GUIDELINES FOR COMMON BEAN QTL NOMENCLATURE

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Quantitative trait locus (QTL) analysis has become an important tool for the characterization and breeding of complex traits in crops plants, such as common bean (*Phaseolus vulgaris* L.). A standard system for naming QTL in common bean is needed for effective referencing of new and previously identified traits to more effectively differentiate QTL. A similar nomenclature system for chromosome identification in common bean was adopted (Pedrosa-Harand et al., 2008).

Although QTL for disease, abiotic, and pest resistance have been identified in common bean, the comparison of QTL across studies, populations, and locations is occurring more frequently with the proliferation of QTL studies. This QTL information serves to test the effects of loci across different genetic and environmental backgrounds, and thus to estimate GxE interactions. With this information available, those stable and consistent QTL can be used for marker-assisted selection in breeding programs. For example, a common bacterial blight QTL, linked to the BC409 marker, was shown to have significant effects across four different common bean populations and with three different *Xanthomonas axonopodis* strains, making it a broadly effective and stable QTL (Jung et al. 1999). Recent work with white mold resistance (Soule et al., 2011) in common bean is another example whereby QTL with stable expression across environments and genetic backgrounds have been identified and used for marker-assisted selection (Kolkman and Kelly, 2003; Miklas et al., 2003, 2007; Ender et al., 2008; Miklas, 2009).

Considering the need for a common nomenclature, the Common Bean Genetics Committee approved the adoption of QTL nomenclature guidelines for use in future QTL publications, described below, during its 2009 Isabela, Puerto Rico, meeting. White mold QTL are used as an example for describing the nomenclature.

Guidelines for common bean QTL nomenclature:

1. To identify each trait, use capitalized letters in a 2-3 letter abbreviation. The 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 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 linkage group 1 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 A55/G122 RIL mapping population, and 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 should 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. The population abbreviations need only be cited in the first mention of the QTL in a publication. Thereafter, the shortened version, e.g. WM1.1, can be used.

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 that if this occurs then the original number (2 in this case) representing chronological order is not used again.

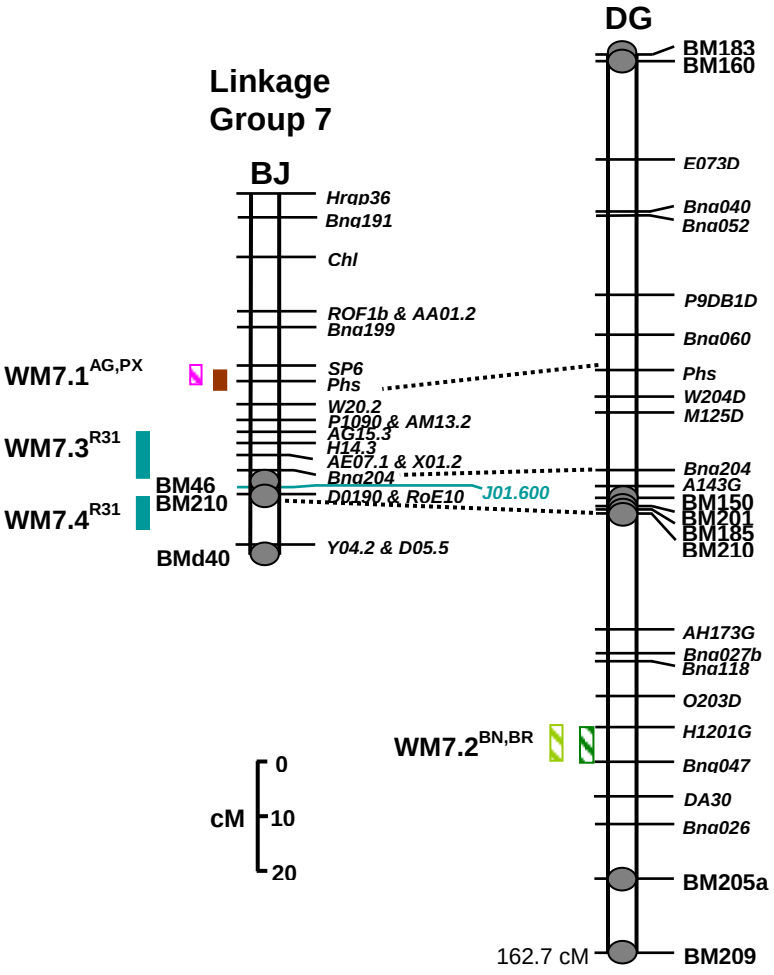

Figure 1. Comparative mapping in BJ-DG core maps (Blair et al., 2003) of QTL for resistance to white mold identified to date on linkage group 7 in different populations. PX, PC50/XAN159, Park et al., 2001; AG, A55/G122, Miklas et al., 2003; BN, Bunsi/Newport, Kolkman and Kelly, 2001; BR, Bunsi/Raven, Ender and Kelly, 2005; R31, Raven/I9365-31, Miklas et al., unpublished).

For example, the first QTL discovered on linkage group 7 (Fig. 1) was identified in the AG population (Miklas et al., 2001) near the phaseolin seed protein locus (*Phs*). Subsequently, the same QTL was identified in population PX (Park et al., 2001); thus, this QTL is designated WM7.1^{AG,PX}. The second QTL found on linkage 7, near the Bng047 marker, was identified first in the BN population (Kolkman and Kelly, 2003) and subsequently in the BR population (Ender and Kelly, 2005); thus, this QTL is named WM7.2^{BN,BR}. In the recently published study (Soule et al., 2011), two independent QTL in R31 were mapped to linkage group 7 on alternate sides of the Bng204 marker; thus, these QTL are named WM7.3^{R31} and WM7.4^{R31}.

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