

## High-density genetic mapping using GBS in *Chrysanthemum*

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### Abstract

*Chrysanthemum* is one of the most important floral crop in Korea produced about 7 billion dollars (1 billion for pot and 6 billion for cutting) in 2013. However, it is difficult to breed and to do genetic study because 1) it is highly self-incompatible, 2) it is outcrossing crop having heterozygotes, and 3) commercial cultivars are hexaploid ( $2n = 6x = 54$ ). Although low-density genetic map and QTL study were reported, it is not enough to apply for the marker assisted selection and other genetic studies. Therefore, we are trying to make high-density genetic mapping using GBS with about 100 F<sub>1</sub>s of *C. boreale* that is a diploid ( $2n = 2x = 18$ , about 2.8Gb) instead of commercial cultivars. Since *Chrysanthemum* is outcrossing, two-way pseudo-testcross model would be used to construct genetic map. Also, genotype-by-sequencing (GBS) would be utilized to generate sufficient number of markers and to maximize genomic representation in a cost effective manner. Those completed sequences would be analyzed with TASSEL-GBS pipeline. In order to reduce sequence error, only first 64 sequences, which have almost zero percent error, would be incorporated in the pipeline for the analysis. In addition, to reduce errors that is common in heterozygotes crops caused by low coverage, two rare cutters (*NsiI* and *MseI*) were used to increase sequence depth. Maskov algorithm would also be used to deal with missing data. Further, sparsely placed markers on the physical map would be used as anchors to overcome problems caused by low coverage. For this purpose, markers were generated from transcriptome of *Chrysanthemum* using MISA program. Among those, 10 simple sequence repeat (SSR) markers, which are evenly distributed along each chromosome and polymorphic between two parents, would be selected.

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