MATERIAL AND METHODS

Plant material and markers molecular The Mimulus population (287 F_2 individuals) was genotyped with 418 molecular markers, which 213 markers are codominants and 205 markers are dominants. Genetic linkage maps were determined using the OneMap software (MARGARIDO *et al.*, 2007; MARGARIDO *et al.*, 2011) implemented in the statistical software R (R Development Core Time 2015). The map has 398 markers distributed in the 14 chromosomes. The phenotypic trait analyzed was **ww**.

Multiple Interval Mapping Information about the Composite Interval Mapping and the Two-dimensional Mapping was considered to formulate the initial model of the Multiple Interval Mapping, using the package R/qtl (BROMAN *et al.*, 2003). The initial model was constructed with the function *makeqtl*, considering four QTLs. The significance of the QTLs was verified with the function *fitqtl*. No significant QTLs was droped with the function *dropfromqtl* and the function *refineqtl* was used to improved estimates of the locations of the significant QTLs. The interaction between the QTLs and the addition of new QTLs was evaluated with the functions *addint* and *addqtl*.

LITERATURE CITED

BROMAN, K. W., H. WU, Ś. SEN, and G. A. CHURCHILL, 2003 R/qtl: QTL mapping in experimental crosses. Bioinformatics, 19: 889-890.

MARGARIDO, G. R. A., M. MOLLINARI, and A. A. F. GARCIA, 2011 OneMap Tutorial: Software for constructing genetic maps in experimental crosses: full-sib, RILs, F2 and back- crosses. Available: http://cran.r-project.org/web/packages/onemap/onemap.pdf. Accessed 22 April 2015.

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