**RosEXEC Minutes**

**January 13, 2013; 8-10 am**

**Town and Country Hotel, International Plant and Animal Genome Conference**

**Attendees:** Chris Dardick (Chair, USDA-ARS-AFRS); J-D Swanson (Vice-Chair, Salve Regina U); Gayle Volk (Secretary, USDA-ARS-NCGRP); Tim Artlip (USDA-ARS-AFRS); Pere Arús (IRTA); Michele Barefoot (Plant and Food Research, NZ); Carole Bassett (USDA-ARS-AFRS); Nahla Bassil (USDA-ARS-NCGR); Douglas Bielenberg (Clemson U); Anna Blenda (Clemson U); Sue Brown (Cornell NYSAES); Jill Bushakra (USDA-ARS-NCGR); José Campoy (INRA Bordeaux France); David Chagné (Plant and Food Research, NZ); Matt Clark (U Minnesota); Stephanie Cornelissen (ARC-South Africa); Danny Cullen (James Hutton Institute, UK); Kate Evans (WSU); Marco Galli (Washington State U); Sue Gardiner (Plant and Food Research, NZ); Amèlia Gaston (INRA Bordeaux France); Ying Zhu Guan (Washington State U); Sook Jung (Washington State U); Takashi Kawai (Kyoto University); Tyson Koepke (Washington State U & Phytelligence); Lisa Mahoney (U of New Hampshire); Jim McFerson (WTFRC); Lee Meisel (INTA-University of Chile); Diego Micheletti (IRTA); Nndozie Oraguzie (Washington State U); Ariel Orellana (Andres Bello University); Dan Parfitt (UC Davis); Cameron Peace (Washington State U); Sushan Ru (Washington State U); Cari Schmitz (U Minnesota); Janet Slovin (USDA-ARS Beltsville); Ryutaro Tao (Kyoto University); Michela Troggio (FEM-IASMA); Judson Ward (Driscoll’s); Mike Wisniewski (USDA-ARS AFRS); Kenong Xu (Cornell U)

**Introductions**

Minutes from RGC6 were accepted.

**Membership**

Current officers: Chris Dardick (Chair), J-D Swanson (Vice-Chair), Gayle Volk (Secretary)

Announcement of departing members: John Clark, Kevin Folta, Ksenija Gasic, Amy Iezzoni, Jim McFerson, Michela Troggio, Thomas Debener

Announcement of new members (term ends Jan 2016): Desmond Layne, Stan Hokansen, Mike Wisniewski, Judson WSard, Gayle Volk

Other committee members: David Byrne (2015), Thomas Chao (2015), Bob Curtis (2015), Sook Jung (2015), Cameron Peace (2015), Chris Dardick (2015), Kate Evans (2014), Mercy Olmstead (2014), Janet Slovin (2014), JD Swanson (2016), Vance Whitaker (2014).

Discussion of RosEXEC meeting frequency: ASHS RosEXEC meeting was successful and should be repeated. RGC6 meeting was successful. Minutes should be uploaded to GDR soon after the meeting.

**Standardized Gene Naming Scheme**

 Discussion of Robert Schaffer’s proposal (See attached report).

Concerns and comments:

* Why not do what is proposed for other species (such as Arabidopsis, wheat, barley)?
* What about gene duplications (artifacts of sequencing vs real duplicates)? A vs B? 1 vs 2?
* BLAST to NCBI and then BLAST NCBI sequence back to genome of interest to determine which gene is most similar.
* What about gene families?
* How to handle species with 2 subgenomes?
* Submit proposed name to GDR prior to publication?
* Could GDR record the history of gene names (aliases)?
* In literature, denote the gene accession number in parentheses after the name of the gene (AT\_\_\_\_).—concern: sometimes the whole gene is not sequenced, and thus is not given a gene name for NCBI
* What about splice variants?
* Use of two letter abbreviations is difficult due to name similarities of genus/species.

A subcommittee was proposed to address the issues listed above. Discussion will include non-Rosaceae researchers as well. Subcommittee members: Sook Jung (chair), Robert Schaffer, Lee Meisel, Doug Bielenberg, Carole Bassett, Michela Troggio, Pankaj Jaiswal(?). It was suggested that recommendations should be published and presented at a conference.

**Rosaceae Nomenclature**

Jay Norelli presented the revised Potter classification of Rosaceae Taxonomy as is now accepted by GenBank. Spiraeoideae has been changed to Amygdaloideae. This information is also posted on GDR.

**GDR Updates**

GDR is preparing species tabs for each of the Rosaceae species. The information will be in bullet format and “timeless”. Jay Norelli will work with GDR and RosEXEC to design a framework and CGCs will help provide the necessary information to GDR for implementation. Possible information includes: basic horticultural information, scientific name, common name, image, genome size, ploidy, # linkage groups, intrafamilial taxonomy, fruit type, linkage to GRIN taxonomy for center of origin, economic uses, etc?

GDR Update (Sook Jung): Presented in Fruit and Nut Workshop. Transcriptomes are in GBrowse, Reference genome assemblies available, Possible to include partial sequence assemblies in GBrowse(?). Recommended that GDR make reference to the publications which users of the database should cite to demonstrate value. GDR currently has funding until August 2014. Expansion of database resources to include cotton, cacao, Citrus, and blueberry has helped.

**Industry Update** (Jim McFerson): Almonds have surpassed grapes as the most valuable crop in California. Weather affected harvests in NY and MI. Washington had a record harvest for apple, cherry, and pears. Strawberries did well also. Roses are doing poorly due to the economic downturns and less landscaping. The SCRI funding is considered discretionary. It has been considered a good program, but funding has not been authorized yet. The SCRI RFP will not be released until funds are available. National Clean Plant Network also has funding concerns. The Specialty Crop Block Grant Program funded through state Experiment Stations has been allocated. The Arctic Apple has been proposed for deregulation. Industry is not supportive of these efforts. Honeysweet Plum has been deregulated in the US and is undergoing deregulation in the EU, sponsored by the Czech Republic. Bob Curtis is pursuing sustainable funding of GDR through State Experiment Station funds (NRSP). A letter of support may be sought.

**New Projects**:

Genomic Tools for Black Raspberry: Nahla Bassil, Chad Finn,

RosBREED II is in the planning/writing stages. International collaborations are sought.

The apple/cherry/peach Infinium chip developed in RosBREED I will continue to be available until Dec. 2013. Information is sought by the manufacturer to determine what is preventing its use (cost!). Please provide feedback to Nahla Bassil. Other concerns: polyploidy, usefulness across diverse germplasm.

FruitBreedomics: Comparing chips vs GBS approaches for genotyping and marker identification.

EUBerry:

**White Paper Revision will be coordinated by Chris Dardick.**

**Meeting Reports and Announcements:**

Gayle Volk is the new Apple CGC Chair.

RosBREED strawberry breeders workshop will be Jan 31, 2013. Organized by Nahla Bassil and Chad Finn.

RGC7 will be held in Seattle in the summer (June) of 2014.

RosBREEDS 4th annual meeting will be held in East Lansing, MI on May 28-30.

USDA-ARS-AFRS (West Virginia) is holding a conference on Genetic Engineering for Rapid Breeding: Challenges and Directions in Late November 2013.

**Subcommitees:** Phenotyping (no report), Enabling technologies (no report), QLT Nomenclature (project underway by Anna Blenda)

**Other Information:**

Sequencing effort underway for doubled haploid of sweet cherry, apple, and pear.

# It is all in the name: naming convention in *Rosaceae* species

Robert Schaffer - on behalf of the Rosaceae International Genomics Initiative RosIGI

In the last few years a considerable effort has yielded the complete genome sequence of 3 key Rosaceae species, Apple (Velasco et al 2010), Strawberry (Vladamir et al 2010), and Peach (website) with more to come. As currently only a few of the 30 - 60,000 predicted genes in the genome have been described, the Rosaceae community has a unique opportunity to standardise gene names within and across the Rosaceae species. With this in mind we respectfully urge the Rosaceae community to follow a standardised naming convention for genes in the Rosaceae species. By doing this the community will benefit from simplified literature reading, and less confusion when looking at genes. For this to happen we encourage people to check with the current literature and within the gene databases that the gene they want to name (and publish) has not already got a name assigned. When dealing with heterozygous species it is occasionally hard to know whether differences in sequence are allelic differences, or a result of gene duplication, or in the case of Maloideae, genome duplication. Through standardising the name we will reduce the incidence observed in models species where the same gene name has been used for different genes and occasional genes being assigned different names.

Here we propose a naming convention for Rosaceae genes at the time of publication. When choosing a name, if possible try and give it ontological relevance. For example if the sequence contains a motif conferring a likely function, such as enzyme action, then ideally you would name it after that enzyme followed by a number to allow other enzymes encoded in the same genome of similar function to be differentiated. If the function of the gene has not been characterised, the ontological reference would be to genes that have been previously characterised in model species, such as the *LEAFY* gene (*LFY*) in Arabidopsis. Here you could name it *LEAFY-Like* (*LFL*), or *LFY*, which can be differentiated in the literature from the *Arabidopsis* gene by inserting the species name in front (*MdLFY*).

Sequencing and marker assessment has shown a common ancestral genome between Rosaceae species containing 9 chromosomes. Both Peach and Strawberry have maintained this number, whereas apple has a genome duplication, followed by a rearrangement leading to a 17n genome (Velasco et al 2010). The linkages between these species is apparent when comparing phylogenetic relationship between these species, with often a single strawberry and peach gene being represented by two apple genes. When dealing with duplicated genomes such as apples, as expected, a clear phylogenetic relationship is often observed within the rosaceae species, with a single gene being observed in the unduplicated genomes strawberry or peach, and 2 copies in the apple gene (Figure 1). When possible we propose that the homeologous genes have a name showing this phylogenetic linkage. Devoghalaere et al 2012, suggests a naming convention as follows,

1. If the gene has been published in Genbank, or GDR, then this name should be used. If there is more than one name for the same gene then bring attention to this in the paper.
2. If one of the species has a name assigned to the gene, then this should be used within the cluster, eg FvARF1, with the closely linked peach gene being named (PpARF1). When dealing with species with a duplicated genome such as apple, to link the two names we propose that one of the homeologues be named the same (MdARF1) and the second homeologue be named MdARF101, clades with gene expansion caused by local duplications can be named MdARF201, MdARF301 etc. to link the common genetic route of these genes.
3. If none of the genes in a subclade have been named then we suggest using phylogenetic relationship with published genes in the literature is desirable especially from the model organisms tomato or Arabidopsis. However due to the evolutionary separation of these species clear distinction of the individual genes within a family is often not clear. When this occurs then authors are encouraged to use their discretion. Finally, once you have named a gene it please up load the name within GDR ([www.rosaceae.org](http://www.rosaceae.org)), to allow other researchers to be aware of the name and not to use it in other publications.

We encourage researchers to upload the gene names into GDR prior to publishing, so no conflicting names are published in the same period. By putting a little extra effort at this stage will mean that there will be less confusion in the literature and allow researchers the ability to make fast cross comparisons of species. As a final note, there is also an opportunity when reviewing papers describing novel genes, please check that they are following this nomenclature before accepting the paper.

**Attachment: Current RosEXEC members**

RosEXEC Membership 2013

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| **TERM STARTS(JAN)** | **TERM ENDS(JAN)** | **LAST NAME** | **FIRST NAME** | **INST** | **REGION** |
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| 2012 | 2015 | [**Byrne**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Byrne_David_bio_vision.docx) | David | Univ  | S |
| 2012 | 2015 | [**Chao**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Thomas_Chao_bio_vision.docx) | Thomas | Govt | E |
| 2012 | 2015 | [**Curtis**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Curtis_Robert_bio_vision.docx) | Bob | Ind | W |
| 2012 | 2015 | [**Jung**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Jung_Sook_bio_vision.docx) | Sook | Univ  | W |
| 2012 | 2015 | [**Peace**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Peace_Cameron_bio_vision.docx) | Cameron | Univ | W |
| 2008 | 2015 | [**Dardick**](http://www.rosaceae.org/sites/www.rosaceae.org/files/gdr_rosexec_2012/Peace_Cameron_bio_vision.docx) | Chris | Govt | E |
| 2011 | 2014 | [**Evans**](http://hortla.wsu.edu/people/evans.html) | Kate | Univ | W |
| 2010 | 2014 | [**Norelli**](http://hortla.wsu.edu/people/evans.html) | Jay | Govt | E |
| 2011 | 2014 | [**Olmstead**](http://hos.ufl.edu/faculty/maolmstead.%20%20) | Mercy | Univ | S |
| 2011 | 2014 | [**Slovin**](http://www.ars.usda.gov/pandp/people/people.htm?personid=5233) | Janet | Govt | E |
| 2011 | 2016 | [**Swanson**](http://www.salve.edu/academics/faculty/facultyDetails.aspx?Channel=%2FChannels%2FSite+Wide+Content&WorkflowItemID=2cfdcee0-b9b4-41ba-8fc2-fc1ec7086cdb) | JD | Univ | E |
| 2011 | 2014 | [**Whitaker**](http://gcrec.ifas.ufl.edu/Whitaker/Whitakercv.htm) | Vance | Univ | S |
| 2013 | 2016 | **Volk** | Gayle | Govt | W |
| 2013 | 2016 | [**Layne**](http://www.arabidopsisthaliana.com/) | Desmond | Univ | S |
| 2013 | 2016 | [**Hokansen**](http://www.clemson.edu/cafls/departments/horticulture/faculty_staff/faculty/gasic.html) | Stan | Univ | W |
| 2013 | 2016 | **Wisniewski** | Michael | Govt | E |
| 2013 | 2016 | **Ward** | Judson | Ind | W |
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**RosEXEC Input for the New Five Year Plan for the National Plant Genome Initiative**

* [**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)
	+ Algorithms capable of 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 germplasm resources and databases including both quantitative phenotypic and genotypic information.
	+ Cost-efficient technologies to identify single-cell metabolites
	+ Prediction programs based on cross-species systems biology analyses, to predict global transcript/proteome/metabolome changes in response to single and/or multiple gene modifications (i.e. transgene stacking).
	+ [**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.
	+ Improve pollination of crop species, such that crops are not jeopardized by suboptimal bee densities.
	+ Improved understanding of the key regulators of developmental, defense, 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.
* [**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.