Comparative analyses of pseudomonads based on the genomic, metabolic and protein contents

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Abstract

Three of the genus *Pseudomonas* (*P. aeruginosa, P. putida, P. syringae*) show highly different phenotypic characteristics among them. Two of the three members are pathogenic and the other is non-pathogenic. Comparative analyses of the complete genomes can elucidate the genomic similarities and differencies among them. We analyzed the three genomes and the genes of them to reveal the degree of conservation of chromosomes and similarity of the genes. The 2-dimensional dot plot between the pathogenic *P. aeruginosa* and non-pathogenic *P. putida* shared higher portion of the nucleotide sequences than other two combinations. Comparison of the nucleotide compositions by calculating the genome-scale plot of G+C contents and GC skew showed the variation of nucleotide composition according to the genomic location. Comparison of the metabolic capabilities using the functional classification of KEGG orthology revealed that the differences in the number of genes for the specific functional categories resulted in the phenotypic differences. Finally combination of the analyses using the protein homologs supported the evolutionary distance of the *P. putida* obtained from other genome-scale comparisons. [This work was supported by the Korean Systems Biology Research Grant Program from the MOST. Further supports by the BK21 program, LG Chemicals Chair Professorship, and IBM SUR program are appreciated.]

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