



P0672: NGS Analysis Reveals a Possible Causal Mutation Conferring Self-Compatibility in a Sweet Cherry Cultivar Cristobalina

Self-incompatibility (SI) is an important reproductive mechanism to maintain genetic diversity within a plant species. However, SI can be a limiting factor for efficient production and breeding of cultivated plants. *Prunus* exhibits the S-RNase-based gametophytic SI system. Many self-compatible (SC) mutants of *Prunus* fruit tree species were found during a long history of the cultivation and have been utilized extensively for commercial production. 'Cristobalina', an SC sweet cherry (*Prunus avium*) cultivar, is one such example and presumed to have arisen by a mutation of a pollen-part modifier gene that is located on LG3, outside of the S locus. In this study, we conducted a subsequence analysis on whole-genome sequences obtained by Illumina sequencing to identify a causal mutation in 'Cristobalina'. Two 'Cristobalina' F₁ populations, both segregating for SC and SI individuals, were subjected to Illumina sequencing. Obtained reads were subdivided into 35-bp subsequences called k-mers. K-mers thus obtained were cataloged into 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 utilizing Illumina genomic reads from various sweet cherry cultivars and 'Cristobalina' progenies. Comparisons of the SC-specific genomic contigs obtained and pollen mRNA-Seq data revealed a possible causal mutation for SC in 'Cristobalina'. Functional characterization of the modifier gene would lead to further understandings of the SI reaction in S-RNase-based gametophytic SI system in *Prunus*.

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