

Assembly and annotation of genomes of some species from the apomictic genus *Boechera* and evolutionary analysis of apomixis-associated genes

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Apomixis is asexual way of plant reproduction through seeds, which could be found in more than 400 plant species representing almost 40 families. It is believed that apomixis evolved independently in several taxa from sexual ancestors. Apomixis could be considered as a developmental variation of sexual reproduction in which some steps are lost, reduced, deregulated, desynchronized or changed. Thus, apomictic and sexual reproduction are closely related and they share many regulatory components. Molecular and genetic basis underlying apomixis and amphimixis (sexual reproduction) regulation still remains poorly understood. The ability to produce maternal clones and therefore to fix useful traits in the further generations of various crop plants could streamline agricultural breeding strategies based on the genetic aspects of apomixis. The potential of apomixis as a next generation technology for plant breeding attracts huge interest to elucidate molecular and genetic mechanisms of its regulation. Closely related to the model plant *Arabidopsis thaliana*, the genus *Boechera* is known to contain both sexual and apomictic species or accessions. *Boechera retrofracta* is a diploid sexually reproducing species and is thought to be an ancestral parent species of apomictic species. In the presentation will be reported the *de novo* assembly of the *B. retrofracta* genome using short Illumina and Roche reads from 1 paired-end and 3 mate pair libraries. The distribution of 23-mers from the paired end library has indicated a low level of heterozygosity and the presence of detectable duplications and triplications. The genome size was estimated to be equal 227 Mb. N50 of the assembled scaffolds was 2.3 Mb. 27048 protein-coding genes were predicted using a hybrid approach that combines homology-based and *de novo* methods. Also repeats, tRNA and rRNA genes were annotated. Finally, genes of *B. retrofracta* and 6 other Brassicaceae species were used for phylogenetic tree reconstruction. Also, we explored the histidine exonuclease *APOLLO* locus, related to apomixis in *Boechera*, and proposed model of its evolution through the series of duplications. An assembled genome of *B. retrofracta* will help in the challenging assembly of the highly heterozygous genomes of hybrid apomictic species such as *B. divaricarpa*. The *B. retrofracta* genome will also provide a basis to decipher the hybridogenesis events that led to the formation of apomictic *Boechera* accessions.