Linkage map of *Mimulus spp.*

A genetic linkage map was constructed by Fishman *et al.* and published in the Genetics Journal in 2001. Knowing that more markers were genotyped after it was published, and that this information is available, the objective of this exercise is to reconstruct the genetic linkage map using the whole dataset. The F2 population is composed by 287 genotyped individuals and 418 markers. The softwares used to build this new map were R and *Onemap*.

Material and Methods

A genetic linkage map of an interspecific crossing between *Mimulus guttatus* and *M. nasutus* was constructed by Fishman *et al.* (2001) and updated with posterior information of new markers. Fishman *et al.* (2001) had constructed the prior map with 255 markers and using the program MAPMAKER 3.0. The new linkage map was built using the program *Onemap*® (version in development -Margarido *et al.*) and Rstudio® version 3.4. A total of 287 genotyped individuals of an F2 population and 418 markers were analyzed. Among these markers, 213 were codominants and 205 dominants. In order to build the final map several rounds of mapping, grouping and ordering within each linkage group were necessary, and relocation of markers to correspond with was published before. Within the *Onemap* package, the type of the molecular markers and their segregation pattern, as well as the missing data were graphically analyzed through the function plot.onemap(). After, the segregation test was performed to verify if the markers segregate in accordance with the expected Mendelian segregation pattern. All the markers, including those with distorted segregation pattern were subjected to the two point test, which calculate the recombination fraction between all pairs of markers. It was performed using the *Onemap* function rf_2pts(). To create the linkage groups first the markers were organized into a unordered sequence using the command make_seq() and them they were assigned into linkage groups with the function group(). In the first attempt it was used the suggested LOD and the default recombination fraction, resulting in ten linkage groups. Then, the markers were ordered within each group. The mapping function choosen was Kosambi, implement by the function set_map_function ().The functions *compare*, *Rapid Chain Delineation* and *try*, were applied through the order_seq() command, which automate the process of mapping a sequence of markers, combining compare and try.seq functions. The algorithm *Ripple* was used to check for plausible alternative orders. By analyzing the *heatmaps* plotted for these groups it was decided that the group one and the group three should each one be split in three new groups. Also, markers lacking appropriate recombination evidence were excluded. A total of 29 markers were discarded and the final map has 14 linkage groups, as well as the map published previously. This final map figure containing the linkage groups was built using the program *MapChart* ®.

References

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