Mapping QTLs in a *Mimulus* F_2 population with multiple-interval mapping method

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1 Material and Methods

The analysis here considered a previously built genetic map from a F_2 population obtained from an interspecific biparental cross between two inbred lines, IM62 (*Mimulus guttatus*) and SF5.4 (*Mimulus nasutus*). All the procedures for obtaning the genotypic and phenotipic data are described in Fishman et al. (2001) and Fishman et al. (2002). The description of the procedure to build the genetic map was not formally published, but can be acessed at this link.

Here we mapped QTLs for only one of the sixteen evaluated phenotipic characteristics: the number of nonviable pollen grains. We considered the measures were normally distribuited. We tested the first multiple-interval mapping (Kao et al., 1999; Zeng et al., 1999) model including QTLs suggested by composite interval mapping , bi-dimensional QTL scan and stepwise regression. All analysis were made in R package R/QTL (Broman et al., 2003).

Composite interval mapping (Jansen and Stam, 1994; Zeng, 1994) was applied previously, details can be accessed at this link. We reduced the threshold from 3.96 to 2.5 to suggest more QTLs for multiple-interval mapping. The five QTLs suggested were located in chromossomes 3, 5, 6 and 13. Bi-dimensional QTL scan was performed by *scantwo* function. The threshold was defined by 1000 permutation tests. The analysis suggested five QTLs located at the same chromossomes suggested by composite interval mapping and also three interations between them. Moreover, the heatmap generated by the function suggested some epistatic effect between QTLs in chromossomes 3 and 14. We use the *stepwiseqtl* function to perform stepwise regression, wich suggested only three QTLs, located at chromossomes 3, 5 and 13, and one epistatic effect between QTLs in chromossome 3 and 13.

Therefore, we tested the first model for multiple-interval mapping using *makeqtl, fitqtl* and *refineqtl*, and considering all the QTLs and interations suggested by the analysis, totalizing 6 QTLs and 5 interations between them. This model showed no significant effects at 5% level for QTL in chromossome 14, also for the interations between QTLs in chromossomes 3 and 14, 5 and 13. We removed them and tested a second model. All the QTLs and interations in the second model were significant, but the QTL in chromossome 6 had a small effect compared with others, then we decided to remove this QTL from the analysis. Our decision was reinforced by stepwise regression results, which did not suggested this QTL. We tested a third model only with 4 QTLs, with two of them located at chromossome 13. By the LOD profile graphic generated, we observated a lack of markers between this two QTLs, which suggest that, probabily, they refers to only one QTL. We removed one of them and tested a fourth model, which showed no significance at 5% level for interation between QTLs in chromossomes 5 and 13, suggesting a final model with 3 QTLs and one interation between QTLs in chromossomes 3 and 13, the same model suggested by stepwise regression.

Finally, the interval mapping, composite interval mapping and multiple-interval mapping methodologies were graphically compared.

References

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