**MINUTES**

**RosEXEC Conference Call**

**1:00 – 3:00 pm (EDT) Friday, 23 August 2013**

Introductions

* Chris Dardick, 2013 Chair (chris.dardick@ars.usda.gov)
* JD Swanson, 2013 Vice-Chair (jd.swanson@salve.edu)
* Gayle Volk, 2013 Secretary (Gayle.Volk@ars.usda.gov)
* Minutes (G Volk)

Attendees: Bob Curtis, Chris Dardick, Kate Evans, Stan Hokanson, Sook Jung, Des Layne, Lee Miesel, Jay Norelli, Mercy Olmstead, Janet Slovin, J.D. Swanson, Gayle Volk, Vance Whitaker, Mike Wisniewski

Recruitment and Elections- JD Swanson, 2013 Chair of Governance and Membership Sub-Committee

Nominations will be requested in Early October and elections will be held in Early December. A short biography and picture will be needed for each nominee. Nominees from the south, east, and industry are particularly needed.

Adoption of minutes, May 2013

Minutes were accepted and will be posted to GDR

New Five Year Plan for the National Plant Genome Initiative

Document (attached) was received by Jack Okamura on May 16th, 2013

Report from the Rosaceae Gene Naming Standardization subcommittee (Sook Jung)

Subcommittee members: Sook Jung (chair), Robert Schaffer, Lee Meisel, Doug Bielenberg, Carole Bassett, Michela Troggio, Janet Slovin, Dorrie Main, Chris Dardick).

* Committee Goal: To come up with Rosaceae gene naming principle and mechanism for enforcement
* Two subcommittee meetings have been held, and another is scheduled for September. The minutes from the subcommittee meetings will not be posted online, but instead a final committee recommendation will be made available. Discussions summarized below.
* Focus themes for discussion: Gene naming convention, Species abbreviations, Gene names, How to enforce/advertise

Naming convention similar to Arabidopsis community:

PROTEIN: CAPS NON ITALIC

*GENE: CAPS ITALIC*

*mutant: lower case italic*

* Gene names can be sent to GDR (Dorrie and Sook; gene editors) to ensure names are novel prior to publication.
* Three letter prefixes will be used for species nomenclature: An official list will be made available for Rosaceae species
* Proposed naming system will be published
* GDR will maintain a community annotation and numbering system

GDR Update (Dorrie Main, Sook Jung)

* QTL curation: All the QTLs from the literature will soon be available online.
* A new Gene-sequence interface has been developed.
* New data pages for germplasm and diversity are underway.
* Grower database is in development: info about cultivars. Gateway to Growers: Training provided. Breeders input the data? Trial data? Phenotypic data? New Research? Climate data will be added including growing degree days & chilling hours.
* New funding will be sought from the National Research Support Project in January
* General species pages have not been updated yet. Jay Norelli, Janet Slovin, and Gayle Volk will discuss and follow up with this project after the conference call.

Genome Sequencing Updates

* *Malus sieversii* genome sequencing and RNA-seq underway.
* Chris Dardick: Illumina sequence available for pooled individuals of segregating population in peach, attempting to submit data to NCBI.
* How/where to store large amounts of data? GDR may just store the polymorphism data. How to best compress the data

Updates for grants, awards, and new projects

AFRI program is starting to send out program responses.

SCRI: October release of RFP? Tom Bewick contact.

Meeting reports and announcements for upcoming meetings

* ASHS meeting: RosBreed workshop: wrap-up of project was well received, including presentation on apple breeding: Broad implementation of Marker Assisted Selection by Jim Luby
* Apple CGC Sept 10-11, 2013 Geneva (Volk)
* Small Fruit and Viticulture Coordinating Committee: Beltsville Oct 21-25 (Lewers)
* Plant Genomics Conference in St Louis: Sept 23-24: Next generation sequencing and application
* 1st International Conference on Rapid Cycle Crop-Breeding: Ann Callahan: Jan 7-10 Leesburg VA
* RGC7: Seattle, Last week in June, 2014.

Next RosEXEC Meeting

Conference Call in November 2013

**RosEXEC Input for the New Five Year Plan for the**

**National Plant Genome Initiative**

***(sent to Jack Okamura, USDA ARS National Program Leader, Plant Biology 5-16-2013)***

[**What areas of basic research, tools and resources are needed to advance biological innovation and breakthrough discovery that are not currently available?**](https://extwiki.nsf.gov/pages/viewpage.action?pageId=17694750)

* + Tools for fast and accurate assembly of complex genomes including polyploids.
	+ NexGen sequencing innovations including cheaper/better long read sequencing and single molecule sequencing.
	+ Improved software for mining and visualization of genome scale data and cross-species genome comparisons; especially for researchers who do not routinely work with –omics scale data.
	+ Enhanced availability of phenotypic and genotypic data for plant genetic resources, including mapping populations, crop wild relatives, and cultivar collections.
	+ Tools for high-throughput phenotyping of organoleptic traits in perennial Rosaceae species including imaging, physiological, metabolomics, or other techniques to study and assess complex traits.
	+ Prediction programs based on cross-species systems biology analyses, to predict global transcript/proteome/metabolome changes in response to specific stimuli, the environment, or transgene modification.

[**What areas of research, tools and information are needed to accelerate the development of sustainable systems for food, bioenergy and industrial feed stock production?**](https://extwiki.nsf.gov/pages/viewpage.action?pageId=17694753)

* + Development of plant transformation technologies for recalcitrant crop species.
	+ Technologies that reduce plant juvenility time and improve overall breeding efficiency and speed.
	+ Easy to use resources and tools for breeders that enable the integration of genomics data and molecular markers into parent/offspring selection.
	+ Molecular marker platforms for breeders that are user friendly, robust, and cost effective.
	+ Improved understanding of the key regulators of developmental, defense, abiotic stress, sexual compatibility, and metabolic pathways.

[**What areas of research training and skills are not currently being met?**](https://extwiki.nsf.gov/pages/viewpage.action?pageId=17694757)

* + Many traditional plant biology fields have an aging workforce including plant breeding, horticulture, plant physiology, phytopathology, and biochemistry. Young scientists with interdisciplinary training in these fields are needed.
	+ Integrative research programs that unite the traditional plant biology fields with the tools and information that genomic analyses provide.

[**What information and resource repository needs are not currently being met? In this regard, are there opportunities to leverage existing datasets and resources?**](https://extwiki.nsf.gov/pages/viewpage.action?pageId=17694755)

* + Increased support for the Genome Database for Rosaceae (GDR) to keep pace with the rapid expansion of –omics scale data being produced by the Rosaceae community.
	+ Integration and enhanced interoperability of existing databases and webservers in order to more efficiently link genomic information with germplasm, phenotyping, literature, and other related databases.

[**What opportunities do you see for leveraging investments through international coordination?**](https://extwiki.nsf.gov/pages/viewpage.action?pageId=17694759)

* + More/better funding opportunities for cooperative international research teams to promote enhanced scientific collaborations.