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Whole genome sequencing approach to identify pollen-part modifier conferring self-compatibility in sweet cherry 'Cristobalina'

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Abstract

Self-incompatibility (SI) is an important reproductive mechanism to maintain the genetic diversity within a plant species. However, SI can be a limiting factor for efficient production and breeding of cultivated plants. Many of rosaceous fruit tree species exhibits the S-RNase-based gametophytic SI, which uses S-RNase and F-box proteins for pistil S and pollen S specificity determinants, respectively. Although most of the self-compatible (SC) mutants reported to date in the Rosaceae are from mutations in the specificity determinants, SC genes located outside of the S locus have also been reported. SC in *Prunus avium* 'Cristobalina' is such an example and presumed to be conferred by a mutation of a pollen-part modifier gene, which is located outside of the S locus (LG3). Because the modifier gene is necessary for pollen SI reaction, identification and functional characterization of SI modifier is important for the clarification of the whole image of SI reaction in S-RNase-based gametophytic SI system. Furthermore, the obtained knowledge can be utilized to breed SC cultivars and to develop artificial SI controls. In this study, we conducted a whole-genome sequencing analysis to identify the modifier gene candidates of 'Cristobalina'. Two 'Cristobalina' F_1 populations, both segregating to SC and SI individuals, were subject to Illumina genome sequencing with a 5x genome coverage for each individual. Obtained reads were subdivided into 35-bp subsequences called k-mers. K-mers thus obtained were cataloged for SC and SI pools, and SC-specific k-mers were extracted. Then, the original reads containing the SC-specific k-mers were assembled into candidate contigs containing SC locus of 'Cristobalina'. Next, we further checked SC-specificity of the contigs by utilizing Illumina genome reads from various sweet cherry cultivars and 'Cristobalina' progenies. Comparisons of the SC-specific genomic contigs obtained and pollen mRNA-Seq data are now underway to identify a candidate causal gene for SC in 'Cristobalina'.