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FIRST GENETIC MAPS DEVELOPMENT AND QTL ANALYSIS FOR FLOWER COLOR IN RANUNCULUS ASIATICUS L.

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Persian buttercup (*Ranunculus asiaticus* L.; 2x=2n=16; estimated genome size: 7.6Gb) is an ornamental perennial crop native of Iran, Turkey and Greece, marketed both as cut flower or potted plant. At present the development of new varieties relies on controlled mating followed by selection of plants showing segregation and recombination of desirable traits, which are vegetatively propagated by means of rhizomes. To date the application of DNA-based techniques in the species is very limited, thus more knowledge of buttercup genetics and genomics is needed for escalating breeding efficiency and market requests.

Reduced-representation sequencing (RRS) is an advantageous approach to generate genome-wide high-throughput sequencing data and obtain a large number of genetic polymorphisms representative of the whole genome, especially in species characterized by large genome sizes. For this reason, RSS techniques are widely applied for molecular marker development, population genetics, genetic map construction and QTL mapping.

We report on the development of the first molecular-genetic maps in *R. asiaticus*, based on a two-way pseudo-testcross strategy, by applying a RRS approach in two F1 mapping populations sharing a common male parental line characterized by simple flower whose, while female parents were a genotype of a 'ponpon' variety' and a 'double flower' variety,

A double digest restriction-site associated DNA (ddRAD) approach generated a total of ~2Gb demultiplexed reads, resulting in an average of 8,3M reads

per line. The *stacks* pipeline was applied for the development of a mock reference genome based on the RRS data, and SNP markers segregating in only one of the parents were retained for map construction by considering the F1 population as a backcross. The four parental maps (two of the female parents and two of the common male parent) were aligned by means of 106 common markers, identifying 8 linkage groups, which correspond to the haploid chromosome number of the species. From 540 to 680 markers were associated with each parental map, with a marker density ranging from 1 to 4.4 markers/cM.

The two F1 segregating populations were also phenotyped for plant and flower traits, and we validated the developed maps by performing QTL analysis for flower color, leading to the identification of a major locus affecting buttercup flower purple pigmentation. These results shed light on the genetics of Persian buttercup, enabling the development of new technologies that might contribute to future varietal development.