

Recommendations for Standard QTL Nomenclature and Reporting in the Rosaceae

Background

Over the course of the last year, the Rosaceae genomics, genetics and breeding community has made great strides in identifying research directions and priorities. The completion of the U.S. Rosaceae Genomics, Genetics and Breeding Initiative White Paper in March 2006, followed closely by the 3rd International Rosaceae Genomics Conference (RGC3) in Napier, New Zealand, solidified the community atmosphere among research labs and institutions in this group. Integral to this process has been the continuing development and refinement of the Genome Database for Rosaceae (GDR, www.rosaceae.org), a central database of genomic information for rosaceous crops. Currently, the GDR provides an excellent resource for comparative linkage mapping, alignment of the *Prunus* physical map, and EST identification. However, quantitative trait loci (QTL) are one of the key genomic tools not yet archived on the GDR.

The lack of consistency in QTL analysis and reporting formats may contribute to the lag in inclusion of these data. During the *Prunus* workshop at the RGC3 conference, we were charged with developing a uniform nomenclature standard for reporting *Prunus* QTL in publications and at the GDR. The outline that follows is our attempt to bring the *Prunus* community together with a common set of reporting standards for future QTL mapping studies. However, recognizing the movement toward a common Rosaceae language, we have included options that can be adopted by the other Rosaceae species immediately, and will facilitate comparative QTL mapping across all of Rosaceae in the future.

QTL label nomenclature and map reporting

Quick review of a map location should provide as much pertinent information as possible. Therefore, QTL loci should be readily distinguishable from other map features by placement of a “q” at the beginning of the name. Emerging evidence of the colinearity of genomes within Rosaceae allows grouping according to subfamily rather than species for a simplified method of reporting where QTL were identified. Reported traits should be abbreviated as much as possible, leaving one letter abbreviations solely for reporting genes. The QTL location will be permanently identified by linkage group and a serial number according to chronology of reporting. It is often important to distinguish between QTL that appear in multiple years or locations. For this reason, the superscript “m” will be used to identify QTL that meet these requirements. Two QTLs for the same trait from the same clonal genotype (whether or not they are detected in the same study, same year, or same population) that have overlapping 5% confidence intervals (CIs) are to be considered the same QTL. The following is an example:

qP-Mat2.7^m

- q = quantitative trait (to distinguish from major gene)
- P = Prunoideae (or “R” for Rosoideae, “M” for Maloideae), followed by a dash
- Mat = trait code (here it is Maturity) beginning with a capital letter for the start of any abbreviated word, followed by lower case letters of the word, as short as possible (as few as 2 letters, preferably 3, not 1 because that is reserved for genes)
- 2 = *Prunus/Prunoideae* chromosome/linkage group 2
- 7 = 7th chronological QTL for this trait reported on this chromosome
- m = (only if relevant) Same QTL identified in multiple years or treatments or populations derived from the same cultivar

QTL representation

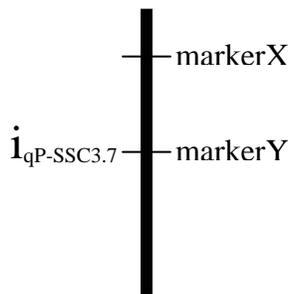
Confidence intervals should be determined by permutation tests and reported as 1% level for “peak”, 5% for determining QTL overlap, and 10% for additional information. These can be graphically depicted in a bar as shown below:



Solid bar is 1% CI, open bar is 5% CI, dotted line is 10% CI

Two QTL for the same trait from the same clonal genotype (whether or not they are detected in the same study, same year, or same population) that have overlapping 5% CIs are to be considered the same QTL.

Loci/QTL with epistatic effects on a QTL can be recorded by placing on the map, to the left of the locus/QTL, a lower case “i” with subscript of the QTL label:



GDR involvement

Because the GDR is one of the two major locations where this information will be accessible, we propose that it become the first stop for reporting QTL data. Therefore, supplementary details similar to those needed for publication will be provided to the GDR along with map and QTL data. A list of pertinent details will be required for each QTL reported, including species, cultivar, population, location of study, how the trait was measured, and when the trait was measured. A master checklist for GDR submission will have the added benefit of standardizing QTL reporting at the publication stage.

The number scheme proposed would be administered by the GDR. We propose that prior to publication, a research group would contact the GDR-QTL administrator to report the new QTL, and using the supplementary details provided, the next consecutive QTL number would be provided for that trait. For this to be efficient, a master list of trait codes should be developed. A simplified searchable method would be to categorize different traits under inclusive categories, for example, as the Gramene database has adopted (www.gramene.org).

GDR vs. Publications

All the above is relevant for both individual publication of QTL and posting of the information on the GDR. However, additional elements can be incorporated on the GDR, such as hyperlinks, drop-down menus, etc.

Immediate priorities for *Prunus*

Fortunately, we are still in the beginning stages of QTL mapping in Rosaceae. For example, a review of the literature indicates only a handful of pertinent publications in *Prunus*. Therefore, we propose a joint publication that reviews all *Prunus* QTL published to date, that brings them all in line with the consensus nomenclature. This gives some incentive to those labs involved in changing the nomenclature of their previously published QTLs

Furthermore, we propose the formation of a **QTL Working Group** that will be Rosaceae-wide, where like-minded researchers can discuss all things QTL. A session devoted to Rosaceae QTL research at RGC4 could be an outlet for all of the pent-up excitement we have over these little bundles of joy.