

## MATERIAL AND METHODS

We used one genetic map previously built from a F<sub>2</sub> population by the cross of two single inbred lines (*Mimulus guttatus* and *M. nasutus*), with 287 individuals genotyped with 418 markers, which 377 markers had type 1:2:1 segregation (codominant) and 205 markers had type 3:1 segregation (dominant). The OneMap package version 2.0-4 (Margarido et al., 2007) and R software version 3.2.0 (R Development Core Team, 2015) with RStudio software was used to do the mapping population.

The R and R/qtl package was used for the multiple interval mapping (MIM) analysis (Broman et al., 2003). The phenotype traits selected were *fl* and *pa*. First, we performed the composite interval mapping method (CIM) for the *pa* and *fl* traits, using LODs thresholds as 3,9 and 3,8 respectively. For the MIM analyzes, first was used the function *scantwo* for the scan the genome looking for more QTL. It was calculated the LOD scores penalties for the threshold (10%) using the *calc.penalties* function and performing 1000 permutations of a two-dimensional genome scan using the Haley-Knott approximation. Next, the function *stepwiseqtl*, that performing a stepwise search forward selection followed by backward deletion, using BIC<sub>δ</sub> criterion (Broman & Speed, 2002), with Haley-Knott approximation, was used for the selection of the best model, with ten QTL maximum. The functions *makeqtl* and *fitqtl* was used for the detection of the effects of the QTL. The same procedures was performed for both traits.

## REFERENCE

- Broman, K. W., H. Wu, S. Sen, and G. A. Churchill. (2003). R/qtl: QTL mapping in experimental crosses. *Bioinformatics* **19**:889-890.
- Broman, K. W., & Speed, T. P. (2002). A model selection approach for the identification of quantitative trait loci in experimental crosses. *Journal of the Royal Statistical Society, Series B*, **64**(4): 641-656
- R Core Team (2015). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.
- Halley, S. and S. A., Knott, 1992 A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* **69**: 315-324.
- Margarido, G. R. A., A. P. Souza, and A. A. F. Garcia, 2007 OneMap: software for genetic mapping in outcrossing species. *Hereditas* **144**: 78-79.