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CHARACTERIZATION OF NOVEL SORGHUM MUTANTS FROM AN EMS-MUTAGENIZED POPULATION

Sorghum (Sorghum bicolor) is ranked as the fifth most important grain crop and serves as a major versatile C4 model crop for research in gramineae. High-quality genome sequence is available for sorghum functional genomics, but the availability of genomic and germplasm resources remains limited for functional validation of genes. Chemical mutagenesis of sorghum germplasm, followed by screening for mutants altered in important agronomic traits, represents a rapid and effective means of addressing this limitation. Ethyl methanesulfonate (EMS) was found to be the most potent mutagen in inducing mutation. Here, we reported that a sorghum mutant population consisting of 3, 000 lines was generated from the cultivar Jiutian1 by treatment with EMS. Numerous phenotypes with altered morphological and agronomic traits were observed from M2 and M3 lines in the field. A dwarf mutant (named SbME6-1) with a pale leaf phenotype and stunted growth and reduced chloroplast contents relative to wild-type (WT) was isolated from this EMS-mutagenized M3 population. To identify the genetic determinant of this trait, four DNA pools (two each from normal and dwarf mutants) were isolated and performed by the Gene Mapping by Sequencing (MBS). Comparison of allele frequency of the single nucleotide polymorphisms (SNPs) between the pools with contrasting phenotype showed that a locus in chromosome 9 between 51M and 57M had an allele frequency of 1. There were 15 mutation genes in the locus, out of which in 5 mutation genes showed unknown function. This finding is expected to contribute to future research on the identification of the causal factor of dwarfing. Our results show an EMS mutant resource as an efficient platform for gene discovery in sorghum, thereby accelerating sorghum breeding.

Country or International Organization

Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, China

Author: Dr ZHU, Li (Biotechnology Research Institute, Chinese Academy of Agricultural Sciences)

Co-authors: Prof. LI, Guiying (Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, P. R. China); Dr LU, Xiaoduo (Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, P. R. China); Prof. LI, Yubin (Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, P. R. China)

Presenter: Dr ZHU, Li (Biotechnology Research Institute, Chinese Academy of Agricultural Sciences)

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