BIC Genetics Committee Meeting Minutes

Location: Virtual meeting hosted by Carlos Urrea (U. of Nebraska, Scottsbluff)

Date: Friday, August 21, 2020, 2:30 - 4:00 pm

Committee Members and Guests present:

Bett, Kirstin (k.bett@usask.ca) – University of Saskatchewan
Cichy, Karen (Karen.cichy@ars.usda.gov) – USDA-ARS, East Lansing, MI
Gepts, Paul (plgepts@ucdavis.edu) – University of California, Davis
Gomez, Francisco (gomez225@umn.edu) – University of Minnesota
Harris, Donna (dharri50@uwyo.edu) – University of Wyoming
Heitholt, Jim (Jim.Heithlot@uwyo.edu) – University of Wyoming
Hoyos-Villegas, Valerio (Valerio.hoyos-villegas@mcgill.ca) – McGill University
Karasov, Alexander (akarasev@uidaho.edu) – University of Idaho
McClean, Phillip (Phillip.mcclean@ndsu.edu) – North Dakota State University
Miklas, Phil (**Chair**; phil.miklas@ars.usda.gov) – USDA-ARS, Prosser, WA
Munoz-Amatriain, Maria (maria.munoz_amatriain@colostate.edu) – Colorado State University
Myers, James (james.myers@oregonstate.edu) – Oregon State University
Osorno, Juan (juan.osorno@ndsu.edu) – North Dakota State University
Ostdiek, David (dostdiek4@unl.edu) – University of Nebraska
Pastor-Corrales, Talo (talo.pastor-corrales@ars.usda.gov) – USDA-ARS, Beltsville, MD
Porch, Tim (timothy.porch@ars.usda.gov) – USDA-ARS, Mayaguez, PR
Raatz, Bodo (b.raatz@cgiar.org) – CIAT, Colombia
Urrea, Carlos (currea2@unl.edu) – University of Nebraska
Wallace, Lyle (lyle.wallace@usda.gov) – USDA-ARS, Pullman, Washington

1. Old Business:

Approval of the Genetics Committee meeting minutes from 2019

Decision: The Genetics Committee minutes were approved from the meeting held at the Hotel Radisson in Fargo, ND on Wednesday Nov 6, 2019. Motion by Paul Gepts, seconded by James Myers, with AIF.

Introduction to the Bean Gene List

Decision: Phil Miklas will review the introductory text at the beginning of the Bean Gene list provided by Phil McClean, that includes new genomic tools such as reference genomes and gene annotation lists and will then share with the committee.

SNP and SCAR markers

Bodo Raatz has agreed to share his SNP marker list developed at CIAT, and Phil Miklas, Phil McClean, and Talo Pastor-Corrales have provided their SNPs pre-publication to make available to the community on the BIC webpage. Bodo Raatz, Tim Porch and Phil Miklas will organize the SNPs for posting with instructions for use with the Intertek platform.

***bc-u* gene identification** (from Phil Miklas)
Three *bc-u* -like loci identified: *bc-u* (original), *bc-ub* (linked with *bc-u*), and *bc-uc* (on another chromosome linked with *bc-2*). Miklas will propose symbols to the committee once the paper is drafted. The *bc-1*^{2} and *bc-2*^{2} symbols will be moved to the Obsolete gene list. A table will be developed with new lines that have all iterations of combinations. New differentials will need to be developed.

***Ppd* candidate gene** (item from Jim Kelly)
The red/far-red photoreceptor gene PHYTOCHROME A3 (PHYA3) was identified as a candidate for the *ppd* gene on Pv01 (Kamfwa et al., 2015; Weller et al., 2019). Jim Kelly proposes that the *ppd* gene be renamed PHYA3.
Decision: The committee proposes to retain the *ppd* gene name and to include PHYA3 as a candidate gene. This candidate could be described as a strong candidate for the gene, but we don't yet have conclusive proof that it is the gene.

QTL naming for rust paper (item from Phil Miklas)
A consensus for appropriate symbols for quantitative resistance to the rust pathogen was requested, while BR, RU, RST, RUST, RUS were mentioned. The manuscript is pending but the authors will likely use RUST1.1, RUST3.1, etc.

Molecular evidence for new gene symbol in rules section (item from Jim Kelly)
Currently, new gene symbol evidence must include the following (i to iv. Below). The suggestion is to make the physical map position (iv) mandatory instead of preferred.

i. data from one generation to formulate a hypothesis
ii. data from subsequent generations to test that hypothesis
iii. for hyper-variable pathogens: family mean testing (F2:3 progenies, or recombinant inbred lines – RILs), and use of multiple, specific races of the pathogen to separate effects of individual genes in gene clusters
iv. molecular marker data and genetic linkage map and physical map (preferred) positions when available

An extensive consultation took place about whether molecular marker data, linkage map and physical map information should be mandatory for a new gene symbol or whether genetic information is sufficient. Should large clusters of genes be approached differently from smaller clusters? You would need recombination within a cluster in order to separate out genes. Resistance specificity can be defined to a specific region of the genome (member of a cluster) instead of specifying by recombination. There is also an issue of defining or naming the clusters since sometimes they are Mbs in size. For example, the Pv04 cluster is full of genes and there is little recombination, so the genes are very difficult to separate. Stavely found recombination between *Ur-3* and *Ur-11*, but in most cases there is no recombination or the required population sizes are extremely large. Decisions were deferred to the new business section (below).

New business

Membership

Current members: Bett, Ferreira, Gepts, Goncalves-Vidigal, Kalavacharla, Kelly, McClean, Miklas (Chair), Osorno, Porch, and Urrea. We thank **Jim Kelly** for his service as member and chair of the Genetics Committee. He will now rotate off the committee as he has now retired. New members: We welcome **Valerio Hoyos-Villegas**.

New Gene Symbol (item from Kirstin Bett)

***P*^{sd}** is an allele of the *P* (Pigment) gene with order of dominance *P*>*p*^{sd}>*p*) (Islam et al., 2020). It replaces the *sd* gene (symbol) that conditions the slow darkening seed coat trait in pinto (Elsadr et al. 2011) and carioca beans (Alvares et al., 2019). *P*^{sd} encodes a bHLH transcription factor with two transcript variants but only one is involved in proanthocyanidin (PA) biosynthesis. An additional glutamate residue in the activation domain, and/or an arginine to histidine substitution in the bHLH domain of the *P*^{sd} -1 transcript in the slow darkening cultivar is likely responsible for the reduced activity of this allele compared to the allele in a regular darkening cultivar, leading to reduced PA accumulation. Unlike small *p* that shuts down pathway, it just scales it down. So replacement symbol would be *P*^{sd}. A linked KASP marker can be used that is presented in the Alvares et al. (2019) publication. The Alvarez publication can be added to the gene list. How does it relate to *p*^{gri}?—they have not looked at this. P. McClean says coding sequence is exactly the same as the wildtype for *p*^{gri}, so it is not likely to be *p*^{gri}.

Decision: Accept *P*^{sd} as a new gene symbol and allele of the *P* (Pigment) gene with order of dominance *P*>*P*^{sd}>*p*). *P*^{sd} will replace the *sd* symbol that conditions the slow darkening seed coat trait in pinto.

New Gene Symbols (item from Maria Celeste Gonçalves)

Maria Celeste Gonçalves has published one paper and they are working on submitting another. She requests adding a single anthracnose and angular leaf spot resistance gene *CoPv01*^{CDRK}/*PhgPv01*^{CDRK} from California Dark Red Kidney to the BIC gene list from a PLOS_One paper, with permission requested post-publication.

Decision: the *CoPv01*^{CDRK}/*PhgPv01*^{CDRK} symbol was not accepted.

The other item was a review of anthracnose genes and candidate genes published in First Look in Crop Science: "Integration of anthracnose resistance loci and RLK and NBS-LRR-encoding genes in the Phaseolus vulgaris L. genome." Two linked clusters with separation of about 100,000bp (<1cm) were characterized, but the segregation data indicates two independent loci with considerable recombination.

The consultation on gene clusters continued. There have been different approaches taken. Juan Jose Ferreira has a proposal for how to handle clusters. Kelly came up with a different method for working with clusters. Are they multiple genes or simply alleles of the same gene is the question?

Phil McClean shared that Prakken was able to define and separate out particular phenotypes, striping from mottling, within the C locus. These appear to be a cluster of MIB genes.

Decision: Add a section to the bean gene list for clusters. These can be delimited by physical map locations. As a work in progress, genes can be moved in and out of this list as studies are completed.