Apple CGC Meeting
Plant Genetic Resources Unit Conference Room
Geneva, NY
Agenda Sept. 10, 2013

In-person attendees: Angela Baldo, Susan Brown, Thomas Chao, John Keaton, Bob Martin, Ian Merwin (morning), Greg Noden, Jay Norelli, Heidi Schwaninger, Steve Van Nocker, Gayle Volk, Mike Wisniewski, Kenong Xu, Mike Chao (afternoon), Joe Davis (afternoon)
Teleconference attendees: Peter Bretting, Gennaro Fazio, Phil Forsline, Kyle Gardner, Gary Kinard, Jim Luby, Jim McFerson, Sean Myles, Gan-Yuan Zhong

Minutes/summary provided by Gayle Volk (Chair)

Apple Collection Report (Thomas Chao)

- See attached pdf of presentation

- Malus collection has 6734 total accessions, of which 5226 are trees in the field and 1508 are seedlots
  Field collections:
  B9: Malus core collection
  M7&E7: Permanent Malus collection, on EMLA 7 rootstock
  K1: Kazakhstan *M. sieversii* seedlings
  W3: Wild Malus species seedlings from Armenia, China, Georgia, Kazakhstan, Russia, and Turkey
  G1: 7 F1 populations of 'Gala" x *M. sieversii* (mapping populations)

- *Malus sieversii* evaluations in progress:
  - Disease evaluation-fire blight and scab (Aldwinckle, Norelli), blue mold (Janisiewicz), post-harvest decay (Jurick), mapping and resistance genes (Aldwinckle, Norelli, Wisniewski)
  - Drought resistance (Bassett)
  - Cold hardiness (Luby)
  - Mapping traits (Xu, Brown, Chao, Fazio, Gutierrez, Zhong)

- Permanent Collection evaluations
  - Digital imaging of fruit, leaves, and flowers (core, wild, permanent)
  - Polyphenolic, antioxidant capacity, juice, red-fleshed, fruit abscission (PGRU) (core)
  - Budbreak, bloom, end of bloom (permanent)
  - Genetic diversity, population structure, core collection, hybrids (Volk, Richards)

- Genotyping by Sequencing project
  - Collaboration: Myles & Zhong, Baldo, Chao, Fazio, Richards, Schwaninger, Volk
  - 1950 Malus accessions: 1403 *M. domestica*, 210 *M. sieversii*, 61 hybrid, 48 *M. baccata*, 23 *M. floribunda*, 22 *M. orientalis*, 16 *M. sylvestris*, and 167 of 24 other Malus species. 'Golden Delicious" was used a reference genome. 60% (near 1,000,000 SNP markers) aligned to the 'Golden Delicious' map, over 50,000 SNPs per chromosome. Investigate: domestication history, breeding history, gene flow, evolution, allele mining, GWAS. The 7 'Gala' x *M. sieversii* F1 populations were added to the dataset in 2013.

- New accesions in 2013
  - 20 Malus accessions from APHIS: 9 cider apples from Northern Spain, 1 *M. sieversii* from 1996 exploration and other varieties around the world.
  - *M. sylvestris* seed accessions from Albania, one *M. paradisiac* seed accession from Azerbaijan
  - 84 *M. fusca* seed accessions from an exploration in Pacific Northwest
  - 9 *M. spontanea* seed accessions from Japan
  - 52 wild Malus seedlings based on drought stress evaluation by Carole Bassett

- Distributions
  - 233 domestic and 46 foreign orders between April1, 2012 and March 31, 2013 for 6,349 samples from 2,313 accessions.
  - There were large orders of leaf samples for DNA isolations; also dormant cutting and pollen requests.
  - The " Botany of Desire" seeds (open pollinated seeds of wild *M. sieversii* seedlings) requests have increased in the past few years especially from Europe such as England, Finland, France and Germany. Over 50,000 seeds in storage and we will collect more seeds in the next few years before the block removal.

- Collection concerns
  - Clonal collection is running out of space for future permanent collection addition
  - *M. sieversii* seedling evaluation block will be removed in 2015
  - Streptomycin resistant strains of fire blight are a concern for the Malus collections – the use of streptomycin is limited when possible.
  - Weather impact on the collection – warm winter, lack of chilling, late spring frost, too much rain, or too little rain.
  - About 1000 accessions in the Apple collection have no ploidy data available. The PGRU was unable o send leaf samples to the previous provider (Plant Cytometry Services in The Netherlands, so Thomas is exploring other opportunities to collect this data).

- Program budget issues
  - $2000-3000 is spent annually on distribution postage, most of which is dormant bud cuttings
  - Sequestration caused a 7.5% cut in the in-house budget for the clonal program, and NE9 also cut funding by 7.5% in 2013. The budget is currently 90% salaries, so most of the discretionary dollars are gone. A 0.5 FTE position was abolished (collection characterization). The program has outsourced pruning of the *M. sieversii* block to Cornell ($20K), but this can not be performed during the 2013-2014 winter, due to budget cuts.
  - Ben Guitterez is in his first year of his SCEP Ph.D. program at Cornell with Susan Brown.
  - Due to budget cuts, the program is focusing on its core mission of preservation and maintenance.

Abbreviated GRIN discussion (Kinard)

- GRIN serves as a portal to Animal, Plant, Microbe, and CGC information, and only the plant portion is being significantly updated.
- The DBMU is in the process of filling 2 vacant positions.

- GRIN-Global is scheduled to be rolled out on Oct 1, 2013, with significant changes to the public web-interface. Trainings are underway.

Rootstock Breeding Program (Fazio)

- Rootstocks are not readily available for distribution, except in the form of dormant buds
- Gennaro Fazio often has some rootstocks in plant-form that can be sent out, if necessary, for materials that are not available commercially
- Breeding program has a number of crosses using wild materials (*M. sieversii*, *M. ioensis*, *M. baccata*, etc.) that are currently being evaluated as rootstocks.

Associated genetic data/genetic coverage (Volk)

- Continued assessment of collection diversity, gaps, and core coverage based on SSR and chloroplast sequence data.
- Contact Gayle for more information

Updates on ongoing research collaborations involving NPGS Apple Collection

- Cornell breeding program (Brown)
    - Crosses have been made between columnar type accessions and 12 different species. Pale Green Lethal was noted (as high as 25%) in these crosses. Interesting results were obtained between *Malus doumeri* and a columnar type. Viney and dwarf phenotypes were also observed.
    - Ben Guitterez is focusing his PhD research on antioxidant levels in the collection and mapping populations, and is studying leaves, fruit, and development.

- Cornell apple genomics (Xu)
    - This program is focusing on apple fruit acidity traits (*Ma* locus) using a Gala x *M. sieversii* mapping population. Markers have been identified. His program is also looking at keeping quality.

- Post-harvest diseases/Blue mold project (Norelli and Wisniewski)
    - 2 QTLs have been identified (LG4 and LG10-colocates with firmness) that are linked with blue mold resistance. Transcriptomics and RNAseq are being used to understand virulence and pathogenicity by *Penicillium expansin*, as part of a BARD project. GBS results will provide additional markers on the map. Materials are being crossed with early flowering materials to validate the markers.

- Identifying and characterizing new sources of resistance to *Erwinia amylovora* in *Malus sieversii* for scion breeding (Norelli)
    - Fireblight CGC/WTFRC project is evaluating the resistance in *M. sieversii* using a Gala x *M. sieversii* mapping population, and identifying if resistance is novel compared to other known forms.

- RosBreed (Luby)
    - This project is in the 4th year and is currently a no-cost extension.
    - See attached pdf of presentation.

- Hard cider varieties (Merwin)

  - Bittersweet and bittersharp cider varieties have been recommended as additions to the NPGS collection (see attached list). Several imports have been attempted to bring materials to the US from France and Spain. Many of the materials were destroyed due to the disease concerns, but 9 were conditionally released from quarantine last year.
  - Recommended that Greg Peck (VA) be added to the committee, since Ian Merwin has retired.
  - The cider industry has an interest in novel varieties from Spain and Portugal, that have not been successfully introduced into the US. Ian Merwin will provide a list of these materials.

- GBS (follow-up meeting to be held 9-11-13) (Miles)
  - Calling SNPs from GBS data is an issue. Golden Delicious reference is a single-stranded representation, which makes data interpretation a challenge. Many SNPs have been identified, but the genotype matrix is sparce, with lots of missing data. Imputation is proposed.

- *Malus sieversii* sequencing (follow-up meeting to be held 9-11-13)
  - Preliminary sequencing has been performed. Data look promising, and more in-depth sequencing will be next.
  - RNA samples are sought for RNAseq.
  - Apple genome size is estimated to be 750 Mb, but may be closer to 800-1000 Mb.

- Michigan State Genomics Program (van Nocker)
  - Using *M. fusca* to determine chromatin structure and gene activity. Has transcription profiles for 40 plant parts at 10 stages. Identifying epigenetic marker and using fusca as a model for genome annotation. *M. fusca* was selected because it has a high number of flowers per cluster. 30x genomes have been sequenced and 150 transcriptional datasets developed.
  - Juvenility is being studied using rapid-cycling *M. hupehensis* (9 month to flower) as a genetic model. 30x genome coverage and 60 transcriptional datasets. Research focuses on age and development of the meristem from the juvenile to adult stage, and genes that are active in repressing juvenility.

Key Topics relating to Apple Collection (discussion of each topic summarized below):

- Apple Crop Vulnerability Statement Update (Volk)
  - A complete rewrite of the Apple Crop Vulnerability Statement using the new NPGS recommended outline is underway
  - **A draft CVS will be distributed for comments in late October or early November**

- Available orchard space for new acquisitions
  - Currently, the orchard has enough space for an additional 150 trees in the permanent collection. This is expected to be enough space for the next 2 seasons.

- Plans for the *M. sieversii* seedling block
  - Thomas has proposed the removal of the K1 (M. sieversii) block after the 2015 harvest season, either in half-block increments or the whole block at one time.

  - **Thomas will make the user community aware of this upcoming event and encourage interested parties to collect materials and data during the next 2 years, in anticipation of the orchard removal.**
  - Additional space will also be made when the W2 wild *Vitis* seedling block is removed, which will allow for additional apple expansion.
  - **Thomas is also accepting recommendations from the user community for materials that should be grafted from the K1 block and added to the permanent collection (even if just for further evaluation).** The 3 core collections (site 6, site 9, other sites) have already been added to the main collection. Materials (>50) tolerant of drought stress recommended by Carole Bassett are currently being grafted and incorporated.
  - **The committee recommended that records be made in GRIN to describe the reason why *M. sieversii* materials were added to the permanent collection.**
  - Additional *M. sieversii* seedlings grown at U. Minnesota were selected and added to the Permanent collection based on their cold hardiness and disease tolerance.
  - Diverse *M. sieversii* accessions collected by Diane Miller in Kyrgyzstan were also added to the permanent collection a few years ago.

- Plans for the W3 Block: Wild seedlings
  - No removal plans for W3 at this time
  - The west end of this block has seedling trees from the *M. sieversii* elites
  - The core collection of *M. orientalis* from this block has been repropagated and added to the main collection.
  - **This orchard has had some die-back, but thinning of this block (removing low-priority trees) didn't seem to be a priority at this time.**

- New Accession Priorities
  - **Additional accessions of wild materials from China are a priority.** GanYuan Zhong is working actively with the Chinese Ministry of Science and Technology to set up some collaborative projects, which will hopefully lead to increased access to wild apple materials. These materials will likely be brought to the US in seed form, and can be kept in cold-storage until field planting space and a grow-out are desired.
  - There are several large heritage apple collections (including the Nick Botner collection in Oregon) that are at risk of being lost. These have hundreds to thousands of additional apple varieties. Lee Calhoun and Tom Burford also have large collections. **Given the very limited orchard space, materials will not be sought from these collections unless there are specific, known, novel, scientifically desirable accessions in these collections that are not available elsewhere.**
  - Nursery cider trees: Nurseries do not maintain many of the cider varieties, due to erratic demands, so large orders must be filled by using materials obtained from private (home orchard) sources, particularly for large-scale cider orchard plantings. In some cases, these materials are available in the PGRU, but even then, ample materials are not available for distribution. This is likely to continue to be a problem in the industry.
  - In situ conservation strategies may be developed for some of the North American Malus species. Habitats for some species (*M. fusca*) may be at-risk due to climate change. This effort may be coordinated with the US Forest Service and BLM using existing agreements between the agencies.
  - **The current collection diversity and representation should be understood to strategically collect novel materials.** Wild apple genetic resources may also be available from future

proposed collection trips by the Global Crop Diversity Trust (in the US and elsewhere). These materials will likely be stored as seeds, and thus field space is not a current concern.
  - **Published scab resistance (and other diseases) standard differentials should be added to the permanent collection so that they are publicly available.**
  - **Publicly available breeding parents (see RosBreed reference set) should be added to the permanent collection.**
  - Hard Cider Types: **Ian Merwin will provide a list of high-priority desired European cider varieties.** The committee recognizes that private industry can bring these materials through quarantine, and should perhaps pursue this if they are in high demand. **Thomas Chao can decide if some of these cultivars would add novelty to the PGRU collection, however they are concerned because cider varieties often bloom late and are susceptible to fire blight.**
  - Other European varieties: **2 accessions are desired from Portugal (contact Susan Brown).** Other European materials may be identified through ongoing collection SSR comparisons.
  - Gayle Volk is doing an SSR comparison of materials in the PGRU to those available at the Morton Arboretum to determine if some of the species materials in the arboretum could be used to supplement the diversity in the NPGS collection.
  - Chloroplast data suggest that there is a lack of diversity represented from Southeastern Asia and India in the NPGS collection. These are likely low-chill varieties. If low-chill materials will be added to the collection in the future, and grown as plants, an alternative grow-out site may be needed at some point.
  - Past discussions have included adding cultivars from China and landraces from Turkey. If opportunities become available to have access to these materials, their priority (and quantity) will be discussed at that time.

- Collection evaluations/GRIN
  - **Photos should be made available for the core collection materials as a highest priority, followed by the main collection.**
  - **The committee recommended that the fire blight and scab resistance data for the *M. sieversii* materials be added to GRIN and made publicly available.**
  - There is interest in having pollen lethal information available for accessions (pollen dwarf, pale green lethal).
  - Fruit quality data should be collected for the parents of the G1 mapping populations, and fruit quality data should be put onto GRIN when available.
  - Angela Baldo described her project plan objectives to aid with interoperability between GRIN and other crop specific databases (such as GDR).

- Peter Bretting requested (via teleconference) that information be provided to Luigi Guarino of the Global Crop Diversity Trust regarding apple accession recommendations and conservation costs for a Global Apple Collection. **The committee discussed this briefly, and some opinions will be provided to the GCDT (Volk and Chao).**

Next CGC Meeting/Teleconference: To be determined

Future CGC Topics:

- Role of public service for collection in times of low budgets
- Trait evaluation priorities
- Follow-up on key discussion items above (particularly those in bold)

- Office of National Programs Report
- National Germplasm Resources Lab/GRIN-Global Report
- APHIS Report

2013 OFFICE OF NATIONAL PROGRAMS REPORT

FOR THE U. S. NATIONAL PLANT GERMPLASM SYSTEM

OFFICE OF NATIONAL PROGRAMS, NATIONAL PROGRAM 301: PLANT GENETIC RESOURCES, GENOMICS, AND GENETIC IMPROVEMENT

(PETER BRETTING, JOSÉ COSTA, JACK OKAMURO, SALLY SCHNEIDER,
ROY SCOTT, GAIL WISLER, DA KAY SIMMONS)

1 Personnel changes:

1.1 Farewell and best wishes to Dave Ellis, who left the NCGRP in Ft. Collins, CO to curate the potato and sweet potato genebank in CIP, Peru; and to Molly Welsh, who retired as the Phaseolus curator at the WRPIS, Pullman, WA. We mourn the loss of Mark Bohning and Gorm Emberland, both staff members of the NGRL Database Management Unit, Beltsville, MD.

1.2 Welcome to Carolyn DeBuse, new Prunus curator at the NCGR-Davis; Josef Pohl, new IT specialist at the NCGRP, Ft Collins; and José Costa, new NPL for Grain Crops, ONP.

2 Site developments and changes:

2.1 Researchers at the USDA/ARS NERPIS at Geneva, New York applied new statistical genetic approaches to identify, from tomato breeding stock, latent genes that originated from tomato wild relatives. They uncovered not only genes from wild relatives introduced into tomato through deliberate breeding, but also other genes genetically-linked to the target traits. Previously-unrecognized hybridizations in nature between tomato and wild relatives were identified. These results will enable these genes from tomato wild relatives to be characterized, and tomato genetic resources more effectively conserved and utilized in breeding.

2. 2 USDA/ARS researchers at the NGRL Beltsville and collaborators from the University de San Carlos in Guatemala, Bioversity International, and the International Center for Tropical Agriculture (CIAT) completed the Guatemalan Atlas of Crop Wild Relatives. The Atlas provides detailed information on 105 species of wild plants--related to 29 different crops--which will support genetic resource conservation efforts. Because Guatemala and adjacent nations are very rich in plant biodiversity, these efforts will also support global efforts to conserve plant genetic resources. Available at http://www.ars.usda.gov/ba/atlascwrguatemala

2.3 USDA/ARS researchers at the WPRIS in Pullman, WA; Children's Nutrition Research Center in Houston, TX; and their university collaborators analyzed the genetic diversity, population structure and genome-wide marker-trait association with seed nutrients for pea (Pisum) accessions in the NPGS pea core subset, identifying 28 significant marker-trait associations for eight of the seed mineral nutrient concentrations, including Ca, Cu, K, Mo, Ni and P. This information could help breeders implement marker-assisted selection in pea for improved mineral nutrient content.

2.4 The USDA/ARS NCRPIS, ONP, and OCIO partnered with the Oregon State University PRISM group and Esri, Inc. to deliver an updated edition of the USDA Plant Hardiness Zone Map (PHZM) on the web at http://planthardiness.ars.usda.gov/PHZMWeb/ Unlike prior editions, the new PHZM is GIS-based, identifies the PHZ for any zip code, and includes an interactive map for exploring variation in PHZ with the resolution of 800 m.

3 Budgets:

The current Administration's research priorities for USDA include climate change, food safety, children's nutrition/health, international food security, and bioenergy.

ARS has implemented the Consolidated and Further Continuing Appropriations Act, 2013 (FY 2013 appropriations) which includes rescissions and other reductions to the ARS's budget due to sequestration. The President's FY 2014 budget proposal, presented on 10 April 2013, would increase ARS's funding by about 2.7% above the FY 2012 appropriated funding level, and specifically would increase the NPGS's budget by $581,000. The House Agriculture Appropriations Subcommittee "mark-up" the FY 2014 budget would provide a 5.6% increase above the enacted FY 2013 operating level, which translates to a total that is 2% lower than the FY 2012 appropriated funding level. The Senate Agriculture Appropriation Committee "mark-up" of the FY 2014 budget would provide a 10.7% increase above the enacted FY 2013 operating level, which would increase ARS's budget by about 2% above the FY 2012 appropriated funding level.

4 National Programs:

ARS's research portfolio is organized as a series of 17 national programs. Plant and microbial genetic resource management, genetic improvement, genomics, molecular and biological processes, biotechnology risk assessment, bioinformatics, and genome database management are incorporated into National Program 301 (see the WWW at: http://www.nps.ars.usda.gov/programs/programs.htm?NPNUMBER=301). NP 301 recently completed its second five year cycle. Based on customer/stakeholder comments, the NP 301 Action Plan, and other input, ARS researchers developed individual Project Plans for its third five-year cycle, 2013-2017. More than 92% of the individual NP 301 Project Plans received "passing grades" during initial external reviews, and will now proceed to implementation.

5 National Plant Germplasm Coordination Committee (NPGCC):

The NPGCC seeks to promote a stronger, more efficient, more widely-recognized and better utilized NPGS. Its goals are to facilitate the coordination of ARS, NIFA and SAES planning and assessment mechanisms for NPGS policy, organization, operations and support; promote awareness and understanding of the NPGS across ARS, NIFA, and SAES and more broadly to the scientific community; and serve as a vehicle for improving communications and discussions about issues impacting the NPGS with ARS, SAES, and NIFA. It will assess, develop and recommend to the SAES, ARS and NIFA strategies for improved coordination of NPGS activities; develop and recommend a process for improved communication of the value of the NPGS; initiate a strategic planning effort for the NPGS to better define and communicate the vision, mission and short- and long-term goals; and to evaluate the current funding models for the NPGS and report findings to the SAES directors, ARS and NIFA.

The current members of the NPGCC are T. Burr (Cornell University-SAES), Chair; E. Young (Executive Director, Southern Region), Secretary; L. Sommers (Colorado State-SAES), J. Colletti (Iowa State-SAES); G. Arkin (University of Georgia-SAES); A. M. Thro (NIFA); E. Kaleikau (NIFA); P. S. Benepal (NIFA); P. Bretting (ARS-Office of National Programs); D. Upchurch (ARS-Southern Plains Area); and G-Y. Zhong (ARS-Geneva). Representatives of the Association of Official Seed Certifying Agencies (AOSCA--Chet Boruff); the American Seed Trade Association (ASTA—Tim Cupka); and the National Association of Plant Breeders (NAPB, David Baltensperger) attend the annual NPGCC meetings as observers.

NPGCC members made a joint presentation on the NPGS to the 2006 Experiment Station Section/State Agricultural Experiment Station/Agricultural Research Directors Workshop September 24-27, 2006. That presentation, plus testimonials from key Directors about the NPGS's value, increased the NPGS's visibility to this important group. In May 2007, the NPGCC recommended to the National Research Support Project Review Committee that it recommend restoring off-the-top funds designated for NRSP-5 (the Prosser, WA virus-free pome and stone fruit project) and NRSP-6 (the potato genebank project at Sturgeon Bay, WI) to their FY 06 levels to sustain these valuable efforts. Since then, funding for NRSP-5 has been assumed by the National Clean Plant Network. Support for NRSP-6 has been maintained at the FY 06 level since then. The NPGCC met on June 5, 2008, in conjunction with the annual PGOC and biennial CGC Chairs meetings. It discussed the NPGS's budget levels, funding for NRSP-5 and NRSP-6, the location of crop collections, and mechanisms for publicizing the NPGS. Similarly, the NPGCC met on 23-24 June 2009, 9 June 2010, 16-17 June 2011, 12 June 2012, and 13-14 June 2013 in Beltsville, MD to continue its work on these priority issues.

6 International germplasm items:

The FAO International Treaty (IT) for Plant Genetic Resources for Food and Agriculture came into force on 29 June 2004, and beginning in 2007 its standard material transfer agreement (SMTA) for plant genetic resource exchange was adopted by Parties to the IT and the CGIAR Centers for distributing plant genetic resources. On 7 July 2008, the White House transmitted the IT to the Senate; ratification would require the advice and consent of a 2/3 majority of the Senate. The Senate Foreign Relations Committee (SFRC) held hearings on the IT on 10 November 2009. During their last Business Meeting of the 111th Congress (30 November 2010), the SFRC voted the IT out of committee, for consideration by the full Senate. Unfortunately, the Senate adjourned on

22 December 2010 without voting on the IT. It is uncertain whether the SFRC will schedule new hearings on the IT during 2013, which might enable vote for consent (or not) to IT ratification to occur during the 113th Congress.

Concurrently, the Convention on Biodiversity (CBD) adopted the voluntary, non-binding Bonn Guidelines on Access and Benefit-Sharing during the sixth Conference of Parties (COP-6) of the CBD at The Hague in April 2002. Starting in 2006, Parties to the CBD began negotiating what became the legally-binding Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization. Adopted by the COP-10 on 29 Oct. 2010, the Nagoya Protocol is quite complicated, with many ambiguous components; its ramifications are currently under analysis (see http://ictsd.org/downloads/2010/11/abs-protocol.pdf for the text).

The preceding developments at FAO and with the CBD will substantially affect international exchange of plant genetic resources, and the NPGS, whether or not the U. S. is ultimately a Party to either or both treaties. Precisely how these treaties will affect U. S. users of germplasm depends on the treaties' implementations.

7 National Genetic Resources Advisory Council (NGRAC):

The National Genetic Resources Advisory Council (NGRAC) includes nine members, was originally established by the 1990 Farm Bill, and had been inactive since 1999. Secretary of Agriculture Vilsack re-established the NGRAC in 2012 to formulate recommendations on actions and policies for the collection, maintenance, and utilization of genetic resources; to make recommendations for coordination of genetic resources plans of several domestic and international organizations; and to advise the Secretary of Agriculture and the National Genetic Resources Program (NGRP) Director of new and innovative approaches to genetic resources conservation. The NGRAC will advise on ways to ensure that the NGRP serves the needs of all farmers for high-quality and diverse seed (both genetically engineered and non-genetically engineered) for their particular farming operations. The NGRAC will also advise on how the USDA can develop a broad strategy for maintaining plant biodiversity available to agriculture, and strengthening public sector plant breeding capacities.

Last year, the NGRAC held an initial organizational teleconference, and its first meeting occurred at Beltsville 5-6 March 2013, and its second at Ft. Collins 25-26 September 2013. The members of the NGRAC include Drs. Manjit Misra (Chair, Iowa State University), Jane Dever (Texas A & M), Karen Moldenhauer (University of Arkansas), Stephen Smith (DuPont Pioneer), Allison Snow (The Ohio State University), Mulumebet Worku (North Carolina A & T), Mr. Matthew Dillon (Seed Matters, Clif Bar Family Foundation), Dr. Herman Warren (Warren and Associates Seeds), and Mr. Terry Williams (Tulalip Tribes). Ex officio members include Drs. Gary Pederson (ARS-Griffin), and Peter Bretting (ARS-ONP), and representatives from other Federal science and technology agencies.

Orientation to Crop Vulnerability Statements

Crop vulnerability statements (CVS) communicate periodic assessments of the challenges that crops face, particularly from reduced genetic diversity resulting from genetic erosion. Collections of genetic resources are key mechanism for reducing crop vulnerability resulting from genetic erosion and uniformity, and for supplying crop breeding and research programs with novel traits and underlying genes to satisfy evolving demands.

Crop vulnerability statements will be reviewed as part of the periodic (usually annual, sometimes biennial) Crop Germplasm Committee (CGC) meetings. During the CGC meetings, the crop-specific curators will be encouraged to communicate a status update for the crop germplasm collection along the lines of CVS section 3 (see outline below).

After the CGC meetings, the CVS will be updated by the CGC chair, secretary, or designate, and submitted to the CGC for review along with the meeting minutes. After internal review by the CGC, the updated CVS text will be provided to the CGC Coordinator at the National Germplasm Resources Laboratory (NGRL). The updated CVS will then be posted on the GRIN-Global website for public access.

Following an initial update according to the outline below, the CVS might change relatively little from one year to another, but considerably over a multi-year time span. CGCs should conduct a more comprehensive assessment of current conditions every five or so years, focused particularly on updating CVS sections 2 and 5.

Maximum page lengths are suggested for the different sections of narrative text. Additional information in the form of text, tables, illustrations, etc. could be included as appendices to the narrative text.

Crop Vulnerability Statement Outline

Summary of key points (1 p. maximum)

1. Introduction to the crop (2 pp. maximum)
  - **1.1 Biological features and ecogeographical distribution**
  - **1.2 Genetic base of crop production**
  - **1.3 Primary products and their value (farmgate)**
  - **1.4 Domestic and international crop production**
    - **1.4.1 U.S. (regional geography)**
    - **1.4.2 International**

2. Urgency and extent of crop vulnerabilities and threats to food security (4 pp. maximum)
  - **2.1 Genetic uniformity in the "standing crops" and varietal life spans**
  - **2.2 Threats of genetic erosion <u>in situ</u>**
  - **2.3 Current and emerging biotic, abiotic, production, dietary, and accessibility threats and needs**
    - **2.3.1 Biotic (diseases, pests)**
    - **2.3.2 Abiotic (environmental extremes, climate change)**
    - **2.3.3 Production/demand (inability to meet market and population growth demands)**
    - **2.3.4 Dietary (inability to meet key nutritional requirements)**
    - **2.3.5 Accessibility (inability to gain access to needed plant genetic resources because of phytosanitary/quarantine issues, inadequate budgets, management capacities or legal and bureaucratic restrictions)**

3. Status of plant genetic resources in the NPGS available for reducing genetic vulnerabilities (5 pp. maximum)
  - **3.1 Germplasm collections and <u>in situ</u> reserves**
    - **3.1.1 Holdings**
    - **3.1.3 Genetic coverage and gaps**
    - **3.1.3 Acquisitions**
    - **3.1.4 Maintenance**
    - **3.1.5 Regeneration**
    - **3.1.6 Distributions and outreach**
  - **3.2 Associated information**
    - **3.2.1 Genebank and/or crop-specific web site(s)**
    - **3.2.2 Passport information**
    - **3.2.3 Genotypic characterization data**
    - **3.2.4 Phenotypic evaluation data**

- **3.3 Plant genetic resource research associated with the NPGS**
  - **3.3.1 Goals and emphases**
  - **3.3.2 Significant accomplishments**
- **3.4 Curatorial, managerial and research capacities and tools**
  - **3.4.1 Staffing**
  - **3.4.2 Facilities and equipment**
- **3.5 Fiscal and operational resources**

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

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

6. References

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

PROGRESS REPORT for APPLE CGC 2013 Meeting

Plant Genetic Resources Unit, USDA-ARS
Geneva, NY 14456
Prepared by C. Thomas Chao, Horticulturist/Curator
Email: c.thomas.chao@ars.usda.gov
September 10, 2013
Apple CGC meeting

Geneva, NY has higher than average rainfall in the spring and early summer of 2013. There was no extreme warm weather early in the season like 2012 and no damaging freeze event. There were more severe thunderstorms in the spring. We had some soil erosion problem at the collections due to high rainfall.

We maintain 6,734 accessions of *Malus* including 5,226 field accessions and 1,508 seed accessions. We distributed 6,349 samples of 2,313 *Malus* accessions based on 233 domestic and 46 foreign requests between April 1, 2012 and March 31, 2013.

We received 7 *Malus* accessions in August, 2012 and 13 *Malus* accessions in February, 2013 from APHIS Quarantine Center. These accessions include 9 cider apples from Northern Spain, one *M. sieversii* from 1996 exploration and other varieties from different countries. We received one *M. paradisiac* seed accession from Azerbaijan, 4 *M. sylvestris* seed accessions from Albania, 84 *M. fusca* seed accessions from Gayle Volk [J. Amer. Soc. Hort. Sci. 137(5):325-332. 2012], and 9 *M. spontanea* seed accessions from Kyushu, Japan through Arnold arboretum. We propagated 52 wild *M. sieversii* or *M. orientalis* seedlings from K1 and W3 blocks based on drought stress evaluation by Carol Basset, Appalachian Fruit Research Station, USDA-ARS. These trees will be in the nursery for two years and they will be planted in spring 2015 at the permanent collection.

We continued the fruit collection of *Malus* in summer/fall 2012 and 2013. We are extracting the juice and conducting fruit quality traits analysis (fruit fresh weight, titratable acidity, anthocyanin, and 28 polyphenolic compounds). We also compare differences in the polyphenolic content between skin and flesh tissue of selected *Malus* accessions. We continue digital imaging of the fruit of *Malus* collection in fall 2012 and 2013, some foliage of the wild *Malus* in fall 2012, and the flower of *Malus* in spring 2013. We received phenological data of our *Malus* accessions from 2010 and 2012 recorded by Steve van Nocker, Michigan State University and we will upload the data to GRIN. I recorded budbreak, full bloom and end of bloom of 2,994 trees in the permanent *Malus* collection on a weekly basis in spring 2013. For our genotype by sequencing (GBS) effort, in collaboration with Sean Myles, Dalhousie University, Canada and Christopher Richards and Gayle Volk of National Center for Genetic Resource Conservation (NCGRP), USDA-ARS, we GBS 1,950 *Malus* accessions. We are analyzing the data to determine the genetic relationships among species and accessions, and answer questions related to domestication and evolution issues. Angela Baldo, computation biologist, is carrying out allele mining of the data for interesting traits such as self-incompatibility and disease resistance. We are also GBS the seven ‘Gala’ x *M. sieversii* F1 populations. A new database for germplasm information–the GRIN Global should be online by end of September 2013.

We restarted the backup cryo-storage of *Malus* accessions last winter. We shipped dormant budwood of 25 *Malus* accessions to NCGRP in January, 2013. We received the cryo-treated budwood back in April and we tested the viability of the cryo-budwood by budding 10 buds per accessions. Two accessions had viability rate of less than 40% (30%) that is considered not high enough viability for long-term storage. We will reship those two accessions to NCGRP for backup storage next season. We will ship 30 accessions of *Malus/Prunus* to NCGRP for backup storage each year.

With the recent budget cuts in the NE9 and ARS in-house projects, we expect to have significant financial constraints to deal with in FY14 and potentially in future years. The reduction in operating budget limits our capability to do certain task such as pruning of the *M. sieversii* seedling block (K1) and the wild *Malus* seedling block (W3).

Publications:

PGRU related publications:

Gross, B.L., G.M. Volk, C.M. Richards, P.L. Forsline, G. Fazio, and C.T. Chao. 2012. Identification of "duplicate" accessions within the USDA-ARS National Plant Germplasm System *Malus* collection. J. Amer. Soc. Hort. Sci. 137(5):333-342.

Gross, B.L., G.M. Volk, C.M. Richards, P.A. Reeves, A.D. Henk, P.L. Forsline, A. Szewc-McFadden, G. Fazio, and C.T. Chao. 2013. Diversity captured in the USDA-ARS National Plant Germplasm System apple core collection. J. Amer. Soc. Hort. Sci. (In press).

Volk G.M., A.D. Henk, C.M. Richards, P.L. Forsline, and C.T. Chao. 2013. *Malus sieversii*: a diverse Central Asian apple species. HortScience (In press).

Geneva germplasm used in the studies:

Potts, S.M., Y. Han, M.A. Khan, M.M. Kushad, A.L. Rayburn, and S.S. Korban. 2012. Genetic diversity and characterization of a core collection of *Malus* germplasm using simple sequence repeats (SSRs). Plant Mol. Biol. Rep. 30:827-837.

Routson, K.J., G.M. Volk, C.M. Richards, S.E. Smith, G.P. Nabhan, and V.W. de Echeverria. 2012. Genetic variation and distribution of Pacific crabapple. J. Amer. Soc. Hort. Sci. 137(5):325-332.

Abstracts:

Fazio, G., C.T. Chao., P. Forsline, C. Richards, and G. Volk. 2012. Characterization of tree and root architecture of *Malus sieversii* seedlings for rootstock breeding. X International Symposium on Integrating Canopy, Rootstock and Environmental Physiology in Orchard Systems. Stellenbosch, South Africa.

Gardner, K.M., H. Schwaninger, S. Cann, A. Baldo, T. Chao, G. Fazio, G. Volk, C. Richards, G.-Y. Zhong, and S. Myles. 2012. Genome-wide survey of genetic diversity in apple using genotyping-by-sequencing. Sixth Rosaceous Genomics Conference, September 2012, Trento, Italy.

Gardner, K.M., H. Schwaninger, S. Cann, A. Baldo, T. Chao, G. Fazio, G. Volk, C. Richards, G.-Y. Zhong, and S. Myles. 2013. Genome-wide survey of genetic diversity in apple using genotyping-by-sequencing. Plant and Animal Genome XXI, January 12-16, 2013. San Diego, CA. (Abstract #W248).

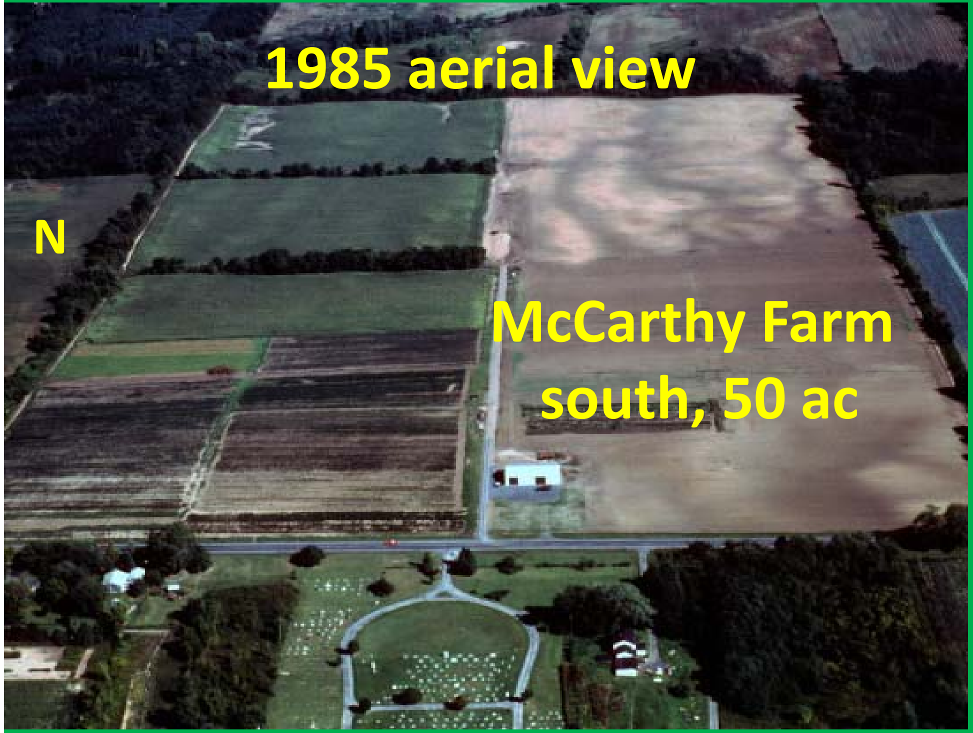
Norelli, J.L., M.E. Wisniewski, S. Droby, V. Hershkovitz, and C.T. Chao. 2013. Genetic analysis of *Malus sieversii* PI613981 for resistance to postharvest apple fruit decay caused by *Penicillium expansium* (blue mold). Plant and Animal Genome XXI. January 12-16, 2013. San Diego, CA. (Abstract # P0418).

Volk, G., C. Richards, B. Gross, P. Forsline, G. Fazio, and C.T. Chao. 2012. The USDA-ARS National Plant Germplasm System *Malus* collection: diversity of cultivars and wild species. Sixth Rosaceous Genomics Conference, September 2012, Trento, Italy.

Malus germplasm collection at Geneva, NY

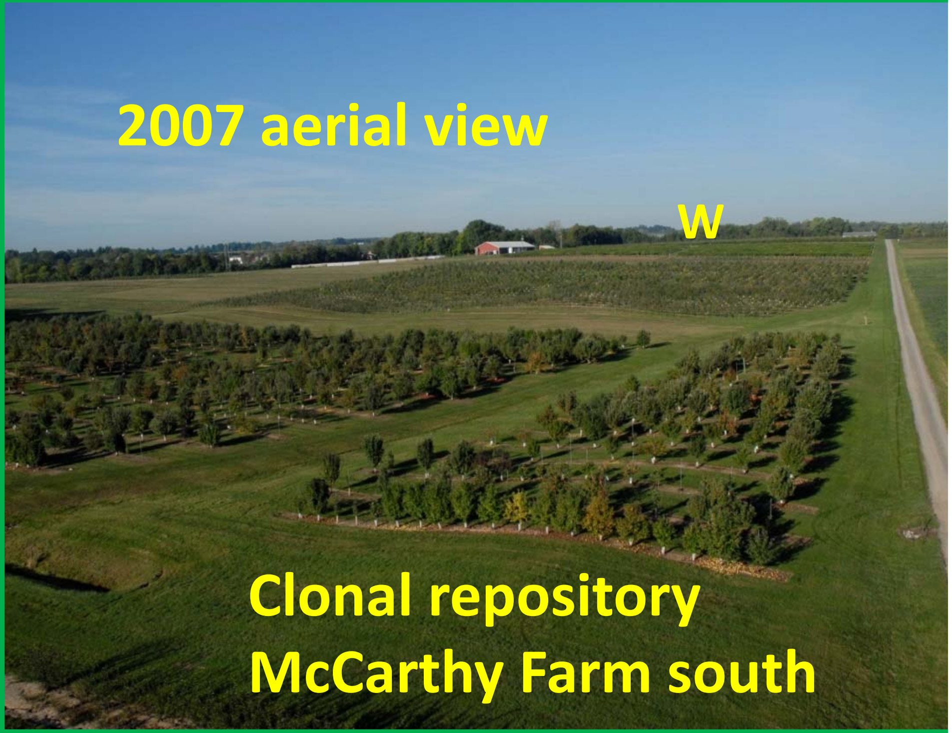
C. Thomas Chao
Horticulturist/Curator
C.Thomas.Chao@ars.usda.gov
Apple CGC meeting
September 10, 2013
Geneva, NY.

Clonally Propagated Collections



1985 aerial view

McCarthy Farm south, 50 ac



2007 aerial view

Clonal repository McCarthy Farm south

Apple (*Malus*)

Cold hardy grape (*Vitis*)

Tart Cherry (*Prunus*)

Genetic Resources Conserved

8,316 accessions of *Malus*, *Vitis*, and *Prunus* in total.

Malus collections:
6,734 accessions in total.
5,226 Field accessions.
1,508 Seed accessions.

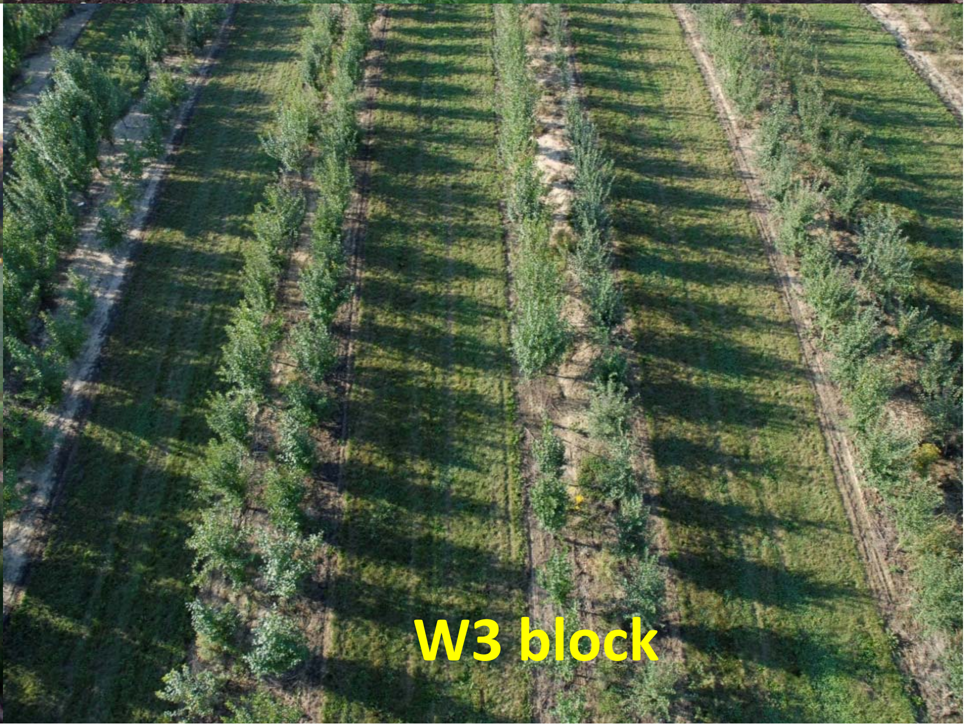
B9 block – *Malus* core collections.
M7 and E7 blocks – permanent *Malus* collections.
K1 block – Kazakhstan *M. sieversii* seedlings.
W3 block – wild *Malus* species seedlings from Armenia, China, Georgia, Kazakhstan, Russia, and Turkey.
G1 block – 7 F1 populations of 'Gala' x different *M. sieversii* with new disease resistance (mapping populations).


10- 30
GMAL 4002.a
GMAL 4002
KAZ 95 18-02P-33
M. sieversii

2004 W3 & K1 blocks

2012 K1 block

2007 W3, K1 & I2 blocks



W3 block

2013 bloom time at the *Malus* collections

2013 bloom time at the *Malus* collection


PI588921
'Alboplena'
M. spectabilis


PI588847
M. x platycarpa


PI613865
M. sylvestris


PI589982
M. coronaria


Large fruited *M. orientalis* from China

12/04/2012

12/04/2012

Malus transitora from China


Malus nursery

10/11/2012


'ButterBall' crab apple

10/11/2012

08/21/2012

New *Malus* planting 2012

10/11/2012

08/21/2012

Thorny juvenile of wild *M. hupehensis* from China

12/04/2012


PI657725
‘Sour Chari’
P. cerasus


PI638735
P. pensylvanica


PI592840
‘Surefire’
P. cerasus


PI632686
P. maackii

Characterization of clonal collections

- All accessions' PI, species, names, general description, source history, pedigrees, and digital images are in GRIN if available.
- Phenotypic and genetic observation are also recorded: chemical composition, ploidy, disease, growth traits, morphological characters, phenology, production description, and SSR loci are also in GRIN if available.
- Future – GBS data, fruit quality data and sequencing data.
- Search GRIN database at: http://www.ars-grin.gov/cgi-bin/npgs/html/croplist.pl

Wild *Malus* germplasm evaluation

- Disease evaluation – fire blight & scab (Aldwinckle, Cornell; Norelli, AFRS); blue mold (Janisiewicz, AFRS); postharvest decay (Jurick, Food Quality Laboratory, ARS); & mapping of resistance genes (Aldwinckle, Cornell; Norelli & Wisniewski, AFRS).
- Drought resistant evaluation (Bassett, AFRS).
- Cold hardiness (Luby, U. Minnesota).
- Genetic diversity and population structure analyses; core determination; identification of interspecific hybrids & duplicates (Volk & Richards, NCGRP).
- Mapping of different traits – ('Gala' x *M. sieversii*) (Xu, & Brown, Cornell; Chao, Fazio, Gutierrez, & Zhong, PGRU).

Genetic analysis of *M. sieversii* PI613981 for resistance to Blue mold

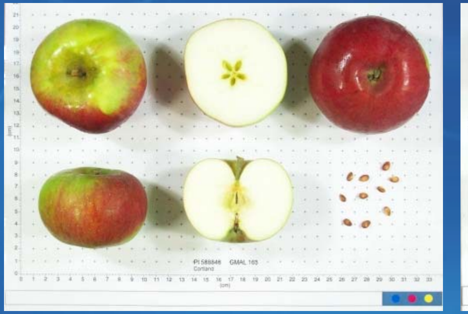
- Collaboration among Norelli, Wisniewski (AFRS), Droby, Hershkovitz (Volcani Center) & Chao (PGRU).
- PI613981 resistant to Blue mold was originally collected from Kazakhstan.
- Fruit collected in 2011 & 2012 from 101 individuals of a 'Gala' x PI613981 (GMAL4593) mapping population were inoculated with *Penicillium expansum* and evaluated 7 days post inoculation (dpi).
- There was significant correlation between resistance ratings in 2011 and 2012.
- The QTL for Blue mold resistance are mapped to linkage group 4.

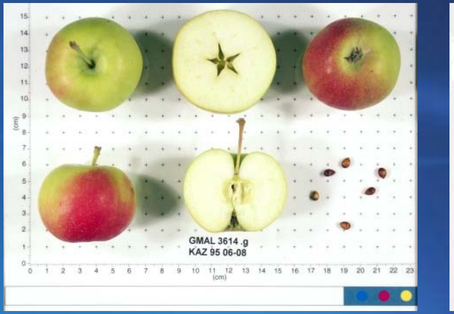

Fruit collection of F1 of 'Gala' x *M.sieversii* population, fall 2012 for postharvest disease resistance mapping. We will collect fruit samples again in 2013.

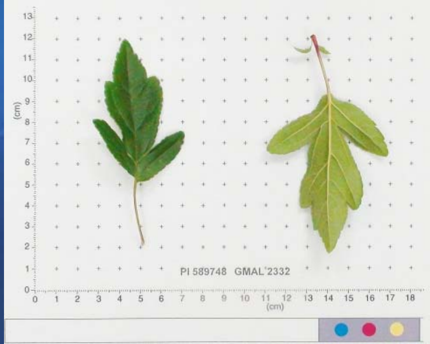
Mature fruit were harvested from 101 progeny of the GMAL4593 genetic mapping population ('Royal Gala' X *M. sieversii* PI613981) and evaluated for resistance to blue mold following controlled inoculation with *Penicillium expansum*. Two representative progeny showing A: susceptible and B: resistant disease responses 7 days post inoculation (dpi). C: Eleven replicate fruit of each accession were inoculated and evaluated 5 and 7 dpi. Plant and Animal Genome XXI, San Diego, 2013, Abstract #P0418.

Horticultural & fruit quality trait evaluation

- Cryopreservation method development and long-term survival rate for *Malus* and *Prunus*.
- Digital imaging of fruit, leaf, and flower.
- Polyphenolic, antioxidant capacity, juice, red-fleshed apples, and fruit abscission.







Malus related characterization work for 2012-2013

- First year evaluation of budbreak, bloom, end of bloom for all permanent *Malus* accessions.
- Digital photos of *Malus* flowering, mature fruit on the tree; wild *Malus* leaf, fruit on grid background.
- Fruit quality of *Malus* core collection and G1 mapping population(s); fruit quality of tart cherry collection.

Malus GBS effort since 2012

- Cooperation: Gardner & Myles, Dalhousie University, NS; Richards & Volk, NCGRP; Baldo, Chao, Fazio, Schwaninger, & Zhong, PGRU.
- 1,950 *Malus* accessions included; 1,403 *M. domestica*, 210 *M. sieversii*, 61 hybrid, 48 *M. baccata*, 23 *M. floribunda*, 22 *M. orientalis*, 16 *M. sylvestris*, & 167 of 24 other *Malus* species.
- 21 plates in total, 100-150 millions good reads per plate.
- We used 'Golden Delicious' genome as reference genome for analyses (Velasco et al. Nature Genetics, 2010, 42:833-839) or use no reference genome in the analyses. About 60%, near one million SNP markers, aligned to the 'Golden Delicious' map; over 50,000 SNPs per chromosome.
- Investigate domestication history, breeding history, gene flow, evolution, allele mining (SI, disease resistance), GWAS and other issues related to *Malus* genome.
- GBS 7 'Gala' x *M. sieversii* F1 populations in 2013.

New accessions for the clonal collection

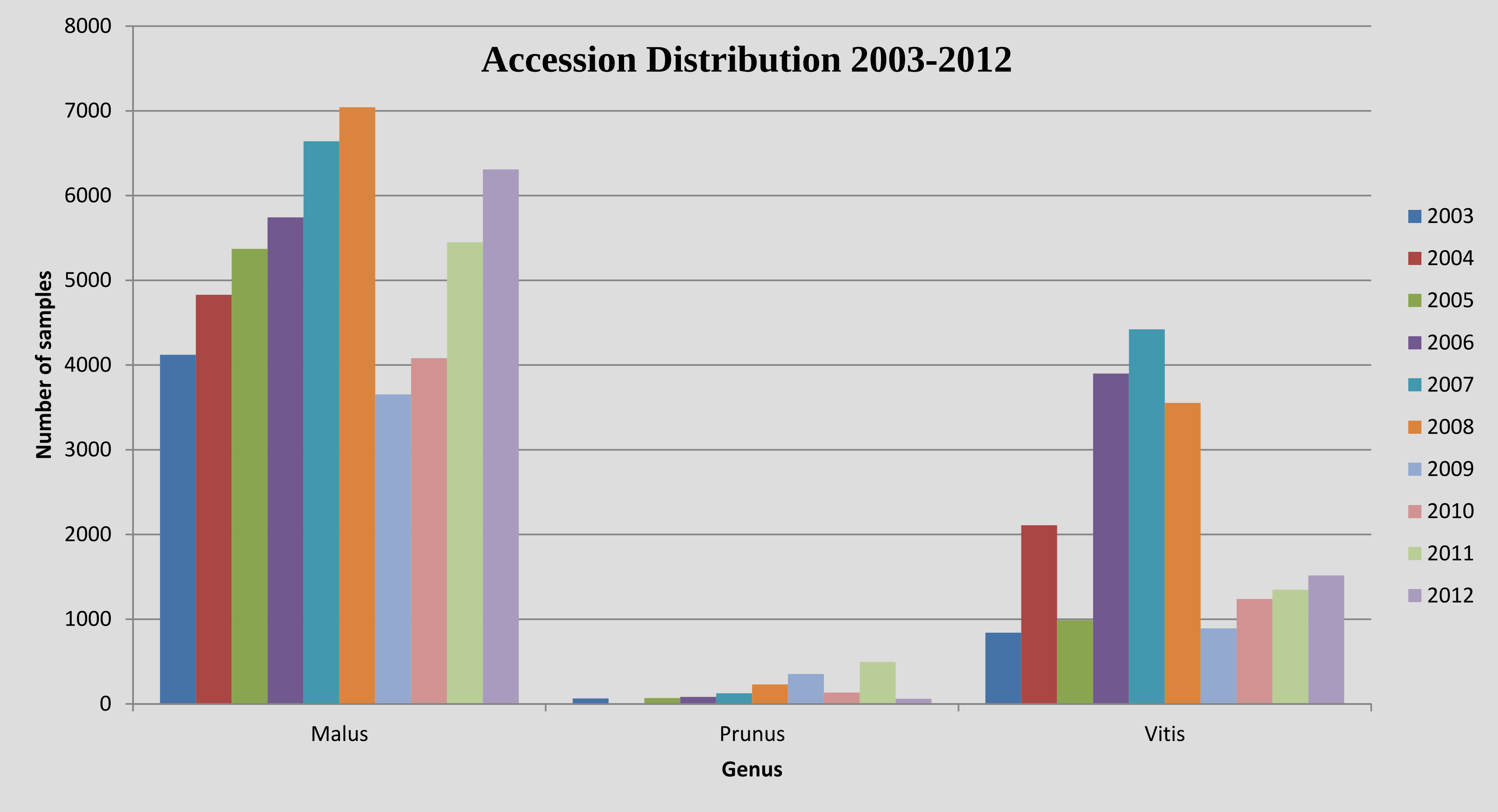
- We received 20 *Malus* accessions from APHIS Quarantine Center including 9 cider apples from Northern Spain, one M. *sieversii* from 1996 exploration and other varieties around the world. We received 4 *M. sylvestris* seed accessions from Albania, one *M. paradisiac* seed accession from Azerbaijan, 84 *M. fusca* seed accessions from an exploration in Pacific Northwest, and 9 *M. spontanea* seed accessions from Japan.
- We propagated 52 wild *Malus* seedlings based on drought stress evaluation by Carol Basset.
- We will continue propagate more wild *Malus* seedlings in the next few years.
- We like to collect additional four North American *Malus* species in the next few years.

Distribution of *Malus* germplasm from 2012 - 2013

- There were 233 domestic and 46 foreign orders between April1, 2012 and March 31, 2013 for 6,349 samples from 2,313 accessions.
- There were large orders of leaf samples for DNA isolation purpose; also dormant cutting and pollen requests.
- The " Botany of Desire" seeds (open pollinated seeds of wild *M. sieversii* seedlings) requests have increased in the past few years especially from Europe such as England, Finland, France and Germany; we have over 50,000 seeds in storage and we will collect more seeds in the next few years before the block removal.

10 years distribution of clonal germplasm

- Apple, grape and tart cherry catalogs at: http://www.ars.usda.gov/Main/docs.htm?docid=10013
- Free of charge for most distribution.



Outreach, educational event and tours of the clonal collections in spring, summer, and fall

Cornell NYSAES summer scholars 2012 visited the Kazakhstan *M. sieversii* seedlings block

Cornell Plant Breeding 4060 class visit

Challenges for the clonal collection

- The clonal collection is running out of space for future permanent collection addition – we need to start remove the wild *Malus* seedling evaluation block(s). The process will take several years.
- Concern of streptomycin resistant strain of fire blight for the *Malus* collections – we try to limit the use of streptomycin when possible.
- Weather impact on the collection – warm winter, lack of chilling, late spring frost, too much rain, or too little rain.
- Overall disease status of the collection – virus problem in *Vitis* collection; for example the new grapevine Red Blotch DNA virus (GRBaV).

Acknowledgement

Bill Srmack
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Angela Baldo
Gan-Yuan Zhong
PGRU, GGRU
FRU, Cornell University

Phil Forsline, PGRU
Herb Aldwinckle, Cornell University
Larry Robertson, PGRU
Gennaro Fazio, PGRU
Susan Brown, Cornell University
Jason Londo, GGRU
Appalachian Fruit Research Station (AFRS), Kearneysville, WV.
Gayle Volk, Chris Richards
NCGRP, Fort Collins, CO.
Sean Myles, Dalhousie University

Map of McCarthy Farm

M1 – Tart cherry
G1 – Gala x *M. sieversii*
I1 – *Vitis* collection
B9 – *Malus* core collection
M7 – *Malus* collection
E7 – *Malus* collection

W3 – Wild *Malus* seedling
K1 – *M. sieversii* seedling
W2 – Wild *Vitis* collection

2013 ANNUAL QUARANTINE REPORT: USDA-APHIS-PPQ-Field Operations

Dr. M.L. Bateman-Lead Plant Pathologist/Program Manager

Pomes and *Prunus* Quarantine Program

SUMMARY

As of September, 2013 the total number of Final Releases Fruit Tree Quarantine Program since 2007 is **1485**. We have introduced changes in molecular, immunological and traditional testing, added innovative tissue culture techniques, heat and chemical treatment and greenhouse management practices that have contributed to a robust program as proven by the numbers of releases in recent years. Below are the numbers that support the aforementioned statements.

Crop Type	***Final Release***	***Provisional Release***	***Conditional Release***	Total Released 2013
Pomes-accessions	*Malus*- 8 *Pyrus*- 16 *Cydonia*-8 Total: 32	*Malus*-27 *Pyrus*-12 *Cydonia*-1 Total: 40	0	Malus-35 Pyrus- 28 Cydonia-9 Total: 72
Prunus-accessions	Prunus-8	Prunus-27	0	Prunus-35
Prunus-seedlings	332	0	0	332
Total	**40**	**67**	**0**	**439**

RELEVANT TERMS

Provisional release-This type of release has restrictions. These are defined as clones that test negative in initial testing. The importer is responsible for obtaining a valid permit to receive and grow provisionally released trees. This permit must be renewed before expiration. The importer is responsible for maintaining the propagated provisionally released germplasm under the conditions specified in their permit. APHIS will complete pathogen testing. Once the material is clean, then it can be given a “Final Release”.

Final Release- This type of release has no restrictions. These are defined as clones that have tested negative for all pathogens of quarantine significance that they have been tested for, as per international Pomes/*Prunus* agreements. APHIS will approve final release of fruit trees after testing is complete and they negative for all known pathogens. There are no further federal restrictions on how these finally released trees may be used.

Permission to destroy- Requested by email from each recipient. Once it is granted in writing, the accession is destroyed.

PATHOGENS INTERCEPTED

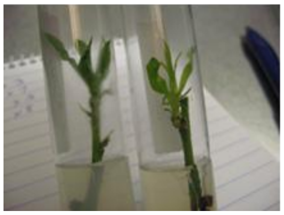
Some of the pathogens intercepted during past years include (but not limited to):

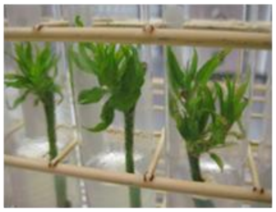
Pomes- PBCVd, AFDVd, AFCVd, ASSVd, ACLSV, ASPV, ASGV

Prunus- APV-1, PBNSPaV, HSVd, PLMVd, PNRSV, PDV, CVA, LCV-1, LCV-2, CGRMV, CNRMV, CMLV, CRLV, APLV, Phytoplasmas.

TISSUE CULTURE LABORATORY: ACCOMPLISHMENTS

We have established and are maintaining several accessions in various stages of therapy treatment. In the case of (A) Pomes: 19 apples, 1 pear, 1 quince; (B) *Prunus*: 13 cherries, 2 plums, 1 peach; (C) small fruits: 1 *Ribes.* Also this year we have successfully established an additional 13 post-therapy accessions through a combination of in vivo tip-grafts (Pomes) and self-rooted plantlets (*Prunus* and small fruits).





As part of the ongoing progressive work conducted in the TC lab we began first trials of a faster method for peach virus-elimination (dubbed “FastTrack”), where shoots are elongated on original stem section in vitro, placed in thermotherapy then the elongated shoot is excised from stem piece and tip-grafted onto GF305 rootstocks following thermotherapy.

In addition, we have purchased a spectrometer to conduct a light quality study in TC growth room with an ultimate goal of providing a more targeted range of illumination (LED) that is closer in simulation to the absorption spectra in photosynthesis.

We have also continued collaboration with ARS on long-term culture maintenance of recalcitrant peaches, almonds.

PROGRESSION OF RELEASES LAST 7 YEARS

Crop	**FY 2007**	**FY 2008**	**FY 2009**	**FY 2010**	**FY 2011**	**FY 2012**	**FY 2013**
Pome Fruits	2	0	23	57	48	100	72
Prunus clones	6	17	33	16	50	41	35
Prunus seedlings	31	70	138	196	111	107	332
Total per year	**39**	**87**	**194**	**269**	**209**	**248**	**439**

CURRENT CHALLENGES

We are in the process of seeking improved cooperation from all stakeholders for the final establishment of released material by recipients so that space is made available faster for new incoming material. This would help us to improve our resource allocation since currently resources are being used to maintain these trees. These resources could be better used elsewhere, including freeing up space for new importations. It is our hope that those involved will be receptive to becoming aware of this information and make a concerted effort to improve the timeliness with which recipients secure their germplasm.

FUTURE ENDEAVORS

We will continue adding new tests for individual viruses and group viruses. We will maintain and continue cooperation with ARS and others in relation to research and development of fruit tree viruses and specific tests.

IMPORTANT DEADLINES

September 30 – Last day to request slots for receiving material.

January 30 – Budwood material from foreign country should be at BLDG 580 to start testing cycle.

List of desirable cider apple varieties (2003) to be added to the NPGS provided by Ian Merwin.

Elite French cider apples not in USDA-PGRU

Avrolles
Biqsuet
Collaos
Calard
Cidor
Clos Renaux
Domaine
Douce Coetligne
Douce Moen
Germaine
Guillevic
Judeline
Judor
Julian
Jurelia
Kermerrien
Locard Vert
Moulin a Vent
Peau de Chien
Petit Juane
Rene Martin
Rouge Duret
St. Aubin

Elite Spanish cider apples not in PGRU

Arbeya, Blanquina
Calabaza
Casado
Coloradona
Collaos
Cristalina
De La Riega
Del Marques
Duron Arroes
Durona de Tresali
Ernestina
Fresnosa
Fuentes
Limon Montes
Maria Elena
Meana
Pachin Torteru
Panquerina
Pepa
Perezosa
Penaflor
Perico
Picona Rayada
Prieta
Rambault
Regona
Raxao
Reineta Santirso
Repinaldo
Solarina
Teorica
Verdialona
Xuanina

RosBREED Summary

Malus CGC

Sept. 10, 2013

Jim Luby and Cameron Peace

RosBREED Products Available

- Apple Crop Reference Set
  - data available at Genome Database for Rosaceae
  - includes phenotype information for 2010,2011, 2012
  - putative pedigrees including some marker based pedigree refutations

- Standardized phenotyping protocols
  - used for fruit traits
  - available at Genome Database for Rosaceae

- International RosBREED 8K SNP array available
  - consistent performing SNPs identified (1700-1800)
  - linkage maps constructed

QTL Discovery/Validation Using RosBREED Reference Germplasm

- Fruit acidity (sensory, instrumental)
- Fruit sweetness (sensory, instrumental – total and individual sugars)
- Fruit firmness
- Fruit crispness
- Fruit juiciness
- Apple scab resistance
- Bitter pit incidence

Predictive DNA Tests Available

1. **Rf locus** – LG09 – SSR and SNP haplotypes characterized – Amount of skin overcolor
2. **“Bl” locus** – LG02 – SNP haplotypes – partially characterized – Amount of skin overcolor, blush vs stripe overcolor
3. **Ma locus** – LG16 - SSR and SNP haplotypes characterized – Acidity, firmness, crispness, juiciness, bitter pit
4. **“A” locus** – LG08 – SNP haplotypes characterized – Acidity
5. **“BP13”** – LG13 – Bitter pit
6. **MdExp7** – LG01 – SSR and SNP - firmness in storage
7. **MdACS1** – LG15 – SCAR – firmness in storage
8. **MdACO1** – LG10 – SCAR – Firmness in storage
9. **MdPG1** – LG10 – SSR and SNP – texture
10. **Vf/Rvi6** – LG01 – SSR and SNP - Scab resistance

Others in development:

- Fructose content
- Other scab resistance loci from EU Fruitbreedomics project and Honeycrisp

Ideas for Future Research with NPGS Germplasm (C. Peace)

- Run all markers across the NPGS collection
- Determine how SNP-based genotypic diversity (random as well as functional alleles) compares between modern cultivars and NPGS material
- Some ancestral cultivars from NPGS collections and a few sieversii accessions, so we could compare them with the more modern breeding material