

Project Number: NC-007

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

Period Covered: 09/2017 through 08/2018

Date of this Report: December 12, 2018

Annual Meeting Dates: August 15-16, 2018

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

Minutes: See 2018 Minutes PDF file

Accomplishments and Impacts:

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

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 specializes 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 70 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.

Germplasm Acquisition, Maintenance and Distribution: North Central Regional Plant Introduction Station (NCRPIS) personnel acquired 362 new accessions (holdings total 54,707 accessions) and distributed 54,700 units of seed to fulfill 1,940 orders from 1,587 requestors, of 22,801 unique accessions. Distribution of 42% of the entire collection holdings reflects very high demand. About 63% of the distributions were to US recipients, and 37% to international recipients. Collection availability overall stands at 76%. More than 2,300 seed health tests were performed to comply with phytosanitary import requirements associated with 122 international seed requests. ELISA testing of all Cucurbita seedlings (2,955) was done prior to transplanting to the field to ensure that seedlings 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 for of those specimens with observable symptoms. Approximately 4,060 accessions were tested for viability as part of routine maintenance activities to ensure the quality of the collections; 40% of the entire collection is in need of viability testing. Backup seed lots were sent of 724

accessions to the National Laboratory for Genetic Resource Preservation (NLGRP) in Ft. Collins, CO and 300 accessions were sent to the Global Seed Vault in Svalbard, Norway.

Approximately 1,200 accessions were grown for seed increase in Ames across all taxa, including 106 perennials that will be maintained until seed increase goals are achieved. Tropical location maize increases for unadapted tropical maize included 250 sent to a commercial nursery provider in Mexico in August 2017 (due to lack of temperate adaptation), with excellent quality seed return, and 25 highland tropical maize accessions with old, low viability seed were sent to CIMMYT for contract increase at their high altitude Toluca site. Sixteen tropical accessions from Kasetsart University, Thailand were grown for increase in a ISU campus greenhouse under APHIS permit. Other Ames regeneration efforts included 172 maize; oilseeds, 591; vegetables, 176; amaranth, panicum, quinoa, etc., 394; and ornamentals, 52. The Ornamentals project is now using other ISU farm locations for tree species regeneration to achieve isolation.

Evaluation and Characterization: More than 564 accessions were grown for various observation trials in 2018; 23,600 observations and 1,040 images loaded to the GRIN-Global database. Sunflower plots were grown for use by an Agronomy class to learn how to evaluate self-fertility. The *Brassica rapa* collection is being evaluated for winter/spring type determination; this will facilitate regeneration management decisions. A new dataset was collected of millet observations for temperate adaptation. Pedigree information of all expired maize PVP lines was added to GRIN.

Software Development: Our development staff released an enhanced Viability wizard, software used for automation of viability testing capture and transfer to the GRIN-Global database, and an enhanced Inventory Attachment wizard for automated mass-loading of accession and inventory file attachments. The latter enables loading of a large backlog of images. The Curator Tool was migrated to the free Open Source WiX installer technology, and to the .NET 4.6.2 framework, providing improved security features. These products support access to information associated with germplasm that facilitates their use.

Accomplishments & Impacts– State Reports:

Ohio (Jourdan)

The Ornamental Plant Germplasm Center acquires, maintains, and develops germplasm of herbaceous ornamental plants. Our primary function is to support the relevant research and development communities by providing appropriate germplasm. In this reporting period, we received 81 germplasm requests and distributed 541 order items. Our collection consists of 5,454 accessions; 23% of the collection (1,068 accessions) is available for distribution and 56% (3,035 accessions) are backed up off-site; these are all stored as seeds. We received 348 new accessions, including a large number collected through the Seeds of Success program. Our clonal collection is currently being backed up and we have 313 accessions from germplasm maintained in the greenhouse backed up in vitro at 4C. We have also managed our collection by regenerating seed of 27 accessions of species in *Phlox*, *Petunia* and *Rudbeckia* and tested seed viability of 36 accessions last year. Seed production has been an ongoing activity with the primarily clonal collection of *Begonia*; we have produced seed in about 25% of the collection and have been validating the consistency of the seedling progeny.

A focused has been establishment of clonal collections in vitro. At present, 418 accessions are stored under sterile conditions at 20C including *Phlox*, *Pelargonium*, *Begonia*, *Chrysanthemum*, *Leucanthemum* and *Dianthus*. We are continuing to explore strategies to reduce maintenance of the in vitro cultures by increasing the time interval between subcultures; these include low temperatures (4C) storage, osmoticum adjustment (higher levels of sucrose or addition of sorbitol), altering light quality (increasing proportion of blue light), and vessel sealing methods (porous vs non-porous).

In the area of seed biology, we've continued work on defining the quality parameters in seeds of perennial species of *Phlox* which have proven difficult to germinate. We have identified the fungi typically

associated with the seed. We have optimized the Tetrazolium test for rapid assessment of seed lot viability, and we have examined the germination potential of isolated embryos. The results point to a typical non-deep physiological dormancy imposed by the residual endosperm as isolated embryos readily germinate. However, Gibberellic acid treatment is not an effective substitute for the moist chilling requirement.

Our germplasm enhancement activities have focused on interspecific hybridization in *Phlox*. Progeny of the reciprocal cross between *P. roemeriana* and *P. drummondii* have been grown to determine the potential for novel flower color combinations. The hybrids were highly sterile, but some backcross progeny with *P. drummondii* have been obtained for further evaluation.

During this reporting period, we trained 3 undergraduate students (as student workers) in the greenhouse and field operations associated with germplasm management and 2 undergraduate students learned tissue culture procedures for germplasm conservation. Our facilities and programs are regular components (tours, demonstrations, labs) of various undergraduate courses at The Ohio State University. The OPGC maintains a website dedicated to sharing information about our germplasm and research/development associated with it. We participate in the annual Cultivate'18 activity, which is the largest horticultural trade show and educational program in North America.

California (Karban)

We continued work on traits of host plants that could provide resistance against herbivorous insects and mites. Emphasis has recently been on physical characteristics of plant surfaces that have received less attention than plant secondary metabolites and other chemical defenses. For example, many grasses have unidirectional hairs, prickles, and spines that point towards the leaf tips and away from meristems. We have tested the hypothesis that these traits may usher small insects away from valuable meristems, making plants more tolerant of loss of leaf tissue. Results from various accessions of oats with and without unidirectional leaf hairs were consistent with this hypothesis. In the future, the role of unidirectional hairs on other species such as rice and wheat that show variability for these traits will be evaluated.

Studies continued for evaluation of potential costs and benefits of inducible defensive traits. A long-standing question is whether plants must experience tradeoffs between defense against herbivores and other desirable traits such as yields. Working with a model plant system, we found that those costs were experienced as reductions in overtopping growth. Since overtopping growth is a valuable trait for wild plants that compete with neighbors but is counterproductive in agriculture, this is a promising observation for breeding host plant resistance.

Michigan (Iezzoni)

The evolution of the key steps controlling the metabolism of the chemical complexity that is exemplified by 48 species of the mint family (Lamiaceae) was elucidated using an integrated chemical, genomic and phylogenetic approach.

Cold weather damage to flower buds is the most important factor limiting yield in sour cherries, and more information about the major loci that affect bloom date is needed to help guide breeders. An analysis of three years of bloom data from 338 individuals from five F₁ populations identified four quantitative trait loci for bloom date, with the locus on chromosome 4 having the largest effect.

An understanding of the genetic variation and underlying genetics of vitamin E levels in maize was advanced in a study using the 5,000-line U.S. maize nested association panel (NAM). The study identified individual genes known to be involved in vitamin E levels along with some genes that suggest novel activities.

The genetic diversity and population structure was analyzed in switchgrass including over a thousand individuals chosen to represent North American germplasm. The seven populations identified were consistent with constraints from glaciation events, ploidy barriers and restricted gene flow due to differences in flowering time.

Cultivated potato was domesticated from wild species native to southern Peru. A genomic analysis of cultivated potato and its wild relatives (n=67), housed in the USDA collection, revealed historic introgressions, hybridization events and genes that were targeted during domestication.

Acylsugar specialized metabolites are one of the most abundant specialized class of metabolites in Solanaceous trichomes where they function as defense against insect herbivores. The chemical diversity of acylsugars observed between three *Petunia* species was described providing insights into the evolution of their specialized metabolism.

Sudden death syndrome (SDS) caused by the fungus *Fusarium virguliforme* is a major disease of soybean in the U.S. Two interacting quantitative trait loci controlling field resistance to SDS were identified and markers were designed that can be used to enable marker-assisted breeding of SDS tolerant soybeans.

A detailed SNP analysis was done using 1,234 cucumber accessions from collection housed at in the U.S. National Plant Germplasm System (NPGS) providing knowledge of genetic diversity, population structure, phylogenetic relationships, linkage disequilibrium, and population differentiation. This knowledge was used to design a core collection of 395 accessions that represents at least 96% of the genetic diversity present at the NPGS. In addition, genomic regions associated with 13 horticulturally important traits were identified through genome-wide association studies.

Iowa (Lübberstedt)

Lübberstedt lab: Improving nitrogen use efficiency (NUE) in maize is one of the approaches to reduce N losses to the environment, as well as improve productivity in nutrient-depleted areas. Doubled haploid lines derived from exotic landraces from the Germplasm Improvement of Maize (GEM) program, backcrossed with ex-PVP inbreds PHB47 and PHZ51, were used. Root system architecture traits at seedling stage, and agronomic traits of the GEM-DH lines grown under high and low nitrogen conditions were investigated, and SNPs associated with these traits were identified. Seedling root traits were examined because of the root system's major role in the water and nutrient acquisition important for the plant's survival and growth. Lines were genotyped based on genotyping by sequencing. Candidate SNPs were identified that were associated with seedling root system architecture in water, and under high and low N conditions.

Lübberstedt received funding (as PI; Paul Scott, Kathleen Delate, Bill Tracy co-PIs) from the USDA OREI program to introduce doubled haploid (DH) technology into 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. A major QTL for spontaneous haploid genome doubling (SHGD) was identified. The usefulness of SHGD is currently evaluated within the USDA OREI project in the background of BS39, a tropical population adapted to photoperiod conditions in Iowa by Dr. Hallauer. First results look promising: success rates for obtaining DH lines from BS39 were higher using SHGD compared to artificial treatment-based DH line development using colchicine.

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. We are developing winter canola cultivars that are released and then licensed to regional and national seed companies. During the reporting period, KSR4723 Roundup Ready winter canola was approved for foundation seed increase with a planned release in summer 2019. In addition, two cultivars, Griffin and HyCLASS225W, were granted Plant Variety Protection certification. Seed of these cultivars will be stored at the NPGS for preservation until the issued PVP certificates expire.

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. Producers continue to employ these cultivars on their farms, improving the overall sustainability and profitability of their cropping systems through crop rotation and diversification.

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.

Kansas (Shapaugh)

Soybean plant introductions continue to be evaluated to identify new genetic variability for response to drought and heat stress, seed composition and improved yield potential. Evaluations were conducted over the past several seasons on over 2500 introductions from maturity groups 3 through 10. Data collected on the plots included traits such as: maturity, lodging, height, seed yield, shattering, 100 seed weight, seed quality, seed protein and oil concentrations, and canopy wilting scores. Based on these evaluations single cross populations will be developed involving a plant introduction that has not previously contributed to the genetic improvement of US soybean varieties. The goal of using these parents is to increase the genetic diversity of US germplasm, or at least, maintain genetic gain.

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.

A new breeding project was initiated for food corn quality traits with a USDA-ARS researcher in Raleigh, NC. Landraces are being evaluated per se and as population hybrids for a large number of traits including agronomic traits, kernel composition traits, and cooking quality traits including texture, flavor, and aroma. Wide germplasm types and target food types are being investigated, ranging from green corn to popcorn to masa-based foods.

New York (Gore)

Sweet corn (*Zea mays* L.), a highly consumed fresh vegetable in the US, varies for tocochromanol (vitamin E) and carotenoid (provitamin A) levels, but makes limited contribution to the recommended daily allowance of these two vitamins. To identify genes controlling natural variation for the content and composition of tocochromanols and carotenoids in fresh sweet corn kernels, we performed a genome-wide association study (GWAS) of six tocochromanol and eight carotenoid compounds and their derivative traits across a sweet corn association panel with ~400 inbred lines. An association was detected between *vte4* (γ -tocopherol methyltransferase) and α -tocopherol (highest vitamin E activity) content, as well as with *vte1* (tocopherol cyclase) and *hgg1* (homogentisate geranylgeranyltransferase) for tocotrienol (antioxidants) variation. Additionally, two kernel starch synthesis genes, *shrunk2* (*sh2*) and *sugary1* (*su1*), were associated with tocotrienols. For GWAS of carotenoids, lycopene epsilon cyclase (*lycE*) and β -carotene hydroxylase (*crRBI*), which encode carotenoid biosynthetic pathway enzymes, were associated with the content of β -carotene (two retinyl groups) and the ratio of β - to α -branch carotenoids, respectively. With consideration of favorable haplotypes for the associated tocochromanol and carotenoid pathway genes, genomic prediction of breeding values was conducted to select promising parents for crossing, thereby contributing to the establishment of a sweet corn vitamin biofortification breeding program. Through these quantitative genetic analyses, our work constitutes an important step for increasing vitamins in fresh kernels of sweet corn for human health and nutrition.

An association mapping population of ~500 sweet corn inbred lines was evaluated in replication for a second year at Cornell University's Musgrave Research Farm. As in 2017, leaf relative chlorophyll content and photosynthetic parameters related to the productivity and health of plants were evaluated at flowering using a non-invasive, handheld and high-throughput phenotyping device (called MultispeQ) in the field. Photosynthetic traits included photosystem II quantum yield (Φ II, qP and qL), non-photochemical quenching (Φ NPQ, NPQt and Φ NO), and light-driven proton translocation (linear electron flow, LEF). A multivariate (multi-trait) GWAS was performed for these phenotypes, resulting in the identification of candidate genes putatively associated with the photosynthesis-related phenotypes. These measurements and analyses allow for the deeper understanding of maize photosynthesis responses in field conditions, dissecting the genetic architecture of these traits, and identifying genetic markers associated with photosynthetic related traits. Eventually, it will help plant breeders to develop new sweet corn germplasm with high performance under stress environments to meet increasing demand for food production.

North Dakota (Johnson)

New, alternative, and principal crops represent areas of tremendous genetic accomplishment and potential for providing food, feed, fiber, and bioenergy for an increasing world's population projected to reach 9.8 billion in 2050. Sources of diverse germplasm such as the National Plant Germplasm System (NPGS) are critical to public and private plant breeding programs for plant/crop improvements and subsequent adaptation to changing regional and global environments. Shifts in regional crops are complex and caused by many factors beyond the agronomy and economics associated with production, but product development, consumer acceptance, and market demand sustained over time can advance a crop's prominence locally and nationally. Crop history indicates soybean [*Glycine max* (L.) Merr.], dry bean (*Phaseolus vulgaris* L.), sunflower (*Helianthus annuus* L.) and canola (*Brassica napus* L.) as new crops in the 1960/1970s in North Dakota with their current national crop rankings at 9, 1, 2, and 1, respectively. The successful transition of these crops from new to principal status was directly involved with plant breeding programs that produced adapted and improved varieties for North Dakota.

The Dept. of Plant Sciences at North Dakota State University has 11 plant breeding programs including hard red spring wheat (*Triticum aestivum* L.), durum wheat (*Triticum turgidum* L.), winter wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), oats (*Avena sativa* L.), canola, dry bean, field pea (*Pisum sativum* L.), flax (*Linum uistatissimum* L.), soybean, and potato (*Solanum tuberosum* L.). These

crop breeding programs utilize genetic resources for variety development and improvement in an integrated approach with university plant pathologists, cereal chemists, entomologists, and soil scientists.

Ongoing screening of agronomic and horticultural crops is important for identifying potential new crops for North Dakota and the surrounding region. New crops often have greater production risk associated with lack of defined production practices and markets which lowers producer appeal, but when major crop commodity prices are poor (currently with corn, wheat, and soybean) producers become more receptive to growing a new crop that could potentially provide greater profits. Faba bean (*Vicia faba* L.), industrial hemp (*Cannabis sativa* L.), Ethiopian mustard (*Brassica carinata* L.), and grain sorghum (*Sorghum bicolor* (L.) Moench) continue ongoing evaluation as potential new crops in the region.

North Dakota adaptation screening of grain sorghum for cold tolerance and maturity, included 106 and 101 genotypes in 2015 and 2016, respectively. The germplasm was sourced from the NPGS and evaluated in 2015 and 2016 at the Carrington and Prosper sites associated with the North Dakota Agricultural Experiment Station/North Dakota State University, Fargo. Twenty-two genotypes were selected for advanced yield performance evaluation and seed increase in 2017. Four cold-tolerant, high yielding, early maturity genotypes were moved forward for evaluation in 2018 and 2019 in a RCBD seeding date/genotype field study at Carrington, Oakes (irrigated), and Prosper. Adapted sorghum genotypes primarily based on yield and seed quality could provide producers an alternative grain crop for drier regions of western North Dakota where corn (*Zea mays* L.) performance is poor. The study also provides research training for graduate and undergraduate students.

Ethiopian mustard yield response to seeding dates resulted in reduced grain yield with delayed seeding at Minot (north/central) and Prosper (east/central). Yield reduction was 80% and 40% at the north/central and east/central locations, respectively, with late seeding compared to the early seeding dates and illustrates the importance of timely seeding and early maturing varieties. Ethiopian mustard yield performance appears higher than camelina (*Camelina sativa* L.), but lower than canola (*Brassica napus* L.) based on previous camelina and canola performance trials in the state. Four years of industrial hemp variety trials at the Langdon Research Extension Center indicate comparable crop performance as for adjacent Canadian production in Manitoba and Saskatchewan.

Evaluation of the winter annual Brassica oilseeds camelina and field pennycress (*Thlaspi arvense* L.) as cover crops and grain crops, for biofuel utility, progresses with relay seeding in corn/soybean/corn and soybean/soybean/corn cropping sequences. Indications show first year corn and soybean yields are not affected by the brassica oilseeds when relay sown as cover crops in Year-1. However, camelina and field pennycress harvested as grain crops in Year-2 reduced soybean yields when relay sown into the brassica oilseeds. Relay seeded second-year soybean yields were reduced for the brassica treatments, but grain value of camelina and field pennycress helped offset the soybean yield reduction. The concept shows potential and would benefit from greater variety selection for both brassica's as well as improved seeding equipment and crop residue management.

Oregon (Liston)

Objective: Characterize plant germplasm using a combination of molecular and traditional techniques and utilize modern plant genetic techniques to help manage plant germplasm.

Findings: In a common garden study, cloned strawberry individuals of 269 genotypes were grown in three climatically diverse locations: Corvallis, Newport and Bend, Oregon. Phenotypic data were collected from 11 species of wild relatives and direct progenitors of the cultivated hybrid strawberry, *Fragaria* × *ananassa*. In a phylogenetic study, plastome diversity was assessed in 81 individuals from 16 populations of the decaploid strawberry *Fragaria cascadiensis*.

Among leaf functional traits, we detected divergence in trait means but not plasticities between polyploids and diploids, suggesting that increased genomic redundancy in polyploids does not necessarily translate

into greater trait plasticity in response to environmental change. Across the heterogeneous garden environments, however, polyploids exhibited fitness advantage, which was conferred by both trait means and adaptive trait plasticities, supporting a ‘jack-and-master’ hypothesis for polyploids. The decaploid *Fragaria cascadiensis* has biparental plastid inheritance and four different plastid donors. Diversification of the *F. cascadiensis* clades occurred in the last 230,000 years. The southern part of its distribution range harbors considerably higher genetic diversity, suggestive of a potential refugium.

South Dakota (Caffe Trem)

Researchers 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 including:

Using yellow-flowered alfalfa (Medicago sativa subsp. falcata) to improve and diversify forage production of rangelands (Xu, Lan). Eight alfalfa populations were selected to assess and characterize variations in their emergence rate, growth, and development for salt-tolerant for 120 days. We found relative emergence decreased as soil salinity levels increased. Relative emergence increased sharply then plateaued in low saline soil. In medium and high saline soils, relative emergence increased gradually and then also plateaued. PI631678 and PI502441 appeared to show characteristics in line with those of drought-tolerant alfalfa under drought stress, having the most promise as potential parent materials. Most populations consisted primarily of growth stage classes one and two, except for ‘Persist II’ and ‘Wind River’, which had a significant amount of advanced development at growth stage class three. Persist II and Wind River populations also had the highest relative emergence despite not being regarded as drought-tolerant populations. We found that drought tolerant alfalfa populations, particularly PI631678, PI502441, and Sholty, grew well in saline soil; this study needs to be repeated to determine if these populations will yield a productive forage crop. In addition, the effect of seed size on germination and growth of drought tolerant alfalfa populations should be determined.

Utilizing genetic resources for the development of oats with improved winter hardiness (Caffe, Melanie). Fall planted crops present several advantages over spring planted crops including higher water use efficiency, better ability to compete with weeds, reduced soil erosion, and potential for higher yield. In addition, winter crops can help producers spread their workload. Currently, only spring planted oats are grown in the Northern Great Plains. Winter oats are only planted in the southern states of the US because winter oats are less winter hardy than rye, wheat, or barley. Our objective is to evaluate the adaptation of winter oat germplasm for winter survival in South Dakota. The winter survival of oat breeding lines and cultivars originating from oat breeding programs in the southern states of the United States and from NPGS was evaluated at three locations in South Dakota. Survival ranged from 0-25% at Winner and 0-80% at Beresford. In Aurora, due to cold temperature following planting, no seedling emerged in the fall and the entire trial winter killed, including the winter wheat checks. In addition to evaluating winter survival, we used winter survival data collected in previous years to perform crosses to develop oat lines with improved winter hardiness.

Utilizing wild ancestral wheat for wheat improvement (Seghal, Sunish). We assessed the diversity in rye by genotyping a panel of 178 geographically diverse accessions of four *Secale* sp. from U.S. National Small Grains Collection using 4,037 high-quality SNPs (single nucleotide polymorphisms) developed by genotyping-by-sequencing (GBS). PCA and STRUCTURE analysis revealed three major clusters that separate *S. cereale* L. from *S. strictum* and *S. sylvestre*, however, genetic clusters did not correlate with geographic origins and growth habit (spring/winter). The panel was evaluated for response to *Pyrenophora tritici-repentis* race 5 (PTR race 5) and nearly 59% accessions showed resistance or moderate resistance. A genome-wide association study (GWAS) was performed on *S. cereale* subsp. *cereale* using the 4,037 high-quality SNPs. Two QTLs (*QTs.sdsu-5R* and *QTs.sdsu-2R*) on chromosomes

5R and 2R were identified conferring resistance to *PTR* race 5 ($p < 0.001$) that explained 13.1% and 11.6% of the phenotypic variation, respectively. Comparative analysis showed a high degree of synteny between rye and wheat with known rearrangements as expected. *QTs.sdsu-2R* is mapped in the syntenic region corresponding to wheat chromosome group 2 where tan spot (*PTR* race 5) insensitivity gene (*tsc2*) and tan spot resistance QTLs were located. Based on the genetic diversity, 32 accessions were selected as the mini core set to represents more than 99% of the allelic diversity with polymorphic information content (PIC) of 0.25. The mini core set could be utilized for genetic characterization of useful traits and genetic improvement of rye, triticale, and wheat.

Evaluating oats and wheat genetic resources for resistance to leaf spot diseases in the region (Ali, Shaukat). Multiple diseases attack and impact oats productivity in South Dakota. Leaf spots and rusts (crown and stem) are the major diseases in the state. Deployment of diseases resistant cultivars is a durable, generally economical, and environmentally friendly approach to disease management. Significant efforts have been made by the SDSU breeding program in the development of crown rust and stem rust resistant oat cultivars. Limited information is available on the reaction of commercial cultivars to *Drechslera avenae* leaf spot in South Dakota. We evaluated 60 diverse oats genotypes from National Plant Germplasm System including commercial cultivars against *Drechslera avenae* leaf spot under controlled conditions. A majority of the commercial cultivars showed moderately susceptible to susceptible reactions. The evaluated genotypes from USDA germplasm exhibited a response to leaf spot ranging from susceptible to resistant. The information was shared with the SDSU oat breeder. The resistant genotypes can be utilized as sources of resistance for developing *D. avenae* leaf spot resistant cultivars. More genotypes are being evaluated. The genotypes that exhibited moderate resistance to resistance to *D. avenae* leaf spot will be further tested against *Stagnospora avenae* leaf blotch, another important leaf spot pathogen of oat in South Dakota.

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 nutrition, health, bioenergy, and economic growth. 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. Examples: Utilizing spontaneous doubling of haploids instead of chemically-assisted doubling would substantially improve capacity to generate maize double haploid inbreds; identifying the genetic basis of the spontaneous doubling trait is key to this effort. 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. Analyses of information on bloom date of cherry populations identified identified four quantitative trait loci for bloom date, needed to help guide breeders in their selections to develop sour cherry varieties with flower buds less susceptible to cold weather damage. Genetic studies related to understanding genetic variation of vitamin E levels in maize identified individual genes involved and some genes that suggest novel activities. Genomic analysis of cultivated potato and its wild relatives provide a genetic history of events during its domestication. Sudden death syndrome is a major disease of soybean in the U.S.; two quantitative trait loci controlling field resistance were identified and markers designed for use in marker-assisted breeding of tolerant soybean varieties.

- Development of new cultivars provides solutions for production challenges as well as introducing novel variation. Examples: The progeny of interspecific hybridizations in *Phlox* help determine potential for novel flower color combinations, of value to the ornamentals industry. Release and licensing of herbicide tolerant varieties of winter canola will provide producers in the southern Great Plains with options for crop rotation and diversification. Identification of sorghum genotypes from the NPGS collection with natural tolerance to factors related to herbicide tolerance advance development of elite varieties with herbicide-tolerance, a valuable technology for weed management. Identification of sorghum germplasm resources with adaptation for cold tolerance and early maturity support development of cultivars for dry, northern environments where corn performance is poor, such as regions of western North Dakota.
- 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 faba bean, industrial hemp, Ethiopian mustard and grain sorghum may identify potential. 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.
- Understanding phenomena associated with natural plant populations' abilities to resist herbivorous insect damage may contribute to our ability to breed crop host plants with resistance.
- 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. 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 will continue 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:

California:

*Karban, R. 2017. Tradeoff between resistance induced by volatile communication and over-topping vertical growth. *Plant Signaling and Behavior* 12:e1309491.

Pezzola, E., S. Mancuso and R. Karban. 2017. Precipitation affects plant communication and defense. *Ecology* 98:1693-1699.

*Karban, R. and J. Orrock. 2018. A judgment and decision-making model for plant behavior. *Ecology* 99:1909-1919.

**Funding from the USDA regional project is acknowledged.*

Iowa:

Carzoli, A.K., Aboobucker, S.I., Sandall, L.L., Lübberstedt, T., Suza, W.P. (2018) Risks and opportunities of GM crops: Bt maize example. *Global Food Security* 19:84-91

Do Canto, J., Studer, B., Frei, U.K., Lübberstedt, T. (2018) Fine mapping of a self-fertility gene in perennial ryegrass. *Theor. Appl. Genet.* 131:817-827

Juan, M., Dengfeng, Z., Yanyong, C., Lifeng, W., Jingjing, L., Lübberstedt, T., Tianyu, W., Yu, L., Huiyong, L. (2018) Heterosis related genes under different planting densities in maize (*Zea mays* L.). *J. Exp. Bot.* 69: 5077-5087

Li, X., Wang, G., Jia, G., Li, L., Fu, J., Lübberstedt, T., Wang, G., Gu, R., Wang, J. (2018) QTL mapping in three connected populations reveals a set of consensus genomic regions for low temperature germination ability in *Zea mays* L. *Frontiers in Plant Science* 9:65

Ma, L., Guan, Z., Zhang, Z., Zhang, X., Zhang, Y., Zou, C., Peng, H., Pan, G., Lee, M., Chen, Y., Lübberstedt, T. (2018) Identification of QTLs for leaf-related traits in an IBM Syn10 DH maize population across three environments. *Plant Breeding* 137:127-138

Sanchez, D., Liu, S., Ibrahim, R., Blanco, M., Lübberstedt, T. (2018) Association mapping of seedling root traits in exotic derived doubled haploid lines of maize. *Plant Science* 268:30-38

Vanous, A., Gardner, C., Blanco, M., Martin-Schwarze, A., Flint-Garcia, S., Bohn, M., Edwards, J., Lübberstedt, T. (2018) Association mapping of flowering and plant height traits in germplasm enhancement of maize doubled haploid (GEM-DH) lines. *The Plant Genome* 11:170083

De la Fuente, G., Frei, U.K., Trampe, B., Nettleton, D., Lübberstedt, T. (2018) A diallel analysis of a maize donor population response to *in vivo* maternal haploid induction. I: Inducibility. *Crop Sci.* 58:1830-1837

Kansas:

Assefa, Y., P.V.V. Prasad, C. Foster, Y. Wright, S. Young, B. Pauley, M. Stamm, and I. Ciampitti. 2018. Major management factors determining spring and winter canola yield in North America. *Crop Sci.* 58:1-16.

Avjinder S. Kaler, Jeffery D. Ray, William T. Schapaugh, Antonio R. Asebedo, C. Andy King, E. E. Gbur, and Larry C. Purcell. 2018. Association mapping identifies loci for canopy temperature under drought in diverse soybean genotypes. *Euphytica* 214:135 <https://doi.org/10.1007/s10681-018-2215-2>.

Avjinder S. Kaler, Jeffery D. Ray, William T. Schapaugh, C. Andy King, and Larry C. Purcell. 2017. Genome-wide association mapping of canopy wilting in diverse soybean genotypes. *Theor. Appl. Genet.* 130: 2203–2217. DOI 10.1007/s00122-017-2951-z.

Channa, S.A., H. Tian, M.I. Mohammed, R. Zhang, S. Faisal, Y. Guao, M. Klima, M. Stamm, and S. Hu. 2018. Heterosis and combining ability analysis in Chinese semi-winter x exotic accessions of rapeseed (*Brassica napus* L.) *Euphytica.* 214(134):1-19.

Maduraimuthu Djanaguiraman, William Schapaugh, Felix Fritschi, Henry Nguyen and P.V. Vara Prasad. 2018. Reproductive success of soybean (*Glycine max* L. Merr.) cultivars and exotic lines under high daytime temperature. *Plant, Cell and Environment.* <https://doi.org/10.1111/pce.13421>

Michigan:

Boachon, B., Buell, C.R., Crisovan, E., Dudareva, N., Garcia, N., Godden, G., Henry, L., Kamileen, M.O., Kates, H.R., Kilgore, M.B., Lichman, B.R., Mavrodiev, E.V., Newton, L., Rodriguez-Lopez, C., O-Conno, S.E., Soltis, D., Soltis, P., Vaillancourt, B., Wiegert-Rininger, K., Zhao, D. 2018. Phylogenomic Mining of the Mints Reveals Multiple Mechanisms Contributing to the Evolution of Chemical Diversity in Lamiaceae. *Mol Plant.* 11(8):1084-1096.

Cai, L., Stegmeir, T., Sebolt, A., Zheng, C., Bink, M., Iezzoni, A. 2018. Identification of bloom date QTLs and haplotype analysis in tetraploid sour cherry (*Prunus cerasus*). *Tree Genetics and Genomes* 14:22.

Diepenbrock, C.H., Kandianis, C.B., Lipka, A.E., Magallanes-Lundback, M., Vaillancourt, B., Góngora-Castillo, E., Wallace, J.G., Cepela, J., Mesberg, A., Bradbury, P.J., Ilut, D.C., Mateos-Hernandez, M., Hamilton, J., Owens, B.F., Tiede, T., Buckler, E.S., Rocheford, T., Buell, C.R., Gore, M.A., DellaPenna, D. 2017. Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. *Plant Cell*. 29(10):2374-2392. doi: 10.1105/tpc.17.00475

Evans, J., Sanciangco, M.D., Lau, K.H., Crisovan, E., Barry, K., Daum, C., Hundley, H., Jenkins, J., Kennedy, M., Kunde-Ramamoorthy, G., Vaillancourt, B., Acharya, A., Schmutz, J., Saha, M., Kaepler, S.M., Brummer, E.C., Casler, M.D., Buell, C.R. 2018. Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. *Plant Genom. Mar*;11(1). doi: 10.3835/plantgenome2017.06.0055.

Hardigan, M.A., Laimbeer, F.P.E., Newton, L., Crisovan, E., Hamilton, J.P., Vaillancourt, B., Wiegert-Rininger, K., Wood, J.C., Douches, D.S., Farr, E.M. and Veilleux, R.E. 2017. Genome diversity of tuber-bearing *Solanum* uncovers complex evolutionary history and targets of domestication in the cultivated potato. *Proceedings of the National Academy of Sciences* 114(46), pp.E9999-E10008.

Liu, X., Enright, M., Barry, C.S., Jones, A. 2017. Profiling, isolation and structure elucidation of specialized acylsucrose metabolites accumulating in trichomes of *Petunia* species. *Metabolomics* 13: article 85. doi:[10.1007/s11306-017-1224-9](https://doi.org/10.1007/s11306-017-1224-9)

Tan, R., Serven, B., Collins, P.J. Zhang, Z., Wen, Z., Boyse, J.F., Gu, C., Chilvers, M.I., Diers, B.W., Wang, D. 2018. QTL mapping and epistatic interaction analysis of field resistance to sudden death syndrome (*Fusarium virguliforme*) in soybean. *Theor Appl Genet* 131: 1729.

Wang, X., Bao, K., Reddy, U., Bai, Y., Hammar, S., Jiao, C., Wehner, T., Ramírez-Madera, A., Weng, Y., Grumet, R., Fei, Z. 2018. The USDA cucumber (*Cucumis sativus* L.) collection: genetic diversity, population structure, genome-wide association studies, and core collection development. *Horticulture Research* Volume 5, Article number: 64.

Missouri:

Bohn, MO, JJ Marroquin, S Flint-Garcia, K Dashiell, DB Willmot and BE Hibbard. 2018. Quantitative trait loci mapping of western corn rootworm (Coleoptera: Chrysomelidae) host plant resistance in two populations of doubled haploid lines in maize (*Zea mays* l.). *J Econ Entomol.* 111:435–444.

Flint-Garcia, S. 2017. Kernel evolution: from teosinte to Maize. In *Maize Kernel Development*. Larkins, B (ed). CABI. Oxfordshire, UK. P. 1-15.

Glowinski, A, and S Flint-Garcia. Germplasm Resources for Mapping Quantitative Traits in Maize. In: Bennetzen, J, Flint-Garcia, S, Hirsch, C, and Tuberosa, R. (eds). *The Maize Genome*. Cham, Switzerland. Springer International Publishing AG. In press.

Vanous, A, C Gardner, M Blanco, A Martin-Schwarze, A Lipka, S Flint-Garcia, M Bohn, J Edwards, T Lubberstedt. 2018. Association mapping of kernel composition traits in germplasm enhancement of maize doubled haploid (GEM-DH) lines. *Plant Genome.* 12(1). doi:10.3835/plantgenome2017.12.0114

Vanous, A, C Gardner, M Blanco, A Martin-Schwarze, A Lipka, S Flint-Garcia, M Bohn, J Edwards, T Lubberstedt. 2018. Association mapping of flowering and height traits in germplasm enhancement of

maize doubled haploid (GEM-DH) lines. *Plant Genome*. 11(2).
doi: 10.3835/plantgenome2017.09.0083.

New York:

Baseggio, M., Murray, M., Magallanes-Lundback, M., Kaczmar, N., Chamness, J., Buckler, E. S., Smith, M. E., DellaPenna, D., Tracy, W. F. and Gore, M. A. 2018. Genome-wide association and genomic prediction models of tocochromanols in fresh sweet corn kernels. *The Plant Genome* In Press
doi:10.3835/plantgenome2018.06.0038

Byrne, P. F., Volk, G. M., Gardner, C., Gore, M. A., Simon, P. W., and Smith, S. 2018. Sustaining the future of plant breeding: The Critical role of the USDA-ARS National Plant Germplasm System. *Crop Science* 58:451-468. doi:10.2135/cropsci2017.05.0303

North Dakota:

Fiedler, J.D., E. Salsman, Y. Liu, M.M. de Jiménez, J.B. Hegstad, B. Chen, F.A. Manthey, S. Chao, S. Xu, and E.M. Elias, X. Li. 2017. Genome-wide association and prediction of grain and semolina quality traits in durum wheat breeding populations. *The Plant Genome* 10(3):1-12.

Lenz, R., and W. Dai. 2017. Mapping X-Disease Phytoplasma Resistance in *Prunus virginiana*. *Front. Plant Sci.* 8:2057. doi: 10.3389/fpls.2017.02057.

Osorno, J.M., A.J. VanderWal, M. Kloberdanz, J.S. Pasche, S. Schroder, and P.N. Miklas. 2017. A new slow darkening pinto bean with improved agronomic performance. Registration of 'ND-Palomino'. *J. Plant Reg.* doi:10.3198/jpr2017.05.0026crc.

Rahaman M., S. Mamidi, and M. Rahman. 2017. Association mapping of agronomic traits of canola (*Brassica napus* L.) subject to heat stress under field conditions. *Aust. J. Crop Sci.* 11(09): 1094-1105.

Simsek, S., M. Ozcan, F. Juhaimi, E. ElBabiker, and K. Ghafoor. 2017. Amino acid and sugar contents of wild and cultivated carob (*Ceratonia Siliqua*) pods collected in different harvest periods. *Chemistry of Natural Compounds* 53:1008-1009.

Somo, M., S.M. Pirseyedi, X. Cai, and F. Marais. 2017. Modified versions of the Lr62 translocation of wheat. *Crop Sci.* 57:1898-1905.

Stenger, J., and H. Hatterman-Valenti. 2018. 'NDMutant1': A novel determinate interspecific grapevine for genetic and physiological study and breeding applications. *HortScience* 53(2):261-263.

Ohio:

Jourdan, P. 2018. Short- and medium-term in vitro conservation and management of germplasm within the USDA's National Plant Germplasm System. *Acta Hort.* 1224, 31-38
DOI: 10.17660/ActaHortic.2018.1224.5 <https://doi.org/10.17660/ActaHortic.2018.1224.5>

Oregon:

Dillenberger, M.S., N. Wei, J.A. Tennessen, T.-L. Ashman, A. Liston. 2018. Plastid genomes reveal recurrent formation of allopolyploid *Fragaria*. *American Journal of Botany* 105: 862-874.

Wei, N., R. Cronn, A. Liston, T.-L. Ashman. 2018. Functional trait divergence and trait plasticity confer polyploid advantage in heterogeneous environments. *New Phytologist* 10.1111/nph.15508.

South Dakota:

Frerichs, Katelin E and L Xu. 2018. Identifying and characterizing salt-tolerant alfalfa (*Medicago sativa* subsp. *falcata*) germplasm. Proc. of the South Dakota Academy of Science.97:152-162.

NCRPIS:

Byrne, PF, Volk, GM, Gardner, CA, Gore, MA, Simon, PW, Smith, S. 2018. Sustaining the future of plant breeding: The critical role of the USDA-ARS National Plant Germplasm System. Crop Science 58(2)451-46. <https://doi.org/10.2135/cropsci2017.05.0303>.

Korus, K, Lang, JM, Adesemoye, AO, Block, CC, Pal, N, Leach, JE, and Jackson-Ziems, TA. 2017. First Report of *Xanthomonas vasicola* causing Bacterial Leaf Streak on Corn in the United States. Plant Disease. 101(6):1030. doi: 10.1094/PDIS-10-16-1426-PDN

Hu, S, Sanchez, D, Wang, C, Lipka, AE, Hin, YI, Gardner, CA, Lübberstedt, T. 2017. Brassinosteroid and Gibberellin control of seedling traits in maize (*Zea mays* L.). Plant Science 263:132-141.

Isbell TA, Cermak SC, Marek LF. 2017. Registration of Elizabeth *Thlaspi arvense* L. (Pennycress) with Improved Non-dormant Traits. Journal of Plant Registrations 11:311-314 doi:10.3198/pr2016.12.0073crg

Mathew F, Olson T, Marek L, Gulya T, and Markell S. 201X. Identification of sunflower (*Helianthus annuus*) accessions resistant to *Diaporthe helianthi* and *Diaporthe gulyae*. Plant Health Progress (PHP10-17-0060-RS; Accepted 06-Dec-2017).

Pal, N, Gardner, C, and Block, CC. 2018. A real-time PCR differentiating *Pantoea stewartii* subsp. *stewartii* from *P. stewartii* subsp. *indologenes* in corn seed (Accepted, Plant Disease).

Seiler GJ, Qi LL, and Marek LF. 2017. Utilization of Sunflower Crop Wild Relatives for Cultivated Sunflower Improvement. Crop Sci 57:1083-1101 doi:10.2135/cropsci2016.10.0860

Vanous, A, Gardner, C, Blanco, M, Martin-Schwarze, A, Lipka, A, Flint-Garcia, S, Bohn, M, Edwards, J, Lübberstedt, T. 2018. Association mapping of kernel composition traits in germplasm enhancement of maize doubled haploid (GEM-DH) lines. Plant Genome. 12(1). doi:10.3835/plantgenome2017.12.0114

Vanous, A, Gardner, C, Blanco, M, Martin-Schwarze, A, Lipka, A, Flint-Garcia, S, Bohn, M, Edwards, J, Lübberstedt, T. 2018. Association mapping of flowering and height traits in germplasm enhancement of maize doubled haploid (GEM-DH) lines. Plant Genome. 11(2). doi: 10.3835/plantgenome2017.09.0083.

Warburton ML, Rauf S, Marek L, Hussain M, Ogunola O, and Sanchez Gonzales, JdJ. 2017. The use of crop wild relatives in maize and sunflower breeding. Crop Sci 57:1227-1240 doi:10.2135/cropsci2016.10.0855