BIC Genetics Committee Meeting

Location: The Westin Poinsett Greenville Hotel, Greenville, SC

Date: Wednesday November 8, 2023, 12:30 to 1:15 PM EST

Committee Members: Brown, Dohle, Ferreira, Gepts, Goncalves-Vidigal, McClean, Miklas (Chair), Osorno, Parker, Porch, Urrea

Members Present: Dohle, Goncalves-Vidigal, Miklas (Chair), Osorno, Parker, Porch, Urrea

A. Old Business:

1. The Genetics Committee 2022 meeting minutes were approved by email and published in the 2023 BIC v66.

B. New Business:

1. Review gene description changes to BIC Gene List—noted in text below with deletions (strikethrough) and additions (in yellow) for *fin*, *ppd*, *stringless*, *Bct*, etc. (Gepts/Parker, Miklas/Soler-Garzón).

a. *Fin Finitus* (Latin): indeterminate vs. *fin* determinate plant growth (Lamprecht 1935b; Rudorf 1958); long vs. short internode; later vs. earlier flowering. Corresponds to *PvTFL1y* (Phvul001G189200, Kwak et al 2008, 2012; Repinski et al. 2012).

b. *ppd* (*neu*) *photoperiod-insensitive* gene found in 'Redkloud' with a syndrome of effects (Wallace et al. 1993); an allele-specific associated primer is now available for *ppd* (Gu et al. 1995); probably the same locus as Neu^{+} for short day vs. *neu* for day *neutral* flowering response to length of day of Rudorf (1958). The red/far-red photoreceptor gene PHYTOCHROME A3 (PHYA3, Phvul.001G221100) was identified as the *ppd* gene on Pv01 (Kamfwa et al., 2015; Weller et al., 2019).

c. *St stringless* pod; *st* gives a complete string (Prakken 1934). Believed to result from gene duplication of *PvINDEHISCENT* (*PvIND*, Phvul.002G271000) and retrotransposon insertion between the tandem repeats, leading to *PvIND* overexpression in stringless types (Parker et al. 2022). Has modifiers.

d. *...,V* is located on Pv06 (McClean et al. 2002). *V* encodes flavonoid 3′5′ hydroxylase (F3′5′H, Phvul.006G018800), a P450 enzyme required for the expression of dihydromyricetin-derived flavonoids in the flavonoid pathway (García-Fernández et al., 2021; McClean et al., 2022).

e. *Bct* (*Ctv-1*) a gene conditioning resistance to *beet curly top virus* discovered by Schultz and Dean (1947). The *Ctv-1* symbol was proposed by Provvidenti (1987) and updated to *Bct* by Larsen and Miklas (2004). *Bct* is located near 2,943,470 to 3,001,466 bp (G19833 v2.1) on Pv07 (Soler-Garzón et al. 2023), and linked markers are listed in the Beyond SCARs table (http://www.bic.uprm.edu/?page_id=91).

Decision: The gene description amendments were accepted. Juan Osorno motioned, Tim Porch seconded, and all were in favor. Travis Parker and Phil Miklas will update the text and include information about the modifiers, reference genome for gene models, chromosomes, as needed.

2. *bc-u*^{d} and *bc-u*^{r} (formerly *bc-4*) are alleles (manuscript sent) noted in text below with deletions (strikethrough) and additions (in yellow).

bc-u^{d} ….. Originally named *bc-u* by Drijfhout (1978b) but renamed by Soler-Garzón et al. (2021b) to reflect Durango race origin and absence from host groups (HG) 2, 4, 5, 7 and presence in HG-10. Gene model Phvul.005G125100, a Vps4 AAAC ATPase ESCRT protein, was identified (Soler-Garzón et al. 2024) as the candidate gene for *bc-u*^{d} ~~*bc-4*~~, and a marker for the putative causal mutation is listed in the Beyond SCARs table (http://www.bic.uprm.edu/?page_id=91).

bc-u^{r} ~~*bc-4*~~ (previously *bc-4*) (Soler-Garzón et al. 2021b) when combined with *bc-2* provides resistance to ~~all~~ BCMV (except PG-5) but not BCMNV (Soler-Garzón et al. 2024) pathogroups. Gene model Phvul.005G125100, a Vps4 AAAC ATPase ESCRT protein, was identified as the candidate gene for ~~*bc-4*~~ *bc-u*^{r} (the 'r' superscript acknowledges discovery in Robust navy bean) and a SNP marker for the putative causal mutation is listed in the Beyond the SCARS Table (http://www.bic.uprm.edu/?page_id=91).

Decision: The gene description and updates for the *bc-u* locus in the BIC Genes List were approved. Travis Parker motioned, Tim Porch seconded, and all were in favor.

3. **Membership** – updates
    a. Phil Miklas will be rotating off as BIC Genetics Committee Chair. We thank him for his service!
    b. Travis Parker was nominated as the new Chair by Phil Miklas, Carlos Urrea seconded and all were in favor.

C: **Other**: How to handle genes that do not fit qualitative conventions (T. Parker will look into this and report back in 2024)

a. Seed dormancy - pectin acetylesterase-8-2 (*Phvul.003G277500*) underlies seed coat impermeability, and 5-bp insertion reduces function, increasing water uptake (Soltani et al. 2021).

b. Pod indehiscence - *PvPDH1* (*Phvul.003G252100*) and other QTL (Parker et al. 2020)

Discussion: Perhaps such genes could be included and maintained on the gene list in a separate section for now.

c. For such genes would classical descriptors or ortholog names be better?

Discussion: Most were in favor of using the ortholog name versus classical descriptors since it aids in comparisons across species. However, gene orthologs for traits with established gene symbols (such as those in the Gene List) should reference the classical descriptor in any publications. Can continue this discussion in the next meeting.