

SUMMARY REPORT

Technology Roadmap Temperate Fruit Genomics, Genetics, and Breeding Workshop

**Marriott Hotel at BWI Airport
1743 West Nursery Road
Baltimore, Maryland**

October 17-19, 2004

**Prepared by the Rosaceae Genomics, Genetics, and Breeding
National Steering Committee**

Meeting purpose:

The purpose of the workshop was to: (1) identify major constraints to the economical production of temperate fruits; (2) identify primary solutions to these constraints, e.g., development of new cultivars and/or rootstocks, pest and disease resistance, tolerance to environmental stresses, developing new plant forms suitable for mechanical or robotic harvesting, etc; (3) determine how genomic technology can help to provide the above solutions; and (4) determine the role of breeding and/or cultural and post-harvest practices in transferring the basic genetic and molecular research findings into tangible benefits for fruit growers. Understanding the basic biology of temperate fruits on molecular and genetic levels is a very important goal. We strongly believe, however, that the research performed must target high priority "problem solving" research for the U.S. fruit industry. Only under these conditions will the undertaking result in tangible benefits to the industry.

This workshop was organized and coordinated by the USDA-ARS National Program Staff in response to a request by fruit industry representatives associated with the National Tree Fruit Technology Roadmap. The Roadmap has identified fruit genomics as a priority research area. The industry and the National Program Staff strongly felt that this research will greatly benefit by the broadening of its scope to include all economically important temperate fruit species, which belong to the botanical family of Rosaceae plants, i.e., apple, pear, peach, almond, plum, apricot, sweet and sour cherry, strawberry, raspberry and blackberry. It is expected that genomic information gained by

studying one species will be extremely useful for the other species as well. This fact strongly justifies a need for cooperation between scientists involved in fruit genomic research within this group of plants.

Participants: List of Participants is at Appendix 1.

Agenda:

The meeting was divided into three components, which consisted of:

1. General plenary presentations by key representatives of the research, industry, and federal funding agencies.
2. Breakout discussion groups of major Rosaceae genera for discussion of the science of genomics and how it will contribute to research focused on solving fruit production problems. These breakout groups consisted of :
 - a. Commodity-Growers Breakout Session. Charge to Breakout Groups:
Jim McFerson, Group Leader.
 - b. Commodity-Scientists Breakout Session. Charge to Breakout Groups : John Radin

Prunus: Bert Abbott, Group Leader

Malus and Pyrus: Herb Aldwinckle,
Group Leader
Fragaria and Rubus: Chad Finn and
Tom Davis, Group Leaders
 - c. The Discipline-Scientist Breakout Session. Functional Genomics: Wayne
Loescher, Group Leader

Breeding and Mapping: James Luby,
Group Leader
3. Final Plenary Report and Discussion Session. Kay Simmons, Moderator.

Charge to All Breakout Groups and Plenary Session Discussions

General

The outline of the United States Rosaceae Genomics, Genetics, and Breeding Initiative should serve as an overarching document that will be used during the breakout group discussions. As these discussions evolve, the outline will start to be filled with the content that will form a basis for preparing a draft of a white paper. The white paper will be prepared by a committee identified during the workshop proceedings and circulated to all workshop participants for their input during the weeks following the workshop. Deadlines for these activities will be decided upon during the workshop.

Specific Instructions

1. The Commodity-Growers Break-Out Session.

This session should identify major problems/constraints to economical production of temperate fruits. Apple, pear and cherry growers can relate to their National Technology Roadmap Vision Statement which ties all their actions to reducing costs by 30 % by the year 2010 while delivering the highest quality fruit. The other groups most likely will also emphasize costs and quality, although their problems/constraints may be different from those that apply to apple, pear, and cherry growers. This workshop is about genomics-genetics-breeding and therefore the industry should prioritize problems that mainly genetic changes to fruit trees will be able to address. One must not discount the possibility, however, that as our knowledge broadens on how plants function on the molecular level, we may be able to activate or suppress the expression of certain genes through cultural and post-harvest management practices. This kind of knowledge will also provide practical benefits to the industry.

2. The Commodity-Scientist Break Out Session.

This session should determine how genomic technology may lead to genetic changes resulting in cultivars/rootstocks to solve the grower-identified problems and constraints. For example these new cultivars and rootstocks may possess the resistance to pest and disease, tolerance to environmental stresses, have canopy forms suitable for robotic harvesting and pruning, etc. Alternatively, the new knowledge gained through the proposed research may lead to gene expression manipulations through cultural and post-harvest management practices. The question is how genomic technology will be used to develop or speed up the development of the above mentioned solutions. What will be specific goals and deliverables in short term (1-5 years), medium term (5-10 years), and long term (10-20 years). The groups should develop intermediate milestone goals which will be indicators of scientific progress. Although these goals may be scientific in nature, they will lead to eventual practical solutions (some of which may be medium term, but many may be long term).

3. The Discipline-Scientist Break Out Session.

This group will look into how various specific goals can benefit from cross commodity interactions among scientists through sharing information, resources, etc. The strategies discussed will seek to minimize duplication of effort, maximize cost effectiveness, and have a synergistic impact on the knowledge generated. Critical topics for discussion will include the strategies to address: comparative linkage mapping including cross species QTL analyses; sequencing; microsynteny; microarray design; and potentially common systems for reverse and forward genetics such as RNAi and transformation.

4. Plenary Session on October 19, 2004. Kay Simmons, Moderator.

This session will consist of reports from the scientist break out groups and also a general discussion across commodity groups and scientific disciplines. Reports from the groups will last one hour and the discussion a total of two hours and fifteen minutes. The moderator will lead the discussion using the United States Rosaceae Genome Initiative, Strategic Planning Document Outline as a guide. Specific goals of research will be discussed: (1) Genome analysis, (2) Functional Analysis of the Genome, and (3) Crop Improvement. Also, deliverables will be discussed: (1) short term (1-5 years); (2) medium term (5-10 years); and (3) long term (10-20 years). Another topic will consist of Resource Centers, specifically genome resources, plant transformation, DNA diagnostics, and bioinformatics. This general discussion will consist, in a large part, of merging the content of the discussions that already took place in commodity and scientific discipline break out sessions. This plenary session is the time when all the participants will come together to generate the foundation of a document that will encompass all commodities and scientific disciplines.

Breakout Session Reports

1. Commodity-Growers Breakout Sessions.

Prunus (Almond, Apricot, Cherry (Sweet and Sour), Plum, and Peach)

Last Name	First Name	Affiliation
Abbott	Albert	University
Baugher	Phillip	Industry
Britton	John	Industry
Carter	John	Industry
Dandekar	Abhaya	University
DeJong	Theodore	University
Heintz	Chris	Industry
Iezzoni	Amy	University
Kaleikau	Edward	CSREES
Korson	Phil	Industry
Liu	Zongrang	ARS
Lott	John	Industry
Main	Dorrie	University
McLeod	Kemp	Industry
Molesworth	Bryce	Industry
Reighard	Gregory	University
Scorza	Ralph	ARS
van Nocker	Steven	University
Watson	Joe	Industry
Whiting	Matthew	University
Woolley	Robert	Industry

Major problems/constraints to economical production in Prunus.

- a. Labor costs.
- b. Tree architecture.
- c. Thinning.
- d. Root/ scion interaction.
- e. Disease resistance (abiotic and biotic).
- f. Fruit quality.
- g. Flower and fruit set.
- h. Post harvest.
- i. Germplasm.

The group generally agreed that the above-listed problems/constraints represented a general list of problems confronting the industry. These can be broadly defined as:

- a. Increased cropping efficiency.
- b. Rootstock development.
- c. Improved fruit quality (at harvest and post harvest).
- d. Improved biotic and abiotic resistance.

Within *Prunus* it was agreed that although these represented the major focus areas of concern, the level of importance on each particular crop for any one of these concerns varied. However, it was agreed that genomic tools could be implemented to improve each of these. In addition, the critical need to develop new breeding capabilities to integrate these tools into the breeding programs was discussed and highlighted as potential problem in the future.

Malus and Pyrus (Apple and Pear)

Last Name	First Name	Affiliation
Anthony	Allyn	Industry
Allan	Dave	Industry
Aldwinckle	Herbert	University
Bell	Richard	ARS
Bewick	Thomas	CSREES
Brown	Susan	University
Cranney	James	Industry
Drake	Dawn	Industry
Fazio	Gennaro	ARS
Jensen	Philip	University
Korban	Schuyler	University
Loesher	Wayne	University
Luby	James	University
Mattheis	James	ARS
McArtney	Steven	University
McFerson	James	Industry
Milne	Brent	Industry
Norelli	John	ARS
Saunders	Bennett	Industry
Simmons	Kay	ARS
Simon	Charles	ARS
Silverthorne	Jane	NSF
St. John	Judith	ARS
Swietlik	Dariusz	ARS
Unruh	Thomas	ARS
Watkins	Christopher	University
Wisniewski	Michael	ARS

Major problems/constraints to economical production in Malus and Pyrus.

- a. Labor cost, availability, safety.
- b. Uniformity and superiority of tree and fruit quality.
- c. Pest and disease resistance.
- d. New and exciting cultivars (scion, rootstock).
- e. Storage quality.
- f. Tree architecture.
- g. Ripening control.
- h. Low browning.
- i. High antioxidants.
- j. Fire blight resistance.
- k. Improved sugar, acid, and volatile properties.
- l. Abscission management.
- m. Replant

The above listed issues were highlighted as those of most critical importance to the apple and pear industries. These are broadly resolved into the following categories:

Apples and Pears:

- a. Labor Costs.
- b. Tree architecture (inc. stock/ scion interactions).
- c. Thinning, uniformity of ripening, abscission.
- d. Fruit Quality (especially consistency).
- e. Disease and Pest Resistance (especially to fire blight).
- f. New and Exciting Varieties.
- g. Storage Quality.

Pears: Dwarfing rootstocks.

The above problems for the industry were grouped into three major research goals:

1. Tree architecture (including new rootstocks).
2. Fruit quality (including new cultivars).
3. Disease and pest resistance.

Fragaria and Rubus (Blackberry, Raspberry, and Strawberry).

Last Name	First Name	Affiliation
Clark	John	University
Davis	Thomas	University
Finn	Chad	ARS
Hancock	James	University
Harrell	Mark	Industry
Johnson	Philip	Industry
Legard	Daniel	Industry
Lewers	Kimberly	ARS
Radin	John	ARS
Sjulin	Thomas	Industry
Slovin	Janet	ARS
Sosinski	Bryon	University
Thro	Ann	CSREES

2. Commodity-Scientist Breakout Sessions:

Prunus: [Almond, Apricot, Cherry (Sweet and Sour), Plum, and Peach]

Last Name	First Name	Affiliation
Abbott	Albert	University
Dandekar	Abhaya	University
DeJong	Theodore	University
Iezzoni	Amy	University
Kaleikau	Edward	CSREES
Liu	Zongrang	ARS
Main	Dorrie	University
Reighard	Gregory	University
Scorza	Ralph	ARS
van Nocker	Steven	University
Whiting	Matthew	University

Develop Genetically Improved Materials:

1. Vegetative Growth Properties of Scion.

Timeline

- 1 -5 years: Developing Mapping Populations
Score characteristics
- 5-10 years: Identifying genes
Transgenics
- >10 years: Development of new germplasm varieties

2. Rootstock Development: Size Control

Timeline

- 1 -5 years: Identifying characters from mapping populations.
- 5-10 years: Comparison with apple.
Identification of genes
- >10 years: Pyramiding of genes
Transformation

3. Flowering Fruit Set/Genetic and Functional Genomic Approaches

Timeline

- 1 -5 years: QTL mapping + single gene
Expression analysis
- 5-10 years: Identification and gene characterization
- > 10 years: Transgenes
MAS for cultivar improvement

4. Fruit Quality/Post Harvest and Fruit Disorders: QTL and single gene

Timeline

- 1 -5 years: Develop mapping populations and maps
- 5-10 years: Characterize gene regions
Potential candidates
Allele discovery and characterization
Physiological Intervention
- > 10 years: MAS application
New cultivar development

5. Biotic Resistance

1. Plum pox resistance.
2. Root knot nematode resistance.
3. Powdery mildew.
4. Leaf spot resistance.
5. Aphid resistance.
6. Borer resistance.
7. Crown gall resistance.

Timeline

- 1 -5 years: Complete mapping of genes. Initiate mapping.
Test gene constructs from other systems.
- 5-10 years: Gene identity studies.
Develop resistant varieties.
MAS.
- > 10 years: Testing of transgenic variety.
Pyramiding resistance genes.
Identification of resistance germplasm.

6. Abiotic Resistance

1. Drought tolerance
2. Heat tolerance
3. Cold tolerance
4. Chilling requirements
5. Waterlogging resistance
6. Alkalinity/Chlorosis
7. Salinity?
8. Sunburn
9. Splitting
10. Pitting

Timeline

- 1 -5 years: Develop populations – maps, QTL, single gene.
Characterize existing populations.
Functional genomics.
- 5-10 years: Candidate gene identification.
Transgenic testing.
MAS.
- > 10 years: Pyramiding resistance genes.
Identification of resistance germplasm.

Malus and Pyrus (Apple and Pear)

Last Name	First Name	Affiliation
Aldwinckle	Herbert	University
Bell	Richard	ARS
Bewick	Thomas	CSREES
Brown	Susan	University
Fazio	Gennaro	ARS
Jensen	Philip	University
Korban	Schuyler	University
Loesher	Wayne	University
Luby	James	University
Mattheis	James	ARS
McArtney	Steven	University
McFerson	James	Industry
Norelli	John	ARS
Simmons	Kay	ARS
Simon	Charles	ARS
Silverthorne	Jane	NSF
St. John	Judith	ARS
Swietlik	Dariusz	ARS
Unruh	Thomas	ARS
Watkins	Christopher	University
Wisniewski	Michael	ARS

Broad definition of genomics including markers, breeding, ESTs, gene regulation, post-translational aspects.

Different applications of genomics:

- Marker development and use in breeding
- Genetic engineering
- Therapeutic treatments

For the problems highlighted in the industry the following solutions and timelines were developed:

Tree Architecture (Need stock/scion approaches)

- a. Robust EST markers (SSRs, SNPs) - short term.
- b. Use of transgenes for apple and pear – *rol* genes; GA insensitivity genes – GA_{20} and GA_2 oxidase - short term.
- c. Use of common mutations/ genes for pillar/columnar for peach, apple, and pear; dwarfing; weeping: markers plus populations -- medium term.

d. Development of new rootstocks – markers; rootstock ESTs; below-ground (root) architecture; anchorage; deep roots for growth without herbicides - medium term.

e. Use of flowering genes implicated in shoot development (Apetala, TF 7- MADS box) - medium term.

f. Genomics of inflorescence architecture and development of flower clusters - short term.

Fruit Quality (including storage quality and new cultivars)

a. Ethylene biology at the genomics level. Ethylene perception and cascades, and integrating them with **texture** and **flavor volatiles**. Cell wall modification; how signals are transduced? Reducing disorders.

(1) Short term goal is determining the regulons in the pathway.

(2) Medium term goal is selecting cultivars.

b. Antioxidants and vitamin C / health benefits. Need to survey antioxidants in diverse germplasm; markers for antioxidants and vitamin C. Can use genomics (transcriptomes for antioxidants and allergens).

(1) This is a short term deliverable.

Disease and Pest Resistance.

Priorities are fire blight (apple and pear), scab, mildew, replant disease, codling moth (apple), and pear psylla

a. Develop robust EST markers - short term.

b. Use new alleles identified for disease and pest resistances in breeding. - medium to long term

c. Clone resistance genes for use in MAB and clean genetics - medium term.

d. In short term use single genes, but in long term pyramid genes for resistances.

Other Issues.

a. Vegetative propagation of rootstocks is expensive. Seed-propagated rootstocks should be investigated, especially in diverse germplasm. Possibility to use doubled haploids in apple, peach, and pear.

b. Productivity and quality are affected by abiotic stress (drought, frost damage to flowers), and genomic solutions should be sought.

Fragaria and Rubus:

Last Name	First Name	Affiliation
Clark	John	University
Davis	Thomas	University
Finn	Chad	ARS
Hancock	James	University
Legard	Daniel	Industry
Lewers	Kimberly	ARS
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Sjulin	Thomas	Industry
Slovin	Janet	ARS
Sosinski	Bryon	University
Thro	Ann	CSREES

For the identified problems, which ones can be helped by genomics research?
There are short-, middle-, and long-term goals as follows:

Short Term

1. Markers and maps for marker-assisted selection (pest resistance, day neutrality etc.)
2. ESTs (libraries first)
3. BACS
 - a. begin construction/make
 - b. transformation-ready
4. Clean transformations for potential cultivar development
5. Transformation systems (clean or not) for gene identification and characterization

Middle-Term

1. Use of markers in seedling evaluation
2. Genechip for each genus
 - a. networks
 - b. tag genes for stress/resistance, etc.
3. BACS in use (position cloning, new markers)
-physical mapping
4. Test ESTs
 - a. candidates
 - b. transformation/complementation
6. Cultivar release transformed plant with useful genes
7. Sequence Rubus and Fragaria genomes

Long-Term

1. Directed mutagenesis (metabolic engineering)

2. Cultivar release utilizing MAS
3. Exogenous gene manipulation

Concurrent Industry Group Breakout Session.

Recommendations and Desirables:

- a. New, significant, long term funding.
- b. Coordinated, accountable research.
 - (1) Avoid duplication of scarce resources.
 - (2) Seek synergy.
- c. Healthful benefits and fruit quality.
- d. IP protection and commercialization.
- e. Technology transfer to and from the United States.
- f. Genetics and genetic engineering has a range of techniques: GMO is one.
- g. Outreach and education:
 - (1) What are genomics, genetics, plant breeding?
 - (2) Why should we care?
- h. Identify and remove constraints,
- i. Moving the initiative ahead – keep it positive, simple, focused, and united.

3. Discipline-Scientist Breakout Session.

Functional Genomics.

Last Name	First Name	Affiliation
Aldwinckle	Herbert	University
Civerolo	Edwin	ARS
Dandekar	Abhaya	University
Jensen	Philip	University
Korban	Schuyler	University
Liu	Zongrang	ARS
Loesher	Wayne	University
Main	Dorrie	University
Mattheis	James	ARS
McArtney	Steven	University
Norelli	John	ARS
Slovin	Janet	ARS
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Unruh	Thomas	ARS
van Nocker	Steven	University
Watkins	Christopher	University
Whiting	Matthew	University
Wisniewski	Michael	ARS

Genetic and Genomic Resources:

Definition of functional genomics: A consensus?

Tools to look at global gene expression and regulation eg microarray and specific expression and regulation eg transformation.

(discussion of which crops can be transformed)

sour cherry

blueberry

apple

strawberry

Should microarray be available and a priority?

Rosaceae microarrays now being considered for production. Some doubt whether this could be representative of all Rosaceous crops, and effectiveness of making array given limited info available especially for minor crops. Limited core of conserved genes could be put on array, supplemented with crop-specific genes. Point made that only 60% of genes will likely be represented given the available and projected EST coverage.

Potential value of doing this is that minor crops (Rubus) could be partially taken care of.

Potential problem of lack of homology among species. Point made that microarrays will never be absolutely comprehensive even with complete genomics sequence and high EST coverage.

What is information to be gained from chips? High error rate, expense, lack of comparability among experiments/different chips, high number of chips involved to do a single experiment.

Another concern is that physiological problems associated with specific crops are not necessarily best addressed by using chips designed with another species. Generally considered that microarray should be available at some time in the future but the degree of comprehension (eg number, species) is arguable.

Discussion of types of chips, which would be the most appropriate?

Given the need to use between species, probably the 'long oligo' type.

Point made that resources that could be put into making chips now should probably be put into genomics (ie more EST sequences, especially for underrepresented species: Rubus, Rose, Fragaria, and underrepresented tissues (roots)).

What other genomic resources?

1. Proteomics. Too much excitement about microarrays. Protein doesn't always follow, and metabolome even less correlated. Only gives info about gene patterns and not useful further.
2. Bioinformatics: databases should be more accessible to user groups (breeders). Point made that the current GDB is not user friendly. GDBR has been developed one year with two more to go. General consensus is that the current GDBR has not been used by the community yet.
3. Systems' approaches to determine gene function (eg heterologous expression, in vitro work, knockout, etc.)
4. Modules' that help us explain/sell the research to user groups (eg growers) and funding agencies. Easily explainable sound bites.
5. Stock centers? This was suggested, response indifferent.
6. Cooperation/collaboration resources (discussion groups, researcher lists)

Tools that would be useful?

1. Transformation systems for recalcitrant crops. Not enough resources to make this go currently.
2. Viral transformation systems. Gets around the regeneration problem.
3. Develop the current low efficiency transformation system for apple into a high-efficiency system suitable for high-throughput functional genomics
4. System for 'rapid throughput' functional genomics.
5. Tilling (strawberry ready first)
6. Tissue and/or temporal-specific promoters
7. Exogenously induced promoters

Summary of session. Most discussions/comments and discussion of future directions were vague and agumentative.' For the purposes of the white paper, must make the perception that the group is cohesive and has common and specific goals.

When pressed the group reached a majority opinion that further EST development and microarrays would be the two top priorities at this time.

Breeding and Mapping:

Last Name	First Name	Affiliation
Abbott	Albert	University
Bell	Richard	ARS
Brown	Susan	University
Clark	John	University
Davis	Thomas	University
DeJong	Theodore	University
Fazio	Gennaro	ARS
Finn	Chad	ARS
Hancock	James	University
Iezzoni	Amy	University
Legard	Daniel	Industry
Lewers	Kimberly	ARS
Luby	James	University
McFerson	James	Industry
Reighard	Gregory	University
Scorza	Ralph	ARS
Sosinski	Bryon	University
Simon	Charles	ARS
Sjulin	Thomas	Industry

Question: What two tools that we need as breeders to achieve our goals?

Consensus responses:

- a. Lab collaborators
- b. More markers
- c. Maps
- d. Peach Genome Sequence
- e. Fish effectively
- f. Linkage breeding/application
- g. Better software for autotetraploid
- h. Common foundation mapping populations
- i. Pear ESTs
- j. Peach Transformation
- k. SNP Informatics
- l. Large insert BAC-Fragaria and Rootstock
- m. Coordination EST development
- n. SSRs
- o. Tissue specific promoters

p. Comparative mapping/sequences

Question: list two traits that you would like to study that have applicability in other Rosaceae?

Consensus Responses:

- a. Dwarfing
- b. Replant
- c. Continuous fruiting
- d. Low light tolerance
- e. Dwarfing or compact stature
- f. Plum pox resistance
- g. Botritis resistance
- h. Fruit firmness and size
- i. Reduced branching
- j. Acidity
- k. Precocity
- l. Harvest index allocation
- m. Antioxidants
- n. Flavor
- o. PPO
- p. Abiotic cold
- q. Rots -post harvest
- r. Nematode response
- s. Abscission
- t. Tree architecture

Question: Out of those traits which ones would be more useful to the Rosaceae as a whole? How do we bridge traits and capabilities for the entire community?

Consensus Responses:

- a. FISH (Fluorescent in situ hybridization) would be useful to identify whole genome relationships.
- b. A set of common markers for Rosaceae would be useful for integrative work.
- c. It was suggested that having a mapping center as a service to plant breeders within Rosaceae as with human genome mapping center. The wheat breeding community has identified four centers that have been funded by ARS. Questions were raised on cost and affordability and timeliness of such a center and the diverse types of services they would be providing. Can it be feasible with the different demands of breeding programs?
- d. There is a need for money to develop marker-assisted selection and it should be funded long term. (sustained support, not just a three year period).

e. On Clemson GDR web site it may be helpful to have parental genotypes as well as accession genotypes available for breeders.

f. It would be helpful to have graphical genotyping software for Rosaceae to facilitate parent selection.

g. What kind of funding would work for supporting applied research? Can federal formula funds be provided?

h. Is there a market that will pay for the development, and if not, make sure that Congress knows about it. Could there be a regional, multistate project to get funding?

i. There was a general out cry for funding that would go directly to breeders trying to apply MAS.

4. Final Plenary Session: Discussion on the Interactions Between Various Fruit Commodities and the Action Plan. Kay Simmons, Moderator.

Fruit Quality:

- Fully sequencing one of the genomes.
- New, unique, exciting cultivars: flavors, quality, outstanding appearance, inter-specific hybrids.
- Diversity in apple consumers: ethnic groups.
- Technology constraints: where are genes clustered? What is the allele diversity?
- Better fruit produced with more sustainable practices.
- Immediate effects: color, quality, health (anti-cancer effects)—basic biochemistry
- Breeding assisted with genomics...skip some basic genomics. Fruit quality and tree architecture.
- Tree architecture: Another goal: unified approach in automation.
- Better transformation systems.
- Reverse genetics technology.
- Sugar and acid metabolism.
- Use existing breeding populations and develop new ones, better support such as analytical capability.
- Ethylene - auxin.
- Predicting genetic recombination.
- More constant production, longer season.

Plant Architecture:

- Genes that control growth habits.
- Scoring the phenotype is easy in peach, harder in strawberry.
- Leaf shape and angle—narrow leaves.
- Role of rootstocks on architecture and fruit quality.
- Useful to identify collinear DNA sequences among Rosaceae.
- Signals between root stocks and scions.
- How to get GE rootstocks to transmit traits to scions.

Disease and Pest Resistance:

- Botrytis as a common disease across species.
- Altering gene regulation to enhance resistance.
- Microarrays to understand resistance mechanisms.
- Pathogen/host interactions.
- Pathogens as targets for manipulations.
- Marker Assisted Confirmation (MAC).
- Diagnostic tools to identify pathogens and virulence.
- Diagnostic tools based on early host responses to pathogens (fire blight).
- Candidate gene markers for resistance.
- Need to identify durable resistance.

Sequencing One Genome from Roseaceae:

- How many species to be sequenced for comparison?
- Fragaria, Rose, Apple, and Peach have been suggested.
- More thorough than ESTs. Explore regions that ESTs do not reflect.
- Sequencing captures control elements.
- Provides physical map, functional genomic information and markers.
- Need root ESTs.
- Important to have ESTs from same tissues from different species.
- Get quality values from ESTs on bioinformatics.
- Comparative genomics is most important.
- Global partnerships essential.

5. Plans for the Future and the Closing Session. Dariusz Swietlik, Moderator.

The following individuals were nominated to form the Steering Committee at the Plenary Session:

Albert Abbott
Herb Aldwinckle
Richard Bell
Susan Brown
John Clark
Amy Iezzoni
Schuyler Korban
Kim Lewers
Dorrie Main
Jim McFerson
Ralph Scorza
Tom Sjulín
Dariusz Swietlik

Technology Roadmap Temperate Fruit Genomics, Genetics, and Breeding Workshop Organizing Committee

Dariusz (Darek) Swietlik, USDA-ARS, Workshop Coordinator
Albert Abbott, Clemson University
Herb Aldwinckle, Cornell University
Phil Baugher, U.S. Apple Association
Abhaya Dandekar, University of California, Davis
Amy Iezzoni, Michigan State University
James McFerson, Washington Tree Fruit Research Commission

Workshop Local Arrangements:

Marilynn Low, USDA-ARS
Valorie Butler, USDA-ARS

6. Post-workshop meeting of the Steering Committee. Presiding: Dariusz Swietlik

This is a summary of the post-workshop meeting of the Steering Committee concerning the future activities of the United States Rosaceae Genomics, Genetics, and Breeding Initiative and also some other events that happened after the workshop. The following individuals participated in the post-workshop meeting: Albert Abbott, Herb Aldwinckle,

Susan Brown, Dorrie Main, Jim McFerson, Tom Sijulin, and Dariusz Swietlik. Also present were non-members of the Steering Committee: Jim Loescher, Gennaro Fazio, Jim Cranney, and Byron Sosinski. Below is the summary of our meeting and the information on some post-workshop activities.

During our deliberations, a suggestion was made and adopted to add to the Committee Abhaya Dandekar of UC Davis and to invite David Byrne of Texas A&M University to represent Rose on the Steering Committee. Dariusz Swietlik was asked to contact these individuals and ask them if they will be willing to serve.

Subsequent to the workshop, Dariusz Swietlik was contacted by John Clark, who requested to be removed from the Steering Committee because of his heavy workload and numerous other commitments. John has recently been elected the Vice President of the Research Division of the American Society for Horticultural Science. Dariusz responded that the Committee understands his situation and will remove his name from the list of its members.

II. It was decided that two documents will be prepared from the workshop.

1. A summary document. Bert Abbott volunteered to lead this effort. This draft will include all the workshop materials plus the reports from all breakout groups, plenary sessions, and all the invited presentations. This document will be e-mailed to all workshop participants.

2. White Paper. It was agreed that the outline of the Strategic Planning Document, The United States Rosaceae Genomics, Genetics, and Breeding Initiative, which was included in the workshop's materials, should be used as a template for preparing this document. It was decided to ask Abhaya Dandekar to coordinate the preparation of the white paper. Dariusz Swietlik indicated that several other individuals gave him a strong commitment to participate in its drafting. These include: Albert Abbott, Richard Bell, Gennaro Fazio, Schuyler Korban, Wayne Loesher, Jim McFerson, and Tom Sijulin. In fact, all of the workshop participants will be given the opportunity to make their input once the first draft of the document is prepared. It was decided that the first draft of the White Paper should be ready by the time the Plant and Animal Genome Conference convenes in San Diego on January 15-19, 2005. Dariusz Swietlik contacted Abhaya Dandekar and asked him whether he will be willing to coordinate the preparation of the white paper. He agreed to do so and Dariusz passed on to him the names of those who agreed to actively contribute to this document preparation.

III. We had a long discussion about a mechanism by which we will further prioritize our research agenda that will enjoy the fruit industry's support. Since no conclusion was reached on this point, the decision on how we will further narrow down and prioritize our research agenda will be postponed until a later date.

IV. The Committee expressed the desire to have two formal contacts during any given year. One of these contacts should be a face to face meeting in association with a

professional society meeting. It was proposed that the first meeting of this kind should be in conjunction with the Annual Conference of the American Society for Horticultural Science that will convene on 18-21 July, 2005 in Las Vegas, Nevada. The other contact should be a conference call. No time was set for this phone conference.

V. It was proposed that the Steering Committee should consist of 10 people. There should be one scientific representative of each genus that is a part of the U.S. Rosaceae Initiative, i.e., *Fragaria*, *Malus*, *Prunus*, *Pyrus*, *Rose*, and *Rubus*; one bioinformatics specialist, two representatives of the industry, and one government representative. It was proposed that each member of the Steering Committee should serve a 2-year-term with a possibility to renew her/his term. It was also proposed that the current composition of the Steering Committee should remain as is, until a further action is taken by the entire group.

VI. It was proposed that the entire group should meet every two years. No date and place was set up at this time.

APPENDICES:

Appendix I

AGENDA

Technology Roadmap Temperate Fruit Genomic, Genetic, and Breeding Workshop

BWI Airport Marriott, Baltimore, Maryland
October 17-19, 2004

Sunday October 17	
7:00 – 9:00 p.m.	Registration and Welcome Reception
Monday October 18	
7:00 – 8:00 a.m.	Continental Breakfast
8:00 – 8:15 a.m.	Welcome Judy St. John , Deputy Administrator, Crop Production and Protection, USDA-ARS, Beltsville, Maryland
8:15 – 8:30 a.m.	Workshop Objectives Dariusz Swietlik , Acting National Program Leader, Horticulture and Sugar Crops, USDA-ARS, Beltsville, Maryland
8:30 – 8:45 a.m.	The Potential Impact of Genomics on the American Temperate Fruit Industry – An Industry Perspective Jim McFerson , Manager Washington Tree Fruit Research Commission, Wenatchee, Washington
8:45 – 8:55 a.m.	U.S. Citrus Genomics Initiative Scott Cameron , National Program Leader, Horticulture and Sugar Crops, USDA-ARS, Beltsville, Maryland
	The Science of Genomics and How It Will Contribute to Research Focused on Solving Fruit Production Problems Presiding: Amy Iezzoni , Tree Fruit Breeder, Department of Horticulture, Michigan State University, East Lansing, Michigan
8:55 – 9:15 a.m.	National and International Efforts in the Rosaceae Genomic Albert Abbott , Plant Geneticist and Molecular Biologist, Clemson University, Clemson, South Carolina
9:15 – 9:35 a.m.	National and International Efforts in Malus Genomic Schuyler Korban , Plant Geneticist and Molecular Biologist, University of Illinois, Urbana, Illinois and Herb Aldwinckle , Plant Pathologist, Cornell University, Geneva, New York
9:35 – 9:50 a.m.	The Role of Breeding in Practical Applications of New Genomic Knowledge in Temperate Fruit Crops Ralph Scorza , Plant Geneticist, USDA-ARS, Appalachian Fruit Research Station, Kearneysville, West Virginia
9:50 – 10:05 a.m.	The Role of Plant Physiology/Horticulture in Practical Applications of New Genomic Knowledge in Temperate Fruit Crops Abhaya Dandekar , Plant Physiologist, University of California, Davis, California

10:05 - 10: 35 a.m.	<ul style="list-style-type: none"> • Break
	<p>Industry Needs Presiding: Jim McFerson, Manager, Washington Tree Fruit Research Commission, Wenatchee, Washington</p>
10:35 – 10:40 a.m.	Charge to Breakout Groups
10:40 – 11:40 a.m.	Meeting in Breakout Groups <ul style="list-style-type: none"> • Prunus • Malus and Pyrus • Fragaria and Rubus
11:40 - 1:10 p.m.	Lunch and Invited Presentation Temperate Fruit Genomics: Forging Links Between Researchers and the Broader Community Jane Silverthorne , Director of Plant Genome Research Program, National Science Foundation, Washington, DC
1:10 – 2:00 p.m.	Industry Needs (continued) <ul style="list-style-type: none"> • Reports from breakout groups, discussion, and summary
2:00 - 2:30 p.m.	National Research Initiative: Plant Genome, Bioinformatics and Genetic Resources in Roseaceous Plants Ed Kaleikau , National Program Leader, USDA-CSREES, Washington, DC
2:30 – 2:35 p.m.	<p>The Science of Genomics and How It Will Contribute to Research Focused on Solving Fruit Production Problems Presiding: John Radin, National Program Leader, USDA-ARS, Plant Physiology and Cotton Production, Beltsville, Maryland</p>
2:35 – 3:30 p.m.	Meeting in Breakout Groups <ul style="list-style-type: none"> • Prunus - Group Leader- Bert Abbott, Plant Molecular Biologist, Clemson University, Clemson, South Carolina • Malus and Pear - Group Leader- Herb Aldwinckle, Plant Pathologist, Cornell University, Geneva, New York • Fragaria and Rubus - Group Leaders - Chad Finn, Geneticist, USDA-ARS, Corvallis, Oregon and Tom Davis, Molecular Biologist, University of New Hampshire, Durham, New Hampshire
2:35 – 4:30 p.m.	Concurrent Activity – Industry Representatives Get Together
3:30 - 3:45 pm	<ul style="list-style-type: none"> • Break
3:45 - 6:10 pm	Meeting in Breakout Groups (continued) <ul style="list-style-type: none"> • Prunus - Group Leader- Bert Abbott, Plant Molecular Biologist, Clemson University, Clemson, South Carolina • Malus and Pear - Group Leader- Herb Aldwinckle, Plant Pathologist, Cornell University, Geneva, New York • Fragaria and Rubus - Group Leaders - Chad Finn, Geneticist, USDA-ARS, Corvallis, Oregon and Tom Davis, Molecular Biologist, University

	<i>of New Hampshire, Durham, New Hampshire</i>
6:10 – 8:00 p.m.	Dinner
8:00 - 10:00 p.m.	Meeting in Breakout Groups <ul style="list-style-type: none"> • Functional Genomics - Group Leader - Wayne Loescher, Michigan State University, East Lansing, Michigan • Breeding and Mapping - Group Leader, James Luby, Geneticist, University of Minnesota, St. Paul, Minnesota
Tuesday October 19	
7:00 – 8:00 a.m.	Continental Breakfast
	The Science of Genomics and How It Will Contribute to Research Focused on Solving Fruit Production Problems (continued) Presiding: Kay Simmons , National Program Leader, Grain Crops, USDA-ARS, Beltsville, Maryland
8:00 – 9:00 a.m.	Reports from Breakout Groups
9:00 – 10:00 a.m.	Discussion on the Interactions Between Various Fruit Commodities and the Action Plan
10:00 – 10:30 a.m.	Break
10:30 – 11:45 a.m.	Discussion on the Interactions Between Various Fruit Commodities and the Action Plan (continued)
	Plans for the Future Presiding: Dariusz Swietlik , Acting NPL Horticulture and Sugar Crops, USDA-ARS, Beltsville, Maryland
11:45 – Noon	Post Workshop Activities; Finalizing the Workshop Document
Noon – 12:15 p.m.	Future Meetings
12:15 - 12:30 p.m.	Closing Remarks Judy St. John , Deputy Administrator, Crop Production and Protection, USDA-ARS, Beltsville, Maryland

12:30 p.m.	Adjourn
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Appendix II

Strategic Planning Document

The United States Rosaceae Genomic, Genetic, and Breeding Initiative

Overview:

Rosaceae species constitute many of the most significant fruit, nut, and ornamental crops including almonds, apples, cherries, peaches, pears, plums, strawberries, and roses.

Fresh and processed products are vital components of diet, human health, urban and rural economies. Crops such as almonds and apples are important export crops.

Global competition, increasing labor costs, loss of effective agricultural inputs, and the advent of alternative products, threaten U.S. domestic industries (e.g., imported apples and juice concentrate, etc.).

National Technology Roadmap strategic planning requested by Congress and coordinated by USDA has identified two research priorities: 1) Genomics, genetics and breeding; 2) Sensors, automation, and precision agriculture.

Critical Issues to sustainability and growth of the fruit industry in the United States:

Improving profitability by optimizing inputs (land, water and chemicals).

Reducing labor costs.

Reducing the dependence on chemical pesticides by improving biological resistance.

Improving fresh and processed product quality, storage, and resistance to abiotic and biotic stress.

Improved competitiveness, globally; e.g., exports such as almonds and apples, etc.
Continued building of knowledge base in basic biology of key species.

Revitalize and build new US tree fruit breeding programs integrating modern molecular breeding technologies and traditional breeding practice.

Germplasm collection, characterization, database management, maintenance, preservation and utilization.

Genomic technology deliverables:

- Marker-assisted selection of new scion and rootstock varieties.

- Genomic tools for early evaluation and quality control.

- Genomic tools to manage diseases, pests and physiological processes in the field.

- Genomic tools for desirable tree growth and architecture.

- Genomic tools for fruit productivity and fruit quality traits.

- Integrate genomic technologies and precision agriculture.

- Development of a high through put transformation system for identification of gene function in index species.

Background:

Economic and dietary significance.
Evolutionary relationships.
Index species
Germplasm diversity in cultivation.

Problems/Challenges:

Pests, diseases, and abiotic stresses.
Quality and storage disorders.
Nutritional quality and food safety.
Plant growth and architecture.
Labor-associated costs.

State-of-the-art Genomics tools:

Diversity genomics
Genotyping and pedigree assessment.
Genetic diversity assessment.

Structural genomics:

- Genetic mapping.
- Physical mapping.
- Genome sequencing.
- Gene-to-Trait determination.
- Genetic transformation.
- Comparative genomics.

Functional genomics:

- EST Development.
- Bioinformatics resources.
- Expression profiling.
- Systems studies.

Specific Goals:

Use of bioinformatics and creation of a system for data management.

Genome Analysis.

- Physical mapping.
- Develop mapping resources.
- Develop and maintain plant populations.
 - Review existing populations and create new mapping populations.
 - Germplasm collection, characterization, database management, and maintenance.

“Universal core” markers useful across different populations and species.

Enriching maps with resistance gene analogs.

Employ technology that is scalable, affordable, and accessible.

Sequencing of Index species.

Comparative genome analysis.

Functional Analysis of the Genome.

EST database.

SNP and SSR database.

Expression analysis (gene chips)/systems studies.

Database development.

Gene delivery systems (Transformation).

Enhancing regeneration.

Multiple selection systems for re-transformation of transgenic lines with additional gene candidates.

Viral vector development.

Agrobacterium vectors.

Reverse Genetics.

Gene silencing (RNAi).

Virus induced gene silencing.

Stable silencing.

Insertional mutagenesis.

T-DNA-tagging.

Tnt1 tagging.

Tilling.

Proteomics.

Metabolomics.

Crop Improvement.

Technologies for existing orchards and post-harvest operations.

Trait or phenotype specific diagnostics.

Protein or RNA based therapeutics.

Enhanced quality control.

New cultivar development.

Introgression of abiotic and biotic stress resistance using marker-assisted selection.

Identification and deployment of allelic variation contributing to superior tree performance and fruit quality.

Deliverables:

Short Term (1-5 years).

Physical mapping.

Development of genetic resources and implementing technologies for mapping.

Index plant genome sequencing.
Rosaceae chip for expression analysis.
Viral vectors for gene silencing.
Regeneration and plant transformation.

Medium Term (5-10 years).

Trait-specific in-field diagnostics.
Gene activity sensors (protein/RNA).
Transgenic cultivars using "clean genetics".

Long Term (10-20 years).

Improved scion/rootstock varieties based upon MAS and introgression of new germplasm.
Trait-specific gene therapy.

Resource Centers:

Genome resources.

Progeny populations.

Microarray.

BACs.

ESTs.

Plant transformation (markerless, and/or with marker excision).

DNA diagnostics.

Bioinformatics.

Future Directions:

Cited Literature:

Appendix:

National Efforts

Region, labs, expertise

International Efforts

Countries, people, expertise

Workshops and Symposia

Appendix III

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