

O-24 (187)**THE USE OF ESTS-DATABASE FOR IDENTIFICATION OF NIC GENE IN TRIGONELLINE PATHWAY IN TRIGONELLA FOENUM-GRAECUM L**

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Recent advances techniques in molecular biology have provided powerful tools for discovery of novel genes relevant to the metabolic compounds. EST database (Expressed Sequence Tags) is an emerging technique for novel gene discovery and it has been successfully applied to the identification of some key genes in secondary metabolite biosynthesis. Trigonelline is the major alkaloid of fenugreek and reported to have protective actions against diabetic peripheral hypertensive. There is several reports focus on therapeutic activities of trigonelline as an anti-adipogen, anti-Alzheimer (in animal model), hypocholesterolemic, neuroprotective, antibacterial and antiviral activity. The present study was undertaken with an objective to analysis EST database on direct searches against public databases and functional assessment of some key enzyme involved in the biosynthesis of trigonelline. The sequence encoding Nicotinamidase gene was isolated from seeds of *T. foenum-graecum* by reverse transcription-PCR. The cleaned PCR products were cloned into pJet vector (CloneJET PCR Cloning Kit) and transformed into *E. coli* strain DH5 α . Plasmid DNA templates were purified using plasmid purification kit and subjected to sequencing. The deduced amino acid sequence of *NIC* gene showed the highest identity (97%) with *Medicago sativa*. Based upon the successful applications of this technique in identification of candidate biosynthetic genes offers access to complete biosynthetic pathways for this valuable specialized metabolite

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