Minutes

BIC Genetics Committee Meeting
University of Delaware, Carvel Research & Education Center, 16483 County Seat Hwy, Georgetown, DE 19947
Tuesday, 08/20/2024, 4:40pm to 6:00pm

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

Participating in person: Sandra Branham, Karen Cichy, Travis Parker, Juan Osorno, Christine Diepenbrock, Ruifeng (Ray) He, David Gang, Emmalea Ernest, Tim Porch
On-line: Phil Miklas, Phil McClean, Celeste Goncalves-Vidigal, Paul Gepts, Jenna Hirshberger, Valerio Hoyo, Carlos Urrea

A. Old Business

The Genetics Committee minutes from the 2023 BIC meeting were approved (1st and 2nd) and were published online.

B. New Business:

1. Review gene list amendments (3:32-3:50)
    a. <u>Seed color updates from Travis:</u>
        i. *T*: Self-colored seed coat and colored flowers (Emerson 1909a; Lamprecht 1934b; Shaw and Norton 1918). *T* is located on Pv09 (McClean et al. 2002). *Phvul.009G044700, a* WD40-repeat gene model homologous to *TRANSPARENT TESTA GLABRA1* in Arabidopsis, has been proposed for control of *T* (Parker et al. 2024, McClean et al. 2024). At least seven characterized independent putative mutations have been identified at the locus.
        ii. t^{cf}: superscript cf, *colored flower*: a seed coat gene (from PI 597984) for partly colored patterns without pleiotropic expression for white flowers; necessary for expression of the two-points pattern (Bassett et al. 1999a). Whole-genome sequencing has identified a putative 22 Mb inversion in the 3' UTR of the *T* candidate gene model in types with the t^{cf} mutation (Parker et al. 2024).
        iii. *Bip: bipunctata* (Latin): *Bip* and *bip* combine with *Arc* and *arc* to form seed coat patterns based on the hilum; extends seed coat color in partly colored seeds (Lamprecht 1932d, 1940b). Genotype *t z bip* expresses the bipunctata pattern of partly colored seed coats; whereas *t z Bip* expresses virgarcus pattern (Bassett 1996c; Schreiber 1940). *Bip* is linked to *J* and is located on Pv10 (McClean et al. 2002). *Phvul.010G098500*, a bHLH-encoding gene model with sequence homology to *P* in common bean, was proposed for its control (Parker et al. 2024).
        iv. bip^{ana}: Anasazi pattern of partly colored seed coats is expressed by genotype *t Z* bip^{ana}; whereas *t z* bip^{ana} expresses the Anabip pattern (Bassett et al. 2000). A non-synonymous SNP in a conserved residue of *Phvul.010G098500* has been proposed for control of the allele (Parker et al. 2024).
        v. p^{hbw}: stippled seed coat (different from p^{stp}) and violet flowers with the lower (superscript hbw) *half* of the *banner* petal *white* (Bassett 1996a, 2003a). A 612 bp intron deletion in the *P* gene model is found in types with this allele and was proposed to control the pattern (Parker et al. 2024). The intron deletion

eliminates conserved sequence motifs and is associated with a 20-fold reduction in *P* expression (Parker et al. 2024).

Co genes

1. Celeste has contacted Travis about Indian paper--Chrom. 10 (Indian group)—New *Co-18* gene symbol requested (used race 3) from KRC-5 (Lateef et al., 2024)
2. *Co* genes and locations—*Co-5* no location others (Pv07 Susa et al.).
3. Contact author after checking on *Co-11, Co-8, Co-12*?—allelism tests.
4. Celeste tried to make *Co-11* and *Co-12* crosses, but no results
5. No isolate information included; Reference information not provided
6. Clusters of genes differ from genotype to genotype, so would need to sequence them.
7. To do: Disclaimer that not confirmed, but do add to gene list.
8. (Travis contacted the authors to discuss in more detail

CoPv01^CDRK/PhgPv01^CDRK: on Pv01; Nomenclature not according to standards

1. From CDRK (Gonzalvez-Vidigal et al., 2020; Lovatto et al., 2023)
2. Separate gene or same cluster?—why not identify it as a separate as Co gene. Need to adhere to consistent nomenclature
3. Transcriptome or QTL mapping results?
4. Review outside of the meeting: Decide by email (Travis will send out the papers and suggestions). Continue with nomenclature, add in other information as details or retain the same symbols as in the publication; Miklas--Indicate that in the Co-1 complex—a bunch of candidate genes that part of the cluster; Several 211kb away from phg-1, so not very highly linked; Organize resources to map out genes/QTL so can serve as a community resource.

2. Discussion: Integrating genomics-based discoveries with classical nomenclature (3:50-4:00)
    a. Genes increasingly being named after homologs or gene models with no other name… how to integrate?
    b. How to handle large-effect QTLs? Should these be included at all?
    c. List in table format? E.g., (*St* | *PvINDEHISCENT* | *Phvul.002G271000* | [description] | Pv02 | flanking markers | population, environment, test on panels across gene pools—MDP/ADP, selectable markers--separate….)
        i. This could possibly help in assessing problematic/useful linkages

1. List in a table format the genes and their locations in a table format to have a more useful resource and reference (from the List of Genes only).
    a. Like the Tm shift table. Keep list for description.
    b. No QTLs—only validated genes from list.
    c. Having two studies confirm results—suggested from other crops.
    d. In Excel to sort and work with and make it useful—Travis will start table and then others can contribute to.
    e. Soltani dormancy genes in grey zone
    f. Shattering could be included…

3. Preferred genotyping strategies (4:00-4:05)?
    a. Best methods for SNP sets in particular; future status of 12K BeadChip

    1. Bead chip great resource, but we are losing these resources and not so available any longer.
    2. Genome sequencing—cheaper, Kmer analysis
    3. SNP chips—Thermo Fisher chip is about \$10/sample for 50-100 markers
        a. Agroseq panel; per marker price; Chickpea 5,000 (85% amplifying regularly). Ion torrent based…
        b. Thermo Fisher--50k for 6,000 samples and then \$10/sample cost. 4,000 SNPs for NDSU for trait-based selection
        c. GS—narrow down to 500 markers certain programs (trait-based efforts); working on 25 traits in barely (quality)—reduce field testing by half.
        d. Illumina chip—more for mapping, broad diversity
        e. Hudson Alpha—been slow for UC Davis; not clean necessarily
        f. Whole genome sequencing—good, but cost higher
        g. Pan-Genome—Valerio using 12k chip work
        h. PACE and KASP markers useful as well
    4. GBS platform another option

4. Discussion (4:05-4:25): Is it worth pursuing a larger grant to take on some of the bigger genetics questions in a coordinated and systematic way?
    a. For example, SCRI SREP? https://www.nifa.usda.gov/sites/default/files/2023-10/FY24-SCRI-Pre-App-RFA-508-P_0.pdf
    b. Topics: divide-and-conquer on the major disease resistances and seed type genes?
    c. Pre-breeding to move a set of major resistances into each major market class?
    d. Improve genomic resources?
        i. Whole-genome sequencing → Expanded MDP, ADP, DDP, SnAP, etc.?
        ii. Improved G19833 reference?
    e. Other priority areas suggestions?
    1. SCRI Popping beans grant has come through
    2. SCRI for Lima bean
    3. AFRI small bean project also funded--shelling
    4. Other opportunities with opportunities for dry beans
        a. Unlikely to get another SCRI after popping bean project
    5. NSF plant genome grant opportunity
    6. Whole-genome sequencing—extracting out MDP, ADP, DDP, SnAP coordinates
        a. Expand work with whole-genome sequencing
        b. Trait of interest—select markers to move phenotype based on background
        c. Include genes that identified—seed coat color McClean.
    7. Improved G19833 reference—telomere to telomere sequence (Phil McClean already working on)

C. Membership updates and other business (4:25-4:30)

-Sandra, Ray, Christine new members
-motioned Juan and 2nd by Tim