

Application of genotyping-by-sequencing (GBS) in plant genome using bioinformatics pipeline

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Abstract

The advent of next generation sequencing technology has elicited plenty of sequencing data available in agriculturally relevant plant species. For most crop species, it is too expensive to obtain the whole genome sequence data with sufficient coverage. Thus, many approaches have been developed to bring down the cost of NGS. Genotyping-by-sequencing (GBS) is a cost-effective genotyping method for complex genetic populations. GBS can be used for the analysis of genomic selection (GS), genome-wide association study (GWAS) and constructing haplotype and genetic linkage maps in a variety of plant species. For efficiently dealing with plant GBS data, the TASSEL-GBS pipeline is one of the most popular choices for many researchers. TASSEL-GBS is JAVA based a software package to obtain genotyping data from raw GBS sequences. Here, we describe application of GBS and bioinformatics pipeline of TASSEL-GBS for analyzing plant genetics data.

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Keywords: plant genomics, Genotype by sequencing (GBS), Genomic selection, Genome-wide association, TASSEL-GBS

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