MATERIAL AND METHODS

Plant material and molecular markers

For this mapping study, were used 282 individuals of the F_2 population originated of interspecific cross between *Mimulus guttatus* and *M. nasutus*. These individuals were genotyped with 418 markers, which 213 markers had type 1:2:1 segregation (codominant) and 205 markers had type 3:1 segregation (dominant). Among these markers, seven (AA208, BB327, BB279, CA392, BC135, CC371, MgSTS23) were discarded because they presented unlike markers, this is, the markers not bound to any linkage group.

Linkage map construction

We used 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 to do the mapping population. Initially, the two points test was used for estimate the recombination fraction between all pairs of markers. Minimum LOD 6.0 and maximum recombination frequency of 0.37 were used to separate markers into linkage groups (LG). To order the markers within each LG, we used the Kosambi function and Rapid Delineation Chain algorithm (RCD) associated with RIPPLE algorithm, which showed satisfactory results in accordance with Mollinari et al. (2009). At this stage, 10 linkage groups were form. However, according to previous work conducted on the same population (Fishman et al., 2001), it is known that this species contains 14 groups. Thus, two major groups (LG1 and LG3) were divided into three other groups with fewer markers. To do this division, these groups were separated from the others and the same analyzes were performed again by changing the criteria for declaring linkage, the maximum frequency of recombination and the minimum LOD. Finally, according to heatmaps generated for each linkage group the markers that showed evidence that did not belong to such linkage group were exclude (MgSTS441, AA153c, AA420, BA125, BD411, CA384, BC125, BD55, AAT233, BA394, CC114, AAT272). Then, 14 linkage groups were formed being renamed according to the aforementioned work. After that the final map was plotted using the software MapChart (Voorrips, 2002).

LITERATURE CITED

Fishman, L., A. J. Kelly, E. Morgan and J. H. Wilis, 2001 A genetic map in the *Mimulus guttatus* species complex reveals transmission ratio distortion due to heterospecific interactions. Genetics **159**: 1701-1716.

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.

Mollinari, M., G. R. A. Margarido, R. Vencovsky and A. A. F Garcia, 2009 Evaluation of algorithms used to order markers on genetic maps. Heredity **103**: 494-502.

R Development Core Team, 2015. R: A language and environment for statistical computing. R Foundation for Statistical Computing, version 3.2.0, Vienna, Austria. URL http://cran.r-project.org/

Voorrips, R.E., 2002. MapChart: Software for the graphical presentation of linkage maps and QTLs. The Journal of Heredity 93 (1): 77-78.