Plant Germplasm Conservation and Research:

A three-way partnership:
ARS--CSREES--SAES

Background Material prepared by Ann Marie Thro with emphasis on CSREES programs in Plant Germplasm

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This document describes the multi-state project structure of CSREES collaboration in the National Plant Germplasm System (NPGS). Included are examples of activities funded; tables of measurable outputs for the most recent available years, FY 2003 and 2004; and tables of funding levels for the years FY 2000-2004. The document also describes additional CSREES-funded activities in the area of plant germplasm.

Summary

The National Plant Germplasm System (NPGS) has responsibility for the conservation, maintenance, preservation, and use of the Nation's plant germplasm resources. The NPGS has its roots in the 19th century; yet converging political and technical factors make its collections more valuable today than at any previous time. The ability to use plant genetic diversity, quickly and with creativity, is an important part of this national asset.

Today's National Plant Germplasm System is a federal-state collaborative program with over 50 years of service to U.S. agriculture, although its antecedents trace back to the beginnings of USDA and the land-grant system. USDA-ARS has primary responsibility for management of the NPGS. CSREES provides significant funding to the NPGS, averaging over $3 million/yr for the past five years, through Hatch Act Funds, both the Multistate Research Fund (MRF) (25% of the Hatch appropriation) and allocations to individual states.

The state agricultural experiment station (SAES) directors allocate an annual off-the-top amount from the annual Hatch Act appropriated funds managed by CSREES. This CSREES/SAES funding for the NPGS has been about 10 % of the total. It is contributed through support to five projects: four multi-state research projects and one national research support project. Over the past five years, these funds to NPGS, plus funds from individual state Hatch allocations, have averaged over $3 million per year. Other funding sources are ARS (about 90% of overall NPGS support) and the individual host state of each project.

Decisions regarding the use of Hatch funds are made at the ESCOP and SAES levels. SAES participation in the NPGS is structured in four multi-state research projects and one national research support project. Members of these projects include the ARS staff of the regional active site, and SAES scientists. Typically, ARS project members conserve and curate plant

germplasm, while SAES members realize its value through characterization, evaluation, and use. SAES project members also contribute advice to the regional active sites.

The state and federal scientists and administrative advisors who participate in the five ESCOP projects constitute a source of advice to NPGS management. They interact with over 40 public/private sector Crop Germplasm Committees (CGCs) and the Plant Germplasm Operations Committee (PGOC) coordinated by ARS.

Beyond the five collaborative projects that form the backbone of the system, the three partners -- ARS, CSREES/SAES-- have significant additional investment in plant germplasm. ARS is the primary investor in plant germplasm conservation and curation. Both ARS and CSREES/SAES invest in research to characterize, evaluate, and use plant germplasm. The CSREES/SAES activities are funded by base (Hatch) funds and other sources, including competitive grants.

As a result of the funding allocation process, including the multi-state committee structure, individual state Hatch projects, and other funding sources, state/federal collaboration in NPGS is supported on various levels,

- in planning and managing the NPGS, and,
- in conducting the research through which the value of the NPGS is realized.

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1. Introduction

The National Plant Germplasm System (NPGS) has responsibility for the conservation, maintenance, preservation, and use of the Nation's plant germplasm resources. **Converging political and technical factors make the plant germplasm collections of the NPGS more valuable today than at any previous time.**

(a) American agriculture has enjoyed an unprecedented era of security and stability. In future, impacts of globalization, terrorism, erratic climate, and other factors will demand a **higher degree of flexibility in agriculture**.

(b) **New molecular tools** make germplasm management and characterization **more efficient** and gene discovery research **more powerful**

(c) Increasing **consumer interest in diverse** fruits, vegetables, and grains is creating new market niches for specialty producers. These new niches create additional value and jobs from a given level of production.

(d) **International markets** are becoming increasingly quality-exigent.

(e) **Access** for collecting additional plant germplasm from different geographic regions is **increasingly restricted**. For example, wild potato species collected by a U.S.–Peru collaborative expedition several years ago have not been allowed to leave Peru. Fewer new accessions will be added to genetic resources now in collections and breeders' nurseries.

As a results of such trends, plant genetic diversity--and the ability to use diversity quickly and in many ways--are increasingly important national assets (e.g., Qualset and Shands, 2005).

2. Legal basis and funding for the National Plant Germplasm System

The Agricultural Marketing Act of 1946 created the legal basis for the federal / state partnership that emerged for germplasm resources, including the major components of the NPGS. The partners are USDA/ARS, CSREES, and the State Agricultural Experiment Stations (SAESs). The NPGS is funded through a partnership diverse of State and Federal resources.

USDA/ARS has primary responsibility for management of the NPGS. ARS also organizes a network of federal-state NPGS committees structured by crop, the Crop Germplasm Committees or CGCs, plus a national administration committee, the Plant Germplasm Operations Committee, or PGOC. The CGCs and PGOC works with five ESCOP projects to coordinate NPGS priorities and activities.

ESCOP, representing the SAES directors, contributes to the funding, planning and management of the NPGS through five projects (Table 1). These include four multi-state projects, one per region: NC-7, NE-9, S-9, W-6; and one national project, NRSP-6, the inter-regional potato introduction project. These five projects correspond to five NPGS "active sites" where crop collections are maintained and curated. The SAES directors in each region decide on an annual off-the-top contribution from the Multi-state Research Fund (MRF) for the project in that region. The contribution amount for NRSP-6 is decided across all regions.

The MRF is itself a proportion, currently 25%, of the CSREES-managed annual Hatch Act appropriated funds, or base funds. The MRF contribution to NPGS ranges from about 8% of all funds in NE-9 to 18% in NC-7 and 22% in NRPS-6 (Appendix 1). Total MRF contribution to the NPGS has averaged about $3.2 million per year over the five years 2000-2004.

Other funding sources for the NPGS include ARS (about 90% of overall NPGS support) and the individual host state of each project. States contributions vary widely and are greatest in states that host an active site (Appendix 1).

Table 1. Projects in the National Plant Germplasm System. There are four multi-state projects and one national research support project.

NE-9: Conservation and Utilization of Plant Genetic Resources (Geneva NY). ***Emphasis:*** Tomato, onion, selected crucifers, celery, winter squash, radish, other vegetables, and buckwheat. The clonal collections include apple, grape, and cherry. Holdings – approx. 11,800 accessions. Current Term: Oct 2003-Sept. 2008.
NC-7: Conservation, Management, Enhancement & Utilization of Plant Genetic Resources (Ames IA). ***Emphasis:*** Maize, sunflower, root and bulb vegetables, forage and turf grass, crucifer, herbaceous ornamentals, woody landscape plants, leafy vegetable, cucurbits, clover and special purpose forage legumes. Holdings – approx. 84,100 accessions. Current Term: Oct 2002 - Sept. 2007.
S-9: Plant Genetic Resources Conservation and Utilization (Griffin GA)**.** ***Emphasis:*** Capsicum, clover, special purpose forage legumes, cucurbit, warm season turf grass, peanut, sorghum, sweet potato, cowpea, vegetables (okra, pepper, watermelon, squash, eggplant, gourds), mung bean, legumes (guar, winged bean), bamboo, castor bean, sesame, pearl millet. Holdings – approx. 47,800 accessions. Current Term: Oct 2003-Sept. 2013.
W-6: Plant Genetic Research Conservation and Utilization (Pullman WA). ***Emphasis:*** Forage and turf grasses, beans, cool season food legumes (pea, lentil, chickpea, fava bean, lupine, etc.), lettuce, safflower, onion relatives, and forage legume crops, selected ornamental and medicinal species. Holdings – approx. 72,400 accessions. Current Term: Oct 2003-Oct 2008.

NRSP-6: Inter-Regional Potato Introduction Project (Sturgeon Bay WI).
Holdings – approx. 5,600 accessions. Current Term: Oct 2005-Sept. 2010.

3. The regional projects

The regional projects (Table 1) are the backbone of the state-federal NPGS partnership. The members of each project include ARS participants from the regional active site and one or more state researchers from each participating SAES in the region. There may be SAES researchers from outside the region, if the active site includes crops with broad geographic importance. For example, the corn breeder from Delaware is a member of NC-7. Each project has an Administrative Advisor from the Director's Office of an SAES in the region, and a CSREES liaison.

NRSP-6 is the only NPGS project with administrative advisors from all four ESCOP regions. Also, NRSP-6 is the only one of the several NPGS single-crop collections that is managed in collaboration with ESCOP, and the only one that receives CSREES funding from Hatch regional funds. This is because the potato crop is important throughout the U.S. Other single-crop collections are of local or regional importance--for example, the date palm germplasm collection in California. The scientists and administrative advisors who participate in the multi-state projects constitute a source of advice to the ARS directors of the regional active sites and the potato collection.

4. Planning and managing the NPGS

The five ESCOP projects interact in matrix fashion with over 40 public/private sector Crop Germplasm Committees (CGCs) and the Plant Germplasm Operations Committee (PGOC), coordinated by ARS. The annual cycle of meetings of the five projects and the various committees are the venues in which ARS and the SAESs coordinate NPGS planning and management.

The USDA Economic Research Service (ERS) contributes economic appraisals that are relevant to planning for the NPGS. For example, a study by Day Rubenstein *et al*., 2005, found benefits of billions of dollars for the U.S. and the world .

5. NPGS research objectives

To achieve benefits such as those documented by the ERS, the NPGS projects work on four objectives. Each project states its objectives somewhat differently (Appendix 2), but they are similar and can be summarized as:

1. Conserve
2. Characterize and evaluate
3 Understand
4 Use and encourage use *(utilization).*

ARS is the primary investor in plant germplasm conservation and curation. Both ARS and CSREES/SAES invest in research to characterize, evaluate, and use plant germplasm. The CSREES/SAES activities are funded by base (Hatch) funds and other sources, including competitive grants.

<u>A note about the terms "characterize", "evaluate" and "use" in the NPGS context</u>. In the NPGS context, to "characterize" germplasm generally refers to assessing characters that tend to be constant over environments, such as flower color. To "evaluate" germplasm generally refers to assessing aspects that must be measured over several seasons and locations, such as adaptation or yield stability. "Use" of germplasm can take several forms:

- Most commonly, germplasm accessions are used as parents to contribute valuable genes to crosses with adapted parents. These crosses are part of long-term germplasm enhancement research.
- Depending on the attributes of an individual accession, germplasm accessions can also be used as parents in crosses from whose progeny varieties will be selected; or even,
- Developed, "as is", into a variety.
- Increasingly, germplasm accessions are used as materials for basic research on aspects of plant biology and genetics.

Examples of SAES/CSREES plant germplasm research activities are presented by region on the following pages. Headings indicate which objective the research addresses.

For ARS research activities, see ARS National Program 301, Plant Genetic Resources, Genomics and Genetic Improvement, on the ARS web page, at (http://www.ars.usda.gov/research/programs/programs.htm?NP_CODE=301). Also see documentation prepared to accompany the ARS National Program 301 Customer and Assessment workshop, October 31, 2005.

6. Base-funded activities in the NPGS

Examples of activities funded by CSREES-managed Hatch funds in NC-7

CONSERVATION, MANAGEMENT, ENHANCEMENT AND UTIIZATION OF PLANT GENETIC RESOURCES

Agronomic crops

Utilize:

Example: UNIVERSITY of NEBRASKA

Foxtail Millet: Test developed advanced lines of foxtail millet derived from adapted by P.I. crosses, in multi-location trials across the region. Similar to proso trials covered in objective one except emphasis is on forage quality, forage yield and forage yield with secondary emphasis on seed yield as well as pest and pH tolerance. Amaranth: Amaranth work is facilitated through cooperation with an amaranth breeder at the Plant Introduction Station at Ames, IA. We have been working to place the non-shattering trait in adapted germplasm. Through an extension approach, we will coordinate with the regional effort to provide germplasm information to producers and colleagues in Nebraska. This will be a part of at least one field day each year. Forty-nine white-flowered sweetclover [Melilotus alba Desr.] genetic stocks and N56, a yellow-flowered sweetclover [Melilotus officinalis (L.) Lam.] genetic stock, were developed jointly by USDA-ARS and the Agricultural Research Division, Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln and were jointly released in May, 2004. Waxy proso haas been approved for release by cultivar relase committee. Decision on how to best balance cost with intellectual property rights has delayed final decision on relase method. Seed has bee increased and should be available for commercial production the spring. Pending approval, a new Canada wildrye cultivar will be released in 2005 as well as several Canada wildrye germplasms that can be grown as source identified and tested cultivars. These germplasms and cultivar trace to plant collections that were made from remnant North American prairies sites in 1989. Germplasm releases of the native legumes, Partridge pea and Illinois bundle flower are pending. **Impact** The genetic stocks were developed over more than three decades of cooperative sweetclover genetic research and contain unique combinations of genes and traits which are described and documented including the presence or absence of coumarin. Seed of these genetic stocks has been entered into the U.S. Department of Agricultures National Plant Germplasm System and is available for research.

Publications: 2004/10 to 2005/09

1. Vogel, K.P., H.J. Gorz, and F.A. Haskins. 2005. Registration of N30-N56, N741, N743, N745, N747, U362, U363, U367, U369-U374, U389-U394, U396-U398, and U500 Sweetclover Genetic Stocks. Crop Sci. 45:1675-1677.
2. Vogel, K. P., D. Tober, P. E. Reece, D. D. Baltensperger, G. Schuman, and R. A. Nicholson. 2005. Registration of NU-ARS AC2 Crested Wheatgrass. Crop Sci. 45(1):416-417. Univ. of Nebraska Agr. Res. Div. J. Series No. 14498.
3. Vogel, K. P., D. Tober, P. E. Reece, D. D. Baltensperger, G. Schuman, and R. A. Nicholson. 2005. Registration of Haymaker Intermediate Wheatgrass. Crop Sci. 45(1):415-416. Univ. of Nebraska Agr. Res. Div. J. Series No. 14497.
4. Vogel, K. P., P. E. Reece, D. D. Baltensperger, G. Schuman, and R. A. Nicholson. 2005. Registration of Beefmaker Intermediate Wheatgrass. Crop Sci. 45(1):414-415. Univ. of Nebraska Agr. Res. Div. J. Series No. 14499.

Utilize:

Example: UNIVERSITY OF WISCONSIN

Corn breeding populations were developed of great value for a silage breeding program; these populations contain germplasm obtained from the PI station at Ames. In cooperation with the Germplasm Enhancement of Maize project at Ames, accessions continue to be evaluated and introgressed that greatly improve forage yield and nutritional quality of the releases from the breeding program. This germplasm is unique for both its forage characteristics and genetic background, and is essential to the success of the Univ. of Wisconsin silage breeding program. Ten sh2 sweet corn inbreds were released that derived from 50% Mexican Dent germplasm. These lines had excellent resistance to MDMV (Maize Dwarf Mosaic Virus) and common rust (*Puccinia sorghi*). The source of the Mexican Dent germplasm was a population that Everett Gerrish at Cargill had developed and donated to the PI collection at Ames. In 2004, three sugary1 alleles were identified in germplasm received from the North Central Regional Plant Introduction Station.

Characterize and evaluate -- Utilize:

Example: KANSAS STATE UNIVERSITY

The entire Brassica napus collection was seeded in the field at Manhattan, KS, spring 2003 with the primary goal of determining spring or winter growth habit. Additional important information will also be collected including taxonomy, flowering date, heat tolerance, and other important traits that the environment will allow differentiation. B. napus not only has importance producing a food grade oil (canola) but also has great potential to contribute to the production of bio- based energy sources. This project, as well as many other similar evaluations, will add value to the germplasm stored at the NCRPIS, encourage its use in cultivar development, and lead to an enhanced crop genetic pool. Information dealing with the accessions stored in the system is made available through the GRIN system. Additional germplasm to enhance the collection and fill voids of important genetic traits will continue to be collected and evaluated. **Progress:** 2004/01 TO 2004/12 Over the past several years, accessions of B. napus from the NCRPIS collection have been important in developing the germplasm base needed to develop canola cultivars adapted to the southern Great Plains. These accessions are included in the pedigrees of many lines in the advanced stages of evaluation. This material will be utilized and reevaluated over the coming years and will help solve some of the problems associated with rapeseed production in the Great Plains. **Impact** The impacts of successful germplasm conservation, management, enhancement and utilization can be measured in the introduction of economically viable new crops and cultivars and new uses for existing crops based on a thorough understanding of their traits and properties. Canola is a crop that will have a major economic impact on Great Plains agriculture. Including canola in a wheat rotation will net about $50 per acre more than growing wheat alone. **Publications:** 2004/01 TO 2004/12

1. Rife, C.L., D.L. Auld, H.C. Minor, W.F. Heer, D.D. Baltensperger, L.A. Nelson, and D. Bordovsky. 2003. Registration of 'Abilene' Rapeseed. Crop Sci. 43:2306-2307.
2. Rife, C.L. 2003. The Consistency of Winter Canola East of the Rocky Mountains. In Proceedings of the US Canola Association Research Conference. Washington, D.C.
3. Rife, C.L. 2003. Evaluation of winter hardiness in oilseed rape in the United States. In Proceedings of the 11th International Rapeseed Congress. Copenhagen, Denmark. Groupe Consultatif International de Recherche sur le Colza. Pp. 999 - 1001.
4. Sidlauskas, G. and C. L. Rife. 2003. The Effect of Agronomic and Climatic Factors on Protein Content in Spring Oilseed Rape (Brassica napus L.). 11th Internat’l. Rapeseed Congress. Copenhagen, Denmark. P. 23.
5. Rife, C.L. 2003. Effects of Environmental Stress on Growth and Development in Oilseed Rape. 11th International Rapeseed Congress. Copenhagen, Denmark. Groupe Consultatif International de Recherche sur le Colza. July 9. Invited Presentation.
6. Rife, C.L., 2003. Research and Production Updates for the Southern Great Plains. US Canola Association Research Conference. Washington, D.C. February 25. Invited Presentation.
7. Rife, C.L. 2003. National Winter Canola Variety Trials. Great Lakes Region Annual Canola Meetings, Carbondale, IL. March 14. Invited Presentation.

Characterize and evaluate -- Utilize:

Example: NORTH DAKOTA STATE UNIVERSITY

Screening of 11 new crop species and three check crops was conducted at the Carrington, Langdon, and Minot Research Extension Centers, and Prosper. New crops included edible grain, oilseed, and fiber crops. A seeding date trial was also conducted that evaluated several oilseed and fiber new crop species. Based on maturity and seed or biomass yield; cuphea (*Cuphea viscosissima* Jacq. x C. *lanceoloda f. silenoides* W.T. Aniton, line PSR23), niger [*Guizotia abyssinica* (L.f.) Cass.], teff [*Eragrostis tef* (Zucc.) Trotter], and kenaf (*Hibiscus cannabinus* L.) indicated moderate to high adaptation. However, the new crops exhibited several agronomic deficiencies including delayed emergence and slow growth (cuphea), plant lodging, late and prolonged flowering, and seed shatter. Fertility studies with spearmint (*Mentha spicata* L.) showed excessive nitrogen fertilizer additions were inefficient in producing yield increases and resulted in nitrogen movement beyond the rooting depth that may cause ground water concerns. **Impact:** Screening of potential new crops and entrance of a selected few into small scale commercial production may require many years, perhaps even decades before any become significant or major crops grown in a new region. This first evaluation of new crops is extremely important and in the past has identified several crops (sunflower, dry bean, soybean, and more recently canola) that are now major crops in North Dakota and the surrounding region. During the transition from new to alternative crop status, definition of best management practices for new crops becomes essential for successful crop production. Spearmint fertility management can approach 20% of annual production costs. Proper management of the nutrient used in the greatest quantities, nitrogen, would improve fertilizer efficiency and prevent ground water contamination with leached nitrates from excessive precipitation.

Horticultural Crops

Understand -- Utilize:

Example: OHIO STATE UNIVERSITY

Germplasm evaluation at The Ohio State University OARDC aims to characterize and develop plant genetic resources for corn, wheat, soybeans and tomatoes. Efforts concentrate on end-product quality, disease resistance, genetic variation, and breeding methodology. This report summarizes recent efforts develop new sources of quality traits, disease resistance, and DNA-based Molecular Markers for germplasm characterization. We developed inbred backcross populations based on Lycopersicon esculentum (Hawaii 7998 and PI 114490), L. pimpinellifolium (PI 128216), and L. hirsutum (LA 407). These populations serve as a resource for simultaneous breeding, trait introgression, and gene discovery. The LA407 population has been evaluated for the improvement of color and lycopene content in red-fruited tomatoes. Within this population we discovered two L. esculentum quantitative trait loci (QTL) associated with improved color. Epistatic interactions were identified between the two L. esculentum loci and between L. esculentum loci and an LA407 introgression on chromosome 7. In addition LA 407 is a source of resistance to bacterial canker caused by Clavibacter michiganensis subsp. michiganensis (Cmm). Two QTL from L. hirsutum, Rcm 2.0 and Rcm 5.1, control resistance to Cmm. Progeny testing of recombinant plants narrowed the QTL location for Rcm 2.0 to a 4.4cM interval between TG537-TG091 and to a 2.2cM interval between CT202-TG358 for Rcm 5.1. In order to develop genetic markers appropriate for the characterization of L. esculentum populations, we developed a bioinformatic pipeline for discovery of Single nucleotide polymorphisms (SNPs) in existing sequence databases. We have identified 101 candidate SNPs in 44 genes for use within cultivated germplasm pools. SNPs between TA496 and Rio Grande have a high probability (53%) of detecting polymorphisms between other L. esculentum varieties. Twenty-six SNPs in 18 unigenes were mapped to specific chromosomes. Two SNPs, LEOH23 and LEOH37, were shown to be linked to quantitative trait loci contributing to fruit color within elite breeding populations. These results suggest that the growing databases of DNA sequence will yield information that facilitates improvement within the germplasm pools that have contributed to productive modern varieties. **Impact** In the Great Lakes region, the lack of resistance to bacterial pathogens in tomato varieties leads to frequent application of copper sprays and the failure of growers to adopt disease forecasting tools that minimize control sprays for fungal pathogens. The disease forecasting models do not predict bacterial infection and growers often default to a calendar application of copper and fungicide tank mixes. The lack of resistance to bacterial spot and bacterial canker therefore adds to the cost of production beyond loss of yield and quality due to disease. The germplasm released from this project will help lead to varieties that contain a higher level of resistance to bacterial disease. A limitation to applying marker-assisted selection to the practice of breeding tomato varieties is that the low level of polymorphism between L. esculentum has precluded map coverage with sufficient density to fully use the power of modern biometrical techniques for trait discovery, genetic mapping and breeding. The lack of genetic markers that detect differences between elite breeding lines of tomato has prevented a detailed study of most traits of economic importance within genetic backgrounds that are relevant to plant breeders, growers, and processors. Results from our studies suggest that it will be possible to develop molecular-marker systems that can be applied to elite germplasm. **Publications:** 2004/01 to 2004/12:

1. Coaker G., B. Willard, M. Kinter, E. J. Stockinger, and D. Francis. 2004. Proteomic analysis of resistance to bacterial canker of tomato. Molecular Plant Microbe Interactions. 17:1019-1028.
2. Coaker G., and D. Francis. 2004. Mapping, genetic effects, and epistatic interaction of two bacterial canker resistance QTLs from Lycopersicon hirsutum. Theor Appl Genet. 108:1047-1055
3. Yang, W., X. Bai, E. Kabelka, C. Eaton, S. Kamoun, E. van der Knaap, and D. Francis. 2004. Discovery of single nucleotide polymorphisms in Lycopersicon esculentum by computer aided analysis of expressed sequence tags. Molecular Breeding. 14: 21-34.
4. E. Kabelka, W. Yang, and D. M. Francis. 2004. Improved Tomato Fruit Color within an Inbred Backcross Line Derived from Lycopersicon esculentum and L. hirsutum Involves the Interaction of Loci. J. Amer. Soc. Hort. Sci. 129:250-257

Conserve -- Utilize:

Example: PURDUE UNIVERSITY.

An apple and a pear are being released and patent application is underway. The apple CrimsonCrisp is a red, very crisp, apple with very high quality that ripens in the middle of September. It has performed well in our experimental farm in Lafayette, and shows excellent performance in Ithaca, New York, Western Italy, and in France. It contains genetic resistance to scab, a serious disease of apple. CrimsonCrisp will be licensed to Adams County nursery. The new pear to be named Ambrosia is a very large pear with excellent quality, ripening in the middle of August with tolerance to fire blight. Ambrosia pear is being licensed to Gardens Alive Nursery. A germplasm exchange trip was completed in Italy for Eruca sativa (cultivated arugula) and *Diplotaxix tenuifolia* (wild arugula); a total of 83 accessions were obtained for the National Plant Germplasm System of the United States. The NewCROP Website received 11, 026, 076 requests for files and a total of 5,380, 719 pages for the year 2003.

Examples of activities funded by CSREES-managed Hatch funds in NE-9

CONSERVATION AND UTILIZATION OF PLANT GENETIC RESOURCES

Horticultural Crops

Utilize:

Example: UNIVERSITY OF NEW HAMPSHIRE

Conventional pedigree breeding techniques, principally backcross and recurrent selection systems, are being used two develop improved germplasm and cultivars within the following taxa: Cucurbita pepo (acorn squash, gourds, ornamental pumpkins, and hull-less snackseed pumpkins); Cucurbita maxima (semi-bush kabocha and processing squash); Cucurbita moschata (round-fruited cultigens that can be used in interspecies crosses with C. maxima); Cucumis melo (cantaloupe, honeydew and Galia melons); and Lycopersicon esculentum (orange-fruited tomato). In melon, resistance to two diseases, Fusarium oxysporum f.sp.melonis (races 1 & 2 of fusarium wilt)and powdery mildew (primarily races 1 and 2 of Sphaerotheca fuliginea) is being incorporated into improved germplasm using the backcross technique and a seedling (root dip) inoculation technique. Tolerance to powdery mildew is being incorporated into pumpkin and acorn squash breeding lines using the backcross technique and field screening. Field screening is being utilized for selection pumpkins and squash with tolerance to fruit rots (principally fruit rots caused by Fusarium solanum and related species and by Xanthomonas campestris pv. cucurbitae. During the summer of 2003, seven experimental hybrids of yellow straightneck squash carrying the glabrous trait (smooth, spineless foliage) were evaluated in replicated tests along with commercial check varieties. Four of the glabrous hybrids were as early and productive as the best commercial hybrid tested. The glabrous trait reduced damage to fruit during harvesting and prevented skin irritation associated with the normal presence of trichomes. These hybrids also performed well in other regional trials, and at least one of these is scheduled for commercial seed production in 2004. Fifteen experimental acorn F1 hybrids with tolerance to powdery mildew were evaluated in 2003. All hybrids had restricted vine growth (semi-bush to bush), and were adapted to close spacing and plastic mulch culture combined with drip irrigation. Several of these hybrids were productive and had superior eating quality to currently available commercial acorn varieties. A gourd breeding program has resulted in the development of several inbred lines of spoon and egg gourd that are earlier and more productive than currently available varieties, exhibit additional color patterns, and have the bush habit of growth for easier culture. Several of these lines are being released for commercial seed production in 2004. A breeding program to develop orange-fruited tomatoes with better flavor and adaptability to short growing seasons has resulted in the production of several experimental F1 hybrids that have been tested over the past 4 years. **Progress:** 2003/10 to 2004/09 An early, determinate, orange slicing tomato, Orange Blossom, was released through the New Hampshire Agricultural Experiment Station (NHAES) in 2003 and seed was offered commercially in 2004. Efforts have been underway to develop semi-determinate and indeterminate midseason orange hybrids that could be used for trellis culture. During the summer of 2004, 20 experimental, orange-fruited tomato hybrids were evaluated for maturity, plant vigor, fruit size, resistance to cracking, fruit firmness, and flavor. Three indeterminate hybrids performed well in 2004 and will be evaluated in multiple locations with trellis culture in 2005. Based on results in 2002 and 2003, the six best NH kabocha squash hybrids were evaluated in 2004 at Woodman Horticultural Research Farm, Durham, NH and also distributed for evaluation at several locations in the Northeast. Based on plant vigor, yield, plant growth habit, fruit size, storage performance, and taste evaluation, three hybrids, NH957, NH964, and NH972, have been selected for release for commercial seed production. These hybrids have restricted vine growth (short internodes) for easier culture. Seed of these hybrids is expected to be available for commercial sale in fall of 2005. Summer squash hybrids carrying the gl-1 glabrous (smooth foliage) gene are being produced commercially for introduction, and breeding work is continuing to expand the number of breeding lines carrying this trait. Cooperative efforts are underway to introduce powdery mildew tolerance into these breeding lines. Several new strains of spoon and egg gourd lines are being produced commercially for introduction into the seed trade. Breeding work continues to expand the number of color and pattern traits in these gourds, especially in the spoon gourds. **Impact** The new tomato variety, Orange Blossom, is the first early slicing tomato in the orange class that has eating quality on a par with red varieties. It not only has 10 times more carotene (provitamin A) than red varieties, but also adds a bright attractive color to salads and other vegetable dishes. The new egg and spoon gourd varieties being released will help extend gourd culture to more northerly regions, and should be an attractive addition for the autumn season at retail roadside markets for use in table decorations and other ornamental purposes. Adoption of the new glabrous summer squash varieties should eliminate much of the harvest injury to fruit from leaf and petiole spines, and eliminate irritation of skin to field workers. The breeding program to develop better eating quality in acorn squash is part of an overall research program to educate growers, consumers, produce managers, and produce distributors about factors that determine eating quality in squash, and to develop quality guidelines for winter squash. Fruit of kabocha squash is similar in size, quality and appearance to the popular buttercup squash, and because of more consistent quality, kabocha varieties are gradually replacing buttercup in supermarkets. Kabocha varieties being developed at the New Hampshire Agricultural Experiment Station are unique in having restricted vine growth and uniform leaf canopies. These varieties are more amenable to sustainable weed control practices and irrigation technologies, and so should fine favor among most vegetable growers. Orange tomatoes are an attractive vegetable and their content of provitamin A is 10 times that of red tomatoes. The entry of these tomatoes into the fresh vegetable market has been impeded by lack of varieties, either modern or heirloom, with good flavor. The new, more flavorful orange tomatoes being introduced through the New Hampshire Agricultural Experiment Station could have a huge impact on consumer acceptance and demand for orange tomatoes.

Utilize:

Example: CONNECTICUT AG. EXPERIMENT STATION, NEW HAVEN

In cooperation with organic growers around the state, we will test vegetable accessions from the Northeast Regional Plant Germplasm Unit, in comparison with standard varieties, for resistance to key insect pests: cucurbits for resistance to squash bugs and cucumber beetles, beans for resistance to Mexican bean beetles and potato leafhoppers, and eggplants and brassicas for resistance to flea beetles. We will increase insect pressure where possible by collecting pest insects on organic farms and releasing them into experimental plots at our research farm: using board traps for squash bugs, attractant traps for cucumber beetles, and vacuuming for flea beetles. **Progress:** 2004/01 to 2004/12 In cooperation with the project "Restoring Our Seed," we have been intercrossing mizuna, tatsoi, and scarlet turnip, with a goal to create a diverse germplasm that will be tested for resistance to flea beetles. In cooperation with the "Public Seed Initiative" project, we sponsored a workshop at our experimental farm on seed saving for farmers, seed savers, and small seed companies. Also, we participated in a farmer/scientist forum to identify needs for vegetable breeding to improve or develop varieties suitable for organic vegetable growers. **Impact** All of these projects will result in increased regional capacity for vegetable breeding and seed production and in selection for traits needed in regional vegetable production, such as resistance to insects. At our workshop on seed saving and processing, 15 farmers and people from seed companies attended and used the equipment in the Mobile Seed Processing Unit to process their own seed.

Characterize and evaluate -- understand -- Utilize:

Example: PENNSYLVANIA STATE UNIV

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During the past several years hundreds of tomato accessions from different species of tomato, including the cultivated species *Lycopersicon esculentum* and wild species *L. hirsutum, L. pimpinellifolium, L. chilense, L. pennellii, L. peruvianum* and *L. cheesmanii,* were screened for various horticultural characteristics, including disease resistance, abiotic stress tolerance and fruit quality. Evaluations were conducted in the greenhouse, growth chamber and under field conditions. Several accessions were identified with one or more desirable horticultural characteristics, including resistance to fungal diseases early and late blight, tolerance to salt, cold or drought stress, and high fruit lycopene or soluble solids contents. Many intra- and interspecific populations were developed for genetic studies such as determination of heritability and mapping of controlling genes and for breeding purposes. The research resulted in gaining a better understanding of the genetic controls of several important horticultural characteristics and facilitated crop improvement through directed plant breeding. Transfer of desirable genes and characteristics from wild species into the cultivated tomato has resulted in the development of improved germplasm, a prelude to the development of improved breeding lines and cultivars. **Impact:** The identification of tomato germplasm with disease resistance, abiotic stress tolerance and excellent fruit quality has provided valuable plant materials for genetic studies and crop breeding in tomato. Characterization of the genetic controls of tomato resistance to early blight and late blight, tolerance to salt, drought and cold stress, and high fruit quality has facilitated breeding tomatoes for improved horticultural characteristics using both traditional protocols of plant breeding and contemporary techniques of molecular genetics. Such investigations as well as the recent breeding efforts have already resulted in the development of improved tomato germplasm, which are useful for development of commercial lines and cultivars of tomatoes.

Examples of activities funded by CSREES-managed Hatch funds in S-9

PLANT GENETIC RESOURCES CONSERVATION AND UTILIZATION .

Agronomic crops

Utilize:

Example CLEMSON UNIVERSITY

Seed of soybean (*Glycine max*) germplasm line, LG00-3372, were obtained from the developer, Dr. Randall Nelson (Curator, Soybean Germplasm Collection), USDA-ARS, Urbana, Illinois. The line was released by USDA-ARS in 2004 because of genetically diverse parentage and high seed yield performance, 2002-2003, in tests in mid-western states. It is a maturity group III line and has an indeterminate growth habit. Parentage is PI561319A x PI574477. Both PI (plant introduction) parents are originally from China. The line was crossed with two elite South Carolina glyphosate-tolerant experimental lines in 2004 with the objective of combining diverse genes for seed yield with genes in the adapted lines which provide nematode resistance and agronomic characteristics suitable for the southeastern U.S.A. F1 plants from both crosses are currently being grown in a winter nursery and seed will be advanced in a F2 nursery in South Carolina in 2005. Another hybridization was made with PI594651-L2, determined by researchers at the University of Georgia to have a high level of resistance to peanut root-knot nematode (*Meloidogyne arenaria*). The PI was crossed with an adapted S.C. cultivar, Dillon, with the objective of combining an improved level of *M. arenaria* resistance with high seed yield and acceptable agronomic traits. Populations from these three crosses will be advanced to the F4 or F5 generation when experimental lines will be derived and evaluated for the specific traits under selection. **Impact:** Plant introductions (PIs) maintained by the USDA Soybean Germplasm Collection supply a source of genetic diversity for soybean breeders. The PIs and germplasm lines developed from them have the potential to improve soybean seed yields and provide an increased level of resistance to economically damaging disease and nematode pests.

Horticultural crops

Conserve--Characterize and evaluate -- Utilize:

Example: UNIVERSITYOF THE VIRGIN ISLANDS

Tropical fruits and rare native plant species are the focus. Papaya varieties from Brazil, Cuba and Uganda were grown and evaluated. Three new papaya varieties were planted and grown that originated from Africa. One variety ‘Redonda’ has been very productive and has good fruit size and quality. The calcareous soils and semiarid environment of the island provides a strong selection pressure for any new variety being evaluated. These new papaya varieties were added to the papaya collection now consisting of 52 varieties that have been evaluated for growth and production in the USVI. New papaya varieties are grown and evaluated for their tolerance to the caliche soils, semiarid environment, for production potential, fruit quality and tolerance to local diseases and pests. Papayas have been repeatedly planted in the same plot that provides for selection to soil borne pathogens. Plants that survive this selection pressure have tolerance to these papaya diseases. A collection of native *Passiflora* species was established consisting of *P. edulis f. flavicarpa, P. foetida, P. laurifolia* and *P. suberosa*. *Passiflora quadrangularis,* barbadine, has been added to the passion fruit evaluation trials. The barbadine produces fruits of over a kilogram and both the rind and pulp have culinary uses. Tissue culture seed germination has been employed to establish a rare native orchid, *Psychilis macconnelliae*. The goal is to produce plants that can be reintroduced in their native environment. Tissue culture has been successfully used to propagate the Sandy Point Orchid (*Phychilis macconelliae*) from seed. This orchid has been listed as an endangered plant species in the USVI. Plants, from tissue culture, have been established under greenhouse conditions and will be re-released into their native habitat. Cassava germplasm is being evaluated for production during the dry season. Tissue culture was used to develop a micropropagation system to increase the number of plants for the lines obtained. In the area of fruit germplasm, work on the in vitro germination of the ‘Sandy Point Orchid’ *Phychilis macconelliae,* on the local Virgin Islands endangered species list, has neared completion. Plants have been successfully transferred from tissue culture to greenhouse-established plants. **Impact,** FY 2003 **:** The seed propagation system developed for the ‘Sandy Point Orchid’ allows for production of this native plant without going into the wild to collect this rare and endangered species. A new fruit with major impact potential is the barbadine fruit. It can be completely used from the rind to the juicy pulp offering little waste for the consumer or public landfill. The new papaya variety ‘Redonda’ has great potential in filling a niche for an early productive medium-large sized fruit that farmers and backyard growers have been requesting. Farmers are growing the papaya varieties and earnestly request seeds yearly to improve their papaya groves. **Impact,** FY 2004 **:** There are two native orchid species remaining in St. Croix, *Epidendrum ciliare* and *Psychilis macconnelliae*, both of which are on the VI endangered species list. *Epidendrum ciliare* is an epiphitic orchid found on trees or cliffsides and requires slight shade. *Psychilis macconnelliae* grows as a terrestrial in the Virgin Islands and prefers full sun. Current research includes media comparison studies to determine the most appropriate method for micropropagation of the plants by seed and developing acclimatization protocols for species which are more difficult to harden off than conventional hybrids. Preliminary results indicate that *E .ciliare* germinates best on a modified Knudson-type media whereas *P. macconnellia* prefers a modified Orchid Replate/Maintenance media. Greater production of in vitro grown native orchids, through the use of specific media for the species, has reduced the cost to local growers.

Examples of activities funded by CSREES-managed Hatch funds in W-6

PLANT GENETIC RESOURCE CONSERVATION AND UTILIZATION **CLASSIFICATION**

Agronomic Crops

Understand -- Utilize:

Example: NEW MEXICO STATE UNIVERSITY

Second year field data, from diallel hybrids derived from 18 high yielding populations of the NPGS alfalfa core collection, detected significant heterosis for forage yield in several hybrids. Several hybrids outperformed the best commercial varieties. AFLP-based assessment of genetic diversity among these populations indicated that hybrid yield was positively associated with increasing genetic diversity among parents. One of the parents, which possessed high general combining ability, also appears to possess high water-use efficiency based on carbon isotope analysis results. First year field results from a commercial alfalfa variety trial indicate that two hybrids, which contain one or more NPGS plant introductions as parents, yielded as well as the best commercial cultivars. **Impact:** Private industry has expressed concern that yield loss may accompany utilization of unimproved germplasms. However, recent diallel analyses conducted by our project have demonstrated that the forage yield of some hybrids derived from NPGS plant introductions can equal, or exceed, that of the best commercial cultivars. Statistical analysis programs for population based diallel analyses have also been developed to help identify alfalfa populations possessing high general combining ability and high heterosis potential. Populations identified in our research as having exceptional merit are being advanced for intrapopulation improvement. Experimental lines derived from two or more of these improved populations will be hybridized to further boost forage yields by exploiting heterosis. Our results also indicate that strategies which incorporate both molecular genetic diversity data, and some degree of agronomic performance data of parents, will likely have the greatest chance of successfully identifying parents to generate hybrid populations with maximum heterosis.

Understand -- Utilize:

Example: UTAH STATE UNIVERSITY

The crested wheatgrass cultivar Hycrest, which consists of germplasm from diploid (2n=2x=14) Agropuron cristatum (L.) Gaertn. and tetraploid (2n=4x=28) A. desertorum (Fisch. Ex Link) Schultes, was hybridized with a promising broadleaf hexaploid (6x-BL; 2n=6x=42) accession of A. cristatum from the USSR. The goal was to combine the wide leaf characteristic and green color retention from the 6x-BL parent into a common gene pool. The crossability between Hycrest (4x) and 6x-BL (6x) was excellent and the progeny had varying levels of fertility. Chromosome pairing in this hybrid was irregular and chromosome numbers ranged from 2n=27 to 41. Leaf morphology in the Hycrest x 6x-BL F1 hybrids was intermediate to that of the parents. Selected F1 pentaploid progenies (2n=5x=35), with leaf widths approaching that of the 6x-BL parent, were backcrossed to Hycrest, and then crossed among themselves [(Hycrest x 6x-BL) x (Hycrest x 6x-BL)]. In the backcross hybrid, chromosome numbers ranged from 2n=28 to 39. Meiotically, 28 chromosome backcross hybrid plants were more stable than aneuploid backcross hybrids. The broadleaf character was readily detected in the backcross progeny. In the [(Hycrest x 6x-BL) x (Hycrest x 6x-BL)] hybrids, chromosome numbers ranged from 2n=33 to 45. Despite the hybrid origin, all aneuploid hybrids had an increased number of univalents and chromosome associations that involved more than four chromosomes. AFLP analysis reflected genetic introgression from the 6x-BL parent beyond that observed in Hycrest. **Impact** The results from this basic research provide grass breeders with the ability to utilize genes from three different ploidy levels within the crested wheatgrasses. From this research several cultivars and breeding lines have been developed that have had significant economic impact on the seed industry and reseeding projects in the Great Basin and Northern Great Plains. **Publications:**

Jensen, K.B., S.L. Larson, B.L. Waldron, and K.H. Asay. 2006. Cytogenetic and molecular characterization of hybrids between 6x, 4x, and 2x ploidy levels in crested wheatgrass. Crop Sci. 46:105-112.

Jensen, K.B., S.L. Larson, B.L. Waldron, M.D. Peel. 2004. Registration of Cache Meadow Brome. Crop Sci. 44:2263-2264.

Jensen, K.B., B.L. Waldron, and M.D. Peel. 2003. Breeding for salt tolerance in NewHy wheatgrass. Agronomy Abstracts. Denver, CO. Nov. 2-7, 2003. CD-ROM.

Jensen, K.B., B.L. Waldron, and K.H. Asay. 2002. Quality or yield: which is most critical. Agronomy Abstracts. Indianapolis, IN. Nov. 10-14, 2002. CD-ROM

Jensen, K.B., K.H. Asay, D.A. Johnson, and B.L. Waldron. 2001. Carbon isotope discrimination of orchardgrass and perennial ryegrass at four irrigation levels. Agronomy Abstract 2001. Charlotte, NC. October 21-25, 2001

Jensen, K.B. and W.H. Horton. 2000. Breeding Meadow Brome for Salinity Tolerance. Abstract ASA 2000, Minneapolis, Minnesota. Nov. 5-9, 2000.

Jensen, K. B., K.H. Asay, and W.H. Horton. 1999. New Plants - Their Adaptation and Uses Under Semiarid Conditions. Abstract. Society for Range Management Annual Meetings Omaha, Nebraska. February 21-26, 1999. Vol 52: pg 36.

Jensen, K. B., K. H. Asay And B. L. Waldron. 1998. Performance of Orchardgrass Cultivars at Five Irrigation Levels. Abstract ASA 1998 meeting in Baltimore, Maryland. October 18-22, 1998.

Understand:

Example: UNIVERSITYOF IDAHO

To better utilize *Aegilops cylindrica* germplasm for wheat improvement, a project was initiated to determine the potential of using the Ph1 gene of wheat and Gc gene of *Aegilops cylindrica* to induce chromosome rearrangements to facilitate the transfer of genes from jointed goatgrass into wheat. Initial results indicate that the absence of the Ph1 gene in wheat x jointed goatgrass hybrids does increase the level of chromosome pairing in meiosis but also reduced the production of the first backcross generation by about 75%. In situ hybridization of BC1 progeny showed potential chromosome rearrangements involving C genome chromosomes in progeny of hybrids lacking the Ph1 gene. **Impact:** In wheat, insects, diseases, and extreme weather conditions are a constant threat to reduce production. One method to mitigate the negative effects of these organisms or conditions is by host genetic resistance or tolerance. Sources of genes for insect, disease or climatic condition resistance/tolerance can be found in many grass species related to wheat, including jointed goatgrass, *Aegilops cylindrica*. Because wheat and jointed goatgrass have unshared genomes it is more challenging to move genes between the two species. If successful, this research will utilize genetic mechanisms found in the two species to induce chromosome rearrangements to rapidly move useful genes into wheat. With additional genes for resistance/tolerance to insects, diseases or extreme climatic conditions, the level of wheat production can be maintained or increased.

Horticultural crops

Understand -- Utilize:

Example: UNIVERSITYOF CALIFORNIA - DAVIS

We continue the advancement of celery lines (*Apium graveolens* var. dulce) containing multiple resistance genes: fusarium yellows, late blight and celery mosaic virus (CeMV). Resistant plants to fusarium were selected in the field and their progeny was tested for resistance to late blight and CeMV in the greenhouse. We are using now marker assisted selection for selection of virus resistant plants in segregating populations. The program aimed to generate celery male sterile lines for hybrid seed production was discontinued for lack of support. Seed increase for twelve depleted accessions of the Apium germplasm collection at UC Davis was carried out under isolation. For *Brassica rapa* we advanced to F3 a segregating population developed by crossing turnip x Chinese cabbage used as a mapping population for glucosinolate analysis. We are advanced to F3 and BC1 (to broccoli) a segregating population obtained by crossing broccoli (*B. oleracea) x B. macrocarpa*, a high glucosinolate content related species. We produced a synthetic *B. napus* hybrid by crossing doubled haploid broccoli x doubled haploid Chinese cabbage. This will be used to resynthesize alien addition lines for the C and A genomes. **Impact:** Maintenance and development of a working germplasm *Apium* collection will assure the availability of sources for desirable traits to breeders. Development of *Brassica* germplasm segregating for traits such as glucosinolate content will allow extraction of lines containing specific glucosinolates for different research purposes such as biological control of pests and diseases and as sources of cancer-protecting agents. Development of genetic stocks, such as alien addition lines are important tools for basic research in genomics.

Characterize and evaluate--Understand:

Example: OREGON STATE UNIVERSITY

Characterize and evaluate hazelnut germplasm. Hazelnut germplasm will be imported as scions and seeds, and evaluated for morphological traits, DNA markers, and susceptibility to eastern filbert blight. Evaluation data will be shared with USDA-NCGR in Corvallis. Representatives from SAES and NPGS units (W-6 participants) will meet annually to evaluate and discuss current germplasm utilization and evaluate future germplasm needs of the Western Region. Oregon researchers will be informed of the plant genetic resources available through NPGS. Those requesting material from NPGS will annually be sent a written reminder of their obligation to report on their use of the plant material. Reports from Oregon researchers will be compiled and presented at the annual meeting of the W-6 Committee.

PROGRESS: 2004/01 TO 2004/12. Forty hazelnut selections from Moscow (Russia) were released from quarantine and planted in the field in October. Cultivars imported in previous years are growing at the Smith Farm. Initial characterization is for response to eastern filbert blight inoculation. Complete resistance was detected for the first time in Serbian selections 'Uebov' and 'Crevejne 3/96' (imported from Cacak, Yugolslavia) and 'Lozovskoi Sharovidnii' (from Kharkiv, Ukraine). Several Turkish selections showed a good level of quantitative resistance to EFB. The complete resistance of an unknown Georgian cultivar is transmitted to its offspring, as is the resistance of Russian selection OSU 495.072. But only two of 40 seedlings of Spanish cultivar 'Closca Molla' remained free of disease. Branches of 17 recently imported cultivars were bagged; fluorescence microscopy will be used to identify the S-alleles that control pollen-stigma incompatibility. **Impact** Oregon residents use the plant collections of the National Plant Germplasm System extensively. The W-6 project maintains the linkage between administrators of the system and its users in Oregon.

Example of activities funded by CSREES-managed Hatch funds in NRSP-6

INTRODUCTION, PRESERVATION, CLASSIFICATION, DISTRIBUTION AND EVALUATION OF SOLANUM SPECIES .

The Inter-Regional Potato Introduction Project

Conserve--Characterize and evaluate -- Understand--Utilize and encourage utilization

Example: UNIVERSITYOF WISCONSIN

Availability of potato germplasm is important to the progress of basic research and breeding. The genebank at Sturgeon Bay, in cooperation with worldwide collaborators, filled this need by providing viable, disease-free stocks in a timely manner, and further evaluating and documenting valuable traits. Materials distributed include 5520 units of seed, 2184 tuber families, 943 in vitro stocks and 153 herbarium specimens to potato researchers and breeders in 24 states of the U.S. and 13 other countries. These stocks will be an important component of future scientific knowledge about potato and its use, and will contribute directly to new cultivars with a positive nutritional and economic impact on U.S. farmers and consumers. Germplasm in a genebank becomes more valuable when it is characterized. With various national and international collaborators, we tested germplasm for disease, pest, and stress resistance, and conducted DNA-based analyses to assure that the genetic diversity is being optimally collected and maintained (both in the wild and in the genebank). Thus, we now have better insights into the best materials for breeding and the best techniques for maximizing technical efficiency in the genebank. Impact is evidenced by the fact that genebank stocks are the subject of over 100 research publications yearly, and that most of the new U.S. cultivars released have exotic potato germplasm in their pedigrees. This year a particular emphasis was made on outreach, as Lead Scientist participated in field days in Mexico (late blight) and Oregon (cultivar selection), and other staff presented posters and talks on the genebank at several professional meetings (PAA, CSSA). The genebank web page was upgraded, and an email list and periodic announcement of new services was initiated (resulting in a substantial surge in germplasm orders). Steps were made to direct more research attention to nutritional quality, continuing screening for antioxidants and taking preliminary steps toward screening for anti-cancer factors. **Impact:** Many units of germplasm are freely distributed to all requesters for research and breeding. In most cases, this is the ONLY domestic source of these stocks, and often the only source in the world in lieu of making re-collections from the wild. Unique germplasm is collected and taxonomic studies set rational species limits. Associated evaluation and characterization data is also distributed. The stocks are the subject of over 100 publications yearly. Use of DNA markers is helping us know the best methods for managing the genetic diversity. We also conduct evaluations on new traits for the improvement of the potato crop, and identify and characterize the sources of these traits for use by other scientists.

7. Other CSREES-funded activities in Plant Genetic Resources and Biodiversity

CSREES funds additional projects that characterize, evaluate, and use plant germplasm for germplasm and variety development and for basic biological or genetic studies. Like the multi-state NPGS projects, these projects fall within the Knowledge Area (KA) 202, Plant Genetic Resources and Biodiversity.

The largest contributor of funds to KA 202 projects, including most of the KA 202 projects involving agricultural plant germplasm, is Hatch funds; followed by Special Grants; “Other CSREES” which includes diverse sources such as the former IFAFS program and Federal Administration grants; and the National Research Initiative competitive grants program (Appendix 3).

NRI programs that may fund research in KA 202 include, but are not limited to:

    52.1 Plant Genome

22.1 Agricultural Plants and Environmental Adaptation
52.2 Genetic Processes and Mechanisms of Agricultural Plants
53.0 Developmental Processes of Agricultural Plants

Excerpts from the text of the current Request for Proposals of an NRI programs that specifically requests proposals involving NPGS germplasm, NRI Program 52.2, is given in Appendix 4.

Examples of additional plant germplasm projects, not part of NPGS, are given here. To illustrate the focus of each, these projects also are listed under headings that correspond to the general objectives of the NPGS. Germplasm used in these projects may come from the NPGS or other sources, such as the collections of the CGIAR centers, or from researcher contacts with collaborators in other countries or the private sector.

The first group of projects receive Hatch funds from the allocation to the individual state. These projects are approved at the SAES director-level. The second group of projects received competitively awarded funding, such as from NRI. Note that ARS is eligible to receive NRI funds, creating an additional form of interagency collaboration in the NPGS: CSREES-funded ARS plant germplasm research. The number of NRI-funded plant germplasm projects is fewer that the number of Hatch-funded projects. Most NRI projects in KA 202 are primarily genomics (KA 201) or basic biology (KA 206) projects using specialized genetic stocks or standard varieties.

Examples of activities in Hatch-funded projects

Agronomic crops

Characterize and evaluate -- Utilize:

Example: TEXAS A&M UNIVERSITY
BREEDING & GENETICS OF CORN

During the 2004 season we have continued the evaluation, characterization and selection of corn germplasm with different origins and genetic backgrounds to develop inbred lines with superior grain quality, reduced susceptibility to aflatoxin, adaptation to Texas, and tolerance to abiotic stresses. We have conducted multilocation testing across the major corn production regions of Texas and evaluated germplasm under drought stress and inoculation with Aspergillus flavus, fungi responsible of aflatoxin contamination in corn. Approximately, 1000 experimental hybrids and testcrosses were evaluated across several Texas environments to identify the most adapted germplasm to the local conditions. Different traits (yield, maturity, moisture, test weight, lodging, ear and plant height, cob and grain color, texture, disease resistance, etc.) were recorded. We have selected the best material in these trials considering its overall performance, local adaptation, and quality. Most of these inbreds have subtropical or tropical origin and hard endosperm (e.g., LAMA lines). In these evaluations we have collaborated with other public programs and agencies, international centers, and private seed companies. During year 2004 we had two nurseries, one during the regular season (summer) at College Station, TX (5,000 plots) and one off-season (winter) at Weslaco, TX (4,000 plots). An approximate of 1000 inbred lines representing a wide range of maturities (early, intermediate and late), adaptation (tropical, subtropical and temperate), color (white, yellow, orange), quality (lysine content), and kernel characteristics (flint, dent) were screened in these nurseries. Traits such as early vigor, maturity, adaptation, plant and ear height, grain color, cob color, texture, disease resistance, and ear characteristics were recorded and ultimately used to classify and select the most promising germplasm for our program objectives. We are searching for new alleles in exotic germplasm for resistance to mycotoxins, tolerance to drought and heat, high test weight, high proportion of hard flinty endosperm, kernel integrity with kernels free of fissures or stress cracks, white cobs, and nutritional value for food or feed. Transitional areas between tropical and temperate areas, such as Texas, represent excellent opportunities to incorporate, combine and introgress exotic germplasm in temperate material and vice versa. By developing inbreds adapted to Southern U.S. we expect to facilitate the connection and genetic flow between these gene pools. Overall, temperate inbreds from northern areas provide high yield, stalk quality, known heterotic response, and early vigor while tropical and subtropical germplasm from southern areas provides resistance and/or tolerance to biotic and abiotic stresses (e.g.,less aflatoxin, drought and heat tolerance) and kernel quality (more flinty endosperm texture). The releases of three parental inbred lines (Tx110, Tx114, and Tx772) and 4 germplasm lines (Tx745, Tx714, Tx732 and Tx770) were published in Crop Science during 2004. **Impact:** With the development of this material we expect to contribute to the diversity of corn germplasm in the U.S. and to the improvement of corn hybrids for sustainable productivity, value-added profitability and food safety.

Understand-- Utilize:

Example: NORTH DAKOTA STATE UNIVERSITY
WHEAT GERMPLASM ENHANCEMENT

Fusarium head blight (FHB) is a fungal disease of small-grain crops that causes yield loss and poor grain quality. The extensive damage caused by FHB has made it necessary to develop resistant lines of durum and bread wheat. We used a previously identified molecular marker, explaining 55% of the genetic variation, to introgress the linked region from *Triticum dicoccoides* into cultivated durum wheat. Additionally, a molecular marker linked to FHB resistance in hexaploid wheat was used to introgress the linked region into durum wheat. The efficiency of marker assisted selection as calculated using only one season of disease screening is more than 85%. Chromosome asynapsis and hybrid sterility are major obstacles to alien gene transfer, and genes affecting nuclear-cytoplasmic (NC) interactions are directly or indirectly involved. A detailed analysis of two genes involved in NC interaction, scs (species cytoplasm specific) and Vi (vitality) genes, located on chromosomes 1A and 1B, respectively, is underway. The scs gene has been mapped using polymorphic populations as well as radiation hybrid mapping approach. We are now pursuing the saturation mapping of 3 cM region surrounding this locus. We have also developed waxy (no amylose) and partial waxy (low amylose) durum wheat lines. These lines have been evaluated for their cereal processing properties and their agronomic potential for release as cultivars. Currently there are two postdoctoral scientists, two Ph.D. students, two M.S. students and three undergraduate students involved in the research projects mentioned above. **Impact:** This project is aimed at developing durum and bread wheat lines better adapted to North Dakota growing environment and tolerant to prevalent diseases. The ultimate aim is to provide North Dakota growers with durum and bread wheat crop having improved resistance and new commercial applications for increased premiums.

Understand

Example: UNIVERSITY OF WISCONSIN
CROSS INCOMPATIBILITY BETWEEN TEOSINTE AND MAIZE

At some locations in Mexico, teosinte, the likely progenitor of corn, now grows principally as a weed in corn fields. In this circumstance, hybridization is restricted because the pollen of corn is unable to fertilize teosinte. This barrier to crossing resembles an incompatibility due to the corn gene Ga1 that prevents pollen of dent and flint corns from functioning on silks of some popcorn varieties. We found Mexican maize to be cross neutral with respect to Ga1 and thus unable to account for the teosinte/maize barrier. Rather, a separate locus unique to teosinte, acting in conjunction with a major enhancing modifier, was discovered in teosinte collection 48703 and is present in six of 12 other collections tested. There appears to be a connection between presence of the teosinte crossing barrier gene (Tcb1) and habitat, with preferential occurrence where teosinte grows in intimate association with maize that is exclusively as a weed. Plants of two collections possessed the pollen-specific property of teosinte but the silk-specific property of maize. In Tcb1 teosinte the pistil and pollen properties regularly are inherited together (8263 meiotic chromosomes tested). Although Tcb1 pistils exclude maize pollen, Tcb1 pollen is disadvantaged on corn pistils. The combined effect implies a bidirectional effect on reproductive isolation of this one locus. **Impact:** The genetic basis of reproductive isolation of closely related, wind-pollinated taxa is now better understood. Transferred into elite breeding lines of corn, this discovery may protect one category of corn varieties from contamination by pollen from others.

Horticultural crops

Characterize and evaluate -- Utilize:

Example: NY AGRICULTURAL EXPT STATION
VEGETABLE BREEDING & GENETICS

Resistance to cucumber mosaic virus, zucchini yellow mosaic virus, watermelon mosaic virus, papaya ringspot virus, and powdery mildew was transferred from wild *Cucurbita* species to squash and pumpkin. Summer squash breeding lines and the cultivar ‘Whitaker’ were bred for parthenocarpic fruit set. New sources of anthracnose resistance were found and introgressed into tomato germplasm. Solanum species were screened for verticillium wilt resistance and resistant eggplant germplasm with good horticultural type was derived from interspecific hybridization. Resistance to cucumber mosaic virus was found in *Lactuca saligna* and was combined with resistance to corky root rot in the lettuce cultivar ‘Onondaga’. Cucumber germplasm bred for dwarf plant habit, good seed production and quality, and multiple disease resistance was evaluated for adaptation to mechanical harvest. **Impact:** The development and release to seedsmen of multiple disease resistant germplasm for summer squash, winter squash, and pumpkin is likely to lead to the introduction of resistant cultivars with increased yield and reduced need for pesticide application. Summer squash bred for parthenocarpic fruit set should improve fruit set and yield when conditions are poor for pollination. The development of tomato germplasm resistant to anthracnose makes possible resistant cultivars with less fruit rot and pesticide use. Breeding eggplants resistant to verticillium wilt will prevent losses from this important disease that cannot be controlled economically by any other means. Lettuce bred for resistance to cucumber mosaic virus and corky root rot provide a means for control for these important diseases and may reduce pesticide use. The development of pickling cucumber germplasm with the dw gene for dwarf pant habit may make possible the use of higher plant populations with increased yield and higher proportion of small size grade pickles in a single mechanical harvest.

Characterize and evaluate -- Utilize:

Example: **U**NIVERSITY OF HAWAII
TRANSFERRING DISEASE RESISTANCE FROM MICRONESIAN TO POLYNESIAN TAROS

Taro cultivars from the Palau Is., found to have resistance to taro leaf blight (TLB) caused by *Phytophthora colocasiae,* were propagated by tissue culture and distributed in the Samoan Is. The most resistant Palau cultivar to TLB was used in crosses with Polynesian taro cultivars to create resistant hybrids with the desired agronomic characteristics of the Polynesian cultivars. From a cross between the Hawaii cultivar Maui lehua (female parent) and Palau cultivar Ngeruch (Male parent) three cultivars were patented by the US Patent Office in 2002, taro cultivar Pauakea PP12342, taro cultivar Palehua PP12361, and taro cultivar Paakala PP12772. These cultivars at plant densities of 6534 produced yields closed to 100,000 lb/A. Paakala yield was higher than Pauakea at sea level elevation, while the inverse was true at 150 m. elevation. Palehua matured in 8 months and averaged 37,000 lb/A. Various density of planting tested during 2003-04 showed that as density increased the size of the corms and yield decreased. **Impact:** Patented taro cultivars Pa'akala and Pauakea at 6,534 plants/A produced close to 100,000 lb/A of carbohydrate rich corms suitable for taro flower manufacture and the creation of a new industry in Hawaii.

Characterize and evaluate -- Utilize:

Example: RUTGERS UNIVERSITY
GENETIC IMPROVEMENT OF UNDERUTILIZED PERENNIAL CROP PLANTS

Over 23,000 plants of pecans, hazelnuts, Persian walnuts, black walnuts, heartnuts, almonds, chestnuts, hickories, hicans and pine nuts are being evaluated in field trials and greenhouses. Additional seed nuts were collected in Kyrgyzstan and southern Russia. Many are new germplasm sources not yet grown in the USA. Evaluations include resistance to diseases, insects, and environmental stresses as well as enhanced nutritional attributes, ornamental characteristics, wide adaptation, and productivity. We are striving to determine the opportunities that exist in the genetic improvement of newly domesticated perennial crops and their role in a New Green Revolution. They could dramatically increase world food and biofuel production, harvest carbon dioxide by dramatically increasing biomass production (perhaps doubling) and improve the environment, lifestyles, health and prosperity of current and future generations. We are using techniques of germplasm collection, evaluation, and population improvement similar to those used in the Rutgers turfgrass breeding program. We continue to evaluate, adapt and utilized new technologies as they become available. **Impact:** Genetically improved tree crops and other perennial species adapted to lands not suitable for sustainable production of cultivated annuals can produce much of the added food, fuel, and timber needed by the current hungry of the world as well as future generations of the world, free us of our dependence on fossil fuels, preserve our precious soil and water resources, and mitigate global warming with its disastrous effects.

Characterize and evaluate -- Utilize:

Example: RUTGERS UNIVERSITY
BREEDING AND GERMPLASM ENHANCEMENT FOR NEW JERSEY CRANBERRY AND BLUEBERRY INDUSTRIES

In spring 2004, 39 blueberry crosses were made among early-ripening selections and cultivars (including southern highbush), and late-ripening blueberries in an effort to extend the growing season in New Jersey; and 9 crosses were made among selections with machine harvestability characteristics. Several thousand field-grown selections, including progeny and advanced selections, were evaluated during June and July for yield, fruit-ripening season, fruit traits and machine harvestability. Over 100 advanced selections were identified as having parental and/or varietal potential. Many of these selections were brought in from the field for use in crosses, either as plants or softwood propagations. The diploid species, *Vaccinium darrowi*, offers potential immunity to the second stage of mummy berry disease, and also possible aphid resistance. Interspecific hybrids of *V. darrowi* by highbush blueberry were produced and used to generate BC (to highbush) and F2 populations in 1997. In 2000, 6000 of these progeny were field planted and this August they were large enough to evaluate. Sixty-three plants were selected based on flavor, crop, plant health, and late season. Over 3000 seedlings from 2003 crosses were grown out for field planting in 2005. Aphid resistance has been evaluated across 8 blueberry species and 13 genotypes of *V. darrowi*, with 5 species and 7 genotypes exhibiting promising resistance, as measured by aphid development, survivorship, and/or offspring production. In spring 2004, 63 cranberry crosses were

made, including 22 crosses to enhance sugar levels, 19 crosses to decrease acidity, and 6 crosses to improve fruit rot resistance. During cranberry fruit ripening period, seedling plots (3380) were rated for productivity, ripening season, fruit color, vigor, and fruit rot. Based on this evaluation, 576 plots were selected for harvest. Eighty-six additional plots were harvested from two trials containing advanced selections, including one in Wisconsin. Fruit samples were evaluated for yield, berry weight, percent rot, scald, total anthocyanin, Brix (soluble solids), and titratable acidity. A new progeny evaluation trial consisting of 1350 progeny from 29 crosses was established. Our germplasm collection of over 500 selections was screened for fruit rot resistance by withholding fungicides during 2003 and 2004. Severe fruit rot was observed in 88% of the selections by early September, similar to 2003, and 10 selections consistently showed resistance to fruit rot. Berries from resistant and susceptible selections were cultured to determine the species of fruit rot fungi present. Progeny of crosses that had previously been made with fruit rot-resistant selections were rated for resistance. Progeny from 13 crosses made with high Brix parents were evaluated for Brix levels to determine the heritability of this trait. A more rapid technique for evaluating proanthocyanidin levels in cranberries has been developed, facilitating the screening of large numbers of selections. Several selections that are being considered for release were planted in large field plots in Wisconsin and New Jersey for evaluation under grower conditions.
Impact: The expected impact of this project is the development of blueberry and cranberry cultivars with improved horticultural characteristics, such as productivity, fruit quality, disease and insect resistance, and optimum human health attributes.

Characterize and evaluate -- Utilize:

Example: WHITE EARTH TRIBAL AND COMMUNITY COLLEGE
WETCC/UMN/BADGERSETT HAZELNUT PROJECT (GITIGAN: BAAGANAG)

Indigenous woody crops such as hazelnuts represent an opportunity for culturally appropriate agricultural and economic development for Native Americans. Success of this venture depends on a healthy state-wide hazel industry in Minnesota. The purpose of this project is to create an indigenous crops research program at the White Earth Tribal and Community College focused on developing hybrid hazelnuts as a commercial crop. The principle challenges to be addressed are the testing of appropriate hazel cultivars for northern Minnesota and developing more economical methods for propagating identified superior varieties. Researchers from the University of Minnesota (UMN) and the Badgersett Research Farm will provide WETCC staff with training in plant propagation and hazel breeding. The staff will use this training to establish research nurseries where various indigenous woody plants will be propagated. The Badgersett Research Farm will propagate 5000 hazel plants representing a number of promising cultivars for northern Minnesota growers (USDA zone 3). These will be established on 5 test plots on and around the reservation. Each plot will represent a different management regime including; a control, conventional tillage, mulch, and two different cover crop systems. Plots will be monitored for establishment success and early growth rates for each cultivar tested. The results of these trials and the training in hazel breeding will be used to plan a long term hazel breeding program at WETCC. Researchers at UMN will test various asexual propagation techniques on BAdgersett hazel stock that has already shown superior characteristics for southern Minnesota (USDA zones 4-5). Both cuttings and micropropagation techniques will be considered depending on the state of the science at the time the project begins. The results of this work will be disseminated to interested scientists, producers, and others across greater Minnesota through and existing Hazel Learning Group.

Understand-- Utilize:

Example: NORTH CAROLINA STATE UNIVERSITY
BREEDING AND GENETICS OF PEACH

Two new peach cultivars, Carolina Gold and Galactica, were released in 2004. Carolina Gold is a late-ripening, yellow flesh peach possessing high flesh quality, resistance to bacterial spot, attractive skin and flesh color, and resistance to oxidative flesh browing after slicing. The pedigree of Carolina Gold includes a Spanish land race of peach called San Miquel, hence Carolina Gold will serve to broaden the narrow genetic base of North American peaches. Galactica is an early-ripening, white flesh peach possessing the peento (donut, saucer) character. Galactica has semi-acid flesh with high soluble solids. It is intended as a specialty peach for niche marketing. Numerous advanced selections from the breeding program have been established in a test plot at the Mountain Horticultural Crops Research Station in Fletcher, NC in order to determine their cropping ability in location deemed marginal for peach production. Genetic interaction of the pillar (PI) and weeping (WE) growth habit genotypes was investigated in peach. Data from F2, BC1P1, and BC1P2 families showed that PI (brbr) was epistatic to the expression of WE (plpl). A unique growth habit not previously described in peach, and referred to as arching (AR), was recovered in the F2 family. Arching trees showed an upright phenotype similar to Brbr heterozygotes, but had a distinct curvature in the developing shoots. Progeny testing of AR trees revealed their genotype is Brbrplpl. **Impact:** Development and ultimate release of late-flowering peach cultivars with high flower bud cold hardiness will reduce the risk of flower bud frost/freeze injury in commercial orchards, reducing the potential for serious crop loss. Development of peach cultivars with distinct characters such as low fruit acidity and flat fruit shape will facilitate the opportunity for producers to target and exploit specialty and niche markets.

Understand-- Utilize:

Example: UNIVERSITY Of CALIFORNIA DAVIS
USE OF WILD *LYCOPERSICON* SPECIES IN BREEDING FOR IMPROVEMENT OF CULTIVATED TOMATO

Our tomato breeding and genetics research has focused on the identification and transfer of genes from wild to cultivated tomato (*Lycopersicon esculentum*) for chilling tolerance (CT), resistance to blackmold (RBM), late blight (RLB) and aphids. The pathogens *Phytophthora infestans* (late blight) and *Alternaria alternata* (blackmold) and chilling temperatures can all cause significant yield and fruit quality losses, while aphids reduce yields. Previously, quantitative trait loci (QTL) for RBM, RLB, and CT were mapped in interspecific populations and QTLs identified for introgression. DNA markers linked to the QTL regions were used to select progeny lines containing the desired wild species alleles at these QTLs (i.e., marker-assisted selection, MAS). RLB QTLs on chromosomes 3, 4, 5 and 11 and RBM QTLs on chromosomes 2, 3, 9 and 12 were transferred into cultivated tomato using backcrossing and MAS. *L. cheesmanii* alleles at RBM QTL conferred resistance in an *L. esculentum* background, and the QTL on chromosome 2 had the largest positive effect on resistance. Selected QTLs were fine-mapped using sub-near-isogenic lines (sub-NILs) obtained via MAS for RBM QTL on chromosome 2 and RLB QTL on chromosomes 3, 4, 5 and 11 (lb3, lb4, lb5b, lb11b). Sub-NILs were tested in replicated field trials, and disease data was used to fine map each of these resistance QTLs to smaller chromosomal segments. QTLs lb4, lb5b and lb11b mapped to intervals of 6.9, 8.8 and 15.1 cM, respectively, resulting in more suitable targets for MAS breeding efforts. Fine mapping of lb3 was not possible due to severe fertility problems in the sub-NILs, but a fertility locus was mapped. RBM QTL on chromosome 2 was located to a 20 cM region. Two CT QTLs from *L. hirsutum* on chromosomes 5 and 9 were individually introgressed into *L. esculentum* using MAS and NILs were developed. The NILs were tested in replicated experiments and CT (measured as shoot turgor maintenance under chilling temperatures) was most strongly associated with the QTL on chromosome 9 (stm9). Sub-NILs were derived from NILs for fine mapping, and stm9 was localized to a 3 cM interval. Sub-NILs are being used for further physiological studies to characterize the basis of CT. Aphid resistance was assessed in two interspecific inbred backcross line (IBL) populations derived from *L. hirsutum* and *L. pennellii*, and the most consistently resistant IBLs over two years of field trials were from the *hirsutum*-derived population. These highly resistant IBLs are a source of aphid resistance for further breeding efforts. An assessment of cultivated tomato germplasm mainly from California indicated that a minimum of 7 AFLP primer pairs revealed unique banding patterns for all 74 cultivars even though some cultivars were genetically related, indicating the value of the AFLP markers for cultivar fingerprinting.

Examples of activities in NRI- funded projects

Agronomic crops

Characterize and evaluate -- Understand

Example: VANDERBILT UNIVERSITY, INDIANA UNIVERSITY, OREGON STATE UNIVERSITY, UNIVERSITY OF GEORGIA
GENETIC DIVERSITY AND GENOME STRUCTURE AND ORGANIZATION OF SUNFLOWER

Compared to wild sunflower, cultivated sunflower shows clear evidence of diversity loss due to domestication. NPGS wild sunflower accessions were found to be a rich source of genetic variation for continued improvement of sunflower. It is likely that association mapping will be able to identify agronomically important genes with a high level of confidence. Mapping of genes controlling seed oil traits in sunflower revealed one or more genes influencing multiple aspects of fatty acid composition in one particular genomic region. There is evidence that this region experienced

strong selection during the modern era of plant breeding. The sunflower genome has extensive rearrangements, which are likely to create reproductive barriers between species. However, large genomic regions devoid of rearrangements exist and suggest wild sunflower can be used for continued improvement of cultivated sunflower.
Publications: Journal of Genetics articles in 2004, 2005 and 2006.

Characterize and evaluate -- Understand

Example: LOUISIANA STATE UNIVERSITY
MOLECULAR DIVERSITY AMONG WILD SACCHARUM SPONANEUM CLONES AND THE PROPORTION OF WILD GERMPLASM REPRESENTED IN THE COMMERCIAL GENE POOL

Modern sugarcane cultivars are genetically vulnerable because the gene pool from which they are derived originated from a few interspecific hybrids. To address this problem in the Louisiana industry, a basic breeding program was established by the USDA at Houma, LA, with two main objectives: 1) to broaden the genetic base of sugarcane and 2) to identify and introgress useful genes from the wild relatives into the cultivated background. Saccharum spontaneum is the most important source of wild germplasm in this effort because S. spontaneum clones are generally better adapted to the range of weather conditions found in Louisiana. Knowledge of genetic diversity is often of crucial importance in maximizing genetic response. Molecular markers will be used to reveal vital information about the level and pattern of genetic diversity present in the S. spontaneum germplasm collection and the extent to which this diversity is represented in the basic and commercial breeding gene pools. This study will provide useful information that will improve the efficiency of our genetic conservation, base broadening and germplasm enhancement programs. **Objectives:** The overall objective is to develop efficient methods for genetic resource management of germplasm belonging to the Saccharum complex. Specific objectives in this project are to assess the level and pattern of genetic diversity among a collection of S. spontaneum clones and to survey the extent to which this diversity has been tapped by the basic and commercial breeding programs. **Approach:** Genetic diversity will be assessed among S. spontaneum clones and clones from the basic and commercial breeding programs using molecular tools. **Progress:** 2004/01 TO 2004/12
Genetic diversity was assessed, using the Amplified Fragment Length Polymorphism (AFLP) technique, among a collection of 54 germplasm accessions comprised mostly of S. spontaneum, and a few representatives of the Saccharum complex and some cultivars. The S. spontaneum clones displayed tremendous amounts of genetic diversity although geographical origin did not seem to influence the pattern of diversity. This has implications in the way in which this germplam can be exploited to improve cultivated sugarcane. Strategies to organize and exploit clones from this collection would reflect these allele frequency differences rather than geographical origin. The extent to which the S. spontaneum diversity has been tapped in the breeding program is being assessed using a different type of marker technique known as Target Region Amplification Polymorphism (TRAP). The TRAP is a Polymerase Chain Reaction (PCR) technique which uses information from known gene sequences from the gene bank for primer design. These gene sequences are derived from sugarcane Expressed Sequence Tags (ESTs) and ESTs from other closely related model species, thus making good use of previously funded information. This new method (TRAP) appears attractive because it supposedly amplifies genome regions linked to traits of interest as opposed to random portions of the genome thus increasing the likely hood of measuring trait related diversity. **Impact:** Results from this study will help answer the following pertinent questions. 1) What is the extent and pattern of genetic diversity represented in our working collection of S. spontaneum clones? 2) Has most of this diversity already been tapped in the commercial breeding program? 3) Does most of the already tapped diversity come from a few clusters or is this diversity uniformly dispersed across clusters. Answers to these questions will improve the efficiency of the germplasm enhancement and genetic conservation efforts. The research may help identify potential sources of germplasm for future exploitation.
Publications:
1. Arro, J., Kimbeng, C.A., Veremis, J.C. and Botanga C.J. 2004. Evaluation of genetic diversity among a collection of S. spontaneum and related species using AFLP markers. Abstract/ Poster Presented at the Plant, Animal and Microbe Genome Conference, San Diego, Ca, January 10 to 14, 2004.
2. Arro, J., Kimbeng, C.A. 2004. Genetic diversity among a collection of Saccharum spontaneum germplasm does not seem to be influenced by geographical origin. Presented at the Annual Meeting of the Louisiana Association of Agronomists, Baton Rouge, April 2004.

Horticultural crops

Characterize and evaluate -- Understand

Example: ARS, USDA
GENETIC DIVERSITY OF WILD APPLE ACCESSIONS IN THE NATIONAL PLANT GERMPLASM SYSTEM

Species of wild apples maintained in the National Plant Germplasm System are not well characterized genetically. Wild apple tree species are often brought to the US as seeds (as a result of fewer quarantine requirements) and maintained as clones in a field. These new genetic materials are valuable for fruit breeding programs. We will determine genetic relationships among accessions of wild Rosaceae species in the NPGS and recommend diverse sets of accessions to represent the diversity of the wider collection. **Objectives:** 1) Quantify and apportion genetic diversity in collections of wild relatives of Malus 2) Identify a group of individuals that represents the overall genetic diversity of wild Malus collections with the fewest number of individuals. **Approach:** Plant exploration trips to China and Turkey have brought valuable Malus hupehensis, M. orientalis, and M. toringoides germplasm of into the US and maintained in the National Plant Germplasm System. Genotypic data from 15 to 20 unlinked microsatellite loci for each individual will be analyzed to calculate a set of descriptive genetic diversity parameters such as observed and expected heterozygosity, number of private alleles, number of group specific alleles as well as hierarchical and pairwise F statistic. AMOVA will be performed using Arlequin to estimate variance components within and among accessions. In addition, we will explore the relationship between divergence (Fst) and diversity (allelic richness) and make estimates, where appropriate, of past genetic bottlenecks. We will graphically represent diversity and structure using network, ordination and Bayesian methods. Core collections will also be identified.

Characterize and evaluate -- Understand

Example: UNIV OF WISCONSIN
A CLADE-BASED SEARCH FOR GENOME REARRANGEMENTS AND USEFUL DIVERSITY IN SOLANUM

The wild relatives of potato present an exceedingly rich and yet largely unexplored resource for potato improvement. Vastly conflicting taxonomies of different workers have hindered a logical search for complimentary sources of resistances, however, especially considering the size of the collections (about 5000 accessions of 200 wild potato species). Recent molecular studies have shown that potato is composed of four well-defined phylogenetic groups (clades). We will conduct a systematic approach to capturing this diversity from one of these four clades (Solanum Piurana), through an examination of comparative genome rearrangements and identification of quantitative trait loci (QTL) for late blight resistance. Objectives: 1) Investigate members of a group of wild relatives of potato taxonomically classified in the Solanum Piurana clade, as potentially important sources of resistance to potato late blight through quantitative trait loci and candidate gene approaches. 2) Contribute to the recognition, characterization, and use of conserved and complementary alleles conferring durable resistance to potato late blight through comparison with quantitative trait loci maps of other solanum species. The cultivated potato, Solanum tuberosum, is affected by a variety of diseases with late blight, caused by Phytophthora infestans, being the most severe. Wild potato species have proven to be a continuing source of resistance, sometimes of an extreme type, to this disease. The present study constructed a genetic map of a previously uncharacterized wild, tuber-bearing South American relative of potato, Solanum paucissectum, using probes for conserved sequences from potato and tomato. Eight probes mapped to unexpected linkage groups, but syntenic differences with prior maps of potato were not supported by any blocks of rearranged chromosome segments. All 12 linkage groups were resolved, and significant associations with late blight resistance were found on chromosomes 10, 11 and 12. A major quantitative trait locus on chromosome 11 accounts for more than 25% of the phenotypic variance measured in a field trial. Crossing of S. paucissectum with cultivated potato resulted in very few seeds indicating partial reproductive barriers. Differential reactions of accessions of this potential donor species with simple and complex isolates of P. infestans suggest that it carries major resistance genes that are not those previously described from the Mexican species, S. demissum. However, the additivity of the quantitative trait loci effects argues for the quantitative nature of resistance in this cross. **Impact:** Late blight, caused by the oomycete Phytophthota infestans (Mont.) de Bary is one of the most important diseases affecting the potato crop (Solanum tuberosum L.) worldwide. Late blight destroys the foliage, stems, and tubers of growing plants, causing severe losses in cultivated potato. The first and most devastating late blight outbreak ever recorded occurred in Ireland in the 1840s, resulting in famine and migration of more than a million people. Control of the disease relies on fungicide application, which increases agricultural inputs and environmental and health risks. Where fungicides are not affordable, total crop loss can result. Resistance to late blight was incorporated into cultivated potato during the first decades of the 20th century by repeated backcrossing with the resistant wild species Solanum demissum. These crosses resulted in the incorporation of at least 11 R (resistance) genes into cultivated potato. Potato has a narrow genetic base and wild species have great potential to improve the crop for a range of traits. Researchers are actively screening additional wild species for sources of new resistance genes and there is a need to continuously develop new sources to keep pace with the dynamic pathogens like P. infestans. This paper reports the first genetic map and late blight resistance loci involving species from a member of the wild potato group Solanum series Piurana, and shows a potential new source of late blight resistance.

Example in an IFAFS - funded project

Horticultural crops

Characterize and evaluate -- Utilize

Example: CORNELL (Plant Breeding + Horticulture Depts; Cooperative Extension);
NE ORGANIC FARMING ASSOC. of NY, Inc.; ARS, USDA
THE PUBLIC SEED INITIATIVE (PSI)

Changes in seed industry have resulted in varieties that are selected for average national growing conditions. There are fewer varieties available selected specifically for Northeaster growers. The PSI worked with farmers and small-scale seed companies, providing training in vegetable breeding and seed production and on-farm breeding. The project helped growers access and evaluate plant materials from the NPGS and from public breeders, and to identify varieties for small seed companies and organic systems. Over 40 community seed days or seed demonstrations were held; 46 varieties made available to farmers and gardeners; 43 commercial licenses were issued (at least 5 via organic seed catalogues); and about 1000 active participants and over 7000 observers attended PSI field days and fairs. The PSI project has the long-term potential to increase the number and quality of varieties offered by remaining and new seed companies; and to improve the productivity and viability of Northeastern agric.

Measurable outputs from CSREES-funded plant germplasm projects

Table 2. Measurable outputs from four NPGS multi-state projects, FY 2003-2004. Data were manually collected from narrative CRIS reports. CRIS does not specifically request these data. Actual totals may vary significantly. Blank cells may signify either zero or not reported.

Proj-ect	**Accessions obtained**	**Accessions characterized or evaluated**	**New sources of valuable traits identified**	**Data entered in GRIN (national electronic database)**	**New/improved conservation/ preservation methods developed/ implemented**	**New introgression populations developed from crosses to breeders materials**	**Advanced inter-specific populations**	**New genetic markers identified-new genes cloned**	**Germ-plasm released or licensed**	**Varieties released**
NC 7		30 plus 15 collections of unspecified size*	3			5		101 SNPs 28 QTLs	10	1
NE 9		148, representing 38 species; two collections of unspecified size	2 or more (sources reported as plural but numbers unspecified)	2333, plus one collection of unspecified size	1	4 or more (‘populations’ reported as plural but numbers unspecified)				2 or more (‘varieties’ reported as plural but numbers unspecified)
S 9	110	2812, plus six collections of unspecified size; 15 species altogether	1	2776, plus three collections of unspecified size; 12 species altogether	2	2	7			17
W 6	12 , plus one collection of unspecified size				2		4			1
Total	**122, plus one collection of unspecified size** **3 species altogether**	**2990 plus 23 collections of unspecified size** **72 species altogether**	**6 or more (some sources reported as plural but numbers not specified)**	**5109, plus, four collections of unspecified size** **76 species altogether**	**5**	**9 or more (some reported as plural but numbers unspecified)**	**11**	**129**	**10**	**21 or more (some ‘varieties’ reported as plural but numbers unspecified)**

“Of unspecified size” indicates that a report did not specify the number of accessions in a collection

Table 3 . Measurable outputs from other CSREES projects coded KA 202, Plant Genetic Resources and Biodiversity, FY 2003-2004. Data were manually collected from narrative CRIS reports. CRIS does not specifically request these data. Actual totals may vary significantly. Blank cells may signify either zero or not reported.

Region	Accessions characterized or evaluated	New sources of valuable traits identified	New populations developed from crosses	Advanced populations developed	New methods developed	New genetic markers identified, new genes cloned	Germ-plasm released or licensed	Varieties released	Patents or Plant Variety Protection Certificates	Species included in reported research	Major journal publications (see list of titles)	Extension bulletins, popular public-cations
North Central	180	17	24	42	4	145	21	30	3	22	203	10
North East	30,000	4	17	28	1	5	8	11	48	32	101	9
Southern	3,294	15	13	23	4	9	51	26	5	34	89	24
Western	112	6	9	21	6	13	9	27	6	25	160	22
Total U.S.	**33,586**	**42**	**63**	**114**	**15**	**172**	**89**	**94**	**62**	**71 (*)**	**553**	**65**

(*) This number is a national total of different species, not a column sum. Some crops are included in more than one region.

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Qualset, C. O. and H. L. Shands. 2005. Safeguarding the Future of U.S. Agriculture: The Need to Conserve Threatened Collections of Crop Diversity Worldwide. Univ. Calif. Genetic Resources Conservation Program. Davis, CA. http://www.grcp.ucdavis.edu/publications/docSafeAgpdf.htm

Acronyms

ARS	Agricultural Research Service, USDA
ASHS	American Society for Horticultural Science
ASTA	American Seed Trade Association
BIC	Bean Improvement Council
CGC	Crop Germplasm Committee
CGIAR	Consultative Group on International Agricultural Research
CSREES	Cooperative State Research, Education, and Extension Service
CSSA	Crop Science Society of America
ERS	Economic Research Service
ESCOP	Experiment Station Committee on Operations and Policy
IFAFS	Initiative for Future Agricultural and Food Systems
KA	Knowledge Area
MRF	Multi-state Research Fund
NAREEEAB	National Agricultural Research, Education, Extension, and Economics Advisory Board
NCCPB	National Council of Commercial Plant Breeders
NPGCC	National Plant Germplasm Coordinating Committee
NPGS	National Plant Germplasm System
NRI	National Research Initiative (competitive grants)
NRSP	National Research Support Project
PAG	Plant and Animal Genome Meetings
PGOC	Plant Germplasm Operations Committee
SBIR	Small Business Innovation Research
USDA	United States Department of Agriculture

Appendix 1. Multistate projects in the National Plant Germplasm System
Funding, in dollars, and scientist-years (SYs) over the five years 2000-2004

Region		**Hatch**	**Multistate Hatch**	**Total CSREES**	**Other federal**	**State approp.**	**Self - generated**	**Industry**	**Other non-fed**	**Total non-federal**	**Total**	**SYs**
NC 7	Total, 5 yrs	290,892	4,205,129	4,496,021	511,651	4,000,092	431,995	1,973,999	407,058	6,813,144	11,820,816	
	Ave/yr	58,178	841,026	899,204	102,330	800,018	86,399	394,800	81,412	1,362,629	2,364,163	4.4
	Ave as % of annual total	2.5%	35.6%	38.0%	4.3%	33.8%	3.7%	16.7%	3.4%	57.6%		
NE 9	Total, 5 yrs	42,689	1,545,552	1,588,241	570,420	1,257,154	377,056	21,933	1,030	1,657,173	3,643,960	
	Ave/yr	8,538	309,110	317,648	114,084	314,289	75,411	4,387	206	331,435	728,792	5.2
	Ave as % of annual total	1.2%	42.4%	43.6%	15.7%	43.1%	10.3%	0.6%	0.0%	45.5%		
S 9	Total, 5 yrs	360,735	5,332,880	5,693,615	391,983	7,130,194	153,987	1,497,188	730,464	9,511,833	15,597,431	
	Ave/yr	72,147	1,066,576	1,138,723	78,397	1,426,039	30,797	299,438	146,093	1,902,367	3,119,486	10.5
	Ave as % of annual total	2.3%	34.2%	36.5%	2.5%	45.7%	1.0%	9.6%	4.7%	61.0%		
W 6	Total, 5 yrs	217,495	3,120,853	3,338,348	717,718	2,660,055	42,366	716,309	35,960	3,454,690	7,510,756	
	Ave/yr	43,499	624,171	667,670	143,544	532,011	8,473	143,262	7,192	690,938	1,502,151	7.1
	Ave as % of annual total	2.9%	41.6%	44.4%	9.6%	35.4%	0.6%	9.5%	0.5%	46.0%		
NRSP6	Total, 5 yrs	94,648	816,231	910,879	140,815	610,422	-	85,019	-	695,441	1,747,135	
	Ave/Yr	18,930	163,246	182,176	28,163	122,084	-	17,004	-	139,088	349,427	0.6
	Ave as % of annual total	5.4%	46.7%	52.1%	8.1%	34.9%	0.0%	4.9%	0.0%	39.8%		
Total				$16,027,104								
Ave/yr				$3, 205, 421								

Appendix 2. Project objectives of NPGS multi-state projects. Objectives are grouped into categories; order may differ from the project proposal.

NC 7 **Conservation and Utilization of Plant Genetic Resources**	**NE 9** **Conservation, Management, Enhancement and Utilization of Plant Genetic Resources**	**S9** **Plant Genetic Resources Conservation and Utilization**	**W6** **Plant Genetic Research Conservation and Utilization**
Cooperate and participate as a key element in the NPGS, a coordinated national acquisition and management program of plant germplasm valued for agricultural, horticultural, environmental, medicinal and industrial uses in the NCR and through the U.S.			
Conserve			
Conserve seed and/or vegetative stock of more than 1700 plant species.	To acquire, maintain/regenerate, characterize, document, and distribute plant genetic resources for use in the Northeast, the United States, and the World.	Conserve genetic resources and associated information for a broad spectrum of crops and related species.	Acquire and conserve cool season food and forage legume, turf and forage grass, vegetable, ornamental and medicinal plant germplasm of over 2,400 species in 268 genera.
Conduct research, and develop an institutional infrastructure needed to attain . . . objectives efficiently and effectively.	To ensure the identity of each accession as to species (or hybrid) and cultivar.		Evaluate and improve seed regeneration protocols and methodologies to both maximize efficiency and quality of germplasm, and to preserve selected beneficial plant microbes and insect-pollinated out-crossing species.
Characterize and evaluate			
Conduct research, and develop an institutional infrastructure needed to attain . . . objectives efficiently and effectively.	To characterize and evaluate plant genetic resources for specific desirable traits	Develop and apply new or improved evaluation procedures and marker-based approaches to assess diversity of genetic resources in the collections and evaluate materials for useful traits.	Characterize & evaluate germplasm by using morphological characteristics and molecular marker technology to enhance conservation management, increase utilization of the germplasm collections, and to incorporate the resulting genetic data into publicly accessible databases
			Evaluate interactions of key associated pathogens, and/or symbionts to improve management and utilization of plant germplasm collections.
			Evaluate interactions of key associated insects to improve management & utilization of plant germplasm collections.
Understand			
Contribute to understanding of plant-environment interactions, including assessment and communication of characteristics that would potentially enable a species to become invasive.	To determine the basis for and the extent of genetic variations, the geographic distribution of cultivated species, and their taxonomic relationships with closely related species.		Conduct research on selected germplasm collections for response to, or relationship with, close organismal associates such as microorganisms, pathogens, and saprophytes.
	To determine the genetic mechanisms controlling the inheritance of important traits.		Conduct research on selected germplasm collections for response to, or relationship with, significant insect pests and disease vectors.
Use, and encourage use			
Within the NCR, throughout the U.S., and internationally, encourage the use of a broad diversity of germplasm to reduce crop genetic vulnerability. Provide resources, information and expertise that foster the development of new crops and new uses for existing crops, and facilitate cultivar improvement of established crops, thus contributing to a sustainable, biobased economy.	To combine genes from diverse sources into germplasm and cultivars	Transfer technology to researchers and plant breeders in the Southern Region and worldwide in the form of plant genetic resources and associated information.	Within the Western Region, throughout the U.S., and internationally, encourage the use of a broad diversity of germplasm to reduce crop genetic vulnerability.
Educate students, scientists and the general public regarding plant germplasm resource issues.			Through different avenues of technology transfer in the form of plant germplasm propagules (seed/clones), research publications and other associated information to scientists world wide, provide resources to scientists world wide for future crop development.

Appendix 3. All CSREES funding for projects in KA 202, Plant Genetic Resources and Biodiversity, including NPGS projects. Funding over the five years 2000-2004.

Fiscal Year	**Hatch**	**Special Grants**	**Other CSREES**	**NRI Grants**	**Evans Allen**	**McIntire - Stennis**	**SBIR Grants**	**Total CSREES**
2000	$6,726, 000	$1,263,000	$1,213,000	$829,000	$269,000	$73,000	$0	$10,372,000
2001	5,943, 000	1,424,000	754,000	1,091,000	487,000	91,000	0	9,789,000
2002	6,276, 000	1,598,000	874,000	442,000	675,000	133,000	59,000	10,056,000
2003	5,787, 000	2,149,000	1,091,000	740,000	813,000	205,000	0,000	10,784,000
2004	5,811, 000	3,048,000	746,000	1,033,000	817,000	189,000	289,000	11,932,000
Total	**30,543, 000**	**9,482,000**	**4,678,000**	**4,135,000**	**3061,000**	**691,000**	**348,000**	**52,933,000**

Appendix 4. Excerpts from the FY 2006 Request for Applications (RFA) for NRI program 52.2: Genetic Processes and Mechanisms of Agricultural Plants.

The full RFA is available on the internet, *http://www.csrees.usda.gov/funding/rfas/nri_rfa.html*

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Basic understanding of plant genes and genetic processes and mechanisms is crucial for the genetic improvement of agricultural plants. The goal of this program is to supply such fundamental knowledge to support the development of genetically superior varieties of crop and forest species that are more cost-effective to grow and will provide more profit for the farmers in the ever more competitive global market. The program also aims at increasing the genetic diversity of crops in the U.S. to meet future threats and challenges and in training new scientists in plant breeding.

To meet these identified needs of agriculture, the long-term (10 year) goals for this program are: obtain a detailed understanding of the regulation of gene expression in agricultural plants to better use agriculturally important genes for improved crop production and quality; and enhance the genetic diversity of existing crop families with the possibility of developing novel crops to meet future challenges.

FY 2006 Priorities for Research

1) Functional studies of agriculturally important genes and gene products, including the development of improved mutational and gene silencing approaches for these studies; and

2) Regulatory mechanisms of gene expression. Research is encouraged that aims at understanding gene regulatory networks at the systems level.

FY 2006 Priority for Integrated Activities (those that combine research, education, and/or extension)

1) Application of plant population and evolutionary genetics to germplasm enhancements with emphasis on increasing the genetic diversity of crops in the U.S. and educating scientists in principles and techniques of crop germplasm enhancement. Applicants are encouraged to utilize germplasm from the National Plant Germplasm System (NPGS).

Other Key Information - Research and Integrated Activities

- Integrated projects should include research, education, and extension/outreach objectives (at least two of three). These include: a) hypothesis-driven research to fill knowledge gaps that are critical to the development of practices and programs to address the problem area; b) create educational deliverables (e.g., interdisciplinary curricula and/or experiential learning for graduate and undergraduate students) that will train the next generation of scientists and educators who will work in the problem area; and/or c) deliver an effective extension/outreach program that will lead to measurable behavior change in an identified audience or stakeholder group. Projects should also include a management plan (developed with input from stakeholder advisory groups) that leads to measurable improvements in the problem area.
- The education component of an integrated application must go beyond the level of laboratory training for graduate students or postdoctoral researchers supported by the grant. Examples of education activities in agricultural plant breeding and germplasm enhancement include curriculum and/or degree program development, multi-college/university approaches to regional or interstate curriculum development, faculty sharing and joint degrees.
- Use of Model Species: Importance of the proposed research to agricultural productivity and sustainability should be clearly indicated in the application. Researchers are strongly encouraged to conduct research directly in a crop or forest species important to agriculture. Use of non-crop model systems is acceptable if tools are not yet available in the crop species of interest. However, the investigator must clearly indicate how such non-crop model studies are relevant to agriculture and food systems or forest species, the strategy for transferring the knowledge to these species for agricultural or forestry benefit, and the potential timeframe for such transfer.

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