Next generation sequencing analysis to identify modifier gene candidates conferring pollen-part self-compatibility in sweet cherry 'Cristobalina'

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The Rosaceae, the Solanaceae and the Plantaginaceae have the S-RNase-based gametophytic self-incomaptibility (SI) system, which uses S-RNase and F-box proteins as the pistil *S* and the pollen *S* determinants, respectively. Despite the commonality of the specificity determinants, SI recognition mechanism in *Prunus* in the Rosaceae is supposed to be distinct from those in the other taxa, and various *Prunus*-specific self-compatible (SC) mutants have been reported. Sweet cherry (*Prunus avium*) 'Cristobalina' is such a Prunus-specific SC mutant of which the pollen-part modifier gene, unlinked to the *S* locus, confers SC phenotype. Here, we performed subsequence cataloging from Illumina HiSeq genomic reads (paired-end 150-bp) in 44 F_1 progeny of 'Cristobalina' segregating for SI and SC phenotypes. The reads including the SC progeny-specific subsequences were assembled into polymorphic contigs covering the candidates of the pollen modifier locus. Most of these contigs showed significant homology to the bottom edge of the peach chromosome 3, to which the syntenic region in the cherry genome has been reported to contain the pollen modifier locus of 'Cristobalina'. Next, we further filtered the polymorphisms specific to 'Cristobalina' by mapping of Illumina HiSeq reads from various sweet cherry cultivars to the candidate contigs. This second screening based on association analysis confined the 66 SC-specific contigs with the average length of *ca.*400-bp. Considering the results from pollen mRNA-Seq analysis together, we could identify the candidates of the modifier genes expressed in the SC-specific genomic contigs.