

SECONDARY METABOLITE PRODUCTION IN PSEUDOMONAS SPP.: A META-ANALYSIS ON ITS ABUNDANCE AND EXPRESSIVITY PATTERN

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In recent decades, there has been an increasing focus on using *Pseudomonas spp.* as biocontrol agents due to its beneficial effects on plants as well as potential insecticidal properties against several pathogens. Secondary metabolites produced by these bacterial groups are one of major factors contributing to protecting crops from pest and disease attacks. In this study, a brief analysis was conducted to determine a broad spectrum of chemical products in genomes of three *Pseudomonas* bacterial species. Genbank files of 149 draft genomes from *Pseudomonas protegens*, *Pseudomonas fluorescens*, *Pseudomonas fragi* were downloaded from NCBI database, then submitted to anti-SMASH 7.0 (a web-based tool for secondary metabolite annotation). A list of annotated genes encoding different secondary metabolites were generated and subjected to comparison using R and Excel. *Arylpolyene*, *Betalactone*, *Hydrogen cyanide* were all highly expressed in three species. In *Pseudomonas protegens*, 2,4-Diacetylphloroglucinol (2,4-DAPG), enantio-pyochelin, pf5-overdine were predicted to be expressed with 100%; orfamide (94%); pyoluteorin (84%); pyrrolnitrin (78%); rhizoxin A and hserlactone (26%); methanobactin (18%); 3-thiaglutamate and alginate (16%). While in *Pseudomonas fluorescens*, a wider range of products were identified: pf5-overdine (100%) viscosin and lokisin (24%); ambactin and pyoverdine SMX-1 (22%); chitinimide (14%); tolaasin and histicorrugatin (12%); thanafactin A (10%); bacilliomycin D and acaterin (8%); syringomycin and nematophin (6%). These compounds might play certain roles in plant protection processes and thus can be tested for their pesticidal activities.