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Virtual prediction of domains in genomes of actinobacteria using NaPDoS, Domain Search Program for NRPS, NP Searcher, and NRPS substrate predictor for bioactive compounds

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Abstract

Natural products are widely distributed and one such source is *Streptomyces* in actinobacteria group. *Streptomyces* are known for producing natural products as secondary metabolites. For predicting domains responsible for production of natural products through NRPS/PKS pathways in actinobacteria by *in silico* approaches there is need of bioinformatics tools for analyzing the growing number of natural products. In the present investigation, thirty six species of *Streptomyces* were retrieved from NCBI and analyzed using four bioinformatics tools (NaPDoS, Domain Search Program for NRPS, NP Searcher NRPS and NRPS substrate predictor), and reporting the findings from the species of *Streptomyces.* Adenylation domain sequences where various domains such as A, KS, T, TE, E and C are predicted that responsible for various natural products. The results revealed 86.1% adenylation domain by Domain Search Program for NRPS, 69.4% condensation domains by NaPDoS, 58.3% by Domain Search Program for NRPS, 13.8% E domains by Domain Search Program for NRPS, 66.7% of T domains, 77.8% of TE domains by Domain Search Program for NRPS are detected. 2.8% KS by Domain Search Program for NRPS and 83.3% by NaPDoS are also detected. Domain Search Program for NRPS predicted maximum number of domains as compare to others. It is suggested to use combination of tools that could support in mining the domains that codes bioactive compounds.

Keywords: Actinobacteria, Virtual prediction, Domains, Natural products, NRPS and PKS

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