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GENOME BASED COMPARATIVE STUDY OF PSEUDOMONAS SPECIES

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ABSTRACT: Genomes of fourteen strains of the Pseudomonas fluorescents the rhizospheric group of bacteria that colonize plant surfaces and function as biological control agents, protecting plants from disease and plant growth promoting bacteria. The genomic diversity of the group by comparing these strains to each that were sequenced collected from NCBI previously has led to the complexity of genome-wide annotation and gene sequence comparison among each strains of pseudomonads. Bioinformatics tools BLAST, ClustalW, ALIGN, PHYLIP and PRIMER3 were used series for sequence the comparison and identifies the genes that are unusual to a particular organism developed, and a phylogenetic tree is constructed. In addition, a common set of primers that can amplify all the sequences are generated. The UPGMA package provides users with a quick and convenient tool to compare genomic sequences among multiple organisms at the whole-genome level with dendrogram constructed.

KEYWORDS: Genome Sequence, Pseudomonas, Bioinformatic tools, NCBI, Comaparasion

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1.INTRODUCTION

Pseudomonas spp. gram-negative bacteria, aerobic, inhabitant of agricultural soils, and are well adapted to growing in the rhizospheric region. They hold many a genetically determined characteristic showed as plant growth-promoting and biocontrol agents. ability to grow rapidly in vitro and to be mass produced; rapidly root exudates and seed utilize; rapidly colonize with the property to a

Jitendra Malviya et al RJLBPCS 2017 www.rjlbpcs.com Life Science Informatics Publications rhizospheric region bacteria and multiply in the rhizosphere and spermosphere environments and in the interior of the plant; they produces a extensive range to produce bioactive compounds (i.e., antibiotics, siderophores, volatiles, production of an array of secondary metabolites and growthpromoting substances); compete aggressively with other microorganisms; and adapt to environmental stresses. In addition, pseudomonads are responsible for the natural suppressiveness of some soils to soil borne pathogens [1]. The major weakness of pseudomonads as biocontrol agents is their inability to produce resting spores (as do many Bacillus spp.), which complicates formulation of the bacteria for commercial use. The genus Pseudomonas currently comprises more than 100 named species that have been divided into lineages, groups and subgroups based on multilocus sequence analysis [1-3]. Many of the plant commensal strains fall into the Pseudomonas fluorescens group, which currently includes more than fifty named species [13]. Plant-commensal strains of Pseudomonas spp. are trapped complicity in plant and soil microbiota through all of these diverse activities, and their functions as biological control agents have distinguished them as microorganisms with significant effects on agricultural productivity. The wide range of ecological, metabolic, and biochemical characteristics of this genus have genomic sequence level, is extend very high due to the diversity among the Pseudomonas spp. The complete genomes of many species have now been sequenced [1-3], and only 25% to 35% of the genome of each strain is composed of core genes shared by all members of the genus. Comparisons among the genomes of four strains within the P. fluorescens group (Pseudomonas protegens biological control agents Pf-5, F113[10] and P. fluorescens strains SBW25, Pf0-1, Pseudomonad PGPR GP72, Rhizobacterium M18, nitrogen fixing strain A1501, Pseudomonas putida CSV86 and WH6 [1-3]) highlight the tremendous extraordinary diversity of these bacteria. Of the 5741-6009 predicted protein-coding genes (referred to herein as the predicted proteome) identified in each genome, only 3115 are present in the entire genus, composing a core genome representing only 52% to 54% of each strain. Allele, nearly a third (1488 to 1833 genes) of the predicted proteome for each strain is ultimately unique to that pseudomonads strain, that shows character of heterogeneity of this group of bacteria. The genomes of Pseudomonas spp., like those of many other bacteria, display a highly mosaic structure, being composed of relatively stable core regions interspersed with regions that vary among the strains [1-3]. Regions that are unique to a specific strain are thought to shape that strain's distinctive characteristics, including its interactions with pathogens causes' disease in the plant and crops that are targeted of biological control agent. The combined repertoire of the core and variable regions of a genome reflects the ecological. Pseudomonas genome, were discovered each genes for the traits which can be explored in the future for their roles in biological control biofertilizer and other heterotrophic interaction who makes fertile soils microbiota. Genomic analysis with phenotypic screens to link the gene statement that ornamentally associated with key phenotypes that exhibited by plant-associated strains in the P. fluorescens group.

Bioinformatics tools for comparisons

UPGMA automates the task of sequence comparison by integrating various bioinformatics tools such as BLASTALL [5] for identifying homologous sequences, ALIGN [6] for calculating sequence identities, CLUSTALW [7] for making multiple sequence alignments, PRIMER3 [8] for designing primers and PHYLIP [9] tool kit for constructing phylogenetic trees.

| Strain | Source | Target disease(s) for biological control | Genome sequence | | | |
|-------------------------------------|----------------------------|--|-----------------|--|--|--|
| P. chlororaphis subsp.aureofaciens: | | | | | | |
| O6 | Soil, Utah, USA | Wildfire of tobacco, target spot of cucumber [7] | | | | |
| GP72 | Green pepper rhizosphere | Antifungal activity | [13] | | | |
| | china | | | | | |
| P.protege | P.protegens | | | | | |
| Pf-5 | Rhizosphere of cotton | Dumping -off caused by P. ultimum Seedling | [5] [13] | | | |
| P.fluoresc | ens | | | | | |
| Pf0-1 | 1 Soil | Massachusetts, USA | [5] | | | |
| Q2-87, USA | Wheat Rhizosphere, | Take-all of wheat | [7] | | | |
| SBW25 | Sugar beet phyllosphere, | Seedling emergence | [13] | | | |
| | Oxford shire, UK | | | | | |
| A506 | Pear phyllosphere, | Fire blight of pear and apple, frost injury, fruit | [7] | | | |
| | California, USA | russeting | | | | |
| SS101 | Wheat Rhizosphere, The | Diseases caused by Pythium spp. and | [7] | | | |
| | Netherlands | Phytophthora spp. | | | | |
| F113 | Sugarcane Rhizosphere | Phytopathogens potato-cyst nematodes, | [10] | | | |
| | | bioremediation | | | | |
| Pseudomonas sp. | | | | | | |
| BG33R | Peach Rhizosphere, South | The plant-parasitic nematode Mesocriconema | [7] | | | |
| | Carolina, USA | xenoplax | | | | |
| M18 | Rhizosphere of sweet melon | Strong antifungal activity | [13] | | | |
| | china | | | | | |
| PAO1 | Rhizosphere of rice based | Nitrogen fixation and mineralize aromatic | [13] | | | |
| | china | compounds | | | | |
| A1501 | Rhizosphere of rice based | Nitrogen fixation and mineralize aromatic | [13] | | | |
| | china | compounds | | | | |
| Pseudomonas | Isolated from soil | bioremediation, biocontrol, and pathogenicity [12] | | | | |
| putida CSV86 | | | | | | |

Table 1. Biocontrol property of PGPR pseudomonas

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| Characters | Size (base | G+C content | Protein | RNA | rRNA genes (5S | tRNA |
|------------|------------|-------------|-------------|-------|------------------|-------|
| | pair) | (%) | coding gene | genes | rRNA,16SrRNA,23S | genes |
| | | | | | rRNA) | |
| Pf0-1 | 6,438,405 | 60.62% | 5,741 | 99 | 19 (6,6,7) | 73 |
| Q2-87, | 6,3663663 | 60.7% | 5597 | 87 | 5 (2,2,1) | 68 |
| SBW25 | 6,722,539 | 60.5% | 6,009 | 88 | 16 (5,6,5) | 66 |
| BG33R | 6,29 | 59.6% | 5511 | 89 | 6 (3,2,1) | 68 |
| M18 | 6,327,754 | 66.50% | 5690 | 79 | 13(5,4,4) | 61 |
| PAO1 | 6264404 | 66.6% | 5677 | 13 | 13(4,4,5) | 63 |
| A1501 | 4567418 | 63.88% | 4135 | 102 | 13 (4,5,5) | 61 |
| A506 | 596 | 60.01% | 5276 | 89 | 6 (1,2,3) | 69 |
| SS101 | 617 | 60.5% | 5370 | 87 | 6 (2,1,3) | 68 |
| F113 | 68458832 | 60.8% | 5862 | ND | 5 (2,1,2) | 66 |
| Pf-5 | 7074893 | 63.30% | 6142 | 115 | 16 (6,5,5) | 71 |
| 06 | 699 | 62.8% | 6224 | 87 | 12 (6,4,2) | ND |
| GP72 | 6663241 | 63.13% | 6091 | 85 | 4 (2,1, 1) | 61 |
| CSV86 | 6,472,491 | 61.85% | 5900 | ND | 7 (3,5,1) | 60 |

 Table 2. General Genome feature of the 14 studied pseudomonad PGPR

Table 3. Nucleotide Sequence Accession from NCBI of 14 studied pseudomonas PGPR

| Name of the strain | Name of the pseudomonads | Nucleotide Sequence Accession No. |
|--------------------|--------------------------|-----------------------------------|
| 06 | P. chlororaphis | AHOT00000000 |
| GP72 | P. chlororaphis | AHAY00000000 |
| Pf-5 | P. fluorescens | CP000076 |
| Pf0-1 | P. fluorescens | CP000094 |
| Q2-87 | P. fluorescens | AHPO00000000 |
| SBW25 | P. fluorescens | AM181176 |
| A506 | P. fluorescens | CP003041 |
| SS101 | P. fluorescens | AHPN0000000 |
| F113 | P. fluorescens | CP003150 |
| BG33R | P. synxantha | AHPP00000000 |
| M18 | P. aeuroginosa | CP002496 |
| PAO1 | P. aeuroginosa | NC002516 |
| A1501 | P.stutzeri | NR076417 |
| CSV86 | P. putida | AMWJ00000000 |

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Genome Ornaments

The genomes of fourteen strains of the Pseudomonas fluorescens group of member that colonize plant surfaces and function as biological control agents, protecting plants from disease. [1] In this study, we demonstrated the genomic diversity of the group by comparing these strains to each other and to three other strains that were sequenced previously. [2] Comparative analysis half of the genes in each bacterial strain are present in all of the other strains, and each strain has hundreds of unique genes that are not present in the other bacterial genomes. We mapped the genes that contribute to biological control in each genome and found that most of the biological control genes are in the variable regions of the genome, which are not shared by all of the other strains. [13] This finding is consistent with our knowledge of the distinctive biology of each strain. Finally, we looked for new genes that are likely to confer antimicrobial traits needed to suppress plant pathogens, but have not been identified previously. Orientation of genome, have many of these new genes, which provide prime avenues for future discovery of new traits with the potential to manage plant diseases in agriculture crop or natural ecosystems. These strains exhibit a diverse range of traits involved in biological control and other multitrophic interactions with plants, microbes, and insects. Multilocus sequence analysis placed the strains in three sub- clades, which was reinforced by high levels of synteny, size of core genomes, and relatedness of orthologous genes between strains within a sub-clade. The heterogeneity of the P. fluorescens group was reflected in the large size of its pan- genome, which makes up approximately 54% of the pan-genome of the genus as a whole, and a core genome representing only 45–52% of the genome of any individual strain. We discovered genes for traits that were not known previously in the strains, including genes for the biosynthesis of the siderophores, achromobactin and pseudomonine and the antibiotic 2- hexyl-5-propyl-alkylresorcinol; novel bacteriocins; type II, III, and VI secretion systems; and insect toxins. Certain gene clusters, such as those for two type III secretion systems, are present only in specific sub-clades, suggesting vertical inheritance.

2. CONCLUSION

Multitrophic interactions of genome map associated with all presented genes on the sequence region present in only a subset of the strains or unique to a specific bacterial strain. Genus is widely high versatile Pseudomonas containing species that can be harmful to humans and plants while others are widely used for bioengineering and bioremediation. Large, conserved region of the core region and a very diverse catalog of accessory regions, and their impressive metabolic capacity, the study of Pseudomonas spp. genomes and their role in shaping these lifestyles is an intense focus of interest. [4-5].

CONFLICTS OF INTEREST

Author has no conflicts interest

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