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Phenotypic and proteomic evaluation of EMS-induced mutants of *Nigella sativa*

Ambreen Asif and M Yunus Khalil Ansari

Aligarh Muslim University, India

Nigella sativa L. (Black cumin) is a small herbaceous plant, belonging to family Ranunculaceae. Seeds of this plant have huge medicinal properties. However, the low seed yield is not fulfilling the demand for pharmaceutical purposes. Therefore, an attempt has been made in this study to develop mutant lines of *Nigella sativa* by using EMS. It has been found that 0.1% EMS resulted in the mutant line which is taller with pro-fused branching with high yield compared to wild type plant. Interestingly 1.0% EMS treatment produced dwarf mutant with few branches and low yield. To investigate the contrasting character of both the mutants, proteome analysis of leaves was carried out through 2D-gel electrophoresis. Analysis of proteome of wild type and mutant lines showed that 32 proteins were differentially expressed. These differentially expressed proteins were sequenced through MALDI-TOF and identified by using MASCOT software. The function and location of these proteins were analyzed by using Uniprot software. These proteins were categorized on the basis of their functions and correlated with the phenotypic characters of mutant lines. Validation of differentially expressed proteins was carried out through studying expression pattern of respective gene through quantitative real time PCR. It has been found that expression of 26 proteins was due to mutation in the mutant lines.

Biography

Ambreen Asif is attending the University of Aberdeen, Scotland, United Kingdom for an Advance Research in Genetic Mapping after being awarded the prestigious Newton-Bhabha Research Fellowship. She is pursuing PhD in AMU with specialization in Genetics and Cytogenetics. She has earlier been awarded the INSPIRE Research Fellowship of Department of Science & Technology (DST), Government of India. She has also been conferred with Anjalina Khan Award and Regularity Award by the Women's College in AMU.

mbreenasif1@gmail.com

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