

A NOVEL APPROACH TO PHENOTYPIC ANALYSIS OF FOREST TREES FOR ACCELERATING BREEDING

Donghwan Shim, Il Hwan Lee, and Kyung-Hwan Jang

Department of Forest Genetic Resources, National Institute of Forest Science, Suwon, Republic of Korea

Genomic Selection (GS) is one of the accelerating breeding methods. With the advent of high throughput molecular technology, numerous molecular markers distributed throughout the whole genome can be produced to characterize many genetic entries involving new perspectives in methodology of selection. In tree breeding the GS could significantly reduce the cost of genetic improvement schemes by limiting the size and number of field experiments. In order to successful performed GS, not only the genetic analysis of trees but also accurate phenotypic analysis is very important. Here, we present a novel approach to automatically measurement of tree phenotypes using drone and ground-based scanner. The actual utility of this scanner depends largely on the efficacy of point cloud data (PCD) analysis. The quantified data of each tree was validated using laborious measurements. The results showed that the individual tree growth was accurately reproduced using our method from three dimension registered scans, with a relative deviation of less than 5%. Therefore, we want to apply this method phenotype analysis for accelerating breeding and management of large-scale progeny test site.

Contact information: Donghwan Shim, National Institute of Forest Science, 39 Onjeong-ro, Suwon 16631, Korea-Republic of (KOR), Phone: 82312901128, Email: shim.donghwan@gmail.com