BIC Genetics Committee Minutes
Meeting held during the 2009 W1150 Meeting
Isabela Substation of the University of Puerto Rico, Feb. 21, 2009

Started: 10AM

Attendance:

	Attendee	**University/Agency**	**Genetics Committee**
1.	Paul Gepts	University of California, Davis	Member
2.	Jim Kelly	Michigan State	Member
3.	Phil Miklas	USDA-ARS	Member
4.	Tim Porch	USDA-ARS (Chair)	Member
5.	Carlos Urrea	University of Nebraska	Member
6.	Molly Welsh	USDA-ARS (ex-officio)	Member
7.	Judith Brown	University of Arizona	
8.	Jim Myers	Oregon State University	
9.	Mark Brick	Colorado State University	
10.	Phillip Griffiths	Cornell University	
11.	Shree Singh	University of Idaho	
12.	M.A. Pastor-Corrales	USDA-ARS	
13.	Steve Noffsinger	Seneca Foods Corp.	
14.	Jim Nienhuis	University of Wisconsin	
15.	A.M. Thro	USDA-CSREES	

Minutes:

1. Topic: Genetic map

Tim Porch presented an updated version of the genetic map, where chromosomes have been rotated top to bottom, based on the new linkage group nomenclature presented in a BIC note by Pedrosa et al. (2008). A recommendation was made to add new microsatellite markers and Phil McClean's gene-based markers to the genetic map.

Decisions

The Genetics Committee decided to eliminate the old Roman numeral chromosome numbers at the bottom of the linkage groups. Paul Gepts will check and determine if additional references are needed for the markers and symbols used in the map, which are mentioned in the legend. Additions and corrections to the map can be submitted by the end of March 2009 after which the map will be posted on the BIC website.

2. Topic: QTL nomenclature

Phil Miklas proposed a QTL nomenclature method for common bean publications based on those used in other species including rice, Rosaceae and soybean. The group consulted and decided on a standard nomenclature for future common bean publications:

Decision

Guidelines for common bean QTL nomenclature:

1. Capitalize 2-3 letter abbreviation for trait. Capitalized trait name should not be italicized. For example, WM for white mold. A preferred list of abbreviations to use for common traits should be generated, and updated periodically.

2. Each QTL will have a linkage group designation directly after the 2-3 letter abbreviation. For example WM1 indicates a QTL for white mold on linkage group 1.
3. QTL should be listed in chronological order. Thus, new publications on a specific trait will initially need to review and number previous QTL designations in order to arrive at a number for new QTL. For example the first QTL identified on linkage group 1 would be named WM1.1, and the second independent QTL on the linkage group would be named WM1.2, and so forth.
4. The population where the new QTL was identified should be indicated by an abbreviation in caps and non-italicized superscript after the linkage group designation. For example, the first QTL indentified on linkage group 1 for white mold resistance was in the RIL mapping population A55/G122, thus would be designated WM1.1^{AG}
5. To distinguish among QTL which co-localize or overlap in the same general region, subsequent population abbreviations would be separated by commas and listed in order of discovery. For example, the overlapping QTL identified first in A55/G122 and subsequently in John/Doe would be designated WM1.1^{AG,JD}, and so forth.

Additional provisions:

6. If upon fine mapping in the future two overlapping QTL are proven to be independent, then the subsequent QTL in the example above could be renamed WM1.1.1^{JD} to distinguish it from WM1.1^{AG}
7. If two independent QTL (Ex: WM1.1^{AG,} and WM1.2^{JD} in the future are proven to co-localize, then the first QTL identified would retain its original name and the second QTL would be incorporated in the name of the first QTL: WM1.1^{AG,JD} . Note if this occurs then original number (2 for this case) representing chronological order is not used again.

3. Topic: Marker development and discovery

Paul Gepts presented a proposal that is being prepared for AFRI for the development of a molecular marker toolbox for breeders. This toolbox would integrate the common bean sequence, marker, and linkage map information into an easily accessible web-based interface to assist breeders in marker discovery and development. This resource will use the soybean genome and will: 1. Map targeted *P. vulgaris* sequences to the soybean genome, 2. Use soybean/common bean synteny for the identification of closely linked *P. vulgaris* sequences, and 3. Assist in the development of new markers and the identification of candidate genes. Paul Gepts has requested input as to the ten most useful target traits and genes to focus on in the proposal. Suggestions were made including regions where QTL for biotic resistance co-localize including regions on chromosomes 2, 4, and 11 as well as the development of additional markers for those SCAR markers that do not function across gene pools. The proposal is integrated with the other two proposals being submitted to USDA involving SNP development and genome sequencing.

No Decision

4. Topic: Manuscript on blue pattern flower color

A new gene symbol, t^{bp}, for a new allele at the *T* locus conditioning blue patterned flowers in the presence of *Prp*^{i}*-2* is being proposed in the manuscript “Blue Pattern

Flower in Common Bean Expressed by Interaction of *Prp*^{i}*-2* with a New Gene t^{bp}” by Mark Bassett and Phil Miklas. Jim Kelly suggested that the placement of *Prp-2* on chromosome 7 be reviewed since the bracketed designation [*C prp*] was used while the C locus is located on chromosome 8.

Decision

Through email and the discussion above, the Genetics Committee has accepted the t^{bp} gene symbol and the evidence provided in the manuscript. It was also clarified that the *Prp-2* locus is independent of the [*C prp*] complex locus.

5. Topic: Committee membership

No changes will be made at this time to the committee membership.

6. Topic: Next meeting

The next Genetics Committee meeting will be held during the BIC meeting on October 28th from 11AM-12PM at the Hilton Garden Inn, Fort Collins, Colorado.

Adjourned: 12PM

Minutes prepared by Tim Porch