Project Number: NC-007

Project Title: Conservation, Management, Enhancement and Utilization of Plant Genetic Resources

Period Covered: 10/2020 through 09/2021

Date of this Report: November 29, 2021

Annual Meeting Dates: August 19-20, 2021 (virtual)

Participants: https://www.nimss.org/projects/view/participant_list/18364

Minutes: https://www.nimss.org/seas/minutes/51849

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 73 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 2019 derecho was responsible for roof damage to the large 4C cold storage building. Roof replacement provided by Iowa State University was completed in February 2021. North Central Regional Plant Introduction Station (NCRPIS) collection holds 54,490 accessions (54,202 in FY2020), grew by 365 accessions and 24 were deactivated. Ames personnel fulfill PGR requests during the pandemic with appropriate safety practices. In FY2021 to date, 39,326 items were distributed, comparable to the 43,432 items distributed in all FY2020, reflecting reduced demand due to challenges associated with the pandemic. About 15,000 items are distributed annually for internal PGR management needs. In FY2021 to date nearly 1,450 orders were received; researchers of the 12

Land Grant institutions of the NCR received nearly 49,406 NPGS distributions, 9,574 (19%) of those from the NCRPIS.

The collections are 79% available. More than 1,500 seed health tests were performed to comply with phytosanitary import requirements associated with international maize and sunflower seed requests. 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 disease-free, and samples were cultured of specimens with observable symptoms. Approximately 7,816 accessions were tested for viability as part of routine maintenance activities to ensure the quality of the collections; about 31% of the entire collection is in need of periodic viability testing. The viability team's "smaller sample/rep, multiple rep testing strategy" rapidly identifies seed lots that potentially have low viability and require more testing; this has greatly increased our testing capacity. Backup seed lots were sent of 1,474 accessions to the National Laboratory for Genetic Resource Preservation (NLGRP) in Ft. Collins, CO; 82% of the collection is backed up. More than 2,008 accessions were also prepared for backup in the Global Seed Vault in Svalbard, Norway.

Approximately 1,514 accessions were grown for seed increase in across all taxa, including perennials that will be maintained until seed increase goals are achieved, about a 50% increase over 2019 plantings, but still below historical averages due to pandemic-related labor issues. Tropical maize increases were again sent to a commercial nursery provider in Mexico due to lack of temperate adaptation in fall, 2020, based on past excellent quality seed return, and 25 highland tropical maize accessions with older, low viability seed await seed increase at CIMMYT's high altitude Tolucca site.

Obj 3: Evaluation and Characterization: Observations for about 2,764 accessions and images for 3,115 accessions were loaded to the GRIN-Global (GG) database. Evaluation of the *Brassica rapa* collection for winter/spring type determination was completed, and the information obtained supports regeneration management decisions and practices. A collection of Hydrangea was field established to evaluate adaptation, disease resistance, and traits such as form and fall color. Optical seed sorters are used to improve seed lots of maize prior to planting, and by ISU campus researchers for sorghum, millet, soybeans, and sorting haploid maize kernels.

Obj 4: Software Development: Our development staff released enhancements to various wizards used by genebank personnel to manage workflows and seamlessly integrate information in GG, and new Curator Tool versions. A new Attach Wizard enables a variety of file and record types to be associated with accessions / accession groups. These products support management of associated information, curatorial workflows, and public access to information associated with PGR that facilitates their use. All enhancements must be coordinated with changes made to the public GG website's functionality. Interoperability to connect GG accession information with information in model organism databases uses BrAPI (Breeding API) a Restful web service API.

Obj 5: Tours were cancelled due to the pandemic. Professional findings were presented at scientific and virtually 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 2021. Development of learning objects and training materials for a Higher Education Challenge Grant is in process.

<u>Accomplishments & Impacts– State Reports:</u>

Illinois (Sacks)

Sacks lab: Miscanthus is of interest as a bioenergy crop; University of Illinois research has examined genetic structure of populations of *Miscanthus* sp; multiple genomes provide advantages for adaptation to unique environment. Previous population structure studies provided insight on distinct genetic clusters from three regions of Japan, the Koreas, and multiple areas of China. Crop persistence from year to year is important for this bioenergy crop; findings indicate second year growth can be used to predict varietal biomass yield performance.

Juvik lab: Genetic, phenotypic, and biochemical analyses have identified flavone-anthocyanin copigmentation compounds from purple corn that can provided for a range of food additive color hues and potentially improve food produce shelf life. The creation of linkage maps of tomatoes, sweet corn, broccoli and more recently for the bioenergy crop, *Miscanthus*, have been used for the identification of favorable QTLs and for marker-assisted introgression of beneficial alleles for improved quality, yield, and other traits into elite germplasm for commercial release.

Kling lab: Research on shrub willow woody biomass indicates that lignin reveals variation in compositional traits such as lignin among species and interspecific hybrids. Yield is negatively correlated with lignin content and positively with cellulose content.

Indiana (Hoagland)

Wang lab: This Purdue University research program examines the processes that underlie genotype by environment interactions that emerge in response to abiotic stress. The group has a particular interest in evaluating and modeling the potential benefits of diverse accessions for breeding for novel climatic scenarios. Team members work on a variety of crop species, including cultivated Asian rice (*Oryza sativa*), upland cotton (*Gossypium hirsutum*), and soybean (*Glycine max*). A major research objective of the group is to improve the predictability of process-based models across genetically diverse materials under contrasting environmental conditions, towards the long-term goal of enhancing the utility of gene bank constituents.

Hoagland lab: The soil microbiome, integral to the crop production system, responds to crop management practices, plant genotype, environmental factors, and impacts / responds to pathogens and pest populations. Fungal endophytes can influence production and post-harvest challenges in carrot. Carrot genotype was found to affect endophyte abundance and the potential for individual soil mycobiota to affect seed germination, seedling growth and tolerance to an important carrot pathogen.

Iowa (Lübberstedt)

Lübberstedt lab: Efforts to understand the basis of spontaneous doubling of the haploid maize genome using GWAS and double haploid breeding method with exotic maize revealed a major locus on chromosome five. This may enable DH line production in exotic populations without use of colchicine or other artificial doubling methods (Verzegnazzi et al., 2021). A range of research activities of a collaborating Chinese group at Sichuan Agricultural University using the IBM mapping population available from ISU has contributed to understanding of the genetic architecture underlying salt tolerance in (Ma et al., 2021), and to quantitative trait loci for tolerance to lead and cadmium soil levels (Hou et al., 2021). These efforts will contribute to the development and cultivation of salt-tolerant maize, and heavy metal tolerant varieties. Efforts to improve seed production in outcrossing grass species focus on identifying candidate genes responsible for self-incompatibility, particularly for perennial ryegrass.

Hufford lab: A maize community effort to sequence the genomes of 26 important, exotic maize founders now provides an unprecedented resource to better understand gene expression and, ultimately, to use these finding to support development of maize genetic resources that can cope with environmental challenges. Maize centromere research has revealed previously unknown variation for gene content, methylation, and more (Hufford et al., 2021).

Kansas (Stamm)

Kansas State University has contributed to the advancement of the NPGS through utilization of PGR stored within the system and placement of germplasm within the system for future exploitation. 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. A new winter canola variety, KS4719, has been registered with superior winter hardiness, greater lodging resistance, and improved (less) pod shattering (Stamm et al., 2021). Both traditional variety improvement and parental line development for hybrid winter canola production are undertaken. Producers want to grow canola if profitable. 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.
Screening diverse PGR collections of sorghum and wheat resulted in identification of herbicide-tolerant traits in these crops. The mechanism and inheritance of herbicide tolerance was investigated in sorghum (Pandian et al., 2020 and 2021). More recently, herbicide tolerant mechanisms are being investigated in wheat. These results help in transferring herbicide-tolerant traits to agronomically acceptable germplasm.

Current wheat germplasm and its interaction with environment and management are being evaluated for traits associated with increased yield. Established experiments investigated physiological traits for increased yield (de Oliveira Silva et al., 2020), increased grain protein concentration (Lollato et al., 2021), and genetic gain in yield (Maeoka et al., 2020).

Wild relatives of wheat have been used to broaden the gene pool of *Triticum aestivum*. Patterns of introgression from *Aegilops tauschii* were explored (Nyine, et al, 2020). Wild materials, including *Ae. tauschii* (Cruppe et al., 2020), *Ambylopyrum mutica* (Fellers et al., 2020), *Triticum dicoccoides* and *Ae. ventricosa* continue to be evaluated and transferred to adapted backgrounds for the purposes of addressing biotic and abiotic stresses and explore the potential of improving wheat quality and nutritional traits.

Genetically diverse soybean association panels are being phenotyped for response to heat and drought stress. Accessions characterized as heat or drought tolerant are being used as parents to develop PGR with the goal of sustaining yield, quality and composition under heat and drought stress conditions while increasing genetic diversity in the US elite soybean germplasm.

Michigan (Grumet)

Grumet lab: Extensive collaborative research program focuses on genetics and genomics of cucurbit crops. RG is the lead for a multi-institutional project with 20 co-PIs developing genomic tools for watermelon (*Citrullus lanatus*), melon (*Cucumis melo*), cucumber (*Cucumis sativus*) and squashes (*Cucurbita pepo, C. maxima, C. moschata*) (Grumet et al., 2020). The full NPGS collections for the above cucurbit species (1000-2000 accessions/crop) were genetically characterized by genotyping by sequencing (GBS) and all data are publicly available on the CuGenDB, http://cucurbitgenomics.org , (Wang et al., 2018; Wu et al., 2019; Wang et al., 2021). Genomically-informed core collections are in development for each crop, which will be re-sequenced to provide broadly available resources for genome wide association studies (GWAS) for important traits of interest. Team members are actively identifying, genetically characterizing, developing makers, and breeding for resistance for 18 crop-disease combinations identified as top priorities by the respective cucurbit industries (Grumet et al., 2020).

Other projects at MSU that utilize NPGS PGR include:
Cichy lab: Research focuses on genetic characterization of seed traits related to consumer acceptance and nutritional quality of dry beans including assessment of genotypic variability, diversity studies, mapping, identification of genomic regions and genes influencing cooking time, seed protein and starch composition, and superior end use quality.
Douches lab: The potato breeding and genetics program optimizes conventional breeding techniques for varietal selection and development of superior potato varieties for the Michigan industry. The program also studies self- compatibility in diploid potato, chip-processing quality, resistance to Colorado potato beetle, and resistance to late blight, and scab. Screening for late blight resistance included testing all accessions of *S. microdontum* and introgression with *Solanum* species from Mexico with interspecific crossing barriers using *S. verrucosum* as a bridge species.
Edger lab: Program on blueberries and strawberry breeding, genetics, genomics program studies the mechanistic basis of subgenome dominance in polyploid crops, largely to guide breeding efforts in blueberry and strawberry.
Hollender lab: Program uses diverse PGR of cherry, apple and peach to investigate genes and pathways that regulate plant size, branch orientation, flower and fruit development, and bloom time. Mitch McGrath used the assembled sugar beet genome to examine diversity in a wide range of beet accessions including 606 publicly available wild (321 accessions) and sugar (285 accessions) beet accessions, 30 other crop types (table, fodder, and leaf), and six crop wild relatives.
Thompson lab: This program studies how maize genotypes grow in different environments and utilizes the Wisconsin Diversity Panel, the Germplasm Enhancement of Maize lines, the Sorghum Association panel, and the Sorghum Conversion lines to find and introgress tar spot resistance in maize, and for quantitative genetics, phenomics, and predictive modeling in maize and sorghum.
VanBuren lab: This program utilized the NPGS collection of teff (372 active accessions) for genome wide association studies and screening of agronomic, abiotic stress, and nutrition related traits. Accessions of other C4 cereals acquired from the NPGS (sorghum, finger millet, proso millet, fonio, pearl millet) are being phenotyped.

Minnesota (Lorenz)

The University of Minnesota Soybean Breeding Program accesses the wide range of genetic variation contained on the soybean collection in several ways. One example includes phenotyping diverse soybean accessions for shoot architecture (SA) features, including branch number, branch angle, petiole length, petiole angle, branch distribution, in addition to others. They are using this information to determine the range in genetic variation for SA properties, which influence canopy structure and hence light capture and light-use efficiency. It has been found that soybean presents a continuous distribution in SA, and that several combinations of SA features can achieve a high degree of light capture and transmittance. A panel of 400 diverse MGI accessions were phenotyped and the data combined with high-density genotypic data in a genome-wide association analysis. Several interesting marker-phenotype associations were made, including a strong association between markers on the end of chromosome 19 and canopy coverage and branch angle. This finding suggests that the well-known QTL on chromosome 19 influences canopy coverage through branch angle. A potentially new branch number QTL was also found closely linked to *Dt2.* These findings will contribute to soybean breeders' knowledge on how shoot architecture can be shaped to influence canopy structure for more efficient light utilization, and to provide information on alleles contained in the germplasm collection that could be mined to breed new soybean varieties with desirable shoot architecture phenotypes.

North Dakota (Johnson)

During the 2017-2021 research cycle the adaptation potential (Research level 1) for Ethiopian mustard (*Brassica carinata* L.) and open-pollenated white sorghum (*Sorghum bicolor* L.) with ongoing efforts for industrial hemp (*Cannabis sativa* L.) and perennial flax (*Linum lewissi* Pursh.) were evaluated in North Dakota and west central Minnesota. Initial evaluations focused on identifying genotypes/varieties with early maturity, good grain yield and quality, and agronomic deficiencies such as low seed/seedling vigor, seed shatter, height extremes and non-uniformity, small seed size, and seed maturity at harvest. Adapted genotypes/varieties were selected for evaluation of stand establishment and harvest management. Additional research will include cover crops, intercropping, and crop rotation components of cropping systems.

Sorghum must be planted early due to lack of early maturing varieties for short, cool growing season areas such as North Dakota. Yields of early maturity hemp varieties do not decline when planted later in June in eastern North Dakota. Timely hemp harvest is important since delays reduce yields from shattering more so than with sorghum. Hemp chemical and biological seed treatments show promise for reducing pure live seed mortality from 30-50% or more as compared to wheat, corn, and soybean, where mortality is commonly 10-15%. Stand establishment challenges were apparent for perennial flax where soil crusting, soil moisture limitations, and seeding depth are problematic. Delayed and extended emergence followed by slow growth reduce perennial flax competitiveness with weeds. Advantages of well-established perennial flax include higher grain value, potential for two harvests per season, stand duration potential for up to five years, and an available market.

Corn and soybean relay intercropping systems were evaluated using the winter annual oilseeds camelina and field pennycress; potential for improved net production and economic advantage was largely dependent on grain yields and prices. The winter annuals reduced soybean yields in the second year in some locations such as North Dakota where the growing season is short and cool in comparison to Minnesota and Iowa. In addition to the potential economic grain value from harvesting three grain crops in two growing seasons, several ecosystem benefits (early pollinator food source, soil protection, carbon fixation, and wildlife habitat) show enhancement

Ohio

At the Ohio State University (OSU), characterization, development, and germplasm release activities on are routinely conducted. These activities are made possible by the Ornamental Plant Germplasm Center (OPGC), (Tay et al. 2004), as well as active breeding programs in crops such as Barley, Tomato, Soybean, and Wheat, a domestication program in rubber dandelion (*Taraxacum kok-saghyz*), an active viticulture program that considers domestic PGR as well as interspecific hybrids of grapevine, a collection of Central Asia apple genotypes, and PGR collections such as *Arabidopsis*, pennycress, and sugar maple. These efforts also encompass obtaining and evaluating the performance of external PGR collections, as well as national and international collaborations that contribute to a more comprehensive characterization of germplasm in the groups of crops previously mentioned. In this regard, OSU activities encompass the six goals of the NC7 project in commercial and developing crops, with the OPGC as the vanguard of such activities. Thus, the OPGC and its personnel are committed to transferring technology, training, and methodology for PGR management, as well as germplasm of herbaceous plants and associated information, conducting germplasm related research, and encouraging the use of PGR and associated information for research, crop improvement, and product development. In its 8000 accessions representing ~300 genera, the current native priority genera are *Coreopsis*, *Lillium*, *Phlox*, and *Rudbeckia*, while non-native genera include *Begonia* and *Viola*. With the new directorship of the OPGC, it is expected that education to students, scientists, and the public will be paramount among OPGC's activities. In addition, OSU active breeding and germplasm development programs will continue with the description, characterization, and release of PGR that contribute to the NGPS and scientific community in the improvement and developing of crops with current and future potential to contribute to the agriculture of the world.

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.

Efforts have primarily focused on the characterization of soybean, sunflower, wheat, wheatgrass, and oat accessions. New sources of resistance to biotic and abiotic stresses have been identified for cultivar development. Examples include soybean accessions with resistance to root rot (Okello et al., 2020), and sunflower accessions with resistance to Phomopsis stem canker (Elverson et al. 2020). Association mapping has also been used to identify genomic regions associated with Bacterial Leaf Streak, Tan Spot, and Spot Blotch resistance in hard winter wheat (Ramakrishnan et al., 2019; Sidhu et al.., 2019; Ayana et al. 2018).

Wisconsin (Tracy)

Sweet corn is a important vegetable, used in both U.S. fresh market and processing industries. The *shrunken2*, or *sh2* allele, is present in 75% of sweet corn germplasm used by the processing industry and nearly 100% of the fresh market industry. Efforts to understand the evolution of modern sweet corn using a high-quality reference-genome assembly of sweet corn inbred line Ia453-*sh2* provide evidence for relationships between sweet and other types of maize, identified genome regions under selection, and candidate genes associated with sweet corn traits (Hu et al., 2021). GWAS studies were devoted to kernel carotenoids (Bassegio etal, 2020), and identification of a gene for resistance to maize common rust, an important and widespread disease that impacts sweet corn yields and quality (Olukolu et al., 2016). Roughly 50% of the inbreds in the GWAS panel were sourced from the maize collection housed at NC-7 in Ames.

Organic plant breeding typically is supported by fewer resources than traditional plant breeding. Genomic prediction may be able to use data for potential hybrids whose parents are not part of a training set, and cannot be evaluated using general combining ability data, but can be modeled using genomic prediction (Zystro et al., 2021). Numerous lines sourced from the NC-& collection are being used in a breeding program to improve earworm (*Helicoverpa zea*) resistance for in sweet corn for organic growers (Moore and Tracy, 2018, 2020).

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 PGR 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 Brassica, soybean, maize, vegetable, and horticultural crop genetic resources that offer traits such as cold hardiness, salinity or heavy metal tolerance, specific chilling and other requirements for flowering (impacts fruit or seed 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 a key accomplishment. 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 crop production success. Multidisciplinary efforts to utilize PGR 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. Identification of quantitative trait loci controlling field resistance is being used in marker-assisted breeding of tolerant crop varieties. The chromosome-scale genome assemblies provide 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. Release and licensing of herbicide tolerant, winter hardy varieties of winter canola provide producers in the southern Great Plains with options for crop rotation and diversification.
- 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, and are now working on perennial flax. 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.

NC-007 Participant Publications: * indicates they were cited

Illinois

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Iowa

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