



Rosaceae Specialty Crops Planning Workshop June 22-23, 2007

Hosts



Final Workshop Report



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WORKSHOP SUMMARY

Rosaceae fruits are vital to human nutrition and well-being, and constitute the backbone of many rural economies. However, the industry faces challenges to profitability and sustainability that require rapid development and deployment of new cultivars. Thus, a key research priority is the translation of genomics science into breeding as a means to significantly enhance this process. A workshop was held at Michigan State University from June 22-24, 2007 to develop a strategy for the integration of genomics science and crop breeding in Rosaceae. Specific workshop goals were to:

- A. Bring together key researchers, breeders, industry representatives, educators, and extension personnel in rosaceous crop agriculture and research
- B. Identify current major barriers and specific problems of the Rosaceae breeding community that impede the utilization of genomics information in rosaceous crop breeding programs
- C. Develop strategies and identify specific infrastructure needs to directly address these major barriers and problems
- D. Identify specific research, breeding, and outreach educational programs capable of implementing these strategies
- E. Identify important research, breeding, and educational partnerships for implementation of workshop goals

Thirty-seven US and three international participants attended this workshop. Of these participants, nine were breeders of rosaceous species, six were growers and/or represented grower organizations, and twenty-one were scientists representing the disciplines of genomics, plant physiology, plant pathology, pomology, and extension.

Considerable discussion on identifying effective ways of working and communicating among various members of the community led to the identification of key issues that must be addressed, as well as, major barriers that must be overcome in order to facilitate crop improvement in Rosaceae. From lengthy discussion of the issues and the barriers, the following three items were identified as major impediments to the utilization of genomics information in rosaceous crop breeding programs: (1) The knowledge gap in our understanding of the genetics of many of economic traits of interest to breeding programs and those molecular markers that are in tight association with these traits for use in marker-assisted breeding, (2) A lack of robust genome-wide anchors for genetic information transfer between Rosaceae crops, and (3) An under-resourced and dwindling Rosaceae breeding infrastructure that is often unable to take advantage of new genomics discoveries. The following key steps were identified that can address these gaps:

- Development of trait-neutral family-wide markers for use in characterizing the genetic nature of economic traits in all breeding programs of Rosaceae crops.

- Germplasm characterization in each species, including the identification of closely linked markers to genes controlling traits of interest, trait phenotyping, and functional analysis of genes.
- Creating and strengthening breeding infrastructure by both new hires and team-building (teams of breeders, genomics researchers, and industry partners that will target crop-specific issues) coupled with education and extension.

Unlike other plant families where one or two globally important problems exist in the family, the key to this implementation plan is based on the premise that each crop has unique traits and problems that must be addressed through integrated genomics and breeding programs. We propose to address this by developing team partnerships consisting of specific crop breeders, research scientists, educators, industry representatives, extension agents, and trainees (young scientists) focused on the critical problem(s) for each major commodity crop. These teams would coordinate efforts to genetically characterize and tag important economic characters in existing germplasm and use this new information to improve the efficiency of Rosaceae breeding programs. This strategy integrates the diverse breeding targets in the different species through a common interface of core family wide genomics capabilities.

KEY OUTCOMES FROM GENERAL WORKSHOP DISCUSSION

Major issues and scope for a strategic plan for “science to the marketplace” in Rosaceae

This discussion with all workshop attendees was centered on defining the problem of how to promote science to the marketplace in Rosaceae. In order to proceed in defining strategies that will move genomics information forward into the marketplace, the group first defined the critical issues facing the industry, based on the crop-specific discussions held earlier in the workshop.

Industry central issue:

There is an industry-wide need for a continuous supply of improved scion varieties and rootstocks that address ever-emerging problems faced by Rosaceae species agriculture. Rosaceae crops face common challenges such as biotic and abiotic stresses, requirements for high fruit quality, and a high energy and labor cost of production. However, from a genetic standpoint, each crop also has unique problems associated with its production (unique pests, unique diseases, etc.). Thus, it was recognized that there is no family-wide research problem addressable by genomics, genetics, and breeding that can meet all needs of the Rosaceae industry.

Following considerable deliberations, the following were deemed as component problems of a Rosaceae-wide strategy for science to the marketplace:

- The knowledge gap in our understanding of the genetics of many of economic traits of interest to breeding programs and those molecular markers that are in tight association with these traits for use in marker-assisted breeding
- A lack of robust genome-wide anchors for genetic information transfer between Rosaceae crops
- An under-resourced and dwindling Rosaceae breeding infrastructure that is often unable to take advantage of new genomics discoveries

To address these component problems, the following were proposed as strategic goals:

1. Development of trait-neutral family-wide molecular markers for use in characterizing the genetic architecture of traits in breeding programs of all Rosaceae species
2. Germplasm characterization in each species
 - a. Identification of closely-linked markers to traits that are of importance to each crop, and achieved through pedigree genotyping (association genetics) together with traditional genetic crosses and mapping of molecular markers
 - b. Phenotyping of germplasm for characters of importance to breeding and industry
 - c. Functional analysis of Rosaceae genes controlling important characters
3. Building of breeding infrastructure

- a. Hiring of breeders (develop positions for breeders)
 - b. Building teams of breeders, genomics researchers, and industry partners that will target crop-specific issues
 - c. Strategic inclusion of young scientists in these teams to ensure the next generation of Rosaceae breeders are able to integrate modern genomics advances into improved cultivar development
4. Enhanced education activities in Rosaceae genomics, genetics, and breeding
 5. Enhanced extension activities in Rosaceae genomics, genetics, and breeding
 6. Address intellectual property issues

Strategic implementation plan: The way forward

Overall implementation plan

The following summary is an integration of the subcommittee reports on the specific nature of an implementation plan for Rosaceae “Science to the Marketplace”.

The plan should consider the following:

1. Some traits and issues are common across multiple Rosaceae crops, and each major crop also has unique requirements or problems that can be addressed through integrated genomics and breeding programs.
2. Although there is no one family-wide central biological problem addressable by genomics, genetics, and breeding that can satisfy all industry needs, there are family-wide technological problems. These problems include lack of:
 - a. Sufficient marker data (genotyping infrastructure) for many species/genomes
 - b. Standardized comprehensive phenotyping of important characters in the diverse germplasm of the family
 - c. Knowledge about the basic biology of many important traits within the species
 - d. Sufficient breeding infrastructure and educational programs to rapidly capitalize on the genetic and genomic discoveries
3. Individual team partnerships composed of specific crop breeders, research scientists, educators, industry representatives, extension agents, and trainees (young scientists) focused on critical problem(s) for each major commodity crop would be valuable. These teams would coordinate efforts to genetically characterize important characters, and use this new information to improve the efficiency of Rosaceae breeding programs and gain a better understanding of existing cultivars. There should also be coordination between teams across Rosaceae.

4. There are unique opportunities for Rosaceae to serve as the model system for studying certain fundamental biological questions, such as the unique genetic pathways underlying perennial fruit production.
5. Maintenance and expansion of core databases and informatics infrastructure (GDR) for the family is necessary, and these informational portals can be integrated with education and extension programs.
6. Rosaceae-wide education and extension programs as part of the broad infrastructure would greatly benefit the sustainability of genomics, genetics and breeding efforts in this family.
7. Intellectual property issues are increasingly important.

Key individuals, organizations, and linkages

1. Centralized genotyping capabilities for all species.
 - a. Integrate genotyping core facilities developed in other genomics programs from other families where possible.
 - b. Utilize specific worldwide expertise available in the family.
2. Teams developed for each representative genus and targeted at species relevant breeding goals.
3. Continued fostering of partnerships with non-US programs to promote cooperation on characterization, preservation, and enhancement of worldwide germplasm and scientific advancement of the rosaceous research community networks.
4. GDR maintenance and expanded functionalities.

Funding strategies and directions

1. Individual coordinated teams have strengths for success with federal funding agencies.
2. Matching investment from industry for team programs.
3. Submission of a Coordinated Agricultural Project for Rosaceae spearheaded by the RosEXEC committee.
4. State support.
5. International cooperative funding opportunities.

WORKSHOP OBJECTIVES, AGENDA AND SCHEDULE

This workshop addresses the economic opportunities for agricultural producers via development of a roadmap for integration of genomics science and crop breeding in Rosaceae agriculture.

Rosaceae fruits are vital to human nutrition and constitute the backbone of many rural economies. However, the industry faces challenges to profitability and sustainability that require rapid development and deployment of new cultivars. Thus, a key priority is the translation of genomics science into breeding as a means to significantly enhance this process. The community is united in advancing this priority through initiatives such as a Rosaceae CAP project but a workshop of stakeholders is required to develop a proposal framework that focuses on the critical integrative pathway to address issues of “science to the marketplace” for rosaceous crops.

Workshop Goals

- A. Bring together key researchers, breeders, industry representatives, educators and extension personnel in Rosaceae crop agriculture and research
- B. Identify the major barriers and specific problems of the Rosaceae breeding community that impede the utilization of genomics information in rosaceous crop breeding programs
- C. Develop strategies and identify specific infrastructure needs to directly address these major barriers and problems
- D. Identify the specific research, breeding and outreach educational programs capable of implementing these strategies
- E. Identify important research, breeding and educational partnerships for implementation of workshop goals

Agenda

Friday, June 22

Morning session facilitator: Bert Abbott

9:00-9:45 AM

Welcome and Overview - Bert Abbott

Participant self-introductions (organization, location, skill set in research, education and /or extension)

Workshop objectives and structure

9:45-10:15 AM

RosEXEC - Kevin Folta

National and international members; Mission and objectives; US White Paper; International White Paper

10:15-10:45 AM

Break

10:45-11:15 AM

Status and Discussion of GDR - Dorrie Main

11:15-11:45 AM

USDA-CSREES Plant Breeding Coordinating Committee (PBCC) - Jim Hancock
Overview of PBCC; Specific issues for Rosaceous crops

11:45 – 1:00 PM

Lunch – provided in adjoining break room

Afternoon session facilitators: Amy Iezzoni and Kevin Folta

1:00-2:30 PM

Key issues in crop production, processing and breeding (*5-10 mins each*)

Peach, nectarine, plum, apricot - Tom Gradziel

Almond - Abhaya Dandekar

Cherry - Amy Iezzoni

Apple, pear - Genarro Fazio, Susan Brown

Strawberry - Phil Stewart

Rose - Stan Hokanson

Raspberry, blackberry - Dan Sargent

2:30 -4:30 PM

Breakout working groups addressing crop-specific key issues with genomics

Breakout group 1: *Malus, Pyrus*

Breakout group 2: *Prunus*

Breakout group 3: *Fragaria, Rosa, Rubus*

Outcomes:

Description of key issues

Highlighted priorities to address issues

4:30-6:00 PM

Breakout working groups: Key issues in application of genomics to breeding

Identification and discussion of major barriers in research, breeding, education and extension

Breakout group 1: *Malus, Pyrus*

Breakout group 2: *Prunus*

Breakout group 3: *Fragaria, Rosa, Rubus*

Outcomes:

- Description of key issues
- Highlighted priorities to address issues

Friday Evening: 7:30 Dinner – Horticulture Gardens

Saturday, June 23

Morning facilitator: Bert Abbott

8:00-9:00 AM

Working group reports

Issues discussed and summaries for each breakout group presented by breakout group facilitators

9:00-9:45 AM

Perspectives on CAP programs, Solanaceae - David Douches, Michigan State University

Overall CAP objectives, Key issues in proposal development and management

9:45-10:00 AM

Break

10:00-11:00 AM

Identify major issues and scope for a strategic plan for “science to the marketplace” in Rosaceae

11:00-12:00 AM

Implementation of strategic plan and breakout group development

- Determine components for implementation of the strategic plan

- Assign participants

- Preliminary implementation plan breakout groups choose leader and reporter

12:00- 3:00 PM

Breakout groups meet over lunch

Breakout working groups divided into implementation plan areas

Develop bullet point structure and working outline for each area

- Genomics and Informatics
- Breeding, Industry, and Education
- Genetics and Germplasm

3:00-4:00 PM

Afternoon Facilitators: Amy Iezzoni and Kevin Folta

Integration of bullet points and working outline for each area into overall plan skeleton

- Reports of breakout groups with group discussion after each

- Amend bullet points and working outline as required

4:00-5:00 PM

The way forward

Discuss overall implementation plan

Identify key individuals, organizations, and linkages

Discuss funding strategies and directions

5:00-5:30 PM

Wrap-up and appreciation

Workshop deliverables:

1) We will develop a final workshop report to summarize the outcomes of the discussions and to serve as a publicly available framework for future efforts by the Rosaceae crop community to enhance research, education, and extension in genomics, genetics and plant breeding. This workshop report will be circulated to the participants of the workshop and showcased online in the Genome Database for Rosaceae (www.rosaceae.org) for general public access. 2) A strategic plan for development of “science to the marketplace” for Rosaceous crops to guide individual future funding efforts in the community. 3) A community framework for a CAP in Rosaceae that can be translated into proposals to relevant agencies.

Workshop coordinators:

Amy Iezzoni, Michigan State University

Albert Abbott, Clemson University

Kevin Folta, University of Florida

Workshop steering committee:

Tom Davis, University of New Hampshire

Sue Gardiner, HortResearch, New Zealand

Renea Hardwick, Clemson University

Schuyler Korban, University of Illinois

Dorrie Main, Washington State University

Jim McFerson, Washington Tree Fruit Research Commission

Cameron Peace, Washington State University

Ralph Scorza, USDA Appalachian Fruit Research Station

PARTICIPANT LIST

Rosaceae Specialty Crops Planning Workshop

Michigan State University, East Lansing, MI

June 22-23, 2007

APPENDIX I

SUMMARIES FROM WORKSHOP DISCUSSIONS

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Key issues in crop production, processing, and breeding in Rosaceae - Reports

Prunus

Peach, Nectarine, Plum and Apricot Breeding

Presented by Tom Gradziel, UC Davis

- 1) Relevance
 - a) These crops are very important economically at the National, State, and community level.
 - b) These crops are widely and relatively uniformly distributed throughout the United States; crop improvement would benefit an extensive spectrum of producers and consumers.
 - c) A long history of genetic and breeding efforts with these crops has established an extensive knowledge base for continued genomic progress.

- 2) Critical Needs. Needs are extensive and in many cases urgent. They are organized here into three major foci.
 - a) Ecological sustainability. Genetic resistance to a number of serious diseases and pests is needed to reduce the use of ecologically damaging agrochemicals, as replacements for lost fungicides and pesticides, to reduce consumer exposure to agrochemicals and natural food-borne toxins, and to provide stable plant communities for ecological stabilization (wildlife habitat, etc.) and remediation (carbons sequestering, etc.).
 - b) National competitiveness. Production costs need to be reduced without losses in food quality. Genetic solutions are urgently needed in the areas of mechanical harvesting (including the control of fruit ripening), the modification of tree size and architecture, and the reduction of agrochemical inputs.
 - c) Consumer value. The frequent and varied consumption of fruits and nuts is now recognized as a major contributor to consumer health. Fruit phytonutrient content needs to be optimized while at the same time maximizing fruit sensory qualities to encourage frequent consumption. Negative contributions associated with food-borne toxins and/or secondary plant compounds need to be characterized and minimized. Finally, the improved phytonutrient/sensory/food safety qualities needed to be managed to optimize value and product consistency to the consumer.
 - i) [A classic example of the importance and urgency of these needs maybe the continuing spread of the Sharka or Plum pox virus in North America. This virus has decimated stone fruit production in Eastern Europe with dramatic losses in economic profitability, orchard sustainability, and availability of quality, fresh fruit to local communities. It's incidence is now global, and while quarantine restrictions have slowed its entrance into North American production areas, the only known control is genetic resistance. No commercial stone fruit cultivars have resistance and usable sources of resistance for breeding are very limited. Resistance has been identified in the closely related almond species that appears to be transferable to stone fruit. The genetic mechanisms and heritability are still poorly understood, however.]

- 3) Foundation for Genomic Research.
 - a) Peach and nectarine have a very small genome size making them very amenable for genomic research. The stone fruits have a well established foundation of genetic

information including genetic maps, a wide array of useful markers, and well established sequence databases, etc.

- b) Because of the global importance of these crops, an extensive network of research collaborations have been established at the national and international level.
- c) Because of the long history of genetic and breeding efforts with these crops, there is already established an extensive genetic knowledge base for continued genomic advancement.

The epigenetic paradigm. The importance of still poorly understood epigenetic mechanisms for determining final genetic expression has become a major obstacle to the full utilization of genomic research at the plant and animal (including human) level. While epigenetic variants in seed propagated crops would be quickly be rogued-out to ensure cultivar uniformity, their presence in vegetatively propagated crops such as the stone fruit has been more tolerated resulting in a small but established knowledge base concerning their activity and in some cases, manipulation (for example Noninfectious Bud-failure in almond). Thus, the stone fruits represent a unique opportunity not only to advance our basic understanding of this very important mechanism controlling plant and animal development, but may represent a powerful and novel breeding tool for the manipulation and capture (through clonal propagation) of useful epigenetic variants.

Almond

Presented by Abhaya Dandekar, UC Davis

Almond: *Prunus dulcis* is a member of the genus *Prunus* in the *Rosaceae* family. In the United States almond production is over a billion lbs/yr, mainly in California where the crop is grown on 615,000 bearing acres and 730,000 total acres valued at \$2.34 billion which is 7.4% of total farm gate value which is currently \$31.7 billion. The value increased from 2000 to 2005.

Almonds are #4 below Milk& Cream (\$5.2 bil), grapes (\$3.2 bil) and Nursery and greenhouse products (\$2.4 bil). It is the #1 export crop valued at \$1.8 bil with a 34% increase during 2004-2005.

Almond Breeding Strategies and vision:

The Almond breeding program at UC Davis is one of the oldest and most effective programs in the world. Currently being directed by Tom Gradziel and previously by the late Dale Kester whom many of you have had the pleasure of meeting.

Traits of interest:

Yield: high kernel yield, less tendency towards alternative bearing, early bearing.

Self-fertility: eliminate self-incompatibility, reduce/eliminate need for bee pollinators, single cultivar orchards.

Late blooming: to avoid spring frost

Resistance to disease and pests: Navel orangeworm, almond bud failure (unknown etiology).

Heat stress tolerance: Reduce/eliminate heat stress and death of vegetative buds

Quality and Safety: Flavor, oil content and composition, antioxidants (vitE and condensed tannins), Aflatoxin contamination, *Salmonella/E.coli* contamination, Acrylamide formation. Improve phytoprotection of seed coat.

Genome Resources and Technology Development for Almond:

Currently nonexistent with only 4200 entries in GenBank. Need physical map to expand genetic mapping resource available in peach-almond mapping populations. Unlike peach, almond has a broad and wild germplasm, because of obligate outcrossing habit is an excellent candidate for association mapping and thus SNP discovery. A small genome, excellent candidate for Genome sequencing. Self-incompatibility locus has been mapped and can be very interesting to characterize genetically especially pollen component that was first discovered in almond. Dissecting the fruit genome of almond would provide valuable insight of both flesh and seed traits that could enable seedling based selection strategies for fruit traits. No efficient *Agrobacterium*-mediated plant transformation for trait introduction or viral-based systems for incorporation/modification of traits in existing trees.

***Prunus* Rootstocks**

Presented by Abhaya Dandekar, UC Davis

Prunus Rootstock Breeding and Selection Strategies:

Almond is a source of stress resistance due to root architecture, peach is resistant to nematodes and plum to fungal disease (oak root and *Phytophthora*) and waterlogging. Hybrid rootstocks combine these traits. The peach-almond hybrid rootstocks such as Hanson are very popular as they promote vigor and early production. Other popular rootstocks are Nemaguard (peach), Lovell (peach) and Mariana2624 (plum).

Vigor: rapid growth and productivity of scion

Pest resistance: Nematode resistance, counter loss of effective soil fumigants.

Disease resistance: crown gall, fungal and replant decline disease, counter loss of effective soil fumigants.

Stress tolerance: Water use efficiency, drought and salinity resistance

Genome Resources and Technology Development for *Prunus* Rootstock:

Currently nonexistent for plum and only 71,000 entries for peach in GenBank. GMO rootstocks are an excellent low profile entry point for technology in *Prunus*. Need to improve the efficiency of transformation *Agrobacterium* and viral methods to enable pyramiding of disease and pest resistance. Dissecting the vigor enhancing trait in Hanson would provide valuable insight of root traits that influence scion and to investigate rootstock-scion interactions.

Almond – Further Perspectives

Presented by Bob Curtis, Senior Manager, Production Research, Almond Board of California

Almond-Peach: Rootstock disease and nematode resistance

- Workshop priority: Counter loss of effective soil fumigants

- In California because of volatile organic constituents (VOCs), this extends to all fumigants -- not just methyl bromide
- Expand beyond current disease resistances to those elucidated as part of the replant complex
- For nematodes, include current array of species of concern

Almond-Peach: An array of flower and foliar disease resistances

- Workshop priority: Reduce chemical pesticide usage
- Needed at bloom time and later in season (and post harvest in peaches)
- Particularly important in light of a number of diseases developing resistance to a number of newer fungicides with single site mode of action

Almond: Further elucidate the genetic basis for self compatibility / incompatibility

- Workshop priority: Reduce cost of production / variability of production
- Especially needed for the “pollen” component and chemical communication between female and male components
- Needed to reduce pollination requirement by bees.

Almond: Resistance mechanisms to navel orangeworm, Aspergillus and aflatoxin, and microbial pathogens

- Workshop priority: Improve quality and safety
- Basis for endocarp shell seal for reduced insect, fungal, and microbial invasion
- Phytochemical protection provided by seedcoat
- Seedcoat phytochemicals are also a positive attribute for consumer nutrition

Almond: Genetic control of bud failure (Epigenetic expression)

- Workshop priority: Develop (heat) stress tolerant plants
- Reduce / eliminate heat stress death of vegetative buds

Cherry

Presented by Amy Iezzoni, MSU

Marketing

Quality traits:

- Firmness**
- Increased size**
- Improved flavor**
- Nutraceutical content (Ex. Red vs. non-red)
- Not prone to doubling
- Rain cracking resistance

Post-harvest/processing quality traits:

- Freestone**

- Not prone to the skin defect called “pitting”

Crop Protection

Diseases:

- cherry leaf spot **
- powdery mildew **
- brown rot
- *Armillaria* root rot

Insects:

- cherry fruit fly
- plum curculio

Other Profitability Issues

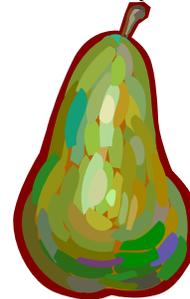
- High density precocious production (rootstocks)**
- Floral freeze tolerance
- Winter hardiness**

** Genetic diversity has been identified, and is in various stages of being characterized. The identification of markers linked to QTL controlling these traits is either underway or could be initiated.

Malus and Pyrus

Presented by Gennaro Fazio, Cornell University, Geneva, New York

There are some unique attributes in apple and pear that are common with other species in the Rosaceae and then some that set them apart. Some of these attributes are: climacteric ripening and response to ethylene, perennial nature, dormancy, rootstock/scion interactions, self incompatibility systems, allergens, antioxidants, disease resistance. These attributes should unify our efforts as a family. Can we develop research that will integrate disciplines (Breeding, Physiology, Genomics, Pathology, Engineering) and deliver a superior product that will attract the consumer and be produced in a sustainable way? How can we develop specific knowledge that will make a tangible impact on the consumer and the production industry?



BREEDING

Marker-Trait associations are needed spanning breeding populations especially for traits that are difficult to measure quantitatively.

Reliable phenotyping methods for traits with high GxE

Lack of streamlined methods for Marker Assisted Selection

Establishing juvenile adult correlations

Intellectual Property Issues

High cost maintaining populations

Need to assess trueness to type for resistance, etc.

Low funding

CROP PRODUCTION

Labor and energy saving technologies

Uniformity in size distribution and quality traits

Biennial bearing

Fruit set and crop regulation

Environmentally friendly crop protection systems

Adaptation to different sites (GXE)

More efficient rootstocks

Risk reduction practices

Industry access to new varieties and rootstocks

PROCESSING and DELIVERY

Uniformity in organoleptic quality

Postharvest quality retention

Polyphenol oxidase activity

Antioxidants

Labor friendly harvest and handling systems

Food safety

Storage systems and treatments

Precision inventory management

Maintenance of superior quality during shipping, delivery and sale



BREEDING TRAITS

BREEDING

Marker-Trait associations are needed spanning breeding populations especially for traits that are difficult to measure quantitatively.

Reliable phenotyping methods for traits with high GxE

Lack of streamlined methods for Marker Assisted Selection

No pear rootstock breeding program

Few breeding programs

Low funding

CROP PRODUCTION

Labor and energy saving technologies

Uniformity in size distribution and quality traits

Juvenility

Environmentally friendly crop protection systems

Adaptation to different sites (GXE)

Dwarfing precocious rootstocks

PROCESSING and DELIVERY

Uniformity in organoleptic quality

Postharvest quality retention

Labor friendly harvest and handling systems

Food safety

Storage systems and treatments

Precision inventory management

Maintenance of superior quality during shipping, delivery and sale



BREEDING TRAITS

Precocity	Precocity – severe lack of precocious genotypes
Compatibility with rootstocks	Dwarfing
Tree shape and growth habit	
Spur habit	
Branch angles (Rootstock and Scion)	
Compactness	
Abiotic stress resistance (Rootstock and Scion)	Abiotic stress resistance (Rootstock and Scion)
Cold hardiness, heat tolerance, drought tolerance	Cold hardiness, heat tolerance, drought tolerance
Clonal propagation (Rootstock)	Clonal propagation (Rootstock)
Burr knots (Scion and Rootstock)	
Biotic Stress Resistance	Biotic Stress Resistance
Fire blight, Powdery mildew, Apple Scab, Rosy apple aphid, Woolly apple aphid, 2-spotted mites, Apple maggot, Oriental fruit moth, Plum curculio, Lepidopteran feeders, Soil replant disease, crown rot (phytophthora spp.),	Fire Blight, Pear Scab, Powdery mildew, <i>Fabraea</i> leaf and fruit spot, Pear Psylla, blue mold (<i>Penicillium expansum</i>), gray mold (<i>Botrytis cinerea</i>), <i>Coprinus</i> spp., Mucor rot (<i>Mucor piriformis</i>), side rot (<i>Phialophora malicortidis</i>), bot rot (<i>Botryosphaeria obtusa</i>), black rot (<i>Glomerella cingulata</i>), brown rot (<i>Monilinia</i> sp.), and sprinkler rot (<i>Phytophthora cactorum</i>).
Flowering, Bud Break and Bloom timing (Scion and Rootstock)	
Self fruitfulness/incompatibility	
Easy to thin, Self thinning (king fruit set)	Easy to thin, Self thinning (king fruit set)
Productivity	Productivity
Fruit ripening – timing consistency	Fruit ripening – timing consistency
Fruit abscission – avoid premature, ease of picking	Fruit abscission – avoid premature, ease of picking
Fruit shape, uniformity	Fruit shape, uniformity
Fruit bloom, skin overcolor	
Fruit skin ground color (skin anthocyanins, carotenoids)	Fruit skin ground color (skin anthocyanins, carotenoids)
Fruit skin wax	
Fruit skin thickness	
Fruit russet type – russet location / intensity	
Fruit skin defects	
Fruit flesh color, texture, firmness, hardness, softness, mealiness, crispness, juiciness.	
Fruit flesh oxidation, Poly-phenol oxidase	
Fruit acidity (malic acid), sugar balance	
Fruit aroma (volatile esters)	
Fruit sweetness (brix, sugar content and composition)	Fruit sweetness (brix, sugar content and composition)
Fruit starch composition	
Fruit phytonutrients (antioxidants, fiber, vit. C)	
Fruit storability (duration, interaction with MCP and other storage practices)	Fruit storability (duration, interaction with MCP and other storage practices)
Shelf life and tolerance to handling	Shelf life and tolerance to handling
Fruit defects – internal browning, bitter pit, scald, water core, stem end cracking, open calyx, surface roughness.	Fruit defects – internal browning, bitter pit, scald, water core, stem end cracking, open calyx, surface roughness.
Rootstock dwarfing, precocity, nutrition	

Rootstock suckering

The above tables are a compilation of contributions from Stuart Tustin, Paul Brookfield, Richard Bell, Susan Brown and Jim McFerson.

Rubus

Presented by Dan Sargent, East Malling UK

Mirror those issues of the Rosaceae community as a whole, with specific issues relating to disease and pest tolerance.

Raspberry

Breeding goals:

- Increased yield
- Plant habit/architecture – presentation of fruit/plantation management
- Season - primocane and floricanes fruiting
- Thornless and thorny
- Adaptation to climate
- Fruit colour: **Red**/Black/Amber/Purple
- Field and tunnel production systems
- Increased nutritional value (not a high priority in Europe)
- Adaptation to climate

Uses of fruit:

- Processing and dessert fruit production

Important pests and diseases:

- Cane blights and other fungal diseases - Verticillium wilt/Powdery mildew/Botrytis/Phytophthora root rot
- Aphid viral vectors – *Amphorophora idae* and *Aphis idae*
- RBDV and other viruses
- Nematodes
- Mites/Thrips/Orange rust/Leaf hoppers (more localised importance)

Other major breeding goals:

- Plant architecture
- Colour post harvest
- Season extension
- Post-harvest fruit quality

Blackberry

Breeding goals:

- Increased yield
- Plant habit/architecture
- Primocane and floricanes fruiting
- Thornless and thorny
- Adaptation to climate

Uses of fruit:

- Processing and dessert fruit production

Important pests and diseases:

- Cane blights and other fungal pathogens - Downy mildew/Anthracnose/Botrytis
- Aphid viral vectors
- RBDV
- Double-blossom/Orange rust/Nematodes/Thrips/White fly

Major environmental stresses:

- UV damage
- Winter root damage
- Low chilling requirement

Other major breeding goals:

- Plant architecture
- Colour post harvest
- Season extension
- Tunnel production
- Post-harvest fruit quality

Foci for future *Rubus* research

Economic sustainability – yield/season extension/fruit quality (both in terms of perception/taste and health benefits [minor]).

Pest and disease resistance in germplasm

Adaptation to climate change:

- Reduced winter chilling
- Waste reduction (increased shelf-life etc.)
- Water usage

Specific goalsBlack and Red raspberry

Yield

Virus tolerance

Remontancy

Thornless

Powdery mildew resistance(for protected cultivation)

Mechanical harvesting (especially for processing)
Heat tolerance (Red raspberry)

Blackberry

Cold tolerance
Frost avoidance
Thornlessness
Remontancy
Orange rust

Climate change may impact on blackberry and raspberry but to a lesser extent than in other fruits

Current genetics and genomics research activities

Marker development

- Main thrust has been at SCRI, UK with lesser inputs from groups in USA and other European countries. Main focus has been on Microsatellite (SSR) development.

Mapping

- First and most comprehensive mapping studies carried out by Graham et al (SCRI, UK). Comprehensive reference map produced of wide intraspecific cross (Latham × Glen Moy) with adequate coverage of nearly all linkage groups. SSRs mapped to all linkage groups in at least one parent.
- Subsequent smaller studies carried out by other groups – Sargent (EMR, UK) published study of mapping of Aphid resistance locus in intraspecific cross (Jewel × Orion).

BAC library construction and physical mapping

- High molecular weight BAC library of *Rubus idaeus* cultivar produced and arrayed at SCRI, UK (Hein et al).
- Subsequent characterisation of *Rubus* BAC library to be carried out at Clemson University, USA by Abbott lab and CUGI.

Biotechnology

- DefH9-iaaM gene fusion in *Rubus idaeus* by Mezzetti et al (Ancona, Italia) promoting increase in number of flowers per inflorescence, number of inflorescences per plant, number of fruits per plant and weight and size of transgenic fruits. Increase in fruit yield was approximately 100% non-GM standard.
- Studies of *Rubus* ripening genes by Kumar et al (University of British Columbia, Canada)

Other relevant information

Raspberries are diploid and the blackberries are tetraploid (and partly tetrasomic but not completely)

Both are highly heterozygous

Maps of tetrasomes won't be as representative of other populations as a diploid map is to other diploid populations.

Rosa

Presented by Stan C. Hokanson , University of Minnesota

Rose and ornamentals

1. Temperate rosaceous landscape plants

Trees - *Amelanchier*, *Crataegus*, *Malus*, *Prunus*, *Sorbus*

Shrubs - *Rosa*, *Spiraea*, *Kerria*, *Aronia*, *Exochorda*, *Chaenomeles*, *Cotoneaster*,
Prinsepia, *Stephanandra*, *Physocarpus*, *Potentilla*, *Sorbaria*

2. Rose (economics)

Most famous landscape plant, most economically important landscape plant. In 2003 8 billion cut stems, 80 million potted plants, 220 million landscape plants worldwide. In 2005, U.S. cut stems worth \$40 million, approximately \$277 million in landscape roses.

3. Rose (biology)

Approximately 200 species recognized. Native from 20-70° N latitude. Basically, seven species utilized in breeding cultivars. Over 10,000 registered hybrid tea roses (this is one of 35 classes of rose). Roses range from diploid $2n = 2x = 14$ to octoploid $2n = 8x = 56$. Most species are diploid, while most cultivars are tetraploid.

4. Rose breeding

Largely carried out in the private sector. There are three large nurseries that support breeding programs, Weeks, Jackson and Perkins, and Bailey Nurseries. Conard/Pyle has an exclusive marketing arrangement with House of Mailland and Bill Radler. Many cultivars are developed by amateur/hobbyists and then picked up by nurseries. Two public breeding programs currently exist in N.A. one at Texas A&M, one at the University of Minnesota.

5. Breeding goals (differ regionally)

Disease resistance (blackspot, powdery mildew, botrytis, leaf spot, downy mildew, rust, spot anthracnose, crown gall, virus, nematodes)

Cold hardiness, heat tolerance

Repeat bloom

Flower color

Increased petal counts

Thornlessness

5. Rose trait inheritance

Blackspot resistance – Dominant qualitative and quantitative reported

Double flowers – Dominant qualitative w/ quantitative additive for petal count reported

Flower color – Quantitative additive reported

Miniature stature – Dominant qualitative reported

Repeat bloom – Recessive qualitative reported

Thorns – Dominant qualitative (stem), quantitative additive (rachis)

Winter hardiness – Quantitative additive

6. Disease resistance breeding/genetics

Blackspot – most important worldwide. Selections generally made in the field with naturally occurring inoculum. Thomas Debener's group (Univ. of Hannover, Germany) first to describe a resistance gene for blackspot *Rdr1*, a major race-specific gene. *Rdr2* is now described. Components of partial resistance have been described. No QTLs for blackspot resistance have been described. Our group (University of Minnesota) have evidence for the existence of race specific partial resistance. Four races of blackspot have been reported for eastern N.A., 6 from Germany, and 3 from England.

Powdery mildew – Most important greenhouse (cutflower) disease for rose. A dominant, race-specific gene *Rpp1* has been reported. Thirty powdery mildew QTLs have been described.

7. Markers and mapping

SCAR markers linked to *Rdr1* and *Rpp1* have been developed. They are not linked. Several maps are in existence, the most advanced being Yan et al., 2005. Created in a diploid population, contains 520 markers including 320 AFLPs, 24 protein kinase, 74 SSR, and 51 RGA markers. The RGAs were found on linkage groups 1,2,4,5, and 7 with some clustering of RGAs noted.

8. Candidate gene approaches

Resistance gene analog primers have been used for tagging and mapping powdery mildew resistance. The Debener group in Germany recently completed an RGA survey. They screened cDNA and genomic DNA with 7 degenerate primers developed from RGAs. They identified 40 families (based on 80% sequence homology). One linkage group contained 37 RGAs. Debener's group is currently doing some expression work with the RGAs.

9. In Minnesota

We have identified 4 races in eastern N.A.

Have obtained 6 races from Germany and will be getting 4 from England.

Developing a composite array (based on Germany, England, Minnesota race ID studies) to standardize the race characterization situation.

Have created populations that are segregating for three of the eastern N.A. races of blackspot (diploid and tetraploid).

Evaluating race specific partial resistance in the populations for inheritance and combining ability.

Used NBS-profiling to isolate 1,000 RGAs from two race resistance characterized rose parents. Seventy-five of these have been sequenced, aligned, and Blasted.

Identified 8 new families

Many top Blast hits were to strawberry and prunus rather than rose

Fragaria

Presented by Philip Stewart, Driscoll's Strawberries

Fruit Quality

Fruit quality in strawberry, as in most fruit crops, is a complex trait that is difficult to quantify or select for in a methodical way. Still, “quality” can be broken down into a number of aspects, though the definition varies between fresh and processing berries:

Fresh Market

- Flavor (sugars, acids, aromatics)
- Appearance (shape, color, gloss)
- Shippability (firmness, resistance to bruising, resistance to puncture)
- Shelf-life (ability to maintain eating quality, including resistance to storage pathogens)

Processing

- Aromatic profile
- Sugars
- Acid level
- Piece integrity
- Ability to maintain stable color
- Uniformity

Reduce Chemical Pesticide Use

The impending loss of methyl bromide as a soil fumigant presents a major challenge for many strawberry growers, and as a result many growing regions may begin to face disease and pest threats that have not in the past been major issues. In most breeding programs, resistance to most or all these diseases has historically been addressed largely after selection has been made for horticultural characteristics, but in some case focused breeding efforts have been directed at specific diseases, including the development of molecular markers for resistance.

Threats affected by loss methyl bromide:

- Verticillium wilt (*Verticillium dahliae*)
- Black root rot (various species)
- Red stele (*Phytophthora fragariae*)
- Crown and root rot (*Phytophthora cactorum*)
- Nematodes and nematode-borne viruses
- Other soil-borne pests and diseases

Other important pest and disease problems:

- Strawberry anthracnose (*Colletotricum acutatum*)
- Crown rot (*Colletotrichum gleosporioides* & *C. fragariae*)
- Grey mold (*Botrytis cinerea*)
- Powdery mildew (*Sphaerotheca macularis*)
- Angular leaf spot (*Xanthomonas fragariae*)
- Two-spotted spider mites (*Tetranychus urticae*)
- Tarnished plant bugs (*Lygus lineolaris*)

Decreasing Costs of Production

One of the most important ways to decrease production cost (in terms of costs per volume) for most growers would be to increase yield. Yields in processing strawberries, in particular, have remained relatively stagnant for many years.

Additionally, labor is in short supply in most major strawberry producing areas, and labor costs are substantial component of production costs.

Characteristics which help to maximize available labor:

- Large fruit
- Uniform fruit shape and size
- Compact plants with exposed fruit
- Even production curve
- Adaptation to mechanical harvesting (processing berries)
- Readily capped (processing berries)

Timing and Controlling the Developmental Cycle

Because of the nature of the plant and the systems used to grow it, strawberry is unusually amenable to manipulations to control the timing of its development, allowing producers to time production for to capitalize on ideal market windows, and to promote vegetative growth in nursery setting as well. An understanding of the factors involved in regulating development might allow growers to do these things more effectively. Only photoperiodic sensitivity, in terms of the everbearing or day-neutral characters, has had much breeding effort directed specifically towards it.

Aspects include:

- Photoperiod sensitivity
- Chilling requirement
- Heat sensitivity

Crop-specific key issues with genomics and application of genomics to breeding – Breakout group summaries

Prunus

Participants: Bert Abbott, Angela Baldo, Bob Curtis, Abhaya Dandekar, Chris Dardick, Tom Gradziel, Bob Gregory, Renea Hardwick, Amy Iezzoni, Cameron Peace, Greg Reighard, Bryon Sosinski, Gary van Sickle

Crops: peach almond, apricot, plum, sweet cherry, tart cherry, *Prunus* rootstocks

Crop-specific key issues with genomics

Various traits of importance to *Prunus* crops (traits that currently limit production or are otherwise of value) were considered under the categories of the Key Issues of the US White Paper. General considerations were value of the trait/problem, existence of useful diversity, heritability and ease of trait measurement, and how general the underlying genetics might be across *Prunus*.

- Fruit & nut quality
 - Quality covers many traits, which are described in the White Paper (sensory quality – appearance, texture, flavor; nutritional quality; processing quality)
 - A table listing important quality traits was begun but not completed – could eventually form the basis of the updated Crop Reports for the next version of the White Paper.

<i>Crop</i>	<i>Desirable quality traits</i>	<i>What happens to grower/consumer if market standards aren't met</i>
Cherry	Size pricing factor for sweet cherry min size, and larger for niche? Color Firmness Pitting ease Not splitting (associated with softness)	downgraded = lower return to growers
Peach (fresh)	Size (but have reached max)	
Peach (processing)	Size range	

- As described in the White Paper, we're interested in improvement *and* maintenance of these attributes until fruit reaches consumers
- Marketable nutritional improvements
 - phenolics?
 - germplasm surveys & metabolic profiling?
- However, fruit (incl *Prunus*) already nutritious, just need to get people to buy/eat more
- Market distinction of superior products
- Minimum quality standards for consumer to recognize?
 - beyond “minimum” - differentiated for consumer
 - includes marketing management

- but begins with breeding of a variety with distinct quality
- As *Prunus* fruit are perishable, need cultivars representing such improved/differentiated quality that stretch across the whole season – a cultivar series
- For all traits, need germplasm surveys to understand the available phenotypic and genetic diversity
 - Survey cultivars, wild / undomesticated trees, breeding selections and populations, experimental populations
 - How to survey the phenotypic / genetic diversity for each trait? Need standardized methods
 - Assess US germplasm, then beyond
- Pest & disease resistance
 - Overall: lots of pests and diseases, some of which may have transferable genetics for resistance across *Prunus* (e.g. plum pox), but few are likely to be transferable, and therefore most pests and diseases in *Prunus* are crop-specific. Some pests and diseases have resistance sources somewhere in *Prunus*, while others have no known resistance source
 - Available diverse germplasm
 - survey for resistance sources to be used as breeding parents
 - Pyramiding for durable resistance
 - Scion diseases
 - powdery mildew
 - not clear if it's transferable
 - peach, nectarine, apricot?, plums, cherries (mostly sweet in Northwest, young tart in MI)
 - almond might be a source of resistance
 - not a problem in moist climates such as Southeast except in greenhouse
 - Plum Pox (Sharka)
 - increasing evidence that it's transferable
 - affects all *Prunus*
 - *Xanthomonas* bacterial spot
 - plum, nectarine peach, , apricot
 - resistance is available in some peach cvs
 - possibly transferable for pathovar that infects all 4
 - more a problem in moist areas
 - one antibiotic is left (otherwise controlled with spraying copper)
 - brown rot / hole rot
 - gradations of susceptibility in almonds
 - extreme problem in southeastern US, Canada & South America
 - infects pretty much all *Prunus*
 - resistance in European species
 - spraying options for control
 - *Alternaria* leaf spot
 - almond, sweet cherry
 - no identified source of resistance, just differences in susceptibility
 - controlled with spray, but options running out

- Cherry leaf spot
 - Cherry scion and rootstock species. Also pest on plum. Causal agent: *Blumeriella jaapii*
 - scab
 - Rootstock diseases, or controlled by rootstock
 - *Armillaria* root rot
 - many genera (most woody plants, kills whole tree)
 - an orchid has resistance
 - not readily controlled – poss. trichoderma
 - crown gall
 - resistance in Spanish material
 - *Pseudomonas*
 - infects scion mostly, but rootstock confers resistance
 - ring nematode feeding increases infection
 - Pests
 - many pests affect *Prunus* crops (no time to list them all)
 - genetic resistance available for some pests
 - greater peach tree borer
 - root knot nematodes
 - aphids
 - very little resistance to anything else
 - generally controlled with sprays
- Reduced energy/cost input for production
 - Tree architecture – overall, there is much diversity in *Prunus*, but interaction with other traits, and rootstocks appear to be the simplest way of managing tree architecture although there is little systematic *Prunus* rootstock breeding in the US
 - compact, weeping – single gene traits or a couple of genes
 - pillar & upright (peach)
 - lots of extra work to keep quality up
 - requires more research
 - rootstocks “simplest” way to control size
 - working well – making good progress
 - Pollination / self incompatibility – overall, a major issue in many *Prunus* (and other Rosaceae) crops that limits production. Useful target for immediate gain - genes are known
 - almond, apricot, plum, sweet cherry, tart cherry
 - same locus across *Prunus* (genes known)
- Abiotic stress resistance (expand growing regions, better performance under existing conditions)
 - Often difficult to screen for resistance/tolerance
 - Juvenility is huge issue in *Prunus*
 - sources of precocity available
 - not a problem in peach, nectarine, Japanese plum – these crops already produce fruit as soon as is desirable (source of precocity for other *Prunus*?)

- genes under study – possible transgenic solutions
- Perennial plants suffer stresses and aging over many years
 - bud failure in almond (epigenetic, aging-related) – would like to understand the heritable component, activity of genes
- Salt tolerance
- Waterlogging resistance
- Drought resistance
 - almond, apricot tolerant
 - other *Prunus* not tolerant
 - often controlled somewhat with peach/almond hybrid rootstocks
- Cold tolerance
 - floral freeze
 - genetic difference in pistil resistance in peach, almond, cherry
 - flower physiology/anatomy
 - sorbitol?
 - flowering time also involved – delayed bloom to avoid frosts
 - fruit freeze
 - has to do with size of fruit – bigger, earlier peaches survived freeze better at the small, green stage
 - tree kill
 - trunks cracking
 - viroid controlled membrane porosity, and conferred some resistance
- Heat tolerance (PSII activity is good indicator)
 - peaches do fine in deserts
 - almonds sometimes tolerant
 - structure of stomata and leaf epidermis
- Reduced chilling requirement
 - expand growing regions to sub-tropical and tropical
 - issues with quality
- Extend season
 - earlier will probably require faster fruit development interval rather than earlier flowering
 - yield issue under 60 days
 - early season peaches (and other *Prunus*) often have poor quality
 - improve particular varieties for earlier picking
 - not necessarily so important when you're dealing with a global economy – but we're trying to improve US competitiveness

Key issues in application of genomics to breeding

Despite the diversity of *Prunus* crops, genomic synteny across *Prunus* is established – therefore, genetic research in one crop is of interest to others. However, functional conservation of specific genes and networks is not assured.

- Genomics training for breeding programs
 - Current breeders are underfunded and therefore not working at capacity
 - New breeder training – breeders can't easily do this themselves as much money is

- spent on technicians
 - Students often interested in molecular biology rather than breeding. In the near future we can emphasize that in Rosaceae we have sequenced genomes that are available for mining. Emphasize similarity with human genetics model
 - Where will all these new breeders be employed when they're done? Monsanto and Syngenta have jobs for people with MS in breeding. We need Rosaceae breeding positions
 - How to keep current breeding positions (following retirements) and create new positions?
 - demonstrate the efficiency of genomics-assisted breeding
 - endowments are sometimes available
 - develop excellent graduates with a curriculum that integrates genomics technology and traditional breeding
 - A CAP-type broad enabling system would free up breeders from becoming molecular themselves (as they have often had to do in recent decades, diverting resources from traditional breeding operations)
- Use of wild material
 - Much breeding effort (e.g. 50%) is spent on disease resistance, especially introgressing resistance from wild material
 - Other traits also look to wild
 - Need to reduce linkage drag associated with useful wild alleles
 - General quality and size are especially reduced with use of undomesticated germplasm
 - Having markers and improved genetic understanding of quality traits (and size) would open up the use of much wider gene pools
 - markers for size and quality would reduce generations to get back elite-type fruit
 - getting the last 10% of quality back is tough without fine maps
- Markers: genome-wide, linked to traits of interest
 - With whole genome sequences available, marker development will be simple
 - Finding alleles will be easy with 454 sequencing
 - Having a shared central resource for genotyping would be useful
 - Would be advantageous to make direct use of a breeder's existing germplasm and phenotypic data – combine with genomics data
 - Need genome-wide markers across Rosaceae
 - Need better resolution on maps (association mapping?)
- Marker-assisted selection: if all the markers were available for all traits of interest, what is required for routine use in breeding?
 - Need money to do the molecular screening (extra costs for collecting leaves, labeling, etc)
 - Need informatics to handle the statistics
 - Need close connection with genomicist
 - etc
 - However, this is an end-game scenario. *Prunus* breeders (public, university) would

- prefer for now that genomics is used to gain a better understanding of the genetic control of and interactions among the traits they are dealing with – increase the knowledge base to aid decisions in:
- parent selection (including wider germplasm surveys)
 - planning crosses
 - phenotypic selection of superior progeny (where knowledge of underlying genetics helps breeders understand progeny performance and weigh up value across many traits)
 - quicker introgression from wild germplasm
- > high-throughput marker assisted progeny selection is perhaps too far off
- Need a pipeline/system for breeding any trait with genomics assistance
 - Association genetics (pedigree genotyping)
 - suits Rosaceae breeding resources – can use existing breeding populations, also germplasm collections and wild populations
 - valuable to better understand genetic control, interactions, linkage drag, and genetic diversity
 - beyond experimental populations – larger numbers of individuals and use of unrelated material enables zooming in on QTLs, validation, survey allelic diversity (allele mining)
 - Germplasm assessment
 - fully assess what we have here in the US
 - then consider worldwide resources
 - need people to score phenotypes where wild germplasm exists
 - Phenotyping
 - make use of breeders' existing germplasm and phenotypic data
 - make use of NPGS / GRIN germplasm and data
 - standardized phenotyping across germplasm is critical
 - doesn't require having all the germplasm in the same place
 - need to understand (and can exploit) GxE

Malus and Pyrus

Schuyler Korban, Susan Brown, Gennaro Fazio, Sue Gardiner, Jim McFerson, Jim Luby, Jim Cranney, Jay Norelli, Michael Wisniewski, Peter Hirst, Wayne Loescher, Eric van de Weg, Yanmin Zhu

Crop specific key issues to be addressed with genomics

In order of preference (based on majority vote), here are the key issues in *Malus* and *Pyrus*:

1. Fruit quality
2. Fruit texture
3. Precision cropping systems (rootstock-scion and tree architecture)
4. Diseases and Insects

Discussion centered around the following:

- Fruit Quality
- Disease and Insect Resistance
- Industry is always looking for profitable new varieties
- There is an interest in consistent fruit quality: what are the attributes? how are they measured? and what has been done?

Issues, resources, and approaches:

- Microarray and chips are available to look at expression profiles
- In New Zealand-QTL & association mapping
- Candidate genes- SNP association mapping
- Replicated apple plantings of ‘Gala’ x ‘Braeburn’ - 600 replicated at three sites - can be used in mapping and utility of robust molecular markers across environments
- In U.S., there are plantings of ‘Gala’ x *M. sieversii* that can be used
- Pedigree genotyping
- Use functional markers for these studies
- Need for phenotypic data
- Texture
- Flavor and aromatics and tying in consumer panels
- If two apples have the same characteristics, then do they get there in the same way?
- Once we have the complete apple genome sequence, how will it be used?
- Texture and flavor go across all members of the Rosaceae
- Need information about robustness of methods
- ACS ethylene - repeat and verify
- Breeder needs to have confidence in his/her ability to cull through their seedlings; for example- sex identification in kiwi allowed breeders to cull young seedlings
- Postharvest
- Biennial bearing
- In pears, there is a need for pear precocity rootstocks
- Consistency of ripening
- Rootstock scion interaction – relating to diseases and pests
- Regulation of cropping
- Tree structure
- High Quality Tree structure will contribute to reduced labor and eliminating ladders at harvest
- Storability and keeping quality
- Apple size
- Apple scab
- Root diseases - replant loss of chemicals is a major problem for both apples and pears
- Allergens
- Quality and scab resistance and appearance
- Scab resistance is available in new apple cultivars that are being marketed in “clubs” in Europe, such as ‘Ariane’ and ‘Juliet’

- Replant disease problems, especially in the westcoast
- Reduce randomness of orchards
- Tree structure to allow for spraying and use of robotics
- To reduce randomness of scion- rootstock
- Reduce variable
- Robotic friendly
- Grower access to varieties
- Improved knowledge
- Breeders we do buy in but need proven markers
- Quality consumer defined by purchased products
- Consistency
- Biotic stress
- Birds
- Rodents
- Flowering and fruit set
- Abscission

Pear industry issues are largely the same as those for apple

Key issues in application of genomics to breeding

How can we convince breeders that the molecular markers are solid enough for use in breeding?

Identification and discussion of major barriers:

A. RESEARCH

- Annotation of the apple genome sequence that will become available soon is a major undertaking which will help in identifying significant numbers of markers
- We should take advantage of the large apple ESTs resource to develop markers
- Our job should be easier in annotating apple than Arabidopsis
- 25% of genes in apple are not present in Arabidopsis, perhaps we better use *Medicago*
- Support for GDR is needed for annotation of the apple genome
- Assessing functionality of genes and gene families
- Need to have a microarray with all apple genes
- Knowing the exact number of genes in a family is very important

Available tools for genomics in apple:

- Microarrays
- Knockouts in apple
- Can use expression in Arabidopsis, tobacco, and yeast
- Availability of germplasm for expression profiling
- Mutant lines
- Transformation systems
- BAC libraries

- ESTs
- Transposons
- Marker-free transformation systems
- Physical map
- SSR markers, SNPs

B. BREEDING

- Should have breeder-friendly genotyping
 - SNP Golden gate Illumina
 - Roche light cycler
 - Cepro 9600
 - PCR-based markers
 - Identify variations associated with genes
- Need to understand whole set of genes that affecting a trait. This explains why breeders are not using some of the identified molecular markers.
- Determine the function of a gene family.
- Resources for breeding programs – the decline in number of breeding programs
- IP issues that prevent transfer of material to industry.

C. EDUCATION

- Need to continue in educating the public in order for them to accept transgenics
- Provide evidence for the utility/robustness of molecular tools in breeding programs
- Complexity of commodity addressing industry problems
- Provide evidence to breeders and growers of the utility and robustness of the techniques
- Educating future communicators (journalists).
- Utilization of information and knowledge and further communication to have more input into creation of knowledge - information need to flow in both directions
- Education of industry groups as well as funding groups

D. EXTENSION

- Facilitating the process of deliverables to the consumer
- Raising an appreciation for the research process
- Few people are competent in education about genomics
- Have good communication between researchers and extension personnel

Fragaria, Rosa, Rubus

Tom Davis, Kevin Folta, Jim Hancock, Stan Hokanson, Dan Sargent, Phil Stewart

Crop specific issues with potential genomic solutions

Disease, temperature, and water use efficiency for all crops, one complete rosoidae genome, one complete transcriptome sequence for *Rosa*, *Fragaria*, and *Rubus*, paucity of ESTs

Fragaria – Soil pathogens, screen wild and old domesticated germplasm for resistance, tag genes move them. Day-neutrality, heat tolerance, anthracnose, phytophthora, sugar and acid levels, nutrition

Rubus – Disease resistance, virus, temperature stress, sugar and acid levels

Rosa – Blackspot resistance, powdery mildew resistance, pyramiding major genes, QTL mapping partial resistance. Repeat blooming in many rosaceous woody crops, cold hardiness, elevated pH tolerance, flower color, architecture

Major barriers to application of genomics to breeding

Center for molecular aided germplasm enhancement? They ID genes, ensure the presence of pyramided genes in a genotype, return it to breeder, breeder shares royalties.

Association type process, simultaneously select for resistance gene and de-select for highest levels of donor germplasm

Research: Lack of adequate genomic resources, lack of screening techniques, (see crop specific issues noted above)

Breeding: Lack of understanding of how to utilize genomics techniques and information to address breeding problems, inability to form complimentary teams between breeders and molecular biologists

Education: Are plant breeding programs capable of training students to utilize cutting edge genomics tools, do current plant breeders have access to training for genomic approaches and technology, lack of funding to bring new graduate students on for degree programs

Extension: Extension programming is lacking for exposing the grower community to the benefits of genomics applications to plant breeding. Does information flow both ways through the extension portal? Does extension communicate with the genomics/breeding community. Are extension personnel trained in genomics techniques, approaches?

Implementation of strategic plan – breakout group summaries

Group 1

Participants: Abhaya Dandekar, Tom Davis, Amit Dhingra, Kevin Folta, Sue Gardiner, Steve Garzynski, Jim Luby, Dorrie Main, Jay Norrelli, Phil Stewart, Steve van Nocker, Mike Wisniewski

Genomics and Informatics

Apple and Peach genome sequence information will be available in the next two years. The group discussion proceeded in the direction where the community can utilize the new information towards development of markers. One of the utilities of having these genome sequences will be identification of orthologues across species.

Another idea that was floated was to use the ribosomal protein genes for trait-neutral markers or for enabling genome scans. The ribosomal proteins genes are highly conserved but the variation arises from introns. These can serve as signposts on the genome landscape. These signposts can also serve in macrosyntenic analysis.

A need for additional EST based SSR markers was brought up. EST based SSR markers are expected to be conserved across different species thus their utility cannot be underestimated.

Integration of currently existing databases with support for extending the functionalities of GDR was discussed. There was a general consensus to federate GDR, AppleBreed and the HortResearch Bioinformatics portals. AppleBreed is currently not publicly accessible but has very useful data from the HiDRAS project that was based on pedigree genotyping and phenotyping. Sue Gardiner from HortResearch suggested opening up their database to the community. Only the IP sensitive data will not be made available but we will have access to their SNP analysis tools. GDR is a publicly available database and has its strengths in physical maps and other pertinent tools and pipelines. Soon transcriptome and pathway analysis data will be added to the GDR. Discussions with Dorrie Main later on revealed that she is already in discussions with Ross Crowhurst at HortResearch to federate the two databases. In the context of the CAP, it was anticipated that funding for bioinformatics would be channeled in two directions. One to support GDR and its activities that include online education and extension modules and the other would be to facilitate federation of two other databases mentioned above.

A strong need for two way education or co-education was felt where Genomics scientists and breeders will have to be educated about each other's activities. "Softening the interface" was the sentiment that was brought out to represent this concept of co-education.

Breeding/Industry/Education

A strong need for establishing a well-structured communication network dominated the discussions. A need was felt to educate the industry regarding the source of new cultivars or genotypes and the impact of genomics on the future of fruit industry. This message should be

spread via grower talks with increasing integration of the existing extension infrastructure and investing in educating the extension faculty. With the focus on industry an input from consumers should be integrated in breeding efforts. These surveys should also collect regional and ethnic data related to consumer preferences. We should be able to fulfill the constant demand for novelty.

Education about fruits has to begin at the K-12 level if the industry has to survive and progress. Ideas about developing an elementary school curriculum as part of the CAP were floated. This should also include teacher training, horticulture extension agents training. At the next level undergraduate student training should be included. This will have a direct impact on breeding programs, job prospects and will help in leveraging additional federal funding.

One of the most important aspects of education should be to inform the industry and consumers and students about the advantages and disadvantages of biotechnology. The issues surrounding transgenics and new strategies to circumvent breeding for faster cultivar development should be brought into the education efforts.

Genetics/Germplasm

This section started with the need for rigorous and standardized phenotyping for any given trait. Also traits that are amenable to biochemical markers need to be identified. Phenotyping is currently available in the GRIN database. CAP should provide for development of additional methods for phenotyping. These methods should be eventually integrated with the GRIN system. CAP should also provide funding for phenotyping traits of interest. Funds should be made available for increasing the capacities of the germplasm repositories for maintaining breeding populations and also there should be additional space for mapping populations. The idea of infusing pedigree genotyping/association mapping in the germplasm collections as brought up. Information from functional and translational genomics efforts should also be utilized in genetics of fruit crops.

Another idea was to develop an International Germplasm exchange system as the current system is impractical. A focus on gene-based markers was brought up. Availability of genomic sequence will expedite development of gene-based markers. A short discussion based on “robust markers” brought out the need for development of a parallel terminology that appeals both to the breeder and the genomics scientist.

A long discussion was centered on genotyping. Should we follow the method used by HiDRAS? There are new methods that are rapid, high-throughput and inexpensive. The new method of pyrosequencing could be integrated. At this point Tom Davis and Kevin Folta mentioned that they will generate pilot data for genotyping using this method. The genotyping could be done at one center or standardized and duplicated at multiple locations. There should be a web-based inventory of genetic resources that is continuously updated. It could be hosted on the federated website.

Group 2

Participants: Bert Abbott, Susan Brown, Bob Curtis, Chris Dardick, Gennaro Fazio, Bob Gregory, Renea Hardwick, Angelo Baldo, Jim Hancock, Bryon Sosinski, Amy Iezzoni, Phil Korsan, Dan Sargent, Ester van der Knaap, Eric Van de Weg, Gary van Sickle.

POTENTIAL COMPONENTS OF IMPLEMENTATION PLAN

- 1. Introduction + Goals and deliverables
 - 2. Breeding & Industry
 - Build breeding-omics-grower teams
 - trait neutrality of umbrella project keeps ALL growers & industries on board
 - individual sub-proposals written for breeding should incorporate specific recognized industry needs, etc.
 - ask for industry matching \$\$ buy-in for proposals?
 - remain cognizant of funding timelines for logistics
 - ask for experiment stations to buy in with matching \$\$ also
 - teams will be sustainable in terms of being able to seek future funding
 - Education (note potential role for minority-serving institutions)
 - graduate or postdoc training programs or fellowships to work in the breeding-omics-grower partnerships?
 - International can be done, but has to be highly justified
 - train current and future breeders about IP issues
 - explore whether K-12 outreach is considered appropriate for this program
 - Extension
 - have these functions sited at several locations spread over the country
 - opportunity for software tools to be developed (see section 3)
 - leverage extension expertise to communicate outcomes of project to consumers, growers,
 - disseminate material to existing facilities and venues
 - conferences
 - websites
 - regional grower, extension, breeding workshops
 - grower newsletters, etc.?
 - possible groups who could do this
 - ? ARS PR department?
 - MSU Plant Breeding group?
 -
 - Cooperative extension agents
- 3. Genomics & Informatics
 - structural
 - functional
 - comparative
 - chemical
 - translational
 - Database and bioinformatics

- need infrastructure to deal with data coming out of genotyping
 - need software developed that traces inheritance through pedigrees, populations, and link with phenotypes
 - need software to help with marker validation
 - use GRIN for managing genotype and phenotype data?
 -
 - use GDR to manage markers, maps, population characterizations
 - check on QTL status?
- 4. Genetics & Germplasm
- Genes and traits
 - Phenotyping
 - do in partnerships creating integrated breeding and functional *-omics teams
 - generates candidate genes/regions for future research
 - NPGS core collections?
 - Mobilize the CGCs to coordinate and standardize the phenotyping among crops at NPGS
 - Use GRIN to manage data (see #3)
 - standardize QTL nomenclature (follow up with RoseEXEC?)
 - Cameron Peace & Jim Olmstead
 - Marker development and implementation
 - Take advantage of European technologies already developed
 - Need validation at the outset for consistent scoring (see #3)
 - Genotyping
 - Utilize the NPGS core collections as a place to start fingerprinting?
 - Facilities – piggyback on an existing one?
 - 3? one each for crop type?
 - Depends on potential demand (# breeding programs using them)
 - Have breeding programs write proposals for this
 - What kind of personnel? 1 PhD & 2 technicians?
 - Strategies
 - pedigree genotyping
 - Allele mining and gene discovery
 - Transformation for functional studies and cultivar improvement/ development
 - How to maintain germplasm?
 - Kick some \$\$ back to breeding programs whose populations are being used
 - vulnerable whenever a breeding program dies
 - use flexi-dollars for some of this? (especially in emergencies)
 - RosPOP?

Group 3

Participants: Tom Gradziel, Peter Hirst, Stan Hokanson, Schuyler Korban, Wayne Loescher, Jim McFerson, Cameron Peace, Greg Reighard, Yanmin Zhu

This breakout group followed a Logic Model (as will be required for at least the extension-based components of the CAP proposal, but is a useful approach for any other components. Thus, it's in our best interests to get familiar with this Model).

Previous discussion in the whole group prior to the breakout had mentioned, and in many cases agreed on, useful ideas for incorporation in any RosCAP. Rather than discussing them over again, we decided to list them as assumptions (=agreed components) of our group's RosCAP plan.

These assumptions were that a RosCAP would:

- be Theme-based, where several traits may fall into a given theme (the actual theme was not chosen, but public health – physical and mental well-being – should be prominent as it suits all major Rosaceae crops)
- be Team-based, to integrate skills from different people/disciplines and institutions
- have Genotyping support – marker development and marker deployment, both ongoing during the CAP term. Marker deployment would be conducted by a genotyping center that may be newly developed within RosCAP or a be third party service, including use of existing such centers
- have Bioinformatics support – central again
- be taxonomically Hierarchical in how crops are involved – subfamily level and within-subfamily level. Apple, peach, and strawberry would represent the three subfamilies for subfamily comparisons and most communication, while the other crops feature primarily at the within-subfamily level
- include Association genetics in some capacity (particularly suggested is the uniting concept of Pedigree Genotyping)
- consider Public-private partnerships important

Teams were considered the center of the conceptual management structure of a RosCAP. A RosCAP will be problem-driven (incorporating the Theme), and the individual teams will address the problem(s) with internal projects that focus on traits/issues of importance to them. Much within-team interaction is expected, such that education of each team member (especially the core members) is integral to a successful team.

Team composition: Core = Breeder, Genomicist, Trainee

- Trainee is a graduate student, postdoc, SRA, or new faculty
- Breeder includes their breeding program with issue(s) of priority to focus on
- Other team members: as appropriate, all the common people/disciplines commonly involved with breeding program (physiologists, pathologists, etc, also could involve ag economists, food scientists – whoever is necessary/useful to work on the issue. Each person may work on only certain aspects within a team (and may be working on other teams too).

Number of teams:

Can all Rosaceae breeding programs be included? We conducted a quick census of Rosaceae breeding programs. Results: see table below. Identified 45 public and well over 18 private breeding programs. We can't have teams on all of them.

Therefore, only a handful of teams would be fundable within the limitations of a CAP program. About 6 teams seems reasonable, and following the hierarchical scheme, would suit

that a team each for apple, peach, and strawberry are included, together with one other crop within each subfamily.

Management committee: ensures there is communication and coordination between support services and teams, and between teams. This between-team interaction is important to bind us together and facilitate synergy

Stakeholder committee: advises teams and informed by teams

Support services and disciplines: Germplasm, Phenotyping, Marker development, Genotyping, Bioinformatics

Education (referring to academic/classroom settings): modules for K-12 school teachers to use, workshops for grad students, online training modules for trainees, postdocs, etc

One or more traveling workshops are held at the beginning of the project – people move around to see the other components/disciplines

Extension and Outreach – try to utilize existing people and resources, but need more - probably need to hire specialists

Quick Survey of Rosaceae Breeding Programs

Apple = 5 public, Pear = 1 public, Strawberry = 10 public, 1+ private, Caneberry = 6 public, 1 private, Rose = 2 public, various private, Peach = 12 public, 6+ private, Almond = 1 public, 4 private, Plum = 2 public, 1 private, Apricot = 4 public, 3+ private, Cherry = 2 public, 2+ private

<p>Apple Cornell Minnesota PRI WSU Geneva ARS</p> <p>Pear Kearneysville ARS</p> <p>Strawberry Cornell MSU UC Davis Minnesota Florida WSU NC State Beltsville ARS Corvallis ARS Ohio State *Driscolls *Other Private</p>	<p>Caneberry Cornell NC State Arkansas WSU Beltsville ARS Corvallis ARS Driscolls</p> <p>Rose Texas A&M Minnesota *Various Private</p>	<p>Peach Florida Byron ARS Clemson Arkansas NC State UC Davis Kearneysville ARS Texas A&M Rutgers Parlier ARS MSU NC State (orntl) *Zaiger *Bradford *Birchell *Sunworld *Paul Friday *Annete Bjorge *Other Private</p>	<p>Almond UC Davis *Utah *Zaiger *Bradford *Birchell</p> <p>Plum Byron ARS Kearneysville ARS *Zaiger</p>	<p>Apricot Rutgers Byron ARS UC Davis Parlier ARS *Zaiger *Bradford *Birchell *Sunworld *Other Private</p> <p>Cherry MSU WSU *Zaiger *Bradford *Other Private</p>
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* = Private

APPENDIX II SUBMITTED PROJECT IDEAS TO FACILITATE WORKSHOP DISCUSSION

NOTE: The following project outlines were circulated to the Rosaceae community prior to the Workshop. Our goal was to encourage groups to brainstorm and share ideas for components of large-scale Rosaceae projects that could potentially unite the community.

Identification and exploitation of genes and alleles of Rosaceous crops for genetic crop improvement

Submitted by Henk Schouten (henk.schouten@wur.nl)

Objective(s)

For several Rosaceous crops many traits have been mapped genetically, using segregating populations and pedigrees. Further, EST databases have been made, and moreover whole genome sequences are being unraveled for *Malus* and *Prunus*. The challenge for the scientific community working on Rosaceae crops for the near future is merging this information for identification of functional genes and their alleles. The second step is exploitation of the knowledge of these genes and alleles for significant crop improvements. Two routes are envisaged here, i.e. marker assisted breeding and cisgenics (= genetic modification using alleles from sexual compatible relatives).

More specific objectives:

- Fine mapping of traits that are important to society
- Isolation of the underlying genes
- Allele mining of these genes in germplasm, and identification of the most beneficial alleles
- Introgression of these alleles into commercial varieties by means of Marker Assisted Breeding and Cisgenics.

Supporters

- Wageningen University and Research Centre (Plant Research International), The Netherlands.
- Inova Fruit Ltd., The Netherlands (to be confirmed)

Pedigree Genotyping for US Rosaceae crop improvement: Establishing a pipeline of genomics knowledge for new cultivar development and enhanced product quality

Submitted by Cameron Peace (cpeace@wsu.edu)

Objectives

- 1) **RESEARCH:** Locate important regions of the Rosaceae genome controlling [suggested: fruit, nut, and flower quality] with the application and improvement of Pedigree Genotyping technology
- 2) **BREEDING:** Establish the enabling infrastructure and a tailored pipeline of perpetual genomics assistance for US Rosaceae breeding programs to enhance breeding efficiency and scope
- 3) **OUTREACH:** Establish an integrated web portal and database to enable efficient stakeholder access to project progress and outputs (phenotypes, pedigrees, QTL locations and effects, and genotypes of predictive genetic markers)
- 4) **EDUCATION:** Develop the next generation of community-minded citizens by providing extensive national and international educational experiences

Synopsis

The overall plan is to develop the knowledge/software/infrastructure that will enable quick implementation of marker-assisted breeding in Rosaceae breeding programs, with the additional benefit of characterizing current cultivars.

Advantages to Pedigree Genotyping:

- The potential to identify multiple alleles for a given QTL locus in one analysis – essentially QTL identification, allele mining, and validation all at once
- Integrates existing data across multiple populations to identify new marker-trait associations – rather than relying on experimental populations on a trait-specific basis – and supports ongoing data collection for present and future generations
- Immediate inclusion of the breeder (and non-breeder) community for generating, cataloging, and maximum utility of phenotypic data

Why Pedigree Genotyping is not implemented right now:

- Lack of suitable multi-allelic markers across Rosaceae crops
- Available phenotypic data are often insufficient for marker identification
- Infrastructure for high-throughput genotyping for each breeding program is not currently available
- Software for integrated genetic analysis over multiple populations has not been previously available
- No database to support research on marker-trait associations
- Breeding community and aligned researchers are not fully aware/trained in the use of Pedigree Genotyping

What RosCAP would do to implement Pedigree Genotyping:

- Develop markers suitable for use in all Rosaceae crops
- Comprehensive and standardized phenotyping for key traits where necessary
- Create genotyping centers to provide Rosaceae breeder access to high-throughput genotyping on a fee basis
- Expand current software to realize Pedigree Genotyping across Rosaceae crops
- Provide a database to access the information generated
- Provide training for breeders to use Pedigree Genotyping into the future

- Illustrate the validity of the above by focusing on a specific trait or set of traits (recommended: fruit/nut/flower quality)

Other components of this core idea:

- Crystallizes the expertise and research of many groups across Rosaceae and across disciplines for the practical application of genomics
- Establishes degree of synteny across Rosaceae
- Responsive to upcoming release of whole genome sequences for Rosaceae species
- Allows focus on specific QTL of industry importance for gene identification and functional validation
- Surveys germplasm collection for useful genetic diversity relevant to the needs of breeders
- Characterizes existing cultivars for greater precision in improving production and handling practices
- Statistics for determining cumulative breeding value with multiple segregating QTLs, and for calculating selection indices across multiple traits combining marker and phenotypic data
- An informative and visually stimulating web portal for industry and public
- Unique educational experiences – domestic and international visits and training for the entire cross-section of participants and stakeholders
- Considerable leveraging of international expertise and resources – so far: Plant Research International, HortResearch, Centre Wallon de Recherches Agronomiques (the AppleBreed database of HiDRAS)...
- Cements the role of Rosaceae as the model for perennial crop breeding and genetics in the 21st century

Alignment with US White Paper and Roadmap

White Paper: This core idea focuses on **one of the four Key Issues** (we feel that to include all would be too diffuse), though the Pedigree Genotyping pipeline will be established so that it is thereafter applicable to any trait. It incorporates **all three Priorities** for addressing Key Issues (Define and exploit the Rosaceae genome, Strengthen the GDR, and Revitalize breeding programs).

Roadmap: Our proposed approach involves **all Impact points** of the Roadmap (Factors that control key traits, Degree of macro- and microsynteny, Apply genomics to industry). **All three points of the broad Roadmap** (Identify genes/QTL, Elucidate gene function, and Cataloging and dissemination) are also fully integrated in this CAP idea.

Through the use of Pedigree Genotyping and the focus on quality traits, this proposed approach also highlights the novelty of Rosaceae and allows these efforts to serve as a model for other perennial crops.

Supporters so far

Bruce Barritt (Washington State University TFREC)
 Marco Bink (Plant Research International, Netherlands)
 Fred Bliss (Davis, California)
 Gennaro Fazio (USDA-ARS Geneva)
 Sue Gardiner (HortResearch, New Zealand)

Amy Iezzoni (Michigan State University)
 Marc Lateur (Centre Wallon de Recherches Agronomiques, Belgium)
 Jim Luby (University of Minnesota)
 Jim McFerson (Washington Tree Fruit Research Commission)
 Jim Olmstead (Washington State University IAREC)
 Cameron Peace (Washington State University)
 Eric van de Weg (Plant Research International, Netherlands)
 Yanmin Zhu (USDA-ARS Wenatchee)

Integrating genomics and breeding initiatives to speed improvement of Rosaceous crop germplasm

Submitted by Chris Dardick (chris.dardick@ars.usda.gov)

This CAP proposal idea is only a template for what the proposal could look like and does not define specific research plans. These would depend on the interests and expertise of the CAP PIs as well as the identified key industry needs.

Marker assisted selection shows great promise for increasing breeding efficiency, especially in members of the Rosaceae with long juvenility times. However, this technology has not yet realized its potential even in well funded, high dollar cropping systems such as wheat, rice, and barley. The funded CAP programs for these crops seem to focus on narrowly defined sets of objectives that target the most critical industry needs. These CAP paradigms may not fit the Rosaceae which comprise a very diverse set of ornamental and horticultural crops with very varying uses, problems, and industry needs. More importantly, the number of Rosaceous crop breeders (and their funding) relative to the collective size of the industry is small and dwindling, threatening the long the term future of cultivar development. This facet presents a significant barrier to effectively integrating genomics technologies, yet the potential positive impact of doing so is substantial.

To leverage the diverse talent and knowledge found across the Rosaceae, some form of inter-disciplinary network will be required that includes Rosaceae crop breeders, germplasm stock centers, industry representatives, molecular biologists, geneticists, and genomicists. I propose this be called the Rosaceae Germplasm Improvement Network (or something like that). This network would be directly funded by the CAP and conduct 3 major activities: 1) They would coordinate efforts on a limited set of key cross-species traits such as architecture, stress tolerance, and flowering time and use innovative methods to establish genomic tools, mapping populations, etc. 2) Provide funding through grants for solicited proposals from breeders, researchers, and the Rosaceae industry. 3) Provide fellowships to train and educate the next generation of Rosaceous crop breeders.

Activity #1—Network directed research. (50-60% of CAP funds)

The Network directed research would be directly conducted by the CAP PIs and specifics are not outlined here, however, the research objectives must target a limited set of critical problems and have achievable goals with strong deliverables. It should also include labs representing the breadth of the Rosaceae community and be integrated as much as possible (ie. a stress group,

fruit quality group, architecture group etc.) This research would be clearly defined in the proposal and directly address key industry needs through practical germplasm improvement. MAS services could also be offered to breeders by some of the network labs. The Network would also be responsible for integrating all germplasm, markers, genomic data etc. into a common searchable database (the GDR) available to all.

Activity #2—Proposal solicitations: (30-40% of CAP funds)

Small narrowly focused proposals would be solicited at regular intervals, ranked and sorted in the same manner as NRI proposals are reviewed. Proposals could be on any rosaceous crop but must focus directly on germplasm enhancement such as phenotyping germplasm, creating mapping populations, conducting MAS on existing populations, solving problems through transgenic approaches etc. but for example, not the creation of an EST library. Supporting MAS in breeding would be the primary interest here. If necessary, a pre-proposal process could direct applicants to appropriate collaborators. (For example, a breeder wanting to develop MAS for his/her traits could be linked with an appropriate genetics lab).

Activity #3—Breeder fellowships: (10% of CAP funds)

These could include costs for training breeders in molecular techniques, training molecular biologists in breeding, scholarships for graduate students focused on breeding, etc.

This type of CAP grant organization would have several advantages:

- 1) It targets funds towards important and achievable goals and leverages the breadth of research talent in the Rosaceae community through proposals.
- 2) It allows for the diversity of the Rosaceae industry and is inclusive of all Rosaceous crops, traits, and germplasm needs.
- 3) It recognizes the fundamental importance and paucity of breeders.
- 4) It provides much needed funding opportunities for breeding programs.
- 5) It provides a forum (and funding) to integrate breeders with molecular biologists.
- 6) It recognizes the long term aspects of Rosaceous crop breeding and supports germplasm solutions at different phases of development that, once initiated, will likely last beyond the duration of the CAP.
- 7) Once working relationships are established, the resulting network and database would provide a permanent center of germplasm information for the entire industry.
- 8) Providing seed money to breeders for MAS will set the stage for practical development and assimilation of the technology.

Deliverables:

- 1) Rosaceous crop selections and releases. (If markers can be used to assist existing mature breeding programs)
- 2) Extensive molecular mapping information for multiple traits and crops.
- 3) Germplasm database including useful phenotypes, markers and mapping populations (similar to RosPOP).
- 4) New mapping populations suitable for molecular breeding and gene discovery.
- 5) The recruitment and training of breeders knowledgeable of and/or skilled in MAS and other genomic techniques.

Comparative Genomics in Rosaceae (peach, apricot, cherry, apple, pear, strawberry, rose)

Submitted by Elisabeth Dirlewanger on behalf of the French Rosaceae research community in Genetics and Genomics:

INRA UREF, GDPP (Bordeaux), INRA-SupAgro, AFEF (Montpellier), PSH, SQPOV, UGAFL(Avignon).
 UMR GenHort (Angers)
 UMR BDP (Lyon)
 Univ. Evry Gen. Veg. (Evry)
 BVPAM (St. Etienne)
 Ciref CV (Douville)
 Hortis (Sainte Livrade sur Lot)

French Rosaceae community is focus on several traits such fruit quality (link with the European integrated project ISAFRUIT), disease resistances, abiotic stress (drought), architecture, floral initiation and development and scent production (see annex for details).

Objective(s)

The main objective is to develop tools useful for all the Rosaceae community and to exploit the information gained by one species to other species in Rosaceae and in link with species models such as *Arabidopsis*, *Populus* or rice.

This main objective can be divided in sub-objectives:

- Macro synteny and comparative mapping.
- Sequencing and micro-synteny study based on the complete sequences of peach and apple available in a near future
- Efficient tools for functional genomics: micro-array, genetic transformation.
- Relationship among species with different level of ploidy
- Genetic resources: construction core-collection, structure of the population, LD survey.
- Tools to identify new genes involved in the control of the studied traits (classical genetics, association or LD mapping, signature of adaptation).
- Way to transfer results from research to breeders / industry or producers.

Different tools are available:

- Genomic tools such as molecular linkage maps, BAC libraries, QTL mapping using meta-analyses
- Important genetics resources (Genetic Resources Center for *Prunus*, *Malus*, *Pyrus*, progenies, genetics maps and molecular markers)
- Functional genomic tools such as microarrays
- Bioinformatics tools such as software for detecting SNP, data bases for genetic resources
- INRA plateforms for sequencing, genotyping, phenotyping, transcriptomic, proteomic...

Alignment with US White Paper and Roadmap

Alignment of the Key Issues for the Industry for the following aspects

- Genomic comparative in Rosaceae
- Improve fresh fruit quality
- Reduce chemical pesticide use
- Develop stress tolerant plants

Original French issue: quality of the flower (roses), flowering

Alignment of the Priorities to Address Key Issues

- Define and exploit the Rosaceae genome: Genomic comparative in Rosaceae
- Enhance Rosaceae genomics database resources
- Revitalize French Rosaceae breeding programs

Supporters

European integrated projects ISAFRUIT, HYDRAS coordinating by INRA-Angers

Genetic Resources project: GENBERRY coordinating by INRA-Bordeaux

GDR Input Information

Submitted by Randy Beaudry

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2007.06.01

13:41:49 PT

Key issues in crop production, processing and breeding

Fruit quality. The means to generate and preserve unique quality traits in protected germplasm and marketing systems will be important for maintaining industry viability. For my part, progress in aroma quality is of interest.

Crop-specific key issues with genomics

Robust and flexible genomics tools are needed by physiologists to identify candidate genes and test specific hypotheses.