

BIC Genetics Committee Meeting Minutes

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

Date: Friday, August 20, 2021, 3:00 - 4:00 pm MST

Committee Members: Bett, Ferreira, Gepts, Goncalves-Vidigal, Hoyos-Villegas, Kalavacharla, McClean, Miklas (Chair), Osorno, Porch, and Urrea.

Present: Ferreira, Gepts, Goncalves-Vidigal, Vazbisneta, Hoyos-Villegas, McClean, Miklas (Chair), Osorno, Porch (Acting Secretary), Heitholt, Urrea, Gomez, Raatz, Pastor-Corrales, Parker

1. Old Business:

The Genetics Committee meeting minutes from 2020 and published in the 2021 BIC v64 were approved.

Bean Gene List: Propose the addition of a modified Introduction section highlighting newly developed genomic tools

Decision: The genomic tools section will be organized in bullet form in the Bean Gene List. Further consultation is needed regarding curation of data on the LIS (Legume Information System; <https://legumeinfo.org/>) database for specific traits of interest. One idea is for each lab group to curate their own data as they publish it and then share it with LIS.

New SNP markers – to replace/complement the SCAR marker Table

This is an effort to replace or complement the **SCAR Table**

http://www.bic.uprm.edu/?page_id=91 with the SNP-based markers for bean community use using the Intertek Company platform (agritech.sweden@intertek.com) for economical and efficient DNA extraction and genotyping. Coordinated by the GIAR Excellence in Breeding Platform (EiB) CIAT, led by Bodo Raatz, and the USDA-ARS-WA, SNP/InDel markers were developed and converted to KASP markers (Intertek-Lab agritech.sweden@intertek.com).

Decision: An excel spreadsheet has been developed with tested and verified markers. Before posting on the BIC webpage, the markers will be confirmed as being based on the G19833 v2.1 genome sequence. In addition, the sequence information and genetic background used for testing will be added to the excel spreadsheet. These same markers can also be used with temperature shift assays. This information will be posted on the BIC website so that users can share their results in different genetic backgrounds, provide suggestions, and decide on which platform to use.

***bc-u* symbol was changed to *bc-u^d* to reflect its origin from race Durango and different interactions.** Namely, *bc-u* was absent from host groups 2, 4, 5, and 7 and present in HG-10 which differs from the Drijfhout (1978) description.

Decision: The committee reviewed Soler-Garzon et al. 2021b and approved that the *bc-u* symbol be changed to *bc-u^d* to reflect its origin from race Durango.

New business

Membership

Decision: Travis Parker was nominated by Paul Gepts and seconded by Phil McClean to be a new Genetics Committee member. All were in favor.

Gene description amendments:

Add the candidate gene PvNAC1 to the description for *bgm* (syn *bgm-1*) based on Soler-Garzon (2021a).

Decision: Add the candidate gene PvNAC1 reference to the description for *bgm* (syn *bgm-1*) in the Bean Gene List based on the evidence in Soler-Garzon (2021a).

Additional updates of candidate genes can be made to those genes below. The candidate, the gene model, and the reference genome used should be included. Mutation analysis is needed within the genes themselves to show a high confidence candidate gene in order to include the gene in the Bean Gene List.

Researchers can send their updates of candidates to Phil Miklas to indicate which candidates or genes have been identified for addition to the Bean Genes List. An initial list of candidates/genes include:

- *fin* gene (Paul Gepts)
- *Ppd* (Paul Gepts)
- Dormancy (Phil McClean)
- Pod Shattering candidate genes (Paul Gepts)

Add the KTR2/3 (truncated CRINKLY4 kinase) candidate gene to the description for *Co-1* cluster alleles (MDRK, *Co-1*; Kaboon, *Co-1*²; Perry Marrow, *Co-1*³; AND277, *Co-1*⁴). It is also found in CDRK but not in Widusa (Richard et al., 2021).

Decision: Phil Miklas will contact Valerie Geffroy to see if she would like to add KTR2/3 (truncated CRINKLY4 kinase) as a candidate gene to the description of the *Co-1* cluster of alleles according to the results of Richard et al. (2021).

New Gene Symbols

bc-4

bc-4 is a new recessive gene locus that interacts with *bc-2* to condition resistance to BCMV. *bc-4* was found in host groups 4, 5, and 7. Genes encoding Vps4 AAA⁺ ATPase ESCRT proteins on Pv11 and Pv05 are candidates for *bc-2* and *bc-4*. A draft of the manuscript was sent to the committee on 7-29-21. Soler-Garzon et al. are planning on submitting this paper in the next several weeks for publication.

Decision: Members were asked to respond by Sept. 10, 2021 regarding their approval of the *bc-4* gene symbol. New symbol was subsequently approved by the committee.

Same gene with different mutations

The use of superscripts in brackets is proposed to denote different mutations for the same gene (ie. the different mutations are not different alleles in the genetic sense). *bc-2*^[d] denotes a 10 kb deletion of Durango origin and *bc-2*^[n] a single SNP deletion found in a navy bean landrace selection (Robust) for the gene encoding Vps4 AAA⁺ ATPase ESCRT on Pv11. Both mutations (frameshift) result in truncated proteins.

Decision: Support the use of superscripts in brackets to denote different mutations for the same gene. These mutations are not different alleles in the genetic sense since different mutations may result in the same phenotype. E.g. $bc-2^{[common\ red]}$ denotes a 10 kb deletion in the common red line of Durango origin and $bc-2^{[robust]}$ a single SNP deletion in the line Robust.

Move $bc-1^2$ and $bc-2^2$ to the obsolete symbol list.

There is only one resistance allele for the $Bc-1$ and $Bc-2$ loci. The differential interaction for $bc-1$ is due to presence versus the absence of $bc-u^d$. The differential interaction for $bc-2$ is due to the presence versus the absence of $bc-u^d$ and $bc-4$.

Decision: Move $bc-1^2$ and $bc-2^2$ to the obsolete symbol list. Consider moving the $bc-u$ symbol to the obsolete symbol list in the next meeting.