2011 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, JACK OKAMURO, SALLY SCHNEIDER, ROY SCOTT, GAIL WISLER, DA KAY SIMMONS)

1 **Personnel changes:**

1.1 Farewell and best wishes to Steve Clement, who retired as Research Entomologist at Pullman; Chuck Simon, who retired as Grape Curator at Geneva; and Doug Cook who retired as IT specialist at Corvallis.

1.2 Welcome to Thomas Chao, new grape, apple, and tart cherry curator at Geneva, NY; Dan Barney, new curator at Palmer, AK; Noelle Barkley, new peanut curator at Griffin, GA; Osman Gutierrez, cacao geneticist at Miami, FL; and Pablo Jourdan, new director of the Ornamental Plant Germplasm Center, Columbus, OH. Kim Hummer, the Research Leader for the Corvallis, OR genebank, is also now providing research and technical leadership for the NAPGRU at Palmer, AK. Roy Pittman, formerly peanut curator, assumed responsibility for the cowpea (Vigna) collection at Griffin.

2 **Site developments and changes:**

2.1 The USDA/ARS-NPGS partnered with Bioversity and the GCDT on a three-year, $1.4 million project to transform GRIN into GRIN-Global, a powerful but easy-to-use, Internet-based, plant genetic information management system that will link world's plant genebanks. NPGS personnel in Beltsville, MD and Ames, IA are leading the project. The nucleus of the system is ARS's existing GRIN, which already houses information about the more than 541,000 accessions of more than 13,000 plant species in the NPGS. Software upgrades will enable GRIN be used by genebanks of all sizes from many countries, making more information about more plants available to researchers. The project concluded in June 2011 but work on several aspects continues.

2.2 Citrus species are highly susceptible to many lethal diseases, damaging pests, and low temperatures. Genetic resources of citrus varieties are often reproduced as clones, and are currently maintained in field orchards and screen houses at the joint ARS-University of California NCGR at Riverside, CA because long-term storage of citrus clonal vegetative tissue has been infeasible. Researchers in the NCGRP at Ft. Collins, CO implemented new "micrografting" recovery methods that enable clonal citrus samples to be stored at the temperature of liquid nitrogen and successfully re-propagated. Storing duplicate clonal samples in secure genebank vaults will safeguard and enable them to be distributed to researchers more efficiently.

2.3 The genomes of wheat, barley and the biofuel crop switchgrass are so large and complicated that analyzing their genetic function and structure requires

special genetic tools. Curators at the WRPIS in Pullman, WA greatly expanded the collection of genetic lines of Brachypodium, a small, rapidly flowering grass, with a relatively small genome which has been completely sequenced. Knowledge gained about this "model plant's" gene content, structure, and arrangement can be readily extended to small grains and bioenergy crops. Thus, by safeguarding and distributing this key "genetic tool," ARS genebanks are catalyzing efforts to map and manipulate key traits for genetically improving major crops.

3 Budgets:

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

3.2 The Federal FY 11 budget was appropriated on 8 April 2011. As a result of the loss to ARS of earmarked projects, and budget rescissions, the overall budget of the NPGS was reduced by about $700,000 from the FY 10 funding level.

3.3 The President's FY 12 budget proposed a substantial budget increase ($3.3 million) for the NPGS. Congress will determine whether to appropriate those funds during the House and Senate "mark-ups" of the President's FY 12 budget and the subsequent Conference Committee budget reconciliation. The House mark-up occurred on 24 May 2011, and it would reduce ARS's budget by more than 12%. The timing for the Senate mark-up is uncertain.

4 National Programs:

ARS's research portfolio is organized as a series of 22 national programs. Plant and microbial genetic resource management, genetic improvement, genomics, 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). During 2007-2008, NP301 Project Plans were developed by ARS scientists and then were reviewed by thirteen peer review panels. 88% of the Project Plans were rating passing during the first review, with a median score of Minor Revision, a substantial improvement as compared to the first review cycle five years ago. NP 301 will undergo its second five-year review in October 2011, which will be followed by customer/stakeholder and ARS scientists workshops in 2012.

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 L. Sommers (Colorado State-SAES), Chair; E. Young (Executive Director, Southern Region); J. Colletti (Iowa State-SAES), G. Arkin (University of Georgia-SAES), T. Burr (Cornell University-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. Pederson (ARS-Griffin).

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. Support for NRSP-6 has been maintained at the FY 06 level for FY 07, FY 08, and FY 09. 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, and 16-17 June 2011 in Beltsville, MD to continue its work on these priority issues.

6 **International germplasm items:**

The FAO 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. The SFRC might schedule new hearings on the IT during 2011, as a prelude to the full Senate for a vote for consent (or not) to IT ratification.

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' implementation.

USDA

United States
Department of
Agriculture

Animal and
Plant Health
Inspection
Service

Plant Protection
and Quarantine

Plant Health
Programs

Registrations,
Identification,
Permits, & Plant
Safeguarding

Plant Germplasm
Quarantine
Program

USDA-APHIS-PPQ-
RIPPS-PGQP
Bldg 580, BARC-E
Powder Mill Road
Beltsville MD 20705
301-504-5700
301-504-6124 FAX

ANNUAL QUARANTINE REPORT
POMES-PRUNUS
Accessions and seedlings
Team Leader: Dr. Margarita Licha

As of August 4, 2011 the total number of Final Releases Fruits Quarantine Program since 2007 is 798.

The quarantine program is at the present a robust program for the quarantine of Pomes and *Prunus* accessions and seedlings as well as Post entry material. Starting in 2007 we introduced changes in molecular, immunological and traditional testing, added innovative tissue culture techniques, heat and chemical treatment for therapy as well as greenhouse management practices that have contributed to a robust program as proven by the numbers of releases in recent years.

During 2011 we received new *Prunus* material for a total of 62 new accessions, 16 new post entry, and over 100 seedlings from different locations including: The Netherlands, The Republic of South Korea, and Georgia. During the same year we have received a total 13 new Pome (Apples and Quince) accessions from New Zealand, Georgia, The Czech Republic, Germany and Tasmania . We have received 131 Post entry *Malus* from the Netherlands.

We have collaborated with the Pomes and *Prunus* Repositories, scientists and private growers to send final releases as budwood and barerooted material when needed. We have requested permission to destroy of the released accessions in order to make space for their present and future accessions in Quarantine at Bldg 580.

The following tables summarize some of the achievements of the last years.

Crop	FY2007	FY 2008	FY 2009	FY 2010	FY 2011
Pome Fruits	2	0	23	57	48
Prunus clones	6	17	33	16	50
Prunus seedlings	31	70	138	196	111
Total per year	**39**	**87**	**194**	**269**	**209**

USDA

United States Department of Agriculture

Animal and Plant Health Inspection Service

Plant Protection and Quarantine

Plant Health Programs

Registrations, Identification, Permits, & Plant Safeguarding

Plant Germplasm Quarantine Program

USDA-APHIS-PPQ-RIPPS-PGQP
Bldg 580, BARC-E
Powder Mill Road
Beltsville MD 20705
301-504-5700
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Crop Type	*Final Release*	*Provisional Release*	*Conditional Release*	*Total Released* 2011
Pomes-accessions	**19**	**29**	**0**	48
Prunus-accessions	**29**	21	0	50
Prunus-seedlings	111	**0**	**0**	111
Total	159	50	0	209

The Program is requesting active collaboration form all stakeholders in relation to the establishment of the material once it has been finally released. Rapid and diligent establishment of this newly released material will assist us in utilizing our available space and resources to the best of our abilities.

We would like to thanks those who have made the effort to assist us in this specific endeavor and look forward to their continued cooperation.

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National Germplasm Resources Laboratory
USDA-ARS
Beltsville, Maryland
2011 Report to PGOC, RTACs and CGCs

The National Germplasm Resources Laboratory (NGRL), Beltsville, MD, supports the acquisition, introduction, documentation, evaluation, and distribution of germplasm by the National Plant Germplasm System (NPGS) and other components of the U.S. National Genetic Resources Program (NGRP). The Laboratory is comprised of the Plant Exchange Office (PEO), the Germplasm Resources Information Network/Database Management Unit (GRIN/DBMU), and the Plant Disease Research Unit (PDRU), whose functions are provided below. Dr. Gary Kinard has been the Research Leader for NGRL since January 2009.

Plant Exchange Office

Plant Exploration and Exchange Program

The PEO supports the collection of germplasm for the NPGS through the management of a Plant Exploration and Exchange Grant Program. Plant explorations involve field collection of germplasm not available in any germplasm repositories, while plant exchanges are expeditions to facilitate the transfer of germplasm already conserved in foreign genebanks. Annual guidelines for developing plant exploration and exchange proposals are prepared by the PEO and distributed to researchers.

An extensive review procedure is used to assess the relevance of the proposals to the NPGS needs and the likelihood that the proposed explorations or exchanges will accomplish their stated objectives. Before submission, proposals are reviewed by the appropriate CGC or other crop experts. After submission to the PEO, proposals are reviewed by a subcommittee of the NPGS Plant Germplasm Operations Committee (PGOC). The PEO then evaluates the proposals and the PGOC reviews and makes recommendations on funding to the ARS Office of National Programs (ONP).

All foreign explorations supported by PEO comply with the provisions of the Convention on Biological Diversity on access and benefit sharing related to genetic resources. Prior informed consent to collect genetic resources is obtained from the appropriate host country before the exploration occurs. The permission includes agreement on the benefits to the host country associated with access to genetic resources. The PEO is involved in most requests to foreign governments for permission to collect and negotiates the terms of agreements when necessary. Foreign explorations are always conducted in cooperation with scientists from the host country and cooperation with their national genetic resources programs is strongly encouraged. Germplasm obtained on explorations is shared by the NPGS and the host country.

Facilitation of Germplasm Exchange

The PEO assists NPGS personnel and other scientists with acquiring germplasm from scientists, foreign national and international genebanks, domestic and foreign explorations, and special projects and agreements. The PEO also helps to expedite the distribution of germplasm from the NPGS to foreign scientists and other international genebanks.

In FY 2009, PEO assisted with the distribution of 754 shipments with a total of 60,323 NPGS accessions to scientists in 67 different countries. PEO also assisted with importing 17 shipments containing 447 items from different 17 countries for the NPGS and ARS.

In FY 2010 PEO assisted with the distribution of 861 shipments with a total of 38,244 NPGS accessions to scientists in 77 different countries. PEO also assisted with importing 33 shipments containing 654 items from 19 different countries for the NPGS and ARS.

In the first quarter of FY 2011 (October-December 2010), PEO assisted with the distribution of 211shipments with a total of 8,963 NPGS accessions to scientists in 47 different countries. PEO also assisted with importing 9 shipments containing 336 items from 4 different countries for the NPGS and ARS. It is estimated that in FY 2011 PEO will assist with more than 900 shipments to 80 different countries.

GRIN Taxonomy for Plants

GRIN Taxonomy provides online current and accurate scientific names and other taxonomic data for the ARS National Plant Germplasm System and other worldwide users. This standard set of plant names is essential for effective management of ARS plant germplasm collections, which now represent nearly 13,400 taxa. GRIN taxonomic data now include scientific names for 26,650 genera (14,120 accepted) and 1,330 infra-genera and 93,970 species or infra-species (55,700 accepted) with nearly 45,760 common names, geographical distributions for 50,340 taxa, 380,820 literature references, and 24,920 economic impacts. A broad range of economically important plants are supported by GRIN nomenclature, including food or spice, timber, fiber, drug, forage, soil-building or erosion-control, genetic resource, poisonous, weedy, and ornamental plants. Most or all species of important agricultural crop genera are represented. Information about the systematic relationships of species is provided, which is critical for optimally determining the disposition or use of individual germplasm samples. Included in GRIN Taxonomy are federal- and state-regulated noxious weeds and federally and internationally listed threatened and endangered plants, with links to information on noxious weed and conservation regulations to ensure unimpeded interstate and international exchange of plant genetic resources. The scientific names are verified, in accordance with the international rules of botanical nomenclature by taxonomists of the National Germplasm Resources Laboratory using all available taxonomic literature and consultations with taxonomic specialists. Generally recognized taxonomic database standards have been adopted in GRIN Taxonomy.

The current focus of GRIN taxonomic work is to ensure that scientific plant names in GRIN continue to reflect recent plant taxonomic and nomenclatural literature, and that new data on classification, synonymy, native and naturalized distribution, economic impacts, and common names for plants and economic use categories currently treated in GRIN are incorporated. Recent efforts have focused on improving the documentation of sources for the information provided in GRIN Taxonomy. We also seek to expand the nomenclatural, classificatory, and ecogeographical information for crop taxa and their relatives. In late 2008 a project to provide thorough coverage in GRIN-Taxonomy to wild relatives of all major and minor crops was initiated. We have now completed work on 38 crops, and an interface to query these data in various ways has been developed (www.ars-grin.gov/~sbmljw/cgi-bin/taxcrop.pl). The breadth of coverage and quality of GRIN taxonomic data has encouraged usage of GRIN-Taxonomy data among genetic resource managers and other agricultural workers worldwide. GRIN taxonomic data are the most requested item on public GRIN, with ca. 800,000 of these reports retrieved monthly.

PI Documentation

Since 1898, Plant Introduction (PI) numbers have been used as unique identifiers for accessions incorporated into the NPGS. In earlier times, PI numbers were automatically assigned to all plant material received by the Plant Introduction Office, a predecessor of the PEO. Currently, before PI numbers are assigned, NPGS curators first evaluate the passport data, and if possible grow and observe new accessions to verify uniqueness and rationale for preservation in the NPGS. For this reason, curators usually assign a local identifying number to an accession until a decision is made to assign a PI number. When the decision is reached to assign a PI number to an accession, the curators contact Mark Bohning in DBMU for assignment of the next sequential number(s).

In FY 2010, the NGRL in collaboration with the National Agriculture Library completed the digitization of the PI Books. The digitized books are now available on the National Agricultural Library (NAL) website http://ddr.nal.usda.gov/, (select United States Department of Agriculture, then USDA/ARS Plant Inventories) and on the NGRL website http://ars.usda.gov/Services/docs.htm?docid=18722. In addition, the Accession records in GRIN have been modified so there is a link (*View original Plant Inventory data*) to the appropriate page in the PI Book. The Plant Immigrant Series is currently under contract to be digitized and should be available to the public in either late 2011 or early 2012.

International Collaboration

PEO works with other U.S. and international programs to support plant germplasm conservation and exchange worldwide. The PEO continues to collaborate with USDA/FAS and USDA/ARS/OIRP to develop joint germplasm collection, conservation and maintenance programs in Guyana, Jordan, Morocco, Tunisia, Georgia and Azerbaijan using US Food for Peace and other programs.

Since 2002, PEO has been collaborating with the plant genetic resources programs of the eight Central Asia and the Caucasus countries: Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan, Uzbekistan, Armenia, Georgia and Azerbaijan. This program is organized by ICARDA (International Center for Research in the Dry Areas) and the focus is on development of national plant inventories, staff training, and plant exploration.

FY 2010 NPGS Plant Explorations

Target Crop	Country	Principal Contacts
Wild beet	Morocco	B. Hellier, L. Panella, Y. Bahloul, N. Qariouh
Small grains	Armenia	K. Tamanian, G. Fayvush
Lettuce	Georgia	M. Mosulishvili, G. Arabuli
Small grains	Georgia	M. Eristave, L. Kobakhidze
Lettuce	Russia	S. Litvinskaya, R. Murtazaliev
Ash	China	W. Kang
Fruits and nuts	Georgia	M. Aradhya, D. Maghradze, Z. Bobokashvili
Cool-season grasses	Russia	D. Johnson, P. Johnson, N. Dzyubenko, E. Dzyubenko
Spanish lime	United States (PR, USVI), Trinidad and Tobago	B. Irish, I. Reyes, C. Bermudez, E. Chichester, P. Perez, E. Ramkhelawan
Sunflower	United States (MO, KS, OK. AR)	L. Marek, G. Seiler
Woody ornamentals	United States (OH)	J. Carstens, M. Scanlon
Carrot relatives	United States (many states)	P. Simon, D. Spooner
Ash	United States (WI, MN)	M. Widrlechner, E. Humenberger
Ash	United States (KS, MO, AR)	J. Carstens, M. O'Hearn
Grain amaranths and bedding plants	United States (AZ)	D. Brenner, S. Stieve
Kentucky coffeetree	United States (MO, AR, TN, KY, IL, IA)	J. Carstens, A. Schmitz
Lesquerella	United States (NM, TX, AZ)	D. Dierig, M. Cruz
Ornamentals	United States (TX)	P. Jordan, S. Stieve
Potato	United States (AZ)	J. Bamberg, A. Del Rio
Juglans spp.	United States (TX)	L.J. Grauke

Database Management Unit

GRIN and GRIN-Global

The mission of the GRIN Database Management Unit (DBMU) is to develop and maintain information systems for the National Genetics Resources Program comprised of plants, animals, microbes, and invertebrates. Recent statistics for data in the plant database include:

Over 95,800 taxonomic names (including synonyms)
535,473 accessions representing 13,388 species and 2,208 genera
1,866,764 inventory records
1,628,283 germination records
7,291,757 characteristic/evaluation records
Over 201,156 images

Germplasm accessions acquired by the National Plant Germplasm System (NPGS) since the effective date of the Convention on Biological Diversity continue to be flagged in the database with appropriate disclaimers and MTAs. The new SMTA issued under the International Treaty is also flagged and tracked through the system. These agreements are displayed with accession passport data and automatically printed on GRIN generated packing slips when accessions are distributed. During the past year, the DBMU continued to provide support to NPGS site personnel and assisted NPGS sites in loading passport data, evaluation data, distribution information and images into the database

The GRIN-Global project is a cooperative effort between the Global Crop Diversity Trust (GCDT), USDA-ARS and Bioversity International to develop a powerful, easy-to-use plant genetic information system that will be freely available to any country throughout the world. NPGS personnel at Ames, IA and Beltsville, MD are leading the project. The international component of the project is almost complete and a test version was released in July of 2011. A demonstration of the new public software was presented at the biennial CGC Chair, Regional Technical Advisory Committees and Plant Germplasm Operations Committee joint meetings in Geneva, NY July 27-29, 2010. The technical steering group (TSG) for the GRIN-Global project held their final meeting in September 2010. They provided important guidance and recommendations to the development team throughout the project. A demonstration of the beta version GRIN-Global public website project was also presented at the Plant & Animal Genome XIX meeting in January 2011. Training sessions for GRIN-Global international trainers (Train the Trainers) was held April 12-23, 2010 in Beltsville, Maryland and November 15-22, 2010 in Ames, IA. Eighteen international participants attended the Beltsville session and 10 attended the Ames session. They all learned how to use the GRIN-Global application and offered their comments and suggestions. Beginning in July of 2011, these international collaborators will assist in providing training and deploying the system to the international community.

The second phase of the project, implementing GRIN-Global for the NPGS, has begun. GRIN-Global will replace the current GRIN system with new site maintenance and public retrieval software. All the NPGS sites will be contacted to ensure all site specific software will be incorporated into the new system.

The development team is always interested in receiving feedback from the user community on the GRIN-Global NPGS public website. A beta version of the GRIN-Global public website can be found at:

http://test.grin-global.org/gringlobal/search.aspx

Comments, ideas and suggestions can be sent to feedback-grin.global@ars.grin.gov

GRIN has been enhanced to handle molecular data. New tables have been added to the database to store this data and software has been developed to display it. SSR data generated on apple, cacao, grape, hazelnut, hops, pear and blueberry, along with AFLP data on Rhubarb, has been loaded into the system.

The GRIN system was available 98% of the time on a 24 hour a day and 7 day a week schedule. Access to the database through the web pages continues at a brisk pace. In 2010, there were 1,928,387 visits to the GRIN database. We always encourage users to send any comments on the current GRIN system by email to dbmu@ars-grin.gov .

Security measures for the hardware and databases are regularly reviewed and constantly monitored for intrusion by those who may attempt to corrupt web pages or to destroy data. New security patches are implemented as soon as they become available. The system is protected by a firewall and all data are backed up at onsite and offsite locations. Backup tapes are kept at several local offsite locations, including one set at Ft. Collins, CO for long term storage. The system has an Uninterruptible Power Supply for short term power outages and a diesel generator for longer power outages. The building housing NGRL is secured with access permitted only by proximity card. The GRIN server room is locked with further limited proximity card access and the room is monitored for temperature fluctuations 24/7/365.

Crop Germplasm Committees

Since June 1, 2010, over 20 of the 42 Crop Germplasm Committees (CGC) have met. An NGRL representative was present at most of the meetings, or participated via teleconference, to help facilitate their activities. Summaries of each meeting are prepared and distributed to appropriate National Program Leaders, NGRL staff and other NPGS personnel. The committees continue to provide advice on all aspects of the NPGS including identifying gaps and duplications in the collections, germplasm maintenance and evaluation, quarantine issues and maintaining updated versions of the crop vulnerability reports. The 13th biennial meeting of the CGC Chairs was held in Geneva, NY July 27-28, 2010 in conjunction with the Plant Germplasm Operations Committee and the Regional Technical Advisory Committees. This meeting provided an opportunity

for the Chairs to hear presentations on the status of NPGS sites, plant germplasm exchange, international issues, preservation and utilization, the molecular characterization of accessions, interactions between curators and CGCs and plant quarantine issues. One of the major topics presented was a demo and discussion of the new GRIN-Global public interface. The meeting also allowed the Chairs to meet and interact with each other, NPGS managers and curators, and invited guests from ARS, other government agencies, and non-governmental organizations. As recommended at the meeting, a video conference/webinar will be held in 2011 to keep the CGC chairs updated on all issues within the NPGS.

Plant Disease Research Unit

Since October 1, 2005, the responsibilities for the quarantine indexing and distribution of prohibited genera germplasm that were performed by the former ARS Plant Germplasm Quarantine Office were transferred to APHIS-Plant Germplasm Quarantine Program (APHIS-PGQP). The quarantine program manager for APHIS-PGQP is Dr. Joseph Foster. For ARS, three SYs (Gary Kinard, Ruhui Li, and Ray Mock) and nine support staff now comprise the Plant Disease Research Unit within National Germplasm Resources Lab (NGRL-PDRU). The mission of NGRL-PDRU is to conduct research to understand the biology of pathogens that infect economically important prohibited genera plant germplasm, including their etiology, detection, and elimination by therapeutic procedures. These projects provide support to the APHIS quarantine programs and help facilitate the safe introduction and international exchange of valuable plant germplasm.

Personnel

Ray Mock works with sugarcane, and deciduous tree and small fruits. Dr. Ruhui Li provides molecular support for all unit projects and works more intensively on sugarcane, sweet potato, grasses, and stone fruits. Whitney Hymes, who was a student employee in PDRU for several years, began working in a permanent position as a Biological Science Research Technician in May 2010 and provides molecular lab support. Sam Grinstead, a Biological Science Research Technician, provides greenhouse support for the unit. Dr. Eun Ju Cheong was hired as a Support Scientist for the unit in December 2010. Her expertise is tissue culture and therapeutic methods. Four International Visiting Research Scholars have joined the lab since February 2008: Dr. Liming Lin, working on viroid detection in stone and pome fruits; Donglin Xu, working on characterization and detection of sugarcane viruses; Ae Rin Jeon, focusing on developing methods for the *in vitro* cultivation of a broad range of small fruit species, and elimination of quarantine pathogens from these 'prohibited' category crops; and Dr. Fan Li working on viruses of potatoes and sweet potatoes.

Research Objectives and Progress

The NGRL-PDRU performs research on viral pathogens of quarantine significance infecting clonally propagated prohibited crop genera, with an emphasis on deciduous tree and small fruits, sugarcane, grasses, and sweet potatoes. The mission is to characterize and investigate the etiology of poorly described diseases and pathogens of quarantine significance, and to develop more reliable detection and elimination methods. Once complete, these protocols will be submitted to the USDA, APHIS quarantine for validation and inclusion in the quarantine testing program. PDRU provides regular updates about its research projects to the CGCs that deal with prohibited genera crops. The staff regularly confers and collaborates with APHIS scientists on matters pertaining to the quarantine of plant germplasm. NGRL-PDRU personnel are glad to discuss potential collaborations with colleagues and stakeholders in the NPGS.

Key NGRL Contacts

Research Leader
Gary Kinard (Gary.Kinard@ars.usda.gov, 301-504-5951 or 5115)

Plant Exchange Office
Ned Garvey (Edward.Garvey@ars.usda.gov, 301 504-7511)
Karen Williams (Karen.Williams@ars.usda.gov, 301 504-5421)
John Wiersema (John.Wiersema@ars.usda.gov, 301 504-9181)

GRIN-Database Management Unit
Quinn Sinnott (Quinn.Sinnott@ars.usda.gov, 301-504-6072)

Crop Germplasm Committees
Mark Bohning (Mark.Bohning@ars.usda.gov, 301-504-6133)

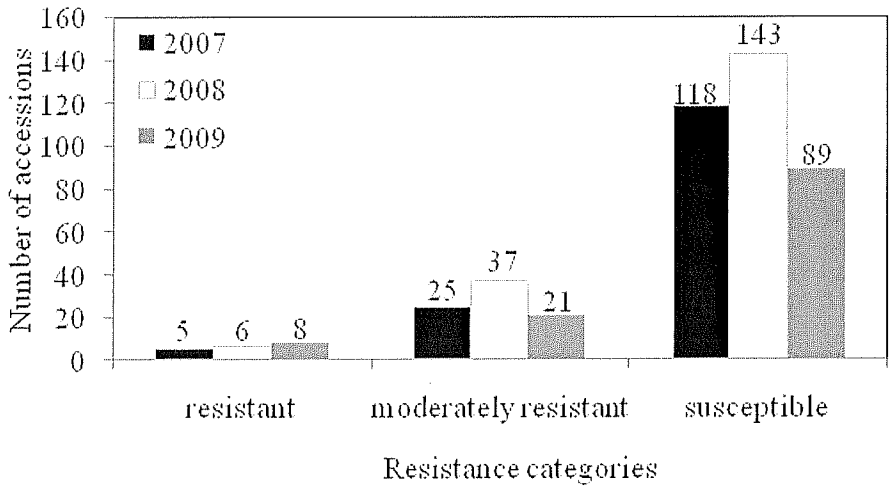
Plant Disease Research Unit
Ruhui Li (Ruhui.Li@ars.usda.gov, 301-504-7653)
Ray Mock (Raymond.Mock@ars.usda.gov, 301-504-8624)

Apple CGC Preliminary Progress Report by Wayne M. Jurick II and Wojciech J. Janisiewicz

Penicillium expansum and *Colletotrichum acutatum* cause blue mold and bitter rot of apples during storage which results in significant economic losses. Resistance to these pathogens in commercial apple cultivars has not been documented in the literature. An apple germplasm collection, from the center of origin in Kazakhstan, is maintained in Geneva, New York. This collection represents a more diverse apple gene pool than commercial cultivars and was evaluated for resistance to the pathogens that cause blue mold and bitter rot. Resistance reactions were skewed toward susceptibility for both fungi and comprised the majority of accessions examined. However, resistance to *P. expansum* was confirmed in select accessions over multiple years. Maturation patterns and quality indices for soluble solids and acidity, which may also affect susceptibility, were highly variable and represent the genetic diversity of the germplasm collection. Resistance in four accessions to *C. acutatum* and two accessions resistant to both *P. expansum* and *C. acutatum*, are reported here for the first time. Data from this study will serve as a foundation for conventional apple breeding programs and molecular genetics investigations to provide resistance against blue mold and bitter rot in commercial apple varieties.

Fig. 1: Distribution of resistance categories from Kazakh apple accessions with various levels of resistance against A. *Penicillium expansum* and B. *Colletotrichum acutatum*.

A.



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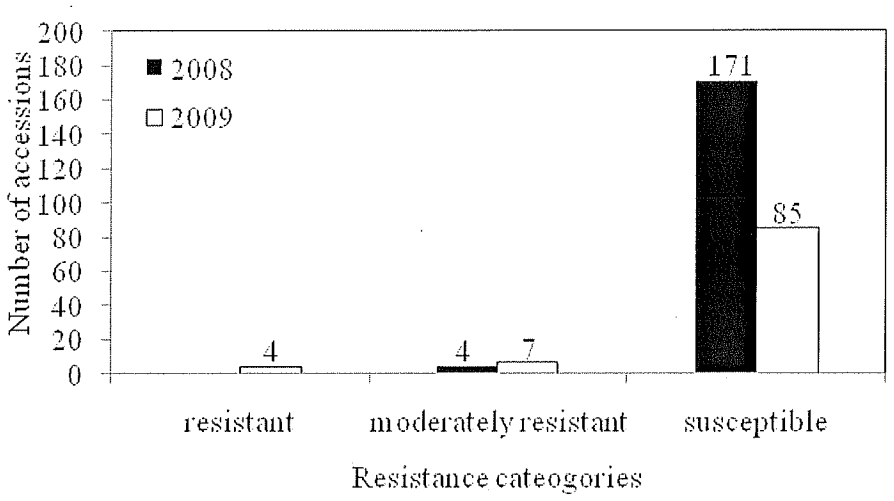
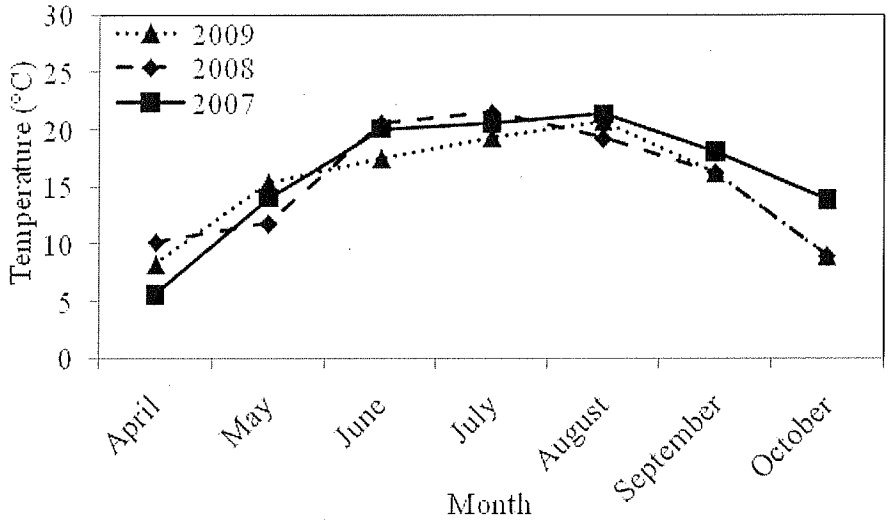


Fig. 2: Weather data from the New York State Agricultural Experiment Station located in Geneva, New York. A. Mean monthly temperatures from April through October 2007-2009. B. Mean monthly rainfall from April through October 2007-2009.

A.



B.

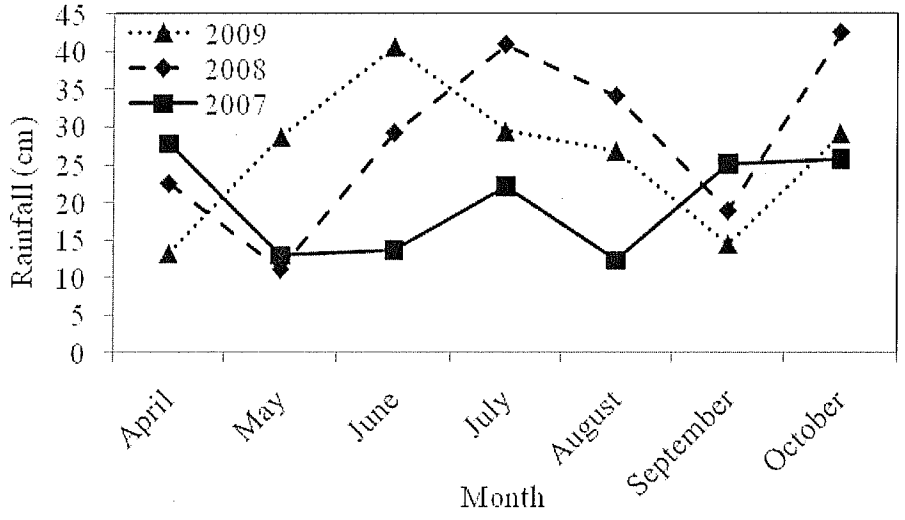
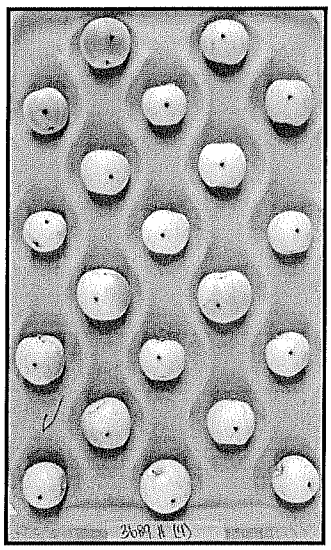
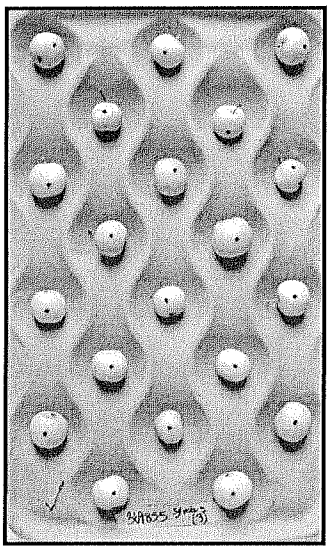


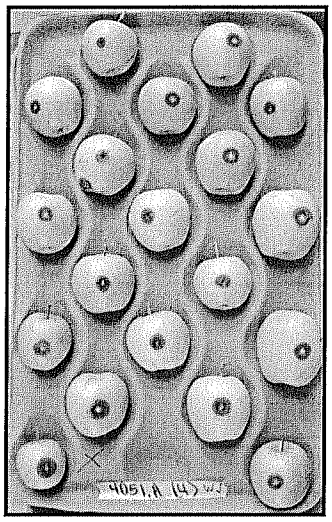
Fig. 3: Bitter rot and blue mold decay development on A. Accession GMAL 3689.h inoculated with 50 µl of 10^4 ml^{-1} conidial suspension of *Colletotrichum acutatum* (resistant) is also resistant to *Penicillium expansum.* B. Accession PI 369855 inoculated with 50 µl of 10^3 ml^{-1} conidial suspension of *C. acutatum* (resistant) is also resistant to *P. expansum.* C. Accession GMAL 4051.a inoculated with 10^4 ml^{-1} conidial suspension of *P. expansum* (susceptible). D. Accession GMAL 3616.b inoculated with 10^4 ml^{-1} conidial suspension of *C. acutatum* (susceptible).



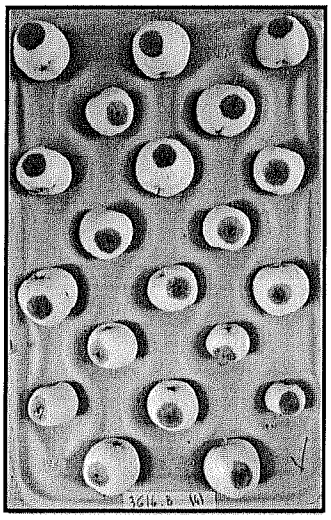
B.



C.



D



Progress Report for Malus CGC Grant 2010
Species differentiation in wild Malus from China
Gayle Volk

We have sequenced 4 chloroplast loci for >500 apple accessions representing the species in the USDA-ARS apple collection. We have extended the project to include several hundred additional samples representing all the Maloideae species in the NPGS. We're filling in missing data and will be analyzing data during the fall of 2011.

In a related project involving species identification, the following manuscript has been submitted:

Gross BL, Henk AD, Forsline PL, Richards CM, Volk GM. 2011. Identification of interspecific hybrids among domesticated apple and its wild relatives. Submitted to Tree Genetics and Genomes.

Abstract

Detecting interspecific hybridization and misclassifications in large, permanent collections can be difficult, because fine scale geographical locations and species-specific phenotypic data is generally unavailable. Thus, there is little *a priori* information available to suggest which individuals might be putative hybrids. Instead, hybrids or misclassified individuals must be identified based on molecular data via population assignment and admixture detection programs. We have applied a variety of programs to over 400 accessions of four closely related *Malus* species held in the USDA national collections genotyped at 19 SSR loci. Our findings indicate that over 10% of the wild species *M. sieversii* and *M. orientalis*, and nearly 20% of the wild species *M. sylvestris*, may be admixed or misclassified. The percentage of admixed or misclassified individuals of the domesticated species, *M.* × *domestica*, was much lower, at less than 5%. These findings have important implications for how to detect hybridization and misclassification in large collections using molecular data, and, ultimately, for the utility of the collections. In addition, the presence of wild-collected individuals that show admixture with domesticated apple suggest gene flow may be occurring in from the crop into natural populations of the wild species.

Additional project updates will be provided in person at the Apple CGC meeting at ASHS.

Cider Apples from Spain-Ian Merwin

PR=provisional release
R=Release

i.e. PR07 was provisionally released in 2007
i.e. R10 was released in 2010

T= Testing
Therapy= Accession is undergoing therapy and more testing

SP	QNUMBER	CLONE	ORIGIN	RECIPIENT	STATUS	RELDATE	COMMENT	DATERCD	Buds Rcvd
A	44131	Blanquina	Spain	Ian A. Merwin	T	PR10		03-Feb-04	>50
A	44132	Clara	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44133	Collaos	Spain	Ian A. Merwin	R	RP07	Released 2010	03-Feb-04	30
A	44134	Cristalina	Spain	Ian A. Merwin	T	PR09	Sent to Field to Prosser 2010 - 12 B44134A	03-Feb-04	>50
A	44135	Coloradona	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	35
A	44136	De la Riega	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44137	Durona de Tresali	Spain	Ian A. Merwin	T	PR10		03-Feb-04	>50
A	44138	Marialena	Spain	Ian A. Merwin	R	RP07	Released 2010	03-Feb-04	30
A	44139	Ernestina	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44140	Limon Montes	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	25
A	44141	Panquerina	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44142	Pepa	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44143	Perico	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	30
A	44144	Peau de Chien	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44145	Piel de Sapo (code 340)	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44146	Prieta	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44147	Raxao	Spain	Ian A. Merwin	T	PR09	Sent to Field to Prosser 2010-12 B44147C	03-Feb-04	>50
A	44148	Regona	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44149	Reineta (code 94)	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44150	Repinaldo (code 106)	Spain	Ian A. Merwin	T	Therapy		03-Feb-04	>50
A	44151	Sangre de Toro (code 84)	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44152	Solarina	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44153	Teorica	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44154	Verdialona	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50
A	44155	Xuanina	Spain	Ian A. Merwin	T	Testing		03-Feb-04	>50

Notes

1 Data for further tests is being generated at this time. Some of these accessions may be sent to the field if all tests are negative.

2 Some other accessions may change status from testing to provisional release depending on the results

3 When provisionally released to the Repository they can start the establishment of the accesion until we issue a final releaes. When we issue the final release there should be enough material established for distribu

I appreciate our mutual interest in having these accessions established at the Repository as soon as we issue a PR. Please feel free to request an update for these next Spring.
I hope you will assist us in moving them into the growers hands faster once we release them.

Apple CGC Preliminary Progress Report by Gennaro Fazio, Phil Forsline, and Gayle Volk

Characterization of Tree and Root Architecture of *Malus Sieversii* seedlings

The success of modern apple orchards is dependent on specific types of tree architecture inherent to varied apple genotypes or imparted by the use of certain rootstocks. Tree size and shape, sylleptic and proleptic growth, columnar habit, spines and the development of fruiting spurs are among examples of inherent characteristics. Additionally, tree size, branch angles, branching and percentage of fruiting wood are examples of architectural characters that can be modified by specialized rootstock genotypes. The ability of rootstocks to modify key architectural features of scions is heritable and derived from a very restricted germplasm pool (Malling series of rootstocks and derivatives) that possesses several weaknesses in traits linked to biotic and abiotic stress tolerance – these weaknesses when exhibited in orchard settings end up costing the apple industry a significant portion of fruit revenues. It is probable that similar root imparted characteristics exist in natural apple populations such as *Malus sieversii* which are known to host traits associated with tolerance to several biotic and abiotic stresses. *M. sieversii* populations could possess genetic factors that can mimic or improve the positive effects of dwarfing, precocity found in Malling germplasm. In addition, it could add characteristcs such as deep root exploration or resistance to diseases and insects already described in *M. sieversii* germplasm to existing rootstock germplasm to create more productive, ecologically and economically sustainable rootstocks.

In an effort to understand the genetic determinism of tree architecture of *M. sieversii* seedlings we utilized a series of genetically related seedlings derived from a project aimed a preserving the genetic diversity of *M. sieversii* through the development of a seed core collection (Volk et al. 2005). This seed core collection was generated by intermating a set of trees representing a very high level of genetic diversity for the species. Several sets of flowers from each mother tree were pollinated with bulked pollen from specific sets of other mother trees from the core set so that each tree in the core set was the donor of both megaspores and microspores. In some cases the core individuals that were selected had a sib relationship (e.g. 3610.b and 3610.l were both seedlings collected from the same seed-lot/mother-tree #3610 collected in site 9 in Kazakhstan). Approximately 500 seeds from Kazakhstan site 6 and site 9 core individuals were germinated and planted in the McCarthy nursery of the USDA ARS PGRU repository in spring of 2008 and allowed to grow for two seasons. Surviving seedlings were harvested in the fall of 2009 and two high resolution TIFF images (the second one with tree rotated 90°) of each tree against a white backdrop were collected between December 2009 and March 2010 (samples displayed in Figures 1 and 2). A total of 1180 high resolution images were then analyzed using the WinRhizo software package resulting in data for average stem diameter, number of growing points (tips), number of biforcations, tree volume and total length of branch canopy. The same images were then visually evaluated for tree architecture characters such as flat branching, presence of spines, root mass, number of primary roots, number of thick roots. Means for half sib families and for bulked pollen pools were calculated using Minitab 15 statistical software and displayed in graphs in figures 3-6.

Table 1. Mother Tree and Pollen Pool designations and S-RNAse alleles of each Mother Tree characterized according to Dreesen et al. 2010, for seedlings in this analysis.

Kazakhstan Site	GMAL Num.	SDLG.	Row	Tree	Pollen pool	S Allele1*	S Allele2
6	3682	.k	6	6	B	359	NA
6	3683	.i	6	15	B	345	NA
6	3683	.n	6	20	A	343	356
6	3684	.a	6	22	B	345	585
6	3684	.b	6	23	B	345	NA
6	3684	.l	6	33	B	345	NA
6	3685	.d	6	40	C	359	545
6	3685	.e	6	41	C	318	585
6	3685	.f	6	42	A	345	545
6	3687	.d	6	55	D	343	NA
6	3688	.n	7	20	B	365	545
6	3689	.c	7	24	A	365	
6	3689	.n	7	35	B	365	545
6	3690	.o	7	53	A	359	585
6	3691	.m	8	7	D	356	359
6	3975	.d	9	36	C	338	345
6	3975	.m	9	45	A	343	362
6	3989	.f	9	52	D	545	585
6	3989	.k	9	56	C	345	365
6	3999	.b	10	2	D	343	362
6	4000	.b	10	17	C	362	545
6	4002	.d	10	33	A	338	359
6	4002	.e	10	34	C	362	NA
6	4002	.h	10	37	A	362	NA
9	3608	.a	1	47	B	343	495
9	3608	.b`	1	48		338	362
9	3610	.b	2	4	D	343	362
9	3610	.l	2	14	D	345	362
9	3614	.a	2	15	A	338	359
9	3614	.g	2	21	A	338	359
9	3616	.d	2	30	B	343	345
9	3619	.j	2	51	B	338	495
9	3619	.m	2	54	B	372	NA
9	3620	.e	3	3	A	345	365
9	3620	.m	3	11	A	338	362
9	3623	.f	3	29	B	338	495
9	3627	.a	4	6	B	318	343
9	3627	.l	4	17	B	318	362
9	3629	.n	4	32	A	343	495
9	3638	.b	5	31	D	343	372
9	3762	.g	8	16	D	338	
9	3762	.n	8	23	B	372	585
9	3764	.e	8	29	D	372	NA
9	3764	.l	8	36	D	362	585
9	3781	.b	8	53	C	362	495
9	3781	.c	8	54	A	NA	NA
9	3781	.n	9	4	B	362	585
9	3785	.b	9	22	A	362	NA
9	4020	.i	11	33	C	NA	NA
9	4024	.n	11	49	C	NA	NA

* NA= Not Amplified

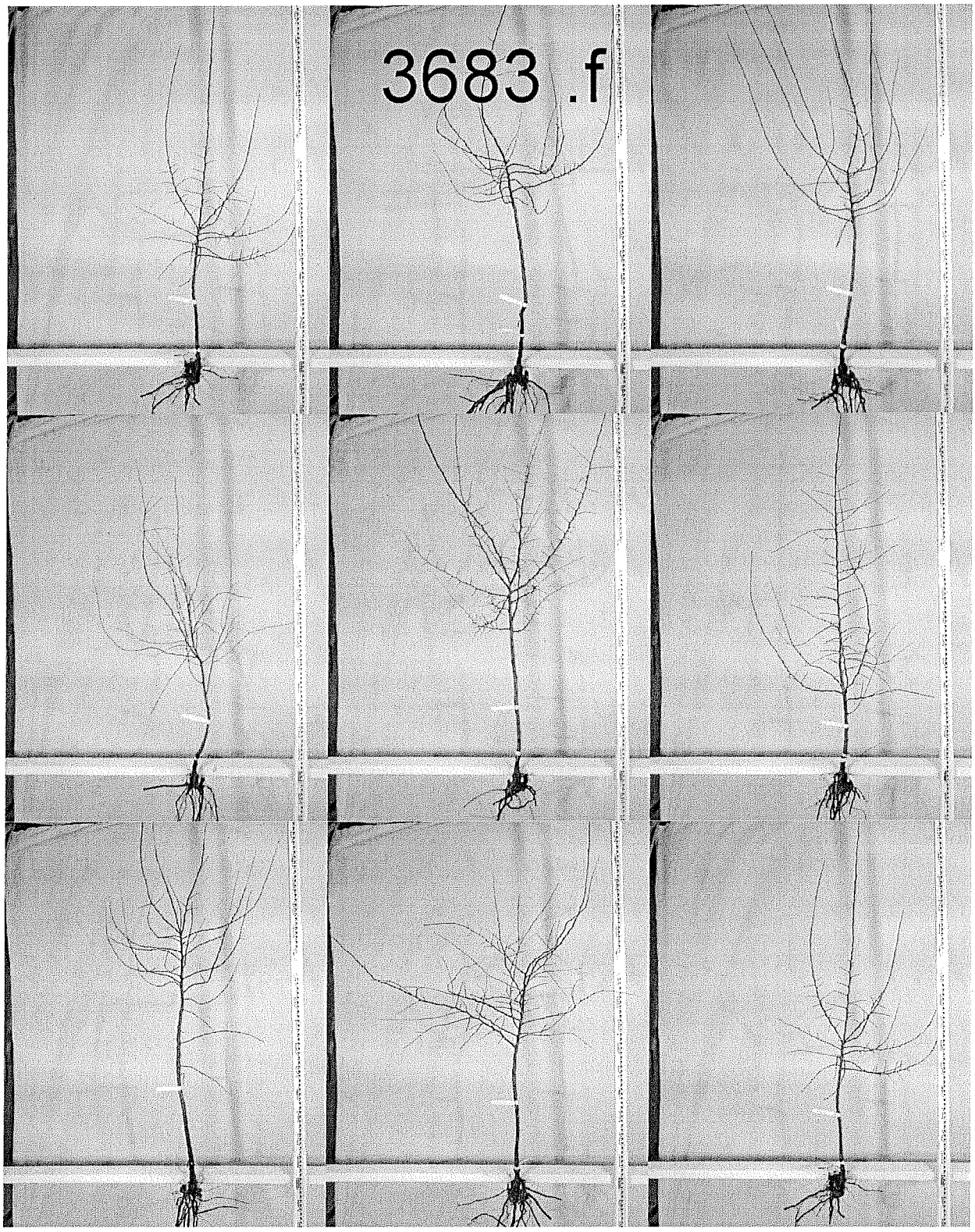


Figure 1. Sampling of high resolution images of seedlings derived from the GMAL 3683.f mother tree. Although the group seems heterogeneous, there are some similarities in tree size, number of branches and general shape of the canopy.

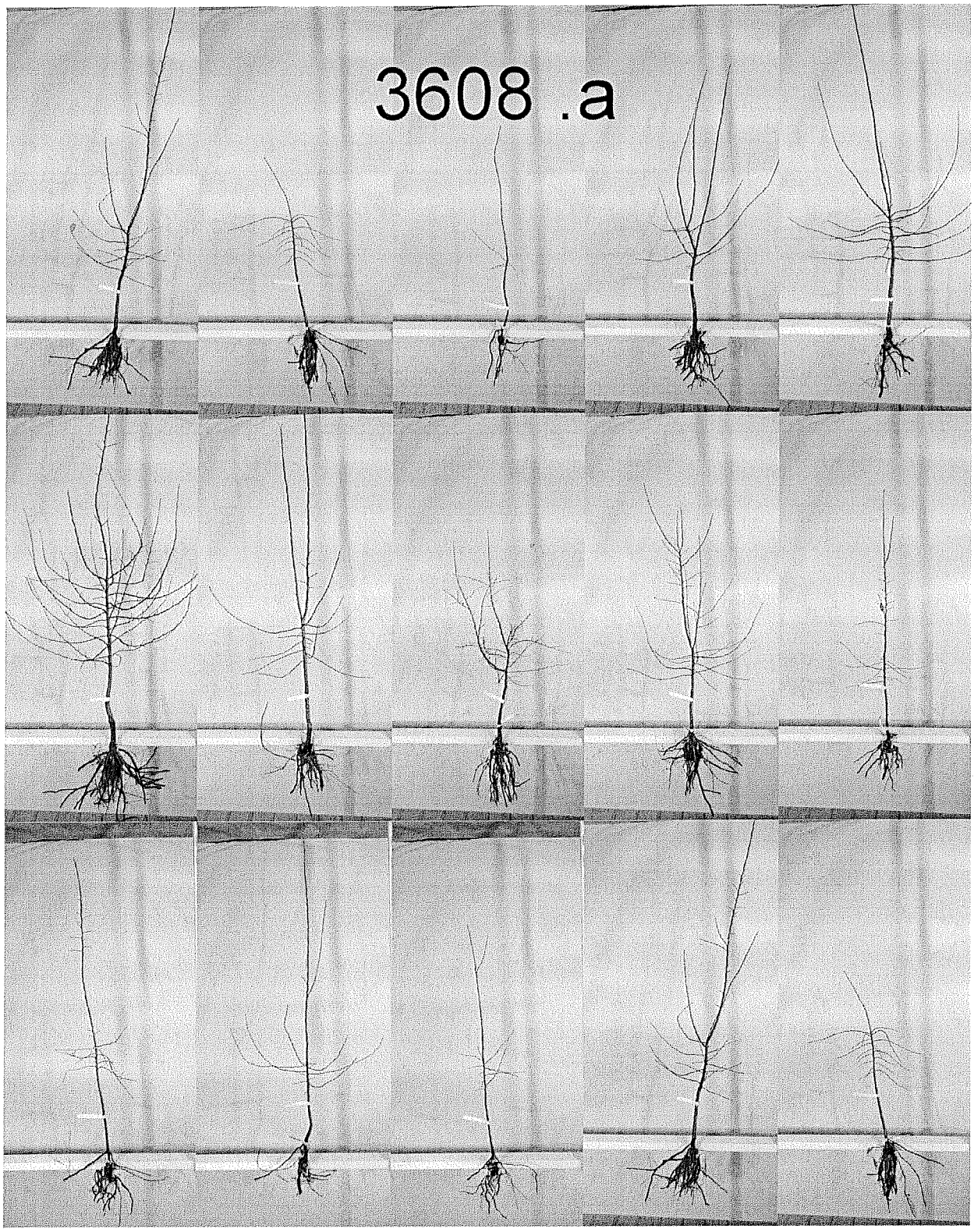


Figure 2. Sampling of high resolution images of seedlings derived from the GMAL 3608.a mother tree and several pollen pools. What is striking about this group of half sib trees is the more flat branching that may be correlated with productive fruiting wood.

Results

Results are summarized in the graphs below.

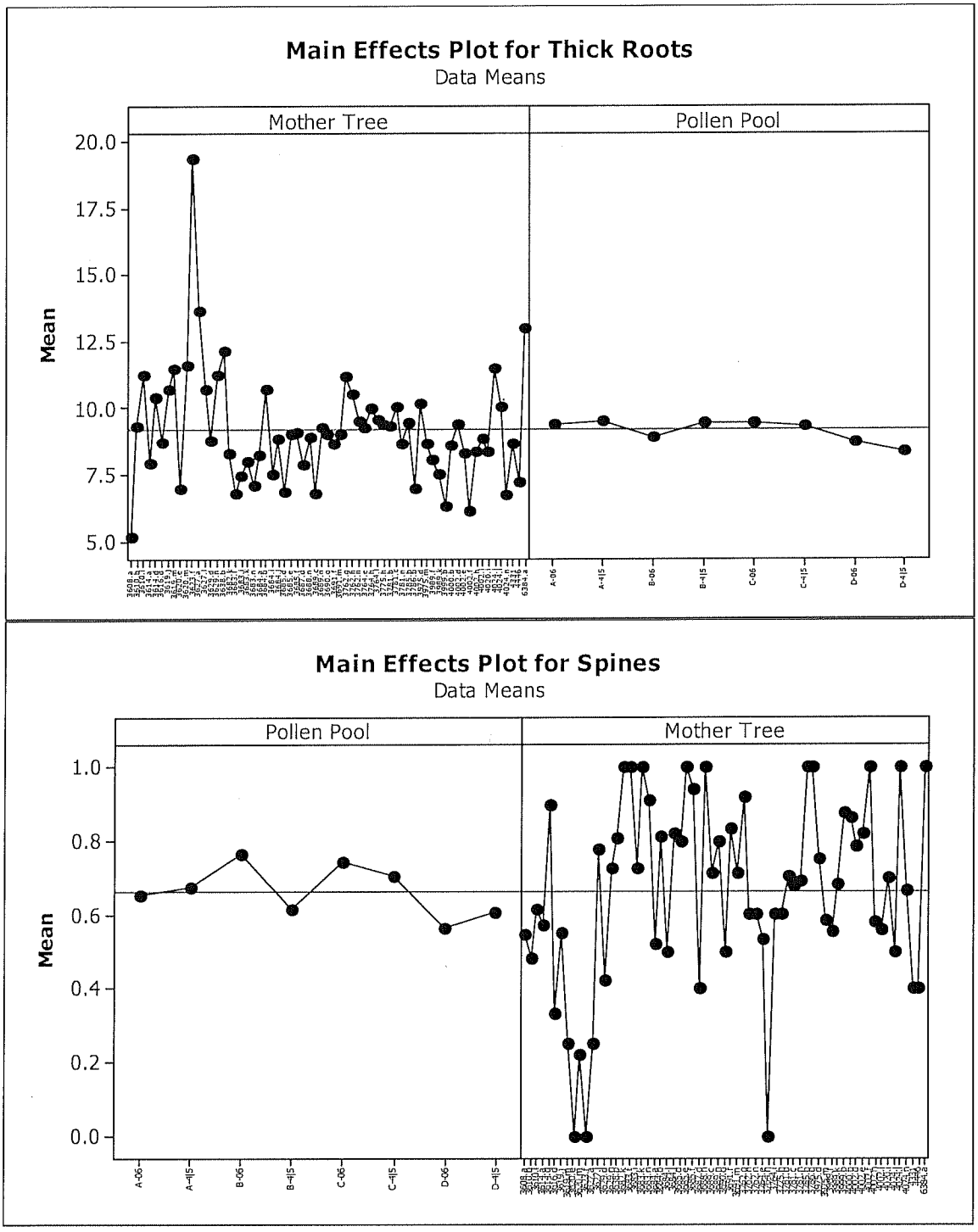


Figure 3. Representation of means for the number of thick primary roots and presence of spines for the individuals grouped by mother trees (half sib means) and pollen pools. The overall mean is represented by the horizontal line. Relative to the mother trees, the pollen pools did not seem to have a significant effect on the above and other traits measured in this study (data not shown). The absence of significant effects of the pollen pools on the phenotypes measured is expected since the pollen pools are composed of pollen from a number of heterogeneous individuals and each individual's heritable contribution is dampened. The effects (variance) caused by the alleles transferred to the progeny from the same mother tree is clearly identifiable and heritable.

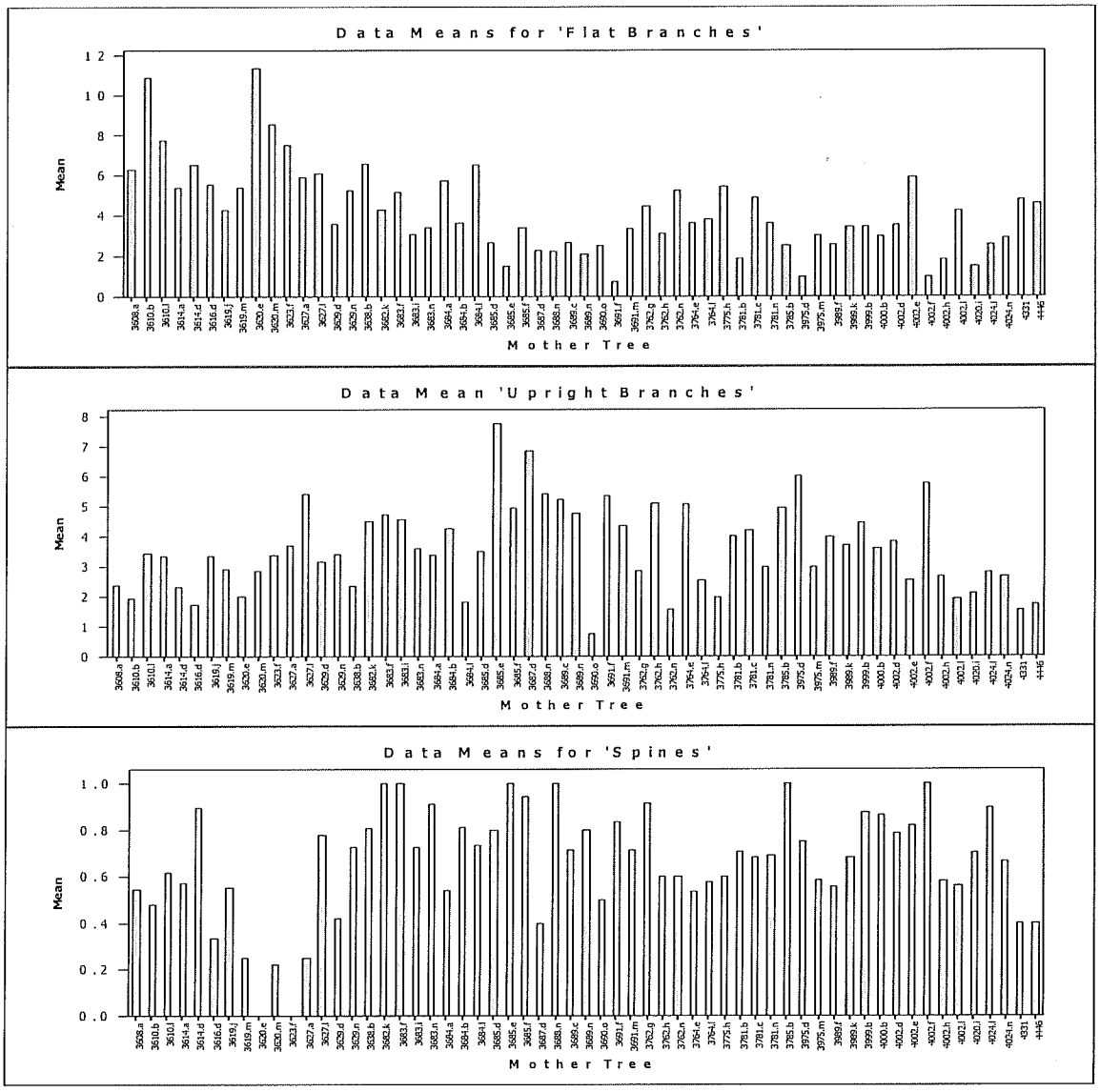


Figure 4a. Half sib family means for visually estimated scion traits: Flat Branching, Upright Branching and Presence of Spines (1=present, 0=absent). The overall mean for each trait is represented by the horizontal line. Genetic variance between half sib families that might be useful for breeding is clearly notable in this panel. For example, individuals of families 3610 might be a good source for flat branching and individuals from 3620 and 3674 might be useful to breed lack of spines. Also noteworthy for the spine trait is the fact that there is variation among some related families (4002 d, e, f, and l) while others are homogeneous (3781 b, c, and n).

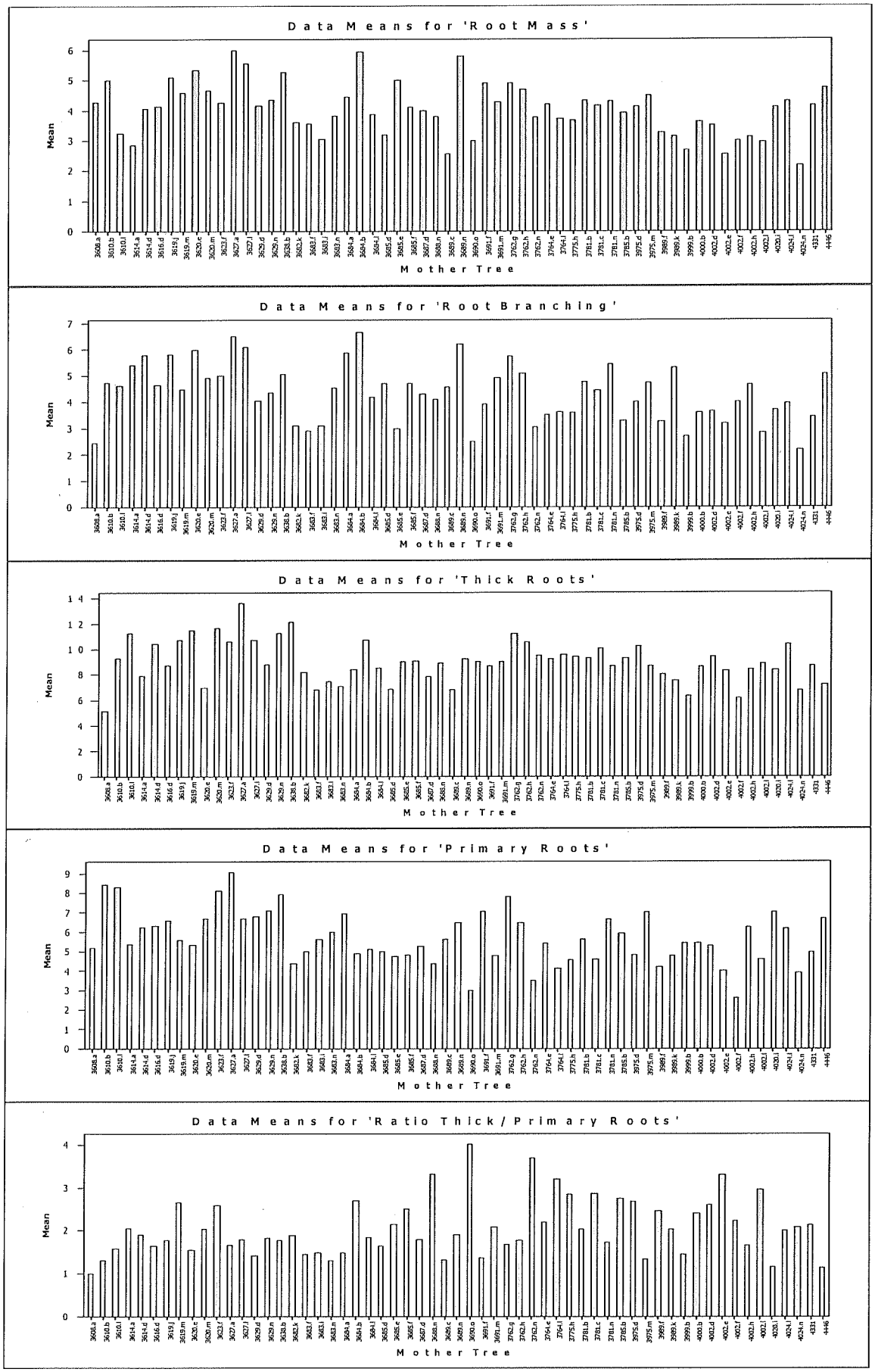


Figure 4b. Half sib family means for visually estimated root traits.

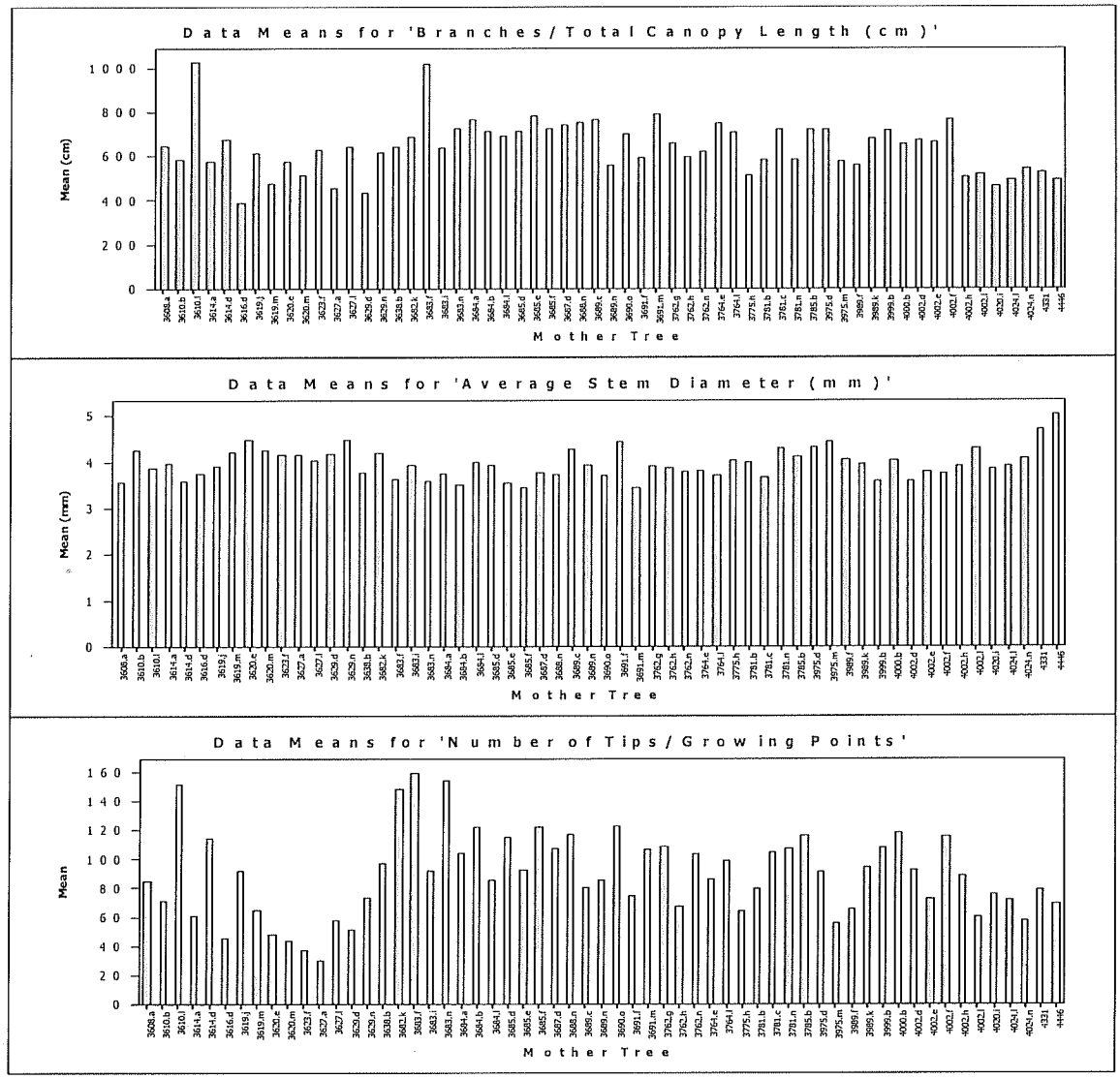


Figure 5. Half sib family means for WinRhizo image analysis scion traits.

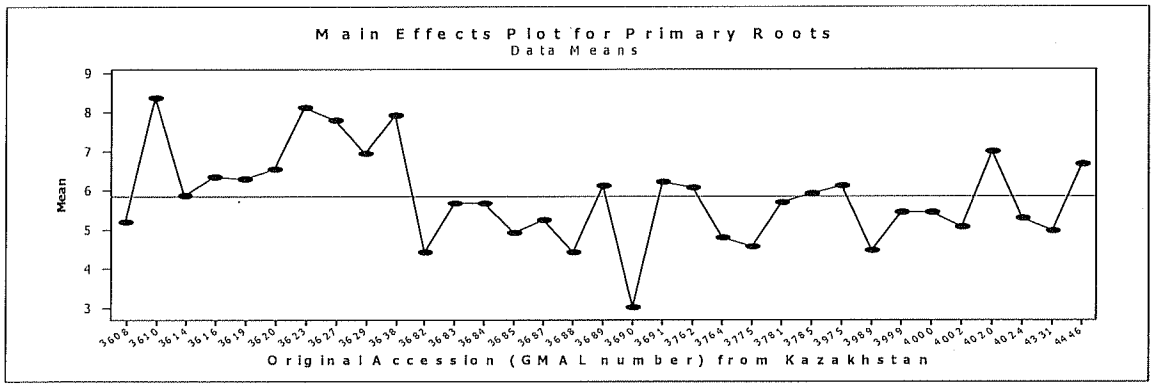


Figure 6. The means represented in this figure are for individuals grouped by the original seed-lot/mother tree (GMAL number) that was collected in Kazakhstan. This particular trait may be of use for increasing root anchorage in apple rootstocks.

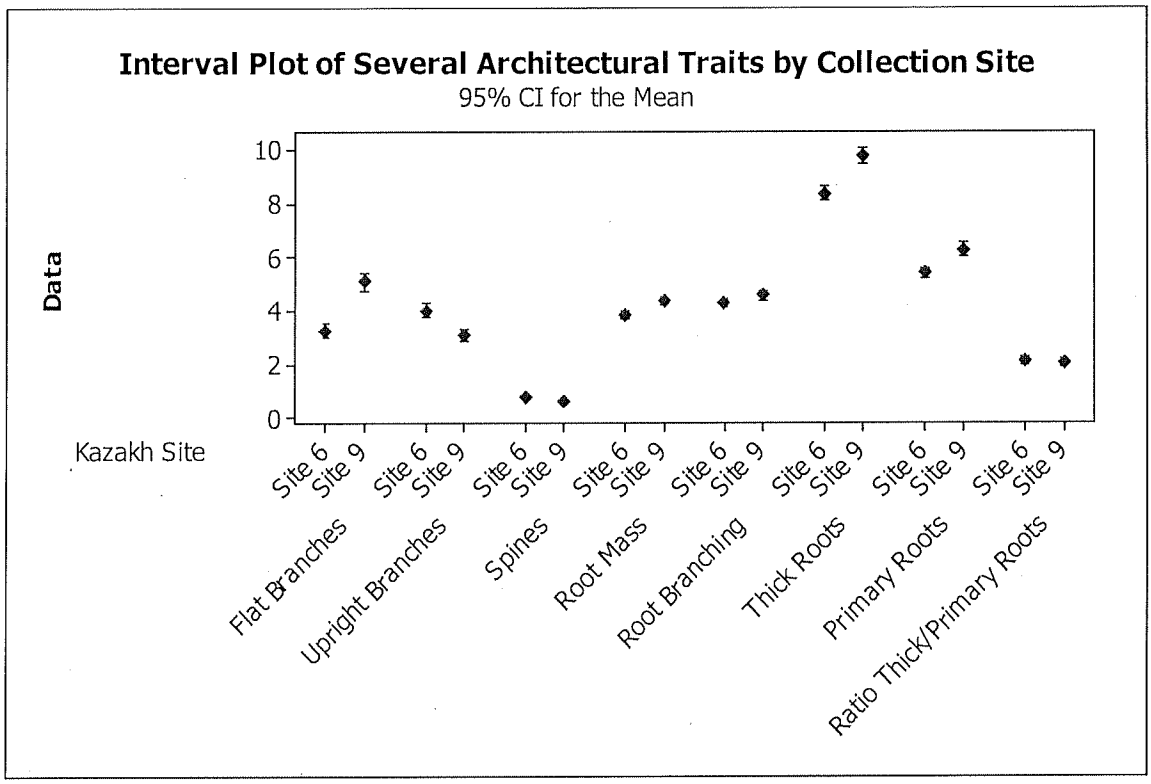


Figure 7. Comparison of means for several apple seedling architectural traits grouped by collection site in Kazakhstan. Trees from Site 9 seem to possess more flat branches, have higher root mass and thicker primary roots. Compared to Site 6, Site 9 was at higher elevation and had less precipitation.

Conclusions

The trees measured in this experiment were not intended at planting to be used for architectural analysis, rather to check the successful preservation of allelic diversity of *M. sieversii* by seed and test for scab resistance. There was no field experimental design intended to minimize variation due to field conditions, however these trees had been planted randomly in the field rows, so that family genotypic effects could be ascertainable. This was a unique opportunity to study the architectural phenotypic diversity of this species and identify genotypes with unique architectural characters for breeding new rootstocks. This analysis revealed substantial genotypic effects on tree and root architecture especially for flat branching, presence of spines, number of primary roots and root mass. Trees will be selected from this study as parents of future crosses with elite Geneva® apple rootstocks.

Acknowledgements: We would like to thank Bill Srmack and the Staff of the Plant Genetic Resources Unit in Geneva for their exceptional work caring for the trees in this study.

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Dreesen, R.S.G., B.T.M. Vanholme, K. Luyten, L.v. Wynsberghe, G. Fazio, I. Roldan-Ruiz, and J. Keulemans. 2010. Analysis of Malus S-RNase gene diversity based on a comparative study of old and modern apple cultivars and European wild apple. Molecular Breeding 26:693-709

Volk G.M., A.A. Reilley, A.D. Henk, C. M. Richards, P.L. Forsline, and H.S. Aldwinckle. 2005. *Ex situ* conservation of vegetatively propagated species: Development of a seed-based core collection of *Malus sieversii.* J. Amer. Soc. Hort. Sci. 130:203-210.

Zhong Report

Uncover the hidden treasures in the *Malus* collection

Over 2500 *Malus* accessions are currently curated at the USDA-ARS Plant Genetic Resources Unit (PGRU) in Geneva, New York. Of these diverse collections, a subgroup of about 250 accessions, representing over 90% of the genetic diversity of the entire *Malus* germplasm, were selected to form the *Malus* core collection. These *Malus* accessions serve as a gene bank for apple breeding and genomics research in the US and around the world. To uncover the hidden treasures in these germplasm, PGRU has been actively collaborating with the apple research community to characterize phenotypic and genotypic variation of the collection. Examples include the work with Herb Aldwinckle on screening the collection for disease resistance and with Gayle Volk on using SSR markers for increasing our understanding of the identity and diversity of the collection.

To further expand our effort on the characterization of these *Malus* accessions, we plan to initiate a pilot phenotyping project on fruit quality traits. Apple fruit quality can be defined by many different physical and biochemical properties, but the composition and concentration of various primary metabolites (sugars, organic acids, and amino acids) and secondary metabolites (phenolic and aroma compounds) in the fruit are the most important ones. We plan to characterize these metabolites in the core collection and establish a comprehensive database of primary and secondary metabolites for the *Malus* collection. In the initial phase of the pilot phenotyping project, we will measure titratable acidity and brix on representative bulk samples from individual accessions in the core collection. Maturity of individual apple samples in each accession will be determined using starch-iodine test and only those apple samples with a maturity range of 4-6 will be bulked for processing and analysis. The same set of bulk samples will also be analyzed for phenolic compounds using established HPLC protocols. The data will be deposited to the GRIN database and shared with the apple research community.

In parallel to the pilot phenotyping project on fruit quality traits, we also plan to explore the opportunity of using next-generation sequencing technologies to further characterize molecular diversity of the collection. This work will be carried out in a close collaboration with Sean Myles, Assistant Professor of Nova Scotia Agricultural College (Canada), who has the needed expertise in processing high throughput sequencing data and recently approached us to initiate this collaborative project. We plan to use the genotyping-by-sequencing (GBS) technique to genotype the entire or major portion of the *Malus* collection. If successful, we will generate tens of thousands of SNP markers for individual accessions with a relatively small cost. GBS has been successfully applied to several annual crops and we believe that it will work as well for perennial crops such as apples.

One of our long-term goals in *Malus* germpalsm characterization is to associate phenotypic and genotypic variation for the traits of interest, which in turn will help apple research community to better utilize these germplasm resources for apple improvement. The phenotyping project on fruit quality traits and the GBS genotyping project proposed above will provide us a unique opportunity to start establishing such trait-genotype association in the *Malus* germpalsm.

Allelic characterization of the *MdACS3a* gene in the *Malus* core collection for long shelf life apples

Kenong Xu, NYSAES, Cornell University

Although controlled atmosphere (CA) storage technology has played a major role in long-term (>10 months) storage of apple fruits, physiological disorders related to CA have been reported for most, if not all, commercial apple cultivars. There is a strong need for new apples of longer shelf life and improved storage ability. The goal of this project is to facilitate the development of long shelf life apples by systematically characterizing the *Malus* core collection (maintained by USDA-ARS, PGRU in Geneva, NY) with the allelotypes of *MdACS3a*, a gene that has recently been discovered to be crucial in regulating apple fruit shelf life (Wang et al 2009). Achieving the project goal will eventually benefit the apple industry with new apple varieties of longer shelf life that could potentially reduce the storage disorders and costs. Data and knowledge gained from this project will be invaluable to our understanding as to how apple fruit shelf life is genetically controlled.

Specific objectives of this project include: 1. Development of allele specific markers for the transcriptionally null allele *Mdacs3a* to simplify the existing detection process that involves cDNA analysis. 2. Development of allele specific markers for the functionally null allele *MdACS3a-G289V* to simplify the existing detection process that needs a two-round nested PCR. 3. Allelic characterization of the *Malus* core collection using the markers developed in objective 1 and 2 to categorize the collection into groups based on the allelotypes of *MdACS3a*. 4. Evaluation of the *Malus* core collection for their fruit shelf life and ethylene production to investigate the range of genetic background in which the two null alleles operate and lead to prolonged fruit shelf life.

Using the existing *MdACS3a-G289V* SSR (containing GA repeats) marker (Wang et al 2009), we have genotyped a total of 243 accessions in the core collection. Preliminary analysis of the SSR marker fragment size data generated by an ABI3730 DNA Analyzer indicated that there are at least 34 fragments different in size, suggesting that there are potentially 34 alleles of *MdACS3a* in the core collection. This number is significantly greater than the number of alleles previously detected from a collection of 48 *Malus* accessions (42 in *M. domestica*, 6 in other *Malus* species), which has been reported at two: one for allele *MdACS3a* or *Mdacs3a*, the other for *MdACS3a-G289V* (Wang et al 2009). The lower diversity in the *MdACS3a* alleles suggested in Wang et al (2009) is likely caused by their lower resolution means in fragment analysis, which is based on PAGE and silver staining. Further examination of the common accessions used in both Wang et al (2009) and this study, such as Gala, Golden Delicious, and Jonathan, showed that the *MdACS3a* or *Mdacs3a* allele in Wang et al (2009) corresponds to fragments of 319-321 bp whereas the *MdACS3a-G289V* allele to 341-349 bp. Based on these results, we concluded that although the *MdACS3a-G289V* SSR marker was developed from the promoter region of *MdACS3a*, more sequencing analyses of the *MdACS3a* genes in the core collection are required in order to understand how the association is between the marker GA repeat polymorphism and the mutation that defines allele *MdACS3a-G289V* from *MdACS3a*.

The frequency of the 34 *MdACS3a-G289V* SSR marker alleles varies greatly in the core collection (Fig. 1). There are six alleles, 319, 321, 337, 349, 341 and 323 bp that are among the most abundant.

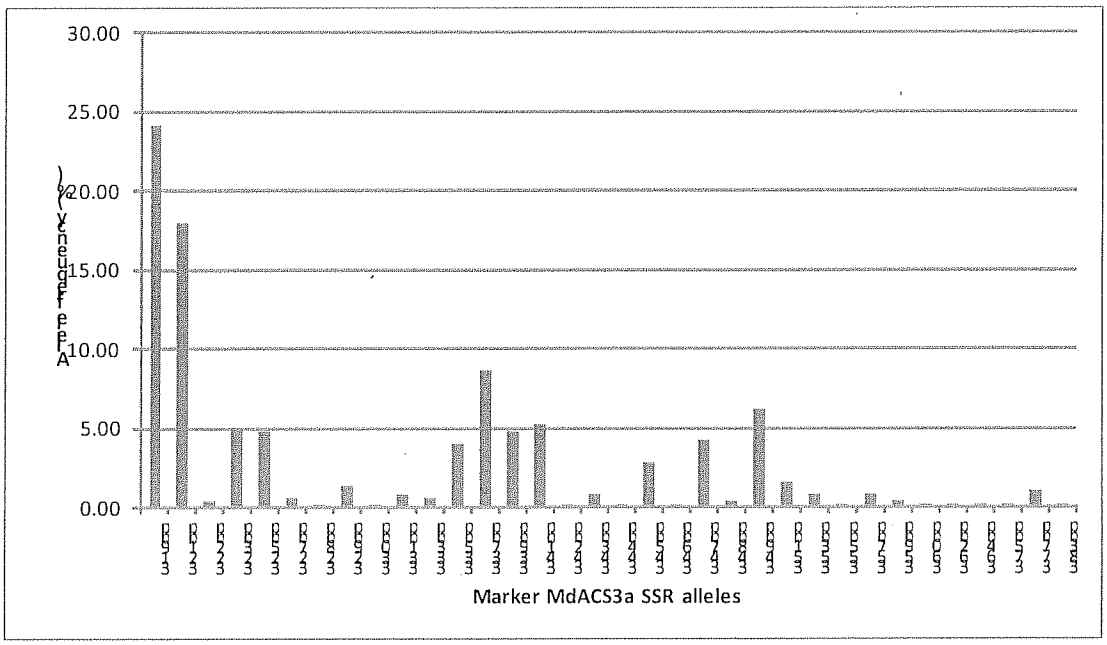


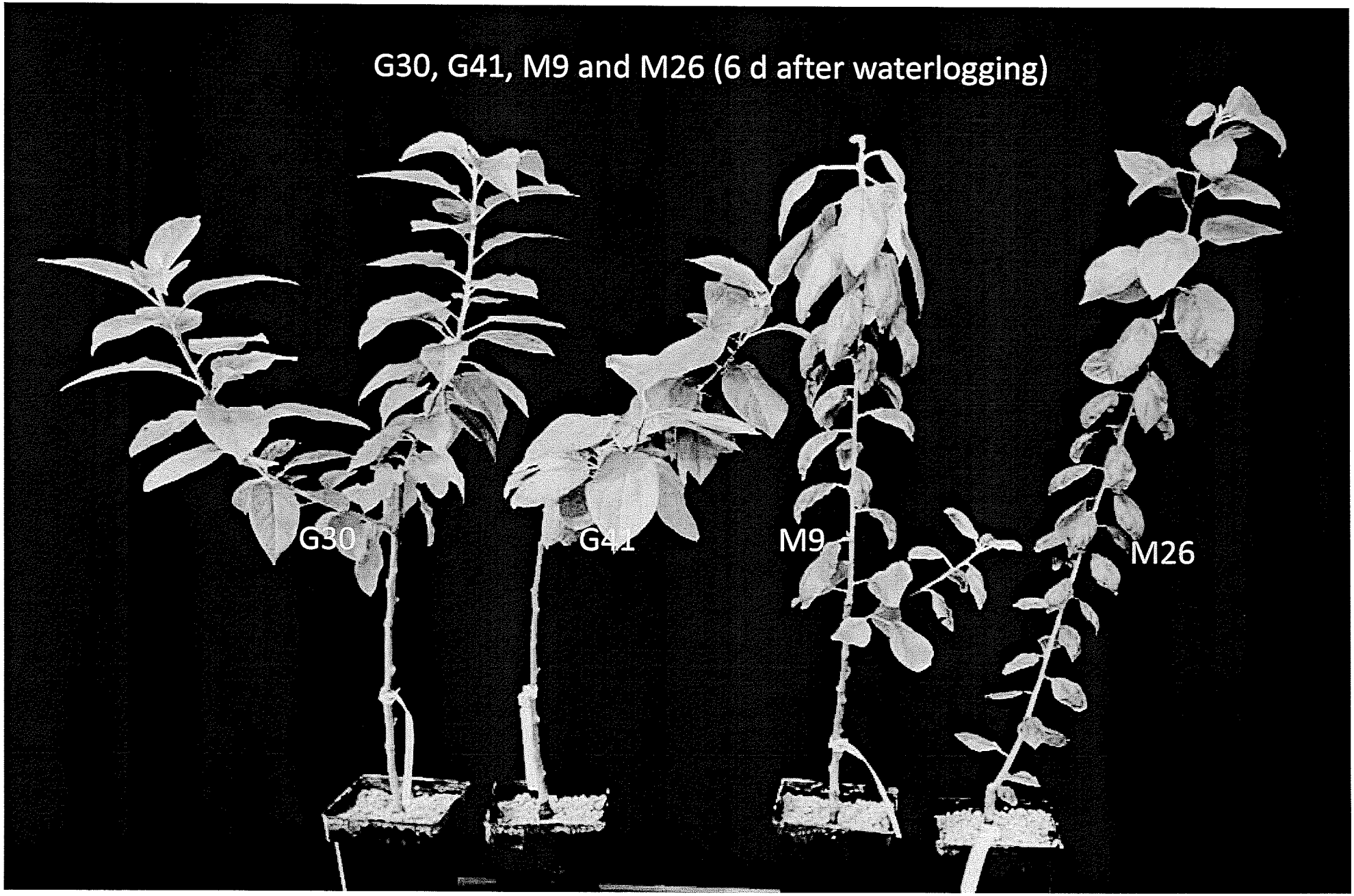
Fig. 1. Allele frequency (%) of the MdACS3a SSR marker in the *Malus* core collections

These six alleles accounted for 67.34% of the *MdACS3a* alleles observed, among which the 319 bp allele is of the highest frequency (24.19%). The rarest alleles are 328, 330, 342, 344, 346, 355, 360, 362, 364, 375 and 383 bp, which presented only once (0.20%) in the core collection.

For fruit shelf life evaluation, we have so far harvested fruits from 48 accessions. These fruits have been stored for 0, 5, 10, 15 and 20 days at room temperature and measured for fruit weight, firmness, Brix and ethylene production levels at the end of each storage period. Additional 50-55 accessions will be evaluated similarly in 2011.

Reference

Wang A, Yamakake J, Kudo H, Wakasa Y, Hatsuyama Y, Igarashi M, Kasai A, Li T, Harada T (2009) Null mutation of the *MdACS3* gene, coding for a ripening-specific 1-aminocyclopropane-1-carboxylate synthase, leads to long shelf life in apple fruit. Plant Physiology 151:391-399


G30, G41, M9 and M26 (6 d after waterlogging)
G30
G41
M9
M26

Prunus Crop Germplasm Committee: Membership and Subcommittee Chairs for 2004 to 2013

Name		Position	Expertise	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	Email/Location	Telephone/FAX
Terry	Bacon	Member	Stone fruit breeding			M	M	M	M	M	M			tbacon@sun-world.com Sun World International, Inc. Research and Development 16350 Driver Road Bakersfield, CA USA 93308	661-392-5100 661-758-3651
Tom	Beckman	Member, Rootstocks Subcomm.	Rootstocks, peach	M	M	M	M	M	M					Tom.Beckman@ars.usda.gov USDA/ARS 21 Dunbar Rd. Byron, GA 31008	478-956-6436 478-956-2929
David	Byrne	Member, Evaluation, Peach Subcomm.	Peach, plum, apricot	M,S Ch	M,S, Ch	M,S Ch	M,S Ch	M,S	M,S	M,S	M,S	M,S	M,S	dbyrne@ag.tamu.edu Dept Hort Sci Texas A&M University College Station, TX 77843-2133	409-862-3072 409-845-0627
David	Cain	Member				M	M	M	M	M	M			d.w.cain@worldnet.att.net International Fruit Genetics 441 Vineland Rd. Bakersfield, CA 93308	(M)661-203-0141 (H)661-399-1559 (F)661-366-4251
Jose	Chaparro	Member	Stone fruit breeding	M	M	M	M	M	M					jchaparro@ifas.ufl.edu Dept Hort Sci University of Florida PO Box 110690 Gainesville, FL 32611-0690	352-392-2134 x300
John	Clark	Member	Peach	M	M	M	M	M	M	M	M			jrclark@comp.uark.edu Dept Hort & Forestry University of Arkansas Fayetteville, AR 72701	501-575-2810 501-575-8619
Ksenija	Gasic	Member	Peach					M	M					kgasic@clemson.edu Dept. Horticulture Clemson University P&A Ctr. E-143, Box 340319 Clemson, SC 29634	864-656-3664 864-656-4960
Joseph	Goffreda	Member, Apricot Subcomm.	Peach, apricots	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	goffreda@aesop.rutgers.edu Dept Plant Biology Rutgers PO Box 231 New Brunswick, NJ 08903	609-758-7311 x13 609-758-7085

M = Membership in Prunus CGC ; S = Subcommittee Crop Chairperson; Ch –CGC Chair.

Name		Position	Expertise	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	Email/Location	Telephone/FAX
Tom	Gradziel	Member, Almond Subcomm.	Almonds, processing peaches	M,S	M,S	M,S	M,S	M,S	M,S					tmgradziel@ucdavis.edu Dept. Pomology Univ. of California Davis, CA 95616	530-752-1575 530-752-8502
Bill	Howell	Member	Plant pathology	M	M	M	M	M	M	M	M			wehowell@wsu.edu WSU-IAREC 24106 North Bunn Rd. Prosser, WA 99350	509-786-9251 509-786-9370
Amy	Iezzoni	Member, Tart cherry Subcomm.	Sour cherry	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	iezzoni@msu.edu A342-B Plant & Soil Sciences Michigan State University East Lansing, MI 48824-1325	517-355-5191 x391 517-355-0890
Jim	McFerson	Member						M	M					mcferson@treefruitresearch.com WA Tree Fruit Research Commiss. 1719 Springwater Ave Wenatchee, WA 98801	509-665-8271
Nnadozie	Oraguzie	Member	Sweet cherry						M	M	M	M	M	noraguzie@wsu.edu	
Cameron	Peace	Member, Chair	Tree fruit genetics					M, Ch	M, Ch	M, Ch	M, Ch	M, Ch	M, Ch	cpeace@wsu.edu Dept.Horticulture & Landscape Washington State University Pullman, WA 99164-6414	509-335-6899 509-335-8690
Margaret	Pooler	Member	Ornamentals			M	M	M	M	M	M			Margaret.Pooler@ars.usda.gov US National Arboretum 3501 New York Ave. N.E. Washington DC 20002-1958	202-245-4568 202-245-4579
David	Ramming	Member Peach Subcomm.	Peach, diploid plum	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	M,S	dramming@fresno.ars.usda.gov USDA, ARS Hort. Crops Res. Laboratory 2021 South Peach Ave. Fresno, CA 93727	209-453-3061 209-453-3088
Gayle	Volk								M	M	M	M	M		
Matthew	Whiting	Member	Stone fruit physiology	M	M	M	M	M	M					mdwhiting@wsu.edu WSU-Prosser IAREC, 24106 N. Bunn Rd., Prosser, WA 99350-8694	509-786-9260

M = Prunus CGC member; S = Crop Subcommittee Chair; Ch = CGC Chair
Year of membership represents through to CGC meeting of that year.

Full email list:

tbacon@sun-world.com; tom.beckman@ars.usda.gov; dbyrne@ag.tamu.edu; d.w.cain@worldnet.att.net; jchaparro@ifas.ufl.edu; jrclark@uark.edu; kgasic@clemson.edu; goffreda@aesop.rutgers.edu; tmgradziel@ucdavis.edu; wehowell@wsu.edu; iezzoni@msu.edu; mcferson@treefruitresearch.com; noraguzie@wsu.edu; margaret.pooler@ars.usda.gov; dramming@fresno.ars.usda.gov; gayle.volk@ars.usda.gov; mdwhiting@wsu.edu

clay.weeks@ars.usda.gov; malli.aradhya@ars.usda.gov; john.preece@ars.usda.gov; cthomaschao@gmail.com; margarita.f.licha@aphis.usda.gov; grghrd@clemson.edu; mark.bohning@ars.usda.gov; gary.kinard@ars.usda.gov; cpeace@wsu.edu

Crop Subcommittees: Chairs

Apricot:	VACANT
Almond:	VACANT
Cherry, Sweet:	Nnadozie Oraguzie
Cherry, Tart:	VACANT
Peach:	VACANT
Plum:	VACANT
Rootstocks:	VACANT

Other standing Subcommittees:

Germplasm Evaluation: David Byrne

Standardized Phenotyping: Ksenija Gasic

Membership: Jim McFerson, Ksenija Gasic

REPORT OF THE NATIONAL CLONAL GERMPLASM REPOSITORY, DAVIS TO THE *PRUNUS* CROP GERMPLASM COMMITTEE

John Preece and Clay Weeks
Research Leader and Horticulturist
Davis, CA
Tuesday September 25, 2011

Introduction

The National Clonal Germplasm Repository (NCGR) at Davis, an entity of the National Plant Germplasm System (NPGS), receives, collects, preserves, evaluates, and distributes genetic resources of assigned fruit and nut crops. These irreplaceable resources are maintained on a long-term basis to support domestic and international research efforts on germplasm enhancement, cultivar development, molecular biology, and other related research. The Repository operates in cooperation with the Plant Sciences, the Viticulture & Enology Departments, and Foundation Plant Services (FPS) at the University of California, Davis.

Staffing

John Preece	Research Leader
Mallikarjuna Aradhya	Geneticist
Mary Parker	Office Automation Assistant
Howard Garrison	Field and Facilities Manager
Jenny Hansen	Agricultural Science Technician
Anne Koehmstedt	Biological Science Technician
Jeff Moersfelder	Greenhouse Manager
Bernie Prins	Grape Horticulturist
Salvador Rivas	Agricultural Science Research Technician
Patty Jo Compton	Biological Science Technician
Clay Weeks*	Prunus Horticulturist
Angela Madina	Biological Science Aid

*retired as of August 31, 2011

Acquisition, characterization, and management

One hundred ninety-six bare rooted almond seedlings germplasm from Azerbaijan collected by Malli Aradhya during 2007 exploration were released from the USDA-APHIS Plant Germplasm Quarantine Program. They were close planted for genotyping and preliminary evaluation and subsequently lost 31 saplings. These progenies have been genotyped using 12 microsatellite loci to select plants possessing diverse set of alleles and horticultural traits. Apart from these

We recently gained access to UC Davis apricot and cherry germplasm and cultivar collections. These collections represent an elite germplasm, breeders' selection, named cultivars, and growers' selections. A total of 190 items have been sampled for microsatellite analysis to

identify and compare with the repository germplasm collections. Unique accessions will be added on to the repository collection. Currently genotyping is in progress.

Corrective dormant and Spring pruning of almond and cherry collections has been undertaken to improve the overall health of the collections. Peach germplasm is currently being re-propagated to establish a new germplasm block. In this effort, a rootstock block was established during 2010 and budding of germplasm accessions has been in progress. During 2011, this block has to be pruned back to regenerate plants suitable for budding again.

Administration

Since the last CGC meeting, Mr. Clay Weeks, horticulturist in-charge of *Prunus* collection has retired as of August 31, 2011 and rehire may be indefinitely delayed as there is hiring freeze.

Other research activities at the repository – Characterization and Utilization of Crop Wild Relatives (Malli et al.)

Figure 1. Interspecific Prunus hybrid from Nemagard by *P. kansuensis* cross in tissue culture. This particular hybrid is undergoing shoot multiplication.

During 2011 Spring season, several thousands of pollinations were made to produce interspecific hybrids involving a number of wild *Prunus* spp. potentially useful for rootstock development. About 150 pollinations yielded hybrid seeds in nine cross combinations (Table 1). Previously during 2010, 116 hybrid seeds were produced from twenty crosses (Table 2). The seeds from 2010 crosses were put into culture at the Davis repository at the end of 2010. The immature fruits produced from 2011 crosses were harvested and delivered to California Seed & Plant Laboratory for culturing in June 2011. Some of the 2010 hybrids in culture at Davis repository are growing (Figure 1) and are entering the shoot multiplication stage. A number of open pollinated seeds collected in 2010 from self incompatible wild almond species in the NCGR collection are also in culture, and are so far the best performers of all the cultured material. Some of the hybrids are still quiescent even after a second round of 30 days chilling in the dark. The most recalcitrant embryos are those from the peach by plumcot cross (see Table 2 for accession details). Most of the *P. dulcis* (Tardy Nonpareil) X *P. argentea* hybrids successfully germinated (Table 2). Contamination is problematic and most genotypes have been rescued through subculturing of non-contaminated shoots as well as additional disinfestation.

Germinated embryos large enough for leaf collection have had DNA extracted and hybrid status confirmed by SSR fingerprinting (Table 3).

Genomic DNA library preparation for next generation sequencing on Illumina HiSeq is in progress. Input is being requested from stakeholders regarding rootstock cultivars widely identified as tolerant or susceptible to soil borne pests and pathogens for preparing cDNA libraries for sequencing and RNA profiling. We hope complete the sequencing of both genomic and cDNA libraries by the end Summer, 2011.

Table 1. Interspecific *Prunus* crosses from 2011. (Immature fruit was collected on June 9, 2011 and delivered to California Seed & Plant Laboratory on June 13, 2011, for embryo culture and multiplication.

Seed Parent	**Pollen Parent**	**Seeds**
Tardy Non-Pareil (UCD)	*P. argentea DPRU 194*	4
Tardy Non-Pareil (UCD)	*P. kuramica DPRU 1467.x*	9
Tardy Non-Pareil (UCD)	*P. tangutica DPRU 2327.x*	2
Tardy Non-Pareil (UCD)	*P. davidiana DPRU 581*	1
Nemared (UCD)	*P. cerasifera DPRU 1511*	9
Nemared (UCD)	*P. tangutica DPRU 2327.x*	23
Nemared (UCD)	*P. fenzliana Pomology*	71
Nemared (UCD)	*P. argentea DPRU 194*	23
P. cerasifera (DPRU 1511)	Nickels DPRU 1511	3
Total		**145**

Table 2. Status of interspecific Prunus crosses from 2010. These individuals are currently in culture at NCGR. Embryos that have germinated and grown to an acceptable size are undergoing the multiplication process. At this time none have had roots initiated. Many have not germinated, especially from the cross of peach (Xin Dia Jiu Bao) x plumcot (NJ-PC5/NJ-PC7).

Seed parent	**Pollen Parent**	**Source of Pollen Parent**	**# Seeds**	**# alive**	**# Lost**
P. dulcis (Tardy Non-Parell)	*P. argentea*	DPRU 194	22	4	13
P. dulcis (Tardy Non-Parell)	*P. fenzliana*	Pomology	3	2	1
P. dulcis (Tardy Non-Parell)	*P. kansuensis*	DPRU 582	2		1
P. dulcis (Tardy Non-Parell)	*P. kuramica*	DPRU 1467.x	5		3
P. dulcis (Tardy Non-Parell)	*P. tangutica*	DPRU 2327.x	3		
P. persica (DPRU2261B)	*P. bucharica*	DPRU 1871.1	2		
P. persica (DPRU2261B)	*P. davidiana*	DPRU 581	2		2
P. persica (DPRU2261B)	*P. fenzliana*	Pomology	3		1
P. persica (DPRU2261B)	*P. tangutica*	DPRU 2327.x	2		

P. persica (DPRU2261B)	*P. triloba*	DPRU 2312.2	1		
P. persica (DPRU2261B)	*P. webbii*	DPRU 196	4		
P. persica (Lard Napier)	*P. kansuensis*	DPRU 582	2	1	
P. persica (Lard Napier)	*P. pedunculata*	DPRU 2329.21	2	1	1
Nemaguard	*P. argentea*	DPRU 194	2		1
Nemaguard	*P. bucharica*	DPRU 1871.1	1		
Nemaguard	*P. fenzliana*	Pomology	1		1
Nemaguard	*P. kansuensis*	DPRU 582	1	1	
Nemaguard	*P. kuramica*	DPRU 1467.x	1	1	
Nemaguard	*P. pedunculata*	DPRU 2329.21	1		1
Nemaguard	*P. tomentosa*	DPRU 2316.5	1		
Nemaguard	*P. webbii*	DPRU 196	1	1	
P. persica (Xin Dai Jiu Bao)	Plumcot	DPRU 2267A	54		6
Total			**116**	**11**	**25**

Table 3. SSR fingerprint data confirming hybrid status of plants in culture. Sampled from crosses of *P. dulcis* (Tardy Non Pareil) x *P. argentea* (cross ID P019), Nemagard (*P. persica x P. davidiana*) x *P. kansuensis* (cross ID P014), and *P. dulcis* (Tardy Non Pareil) x *P. fenzliana* (cross ID P022).

Sample	**E006**		**M012**		**U409**		**MA27**		**pch3**		**TA25**	
Tardy Non Pareil	191	195	185	191	142	142	114	120	169	171	203	203
P. argentea (194)	ND	ND	185	193	124	146	118	142	ND	ND	ND	ND
P019.11	191	191	185	193	124	124	118	120	169	171	203	203
P019.19	191	191	185	185	146	146	114	118	171	175	203	203
P019.3	193	195	185	191	124	124	114	118	169	171	203	203
Nemagard	195	195	174	174	126	126	149	149	175	175	197	197
P. kansuensis (582)	195	195	189	189	142	142	104	110	175	175	201	201
P014.1	195	195	174	189	126	142	110	149	175	175	197	201
Tardy Non Pareil	191	195	185	191	142	142	114	120	169	171	203	203
P. fenzliana	191	195	183	185	128	146	104	134	175	180	203	203
P022.1	191	195	183	185	146	146	114	134	169	175	203	203
P022.2	191	195	185	191	142	146	120	134	171	180	203	203

GLOBAL CROP DIVERSITY TRUST
A FOUNDATION FOR FOOD SECURITY

MILLENNIUM SEED BANK PARTNERSHIP
Kew

ADAPTING AGRICULTURE TO CLIMATE CHANGE:
COLLECTING, PROTECTING AND PREPARING CROP WILD RELATIVES

Background

Adapting agriculture to climate change is one of the most urgent challenges of our time. There is, quite simply, no more important step we can take to prepare for climate change than to ensure that the crops that feed humanity are adapted. The need for new crop varieties that can be productive in the new climates of the future is now widely recognized. It is much less well known that our ability to breed these new varieties cannot be taken for granted. The greatest source of untapped diversity, and in particular the richest source of diversity for *adaptive* characteristics needed to confront the challenges of climate change, are the wild relatives of our crops. Not only are these largely uncollected, and therefore unevaluated and unavailable to plant breeders and thus to farmers, many are also at risk of extinction. This project will ensure that we win the race to collect crop wild relatives, protect them, and prepare them for use in plant breeding programmes in time to breed new crop varieties adapted to new climates.

Objective

A portfolio of plants, with the characteristics required for adapting the world's most important food crops to climate change, is collected, protected and prepared in a form that plant breeders can readily use to produce varieties adapted to future climatic conditions that farmers in the developing world will soon be encountering.

Description

The project is focused on the species related to 26 crops[1] of major importance to food security. It will:

- identify those crop wild relatives that are missing from existing collections, are most likely to contain diversity of value to adapting agriculture to climate change, and are most endangered;
- collect them from the wild;
- provide them to genebanks for conservation;
- prepare these and others already in collections ('pre-breeding') for use in breeding crops for new climates;
- evaluate them for useful traits; and
- make the resulting information widely available.

The pre-bred material incorporating the desired traits will be directly fed into ongoing, active and successful breeding initiatives aimed at helping poor farmers in developing countries increase food production, and made available to on-farm improvement efforts and farmers as appropriate. The project will run for ten years. It will introduce a range of new and exciting adaptive options for agriculture that might otherwise have been lost, whilst helping protect biodiversity from disappearing. The project will help build capacity in developing countries and will produce valuable information to assist in complementary on-farm and *in situ* efforts. Importantly, it will further implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture.

Timeline

Activity	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Research										
Collecting										
Conservation										
Pre-breeding										
Evaluation										
Information										

Partnerships

The project will build bridges across intellectual spheres. It will draw in climate change experts, biodiversity conservationists, and agricultural scientists. The main partner is the Millennium Seed Bank of the Royal Botanic Gardens Kew, with its wide expertise in the *ex situ* conservation of wild species. Implementation will be carried

[1] The 26 crops and their wild relatives are covered by Annex 1 of the International Treaty. They are: alfalfa, apple, bambara groundnut, banana, barley, bean, carrot, chickpea, cowpea, eggplant, faba bean, finger millet, grasspea, lentil, oat, pea, pearl millet, pigeon pea, potato, rice, rye, sorghum, sunflower, sweet potato, vetch and wheat.

out in close partnership with national PGRFA conservation and use programmes in developing countries and the CGIAR Centres. The Secretariat and national focal points of the International Treaty will be involved at all stages.

Beneficiaries
The ultimate beneficiaries of the project will be present and future generations of farmers worldwide, and the people that they feed. Farmers in developing countries will have access to the new and increased diversity in their crops they will need to cope with climate change. National agricultural research and conservation programmes will benefit from the enhanced conservation of the country's crop diversity as well as capacity-building, information and information systems, and partnerships the project will facilitate.

Budget
The budget is USD 50 million over the ten-year lifespan of the project.

Summary of outcomes and outputs

Outcomes	Outputs
1.The collecting and use of novel genetic diversity for crop adaptation to climate change are informed by an assessment of the state of *ex situ* conservation of the wild species related to major crops (Crop Wild Relatives - CWR).	1.1 Database listing CWR taxa in the genepools of at least 60 crops listed in FAOSTAT
	1.2 Database of ecogeographic information for CWR in at least 60 genepools available for analysis
	1.3 Review of germination requirements of CWR in existing *ex situ* collections
	1.4 Identification of the gaps in the diversity available *ex situ* of CWR in at least 60 genepools
	1.5 Strategy for the collecting of 26 priority Annex 1 crop genepools available
	1.6 Guides for collecting in potential partner countries produced and made available
2. Novel and threatened diversity of CWR is collected, shared with breeding programs, and high quality seed safeguarded *ex situ* and accessible to researchers and other users worldwide.	2.1 Projects that engage and strengthen national capacity in CWR collecting in place with partner countries
	2.2 Target CWR taxa collected and seed samples sent to Kew for high quality processing
	2.3 Collected seed is processed, stored by partner national programs and duplicated at Millennium Seed Bank Kew and Svalbard Global Seed Vault, and shared with pre-breeding and breeding programs
3. Germplasm lines incorporating novel, useful diversity from CWR are available to breeders and farmers worldwide for enhancing crop adaptation to climate change.	3.1 Pre-breeding and evaluation strategies for selected priority crop genepools developed with experts
	3.2 Case study on one or more crops produces germplasm lines incorporating diversity from CWR available *ex situ* and recommendations on strategy and methods to guide implementation of pre-breeding and evaluation on other crops
	3.3 Projects in place with national programs and research institutes to analyze the genetic diversity of CWR collections, identify target accessions for pre-breeding, and generate new germplasm lines through pre-breeding
	3.4 Projects in place with national programs and research institutes to evaluate breeding lines for traits of value to climate change adaptation and to make lines available to breeding programs and farmers
4. Researchers, collection holders, breeders and other users of plant genetic resources have access to information and information systems for improved conservation and use of CWR and other plant genetic resources.	4.1 Website giving the global community access to the information from the project's research and collecting activities, showing the impacts on the state of *ex situ* conservation of CWR and giving guidance to *in situ* conservation
	4.2 Capacity of national programs enhanced in the use of genebank data management system (GRIN-Global) for managing PGR collections
	4.3 Global portal to accession level information on plant genetic resources (Genesys) expanded to include data on the collected CWR and evaluated breeding products, plus additional PGR data from programs worldwide