

M-110

Snapshot of DNA methylation changes associated with floral bud distortion in Indian soybean (*Glycine max* L.)

*Jadhav Pravin\**, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Kale Prashant*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Kad Snehal*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Moharil Mangesh*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Dehmukh Amit*, Nagarjuna Medicinal Garden, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Nandanwar Ravindra*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Mane Shyamsundar*, Department of Plant Pathology, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Dudhare Mahendra*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

*Varghese Philips*, Genetics and Plant Breeding, Agharkar Research Institute, Maharashtra, India

*Manjaya Joy*, Nuclear Agriculture and Biotechnology Division, BARC, Maharashtra, India

*Dani Raviprakash*, Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Maharashtra, India

The present study aimed to understand the Epigenetic changes associated with floral bud distortion (FBD) in Indian soybean. The FBD is the abnormal development of plant it is an adverse biological phenomenon that occur during reproductive phase (R5). Although, it occurs frequently, its mechanism remains unknown. To elucidate molecular mechanism underlying FBD, we detected gene expression differences between symptomatic and asymptomatic samples of soybean using Methylation sensitive amplified polymorphism (MSAP). The methylation-sensitive amplified polymorphism technique (MSAP) which is a modification of amplified fragment length polymorphism (AFLP) used to investigate the epigenetic changes associated with FBD in soybean. The samples of genomic DNA were double-digested with either *HpaII* or *MspI* and with *EcoRI*. To analyze epigenetic changes, 25 MSAP primer pair combinations detected a few DNA methylation patterns in the plant tissue of symptomatic and asymptomatic plant. Out of total 495 MSAP sites in the symptomatic plants, 440 (87.96%) were un-methylated, 31 (6.84%) fully methylated and 24 (5.185%) hemi-methylated. However, out of total 432 MSAP sites in asymptomatic plant, 432 (86.04%) were un-methylated, 52 (10.16%) fully methylated, and 35 (7.131%) hemi-methylated sites were amplified. MSAP analysis was effective in detecting differentially methylated sites in the genomic DNA of soybean samples and methylation may be responsible for no pod formation.