

**GWAS for seed color and size in mungbean (*Vigna radiata* (L.) Wilczek)**Siphanh Daovongdeuan<sup>1,3</sup>, Dani Satyawan<sup>1</sup>, Moon Young Kim<sup>1,2</sup>, Haneul Jeong<sup>1</sup> and Suk-Ha Lee<sup>1,2\*</sup><sup>1</sup>Department of Plant Science and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea<sup>2</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea<sup>3</sup>Department of Plant Science, Faculty of Agriculture and Forest Resources, Souphanouvong University, Luang Prabang, Lao PDR**[Introduction]**

Mungbean seed size is one of the most important traits determining the whole production, and seed color greatly affects the price through consumers' preference and acceptability. Although better understanding of the mechanisms of seed size and color determination are crucial for mungbean improvement, few studies have been conducted for the genes regulating seed size and color. The objectives of this study were to investigate phenotypic variations in seed size and color among cultivated and wild mungbean accessions and to identify loci associated with seed size and color using genome-wide association study (GWAS).

**[Materials and Methods]**

In total, 218 mungbean accessions consisting of 200 green mungbean, 12 black mungbean and 6 yellow mungbean were used in this study. Among 218 accessions, 201 mungbeans are originated from 23 countries and the origin of 17 mungbeans are unknown. Mungbean seeds harvested in 2017 have been used for phenotyping of seed size and color. Ten seeds from each accession were used for phenotyping. Seeds were scanned in 3 different directions to measure SL, SH and SW (length, height and width). Seed color was measured as R, G, and B (Red, Green and Blue) using ImageJ 1.50i program. Average value of ten seeds were calculated as mean.

**[Results and Discussions]**

Phenotypic data were collected for seed size and color using 218 cultivated and wild mungbean accessions from more than 23 countries. Principle component analysis (PCA) plots were constructed based on phenotypic data. The cultivated and wild accessions in both seed size and color were clearly separated into two groups. Manhattan plots were constructed with a total 18,171 of SNP markers developed using genotyping by sequencing (GBS) on 222 cultivated mungbean accessions and 187 RILs. General line model (GLM) based on GWAS showed that there were no significant markers associated with the traits at p-value <0.05 and a LOD of 6. The results in this study indicate that the traits were coded by many alleles with small effects.

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