

## Construction of genetic linkage maps of *Allium cepa* using genotyping-by-sequencing

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### Abstract

The onion (*Allium cepa* L.) is the most widely cultivated species of the genus *Allium*, especially it has been valued because of the pungent flavor and aroma. *Allium* species including onion has very large genome sizes ranging from approximately 10 to 20 Gbp, which have complicated genomic studies and precluded genome sequencing until recently. A population of 186 F2 individuals derived from a cross of 'Umjinara' x 'Sinsunhwang' and the two parental lines were used for this study. For the development of framework map, various types of markers including SSRs, RAPD, SNPs, and CAPS makers have been used for polymorphism test. Especially, a lot of SNP and CAPS loci were developed from the onion transcriptome sequence by RNASeq of two parental lines. The GBS libraries have been constructed based on a modified protocol from Poland Lab using a two-enzyme system. We have been developing markers showing polymorphism between two parental lines, and genotyping for all F2 individuals were finished for a number of polymorphic markers. For the construction of GBS libraries, a set of 192 barcoded adapters were generated from complementary oligonucleotides with XhoI overhang sequence and unique barcodes of length 4-8 bp and they have been tested using two parental lines to determine the optimum conditions for GBS analysis.

Keywords: onion, markers, genetic map, genotyping-by-sequencing, GBS libraries,

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