

**PB-56**

## Efficient Determination of Genomic Variants from Sorghum Genetic Resources by HPC

Tae-Ho Lee<sup>1\*</sup>, Myung-Eun Park<sup>1</sup>, Yun-Ho Oh<sup>1</sup>, Da-Hye Jeon<sup>1</sup>

<sup>1</sup>Genomics Division, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea

### [Abstract]

In the digital age, a lot of agricultural R&D is based on data. However, genetic resources are still essential for basic research and agricultural development. Accordingly, many countries are making great efforts to secure various genetic resources. In Korea, the National Agrobiodiversity Center (NAC) has more than 270,000 plant genetic resources so far as part of its efforts. In order to efficiently use the resources for agricultural R&D, it is essential to determine the genotypes of the resources. For this, it is essential to build a system for mass genotyping. For this, sorghum were selected as a model crop considering the genome size, the high-quality reference genome, and the number of resources. To efficiently determine the genotype data from many genetic resources, we developed a GATK pipeline that works efficiently on HPC. The pipeline efficiently and rapidly determined 769 genotypes of 410 genetic resources. Going forward, our team will continue to work to determine genotypes of over a thousand sorghum resources, and the data will be released at the National Agricultural Biotechnology Information Center (NABIC) in order to be used in agricultural R&D.

### [Acknowledgement]

This work was carried out with the support of “Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ01427602)” Rural Development Administration, Republic of Korea

\*Corresponding author: E-mail, thlee0@korea.kr Tel. +82-63-238-4558