and traits that were eliminated from modern maize breeding pools. There has been little breeding effort in the past for non-sweet, non-popcorn food corn, and we have little knowledge about flavor components. Wide germplasm types and target food types are being investigated, ranging from green corn to popcorn to masa-based foods. Initially 100 southeastern US and temperate heirlooms were evaluated, and currently 12 populations are being used in an S1 selection project to improve basic agronomic traits. Landraces and derived crosses are being evaluated for adaptation, agronomic traits, starch/oil/protein content, flavor and aroma compounds, and their applications for use in tortillas, popcorn, and other culinary uses.

Nebraska
A majority of the NPGS germplasm used by scientists in Nebraska was of the *Panicoideae* sub-family of the family *Poaceae*. This includes sorghum, maize, pearl millet, proso millet, foxtail millet, finger millet, etc. Sorghum, maize and proso millet in **Schanable's lab** were used for various projects related to GWAS, image-based high throughput phenotyping and genome sequencing. At **Santra's lab**, the entire set of proso millet germplasm was used for research projects related to proso millet breeding and genomics and was evaluated in the field for morpho-agronomic traits. Ninety-six genotypes were sequenced for population studies and SNP marker development. A sub-set of genotypes was also used for UAV imaging-based high-throughput phenotyping. Selected genotypes with useful traits were used in crossing and the resulting breeding populations are at various stages of variety development. In **Benson's lab**, the millet lines were used to compare the effects of waxy starches from maize, sorghum, millet, and wheat on the gut microbiome. Data showed similar effects of waxy starch across most of these cereal grains with the greatest effect size observed for maize and sorghum. In **Sattler's lab**, sorghum germplasm and genetics stocks were used for EMS mutation followed by sequencing, lines were grown under greenhouse and field conditions, and a second allele of brown midrib 30 (bmr30) was isolated and the gene's identity at the locus.

Soybean lines were used to evaluate response to stalk pathogens in the greenhouse, and assessed for senescence traits (stay-green) and dhurrin levels in greenhouse and field. Other sets of soybean germplasm were used for disease research, testing pathogenicity of various *Pseudomonas syringae pv. glycinea*, *Phytophthora sojae*, and *Heterodera glycines* in greenhouse and field. Strawberry lines were used to complete a 40+ species phylogenetic analysis of the origins of a freezing tolerance mechanism. Various legume species were used to study response of the legume's symbiotic partner and another closely related, but not symbiotic, bacterium to the peptides (short proteins) in vivo. Detection of functionalities in the non-symbiotic bacterium will be used to modify it, enabling it to become a symbiotic partner for the legume. An undergraduate research project used *Brassica rapa* cv. torch to develop a simple and rapid method for enriching mitochondria and chloroplasts DNA; mitochondrial genome enrichment was 100-fold for Brassica.

Several journal publications are expected to result from these investigations.

North Dakota (Johnson)
Commercial production of industrial hemp (*Cannabis sativa* L.) continues in North Dakota and is primarily associated with ongoing grain production since 2016 due to good local grain prices and

crop performance, a growing interest in fiber production tempered by low feedstock value, and a rapid expansion in cannabinoid production fueled by high profit potential in 2019 and 2020.

Initial crop production research for the new/old crop industrial hemp at North Dakota State Univ. was conducted at the Langdon Research Extension Center (REC) in northeastern North Dakota and focused on varietal performance trials to guide varietal selection for growers to attain high grain yield, crop value, and profit. Hemp variety performance trials expanded westward across the state to other RECs including Carrington, Dickinson, Hettinger, and Prosper in 2019 with further expansion to include Williston in northwestern, ND, in 2020. Grain yield performance among varieties varies depending on location and is associated with growing season rainfall which becomes progressively reduced as location becomes more western in the state. Grain yield performance is typically 50 to 60% or greater for high yielding compared with low yielding varieties and accentuates the importance of growers having varietal yield performance information from Research Extension Center trials in the vicinity of their farms.

Hemp agronomy production research pertaining to best management practices has expanded in scope to include chemical and biological seed treatment studies, planting date and harvest date studies, herbicide screening for phytotoxicity, and crop physical injury studies (simulated hail damage).

Perennial flax (*Linum lewisii* Pursh.) field trials were initiated in spring of 2020 to evaluate stand establishment and biological weed control in organic production systems in western Minnesota and east central North Dakota at the Carrington REC. Initial results identified challenges in obtaining successful stand establishment and the sensitivity of perennial flax to soil crusting, soil moisture limitations, and seeding depth; and a delayed and extended emergence period followed by slow plant development. Once established advantages of perennial flax compared with annual grain crops include: higher grain value, moderate yields with potential for two harvests per season, stand duration potential for multiple years perhaps as many as five depending on crop husbandry, and a readably available market with attractive prices.

Ohio (Representative Jourdan retired) A new representative is being appointed.

South Dakota (Caffe Treml)

Researchers at South Dakota State University participated in the NC-7 Hatch Multi-state project by characterizing and utilizing plant genetic resources for crop improvement. Genetic resources were characterized for traits associated with production challenges in South Dakota and the region through diverse research projects. Climate trends, combined with technological, management, and economic interactions are correlated with increasing incidence of disease in sunflower production areas.

Mathew lab: Cultivated sunflower accessions have been screened for an economically important fungal disease called Phomopsis stem canker. The incidence of Phomopsis stem canker of sunflower has been increasing since 2010 in the U.S., particularly in Minnesota, North Dakota and South Dakota, where over 75% sunflower production takes place. To date, management options are limited and hence screening sunflower for resistance to the causal fungi of Phomopsis stem

canker is underway. Studies from Mathew's lab showed that there is a possible impact of growth stage on the Phomopsis stem canker severity and cultivated accessions with resistance to the causal fungi are identified that can be used to breed and develop disease-resistant hybrids. Other work shows that *D. gulyae* and *D. helianthi* can be detected in sunflower samples via qPCR assays even when they cannot be isolated on agar culture. The qPCR assays will facilitate rapid diagnosis of Phomopsis stem cancer and screening of germplasm for disease resistance.

Wisconsin:
Tracy lab: Sweet corn is an important crop with diverse product development needs. The University of Wisconsin program's objectives include improvement for resistance to Northern corn leaf blight (NCLB), Maize Dwarf Mosaic Virus (MDMV) and common rust; ultrahigh eating quality, and a variety of traits required for canning or fresh market or specialized culinary objectives. Tropical germplasm is used extensively as a source of traits and genes in the inbred development and hybrid testing programs. One project focused on resistance mechanisms to corn earworm invasion; silk channel length and maysin content were evaluated in developmental materials with the goal of identifying hybrids with long silk channels, high maysin levels, and high yield. Selection for long silk channels while maintaining ear length was successful but did not improve earworm resistance. Higher maysin content was associated with lower earworm infestation rates.

Genomic prediction has been used in the development of hybrids for organic production. Phenotypic data was used together with marker data to predict the performance of 100 untested hybrids evaluated in 11 organic environments in Wisconsin, California, and Oregon. Traits of interest included plant and ear height, flavor, tenderness, husk protection, tip fill, ear parameters, and flowering date. Predicted and actual values were highly correlated for plant height, flavor, but not for tip fill.

Research associated with the Sweet Corn Coordinated Agriculture Project has illuminated the origins of the multiple sugary and shrunken genes; multiple domestications occurred over time in Central and Northern Mexico, the US Southwest, the US Puebloan culture, and the US lower Colorado River.

Outcomes /Impacts:

- Demand continues to escalate for access to a broad range of well-document, high quality plant genetic resources which enable basic and applied research applications necessary to sustain agricultural productivity and to achieve need advances in supply of food and feed, ornamental and nursery industry stocks, and for nutrition, health, bioenergy, and economic growth. Addition of new resources via collection and exchange is essential for continued innovation.
- Establishment of clonally propagated plant collections in vitro helps assure their survival and maintenance as threats to field survival continue to grow for many of these species.
- Software products that enable collection management, genebank workflows, and public access to plant genetic resource information facilitate use of germplasm to meet well-targeted objectives.

- Efforts devoted to characterization and evaluation of the genetic resources for priority traits and genetic profiles, coupled with information access, help researchers better target those accessions which can best address objectives and realize their potential to contribute. *Examples:* Identifying sunflower, soybean, maize, vegetable, and horticultural crop genetic resources that offer traits such as cold hardiness, salinity tolerance, specific chilling and other requirements for flowering (impacts fruit production), disease and insect resistance, and the potential to contribute beauty to our landscape and important ecosystem services that enhance the quality of life in communities. Utilizing spontaneous doubling of haploids instead of chemically-assisted doubling will substantially improve capacity to generate maize double haploid inbreds; identifying the genetic basis of the spontaneous doubling trait is key to this effort. Identification of germplasm and/or genes that contribute winter hardiness to fall planted crops, or that withstand wide variations in seasonal conditions supports overwintering and drop production success. Multidisciplinary efforts to utilize germplasm resources for disease resistance improvement identified trait loci and markers for use in cucurbit breeding programs for diseases that threaten crop production. Defining quality parameters in seeds of plant species which have proven difficult to germinate or emerge helps agronomists develop best management practices to support crop production, and genebank managers to maintain these genetic resources. Reliable stand establishment is critical, especially with variable climate trends, to achieving populations that support yield goals. Genomic prediction of breeding values is used to select promising parents for crossing, contributing to rapid breeding progress. Example: conventional and organic sweet corn breeding programs to improve human health and nutrition. Development of maize populations that include landraces and wild relative teosinte supports discovery and understanding of traits for which we have little understanding, such as flavor, aroma, nutritional compounds, and culinary uses. Identification of resistance germplasm sources for an array of soybean diseases and cyst nematode, followed by identification of quantitative trait loci controlling field resistance is being used in marker-assisted breeding of tolerant soybean varieties. The first chromosome-scale genome assembly of the octoploid strawberry provides a foundational resource for research and innovation.
- Development of new cultivars provides solutions for production challenges as well as introducing novel variation. Examples: Development of diploid potato breeding systems will accelerate genetic gain and new variety development. Cherry stocks that can evade damage from late freezes reduce production risks for growers. Release and licensing of herbicide tolerant varieties of winter canola provides producers in the southern Great Plains with options for crop rotation and diversification. Production of winter canola hybrids produced using male sterile / restorer systems will greatly expand parental combinations and traits that can support grower objectives. Outcomes of SCRI initiatives provide new disease and pest resistant carrot, cucumber, and melon varieties, and also focus on soil health and microbiome factors contributing to productivity.
- Advanced in application of genomics and high-throughput phenotyping are rapidly advancing identification of useful genes, traits, and enabling more rapid breeding progress.
- Development of new markets for crops and new cropping systems provides value to growers and society. Examples: Identification of new crops, factor posing production risks, need for best management practices are critical to success in establishing new crops that are profitable. North Dakota's work with grain sorghum, industrial hemp, Ethiopian mustard and camelina have resulted in commercial production. Expanded potential for forage in

production in high saline rangeland soils will depend on identification of forage crop resources with promise and incorporation of these traits into elite cultivars. Development of unusual cultivars with unique culinary properties expands producer and consumer options.

- Training of undergraduate and graduate students, postdoctoral candidates, and visiting scientists provides valuable experience with use of plant genetic resources for a wide range of objectives and provides for the next generation of U.S. scientific leadership in agricultural and allied sciences. Providing education and information about genetic engineering of crop plants without advocacy broadens public understanding of the applications of such technologies, their role in our food and potential risks/benefits. Incorporation of genetic resource investigations in development of predictive analytic tools provides a valuable opportunity to develop scientists who can capitalize on technical and analytical advances to realize the inherent value of the plant genetic resource collections.
- Germplasm use continues to contribute to the aesthetics and sustainable management of the world we live in, and the health, welfare and security of the world's peoples.

Publications:

Illinois:

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