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IDENTIFICATION OF PROTON-BEAM INDUCED MUTATIONS IN SOYBEAN BY GENOTYPING-BY-SEQUENCING (GBS)

Mutagenesis using ionizing radiation has been widely used for the development of breeding resources. Because mutation breeding using gamma-rays has been attempted in soybean crop, studies on the effectiveness of different types of radiation are limited. This study carried out to investigate the genetic variation in the soybean chromosome induced by the proton beam irradiation. Twenty M2 plants by proton beam irradiation (10 M2 plants at 118 Gy and 10 M2 plants at 239 Gy) and two plants of original cultivar (Deapungkong) were sequenced using GBS platform. The mapping to the reference genome averaged 30⊠ with high accuracy, and the average length of the mapped region was 125 Mb. Total of 7,453 SNPs was observed in 20 M2 plants. SNP occurred at a frequency of 1 / 36,976 bp at the proton beam irradiation dose of 118 Gy, and 1 / 32,945 bp at the 239 Gy dose. The SNPs induced by proton beam were uniformly distributed in most of the chromosomes. Gene ontology clustering analysis of mutative genes showed that the many mutations induce functional changes. The detection of the mutation loci, types, and rates in genome wide would provide the molecular characterization of mutations induced by proton beam in soybean.

Country or International Organization

Republic of Korea

Author: Dr RYU, Jaihyunk (Chonnam National University)

Co-authors: Prof. HA, Bo-Keun (Chonnam National University); Ms GANG, Ryuli (Chonnam National Univerity); Mr KIM, Sang Hun (Chonnam National Univerity); Dr KANG, Si-Yong (Korea Atomic Energy Research Institute); Mr KIM, Woon Ji (Chonnam National University)

Presenter: Dr RYU, Jaihyunk (Chonnam National University)