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Quantitative Trait Loci (QTL) Related to Microspore Culture in Radish

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Radish is a self-incompatible plant, so it takes a long time to produce homozygous lines. However, it is possible to reduce the time to obtain homozygous plants by using haploid breeding. We performed a quantitative trait loci (QTL) analysis related to microspore culture of radish in a previous study. We performed Genotyping-by-Sequencing (GBS) with 62 F1 individuals derived from a cross of 'GX50' X 'GX71' that represent high and low regeneration rates, respectively, to find SNP markers. We also performed QTL analysis and used the markers to designate genes related to regeneration rate as candidate genes. QTL analysis was performed by ICIM (Inclusive composite interval mapping) and a candidate gene approach was used to find candidate genes. A total of 97,772 SNPs were generated through GBS, and 22,158 SNPs were selected. We found a total of five QTLs through QTL analysis and predicted five candidate genes. Candidate genes are divided into two classes (PRC2 subunits or auxin synthesis). We are planning to perform Quantseq through these results, and we will proceed RNA sequencing in species with high and low regenerate rates, respectively, to see how genes are actually expressed and to validate markers.

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