

Effect of epigenetic modifiers on the secondary metabolite profile of the endophytic fungi of *Datura innoxia* Mill

Vishal Sharma¹, Sundeep Jaglan²

¹Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu (India)

²Academy of Scientific and Innovative Research (AcSIR), Jammu Campus, Jammu (India)

ABSTRACT

Epigenetic modifiers are known to stimulate expression of inactive biosynthetic gene clusters and change secondary metabolite biosynthesis in fungi. Recent studies of the genome sequencing of filamentous fungi have revealed that many gene clusters involved in producing Polyketide synthetases, nonribosomal peptide synthetases, and hybrid PKS-NRPS metabolites does not undergo expression under normal conditions in laboratory. New strategies have been designed to open up the inactive gene clusters and give expression to the latent gene clusters in fungi that would lead to new chemical entities. Epigenetic modifiers such as DNA methyl transferase (DNMT) and Histone deacetylase (HDAC) inhibitors are successfully used by many researchers to discover new natural products or boost the yield of known metabolites by transcriptional activation of silent biosynthetic genes. In this study, seventeen endophytes were screened separately with 5-azacytidine and valproic acid on PDA plates and also in PDB flasks. The change in morphology was observed in plates and the extracts were prepared from the endophytes cultured in PDB and PDB containing epigenetic modifiers. Change in secondary metabolites was observed by using HPLC and GCMS.