

Poster Abstracts



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Unveiling the Genomic Aspects of *Habella chejuensis* KCTC 2396, an Algicidal Marine Bacterium

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Habella chejuensis KCTC 2396T, previously identified as a sole member of a novel genus (Lee et al, 2001, IJSEM 51:661-6) in the class *Gammaproteobacteria*, produces copious extracellular polysaccharides having desirable properties for industrial applications and a red pigment showing the algicidal activity against *Cochlodinium* and other red-tide phytoplanktons. Random shotgun sequences of about 5.3-fold genomic coverage were assembled into 619 contigs (total contig length ≈ 7.3 Mb), and basic annotation was performed. Among the 7,376 ORFs predicted by Glimmer, 45% could be functionally assignable according to the COG categories, and 30% were unique to the genome. Genes potentially involved in synthesis of red pigments were searched throughout the genome, and several were identified in a scaffold consisting of four contigs. Subsequently, a ca. 60-kb region encompassing all of the genes responsible for

the pigment synthesis was completely sequenced and re-annotated. Genome analysis also revealed a multitude of genes possibly involved in biosynthesis and transport of exopolysaccharides, and about a dozen of gene clusters for biosynthesis of polyketides and non-ribosomal peptides. One of the striking features of the *H. chejuensis* genome is the unexpected presence of two gene sets for type III secretion, which functions in injection of effector proteins into eukaryotic cells. This suggests that *H. chejuensis* may occupy a unique ecological position in the marine environment through interactions with other organisms.

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Distribution of Mobile Genetic Elements and Genomic Islands in the Plant Pathogen *Pseudomonas syringae* pv *Tomato* DC3000

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As previously reported, the chromosome of *Pseudomonas syringae* pv *tomato* DC3000 showed a high degree of sequence conservation in ORFs involved in "housekeeping functions" when compared with the genomes of *Pseudomonas aeruginosa* PAO1, an animal pathogen, and the non-pathogenic soil inhabitant *Pseudomonas putida* KT2440. However, significant divergence in genes with unknown function and in mobile genetic elements is present among these fluorescent pseudomonads. With respect to DC3000, the majority of these ORFs do not have a known function yet share other features such as association with regions of