



RESEARCH ARTICLE :

Molecular insights of floral malady prevailing in Indian soybean (*Glycine max* L.)

■ P. V. JADHAV, P.B. KALE, S. KAD, M.P. MOHARIL, M.S. DUDHARE, A.G. DESHMUKH, S.S. MANE, J.G. MANJAYA AND R.S. NANDANWAR

ARTICLE CHRONICLE :

Received :

10.07.2017;

Accepted :

23.07.2017

KEY WORDS :

Soybean, Floral bud distortion, cDNA-RAPD, cDNA-SCoT, Differentially expressed fragment

SUMMARY : Molecular alterations of symptomatic and asymptomatic soybean plants in response to floral bud distortion (FBD) are not completely understood yet. Oilgo-dT anchored cDNA-RAPD and cDNA-SCoT markers were exploited to determine differentially expressed genes in response to FBD. Differential transcriptome analysis using cDNA based oligo-decamer profiling was executed to identify differentially expressed TDFs. The TDFs were further analyzed using computational tools *viz.*, BLAST homology, protein interactome, virtual karyotyping, sub-cellular localization, neighbor joining placement. The *in-silico* studies were used for annotation, structural, functional characterization and protein interaction of TDFs. Differential expression studies (cDNA-RAPD) produced transcript derived fragments (TDFs) in all tissues (leaf bud and node) of symptomatic and asymptomatic plant. Out of 197, only 26 TDFs were found differentially regulated. Amongst them 15 were found completely polymorphic and 11 showed differences in their amplicon intensity. Similarly cDNA-SCoT revealed that total of 36 primers amplified 86 fragments between 200 bp to 1800 bp in length. Amongst them, nine differentially expressed fragments (DEFs) were re-amplified and sequenced. Sequence based studies of DEFs revealed their homology to five known genes; which were functionally involved in DNA repair mechanism, apoptotic, autophagy and pathogen responsive mechanisms in soybean. However, four fragments encode un-clarified proteins with unknown functions. The possible role of unknown genes, along with protein-protein interactome, physical karyotyping and cellular localization were predicted using *in silico* analysis. This study suggests that oligo-dT anchored cDNA-RAPD, cDNA-SCoT differential display approach is a useful tool to serve as initial step for understanding alterations involved in upcoming malady and provide valuable information for further studies.

Author for correspondence :

P. V. JADHAV

Department of
Agricultural Botany,
Biotechnology Centre,
Post Graduate Institute,
Dr. Panjabrao Deshmukh
Krishi Vidyapeeth,
AKOLA (M.S.) INDIA
Email: jpraveen26@yahoo.co.in

See end of the article for authors' affiliations

How to cite this article : Jadhav, P. V., Kale, P.B., Kad, S., Moharil, M. P., Dudhare, M. S., Deshmukh, A.G., Mane, S.S., Manjaya, J.G. and Nandanwar, R.S. (2017). Molecular insights of floral malady prevailing in Indian soybean (*Glycine max* L.). *Agric. Update*, 12(TECHSEAR-2) : 305-327; DOI: 10.15740/HAS/AU/12.TECHSEAR(2)2017/305-327.