JB Journals.ASM.org

GENOME ANNOUNCEMENT

Genome Sequence of the Cycloprodigiosin-Producing Bacterial Strain *Pseudoalteromonas rubra* ATCC 29570^T

Bin-Bin Xie,[a,b] Yan-Li Shu,[a] Qi-Long Qin,[a] Jin-Cheng Rong,[a] Xi-Ying Zhang,[a] Xiu-Lan Chen,[a] Bai-Cheng Zhou,[a] and Yu-Zhong Zhang[a]

State Key Laboratory of Microbial Technology, Marine Biotechnology Research Center,[a] and Key Laboratory for Colloid and Interface Chemistry of the Ministry of Education,[b] Shandong University, Jinan, China

The cycloprodigiosin biosynthetic gene cluster has not been reported. We sequenced the genome of a cycloprodigiosin-producing bacterial strain, *Pseudoalteromonas rubra* ATCC 29570^T. Analysis revealed a probable cycloprodigiosin biosynthetic cluster, providing a good model for the study of cycloprodigiosin synthesis and regulation.

Prodiginines are a family of tripyrrole red pigments which have antifungal, antibacterial, antiprotozoal, antimalarial, immunosuppressive, and anticancer activities (16). Prodiginines can be divided into four structural classes (16): prodigiosin/undecylprodigiosin, butyl-meta-cycloheptylprodiginine, cycloprodigiosin, and cyclononylprodigiosin. The prodigiosin/undecylprodigiosin biosynthetic (*pig*) cluster has been studied in *Serratia* sp. ATCC 39006 (17), *Serratia marcescens* ATCC 274 (9), and *Hahella chejuensisi* KCTC 2396 (10), and the prodigiosin/undecylprodigiosin and butyl-meta-cycloheptylprodiginine biosynthetic (*red*) cluster has been studied in *Streptomyces coelicolor* strain A3(2) (3, 5–7, 13, 15). However, biosynthetic gene clusters for cycloprodigiosin and cyclononylprodigiosin have not been reported.

The genus *Pseudoalteromonas* (*Gammaproteobacteria*, *Alteromonadales*, *Alteromonadaceae*) is a group of wide-spreading marine bacteria, and many species of the genus have been shown to be able to produce series of bioactive compounds (2). Studies have shown that *Pseudoalteromonas denitrificans* (11) and *Pseudoalteromonas rubra* (8) can produce cycloprodigiosin. To uncover the biosynthetic gene cluster for cycloprodigiosin, we sequenced the genome of the type strain of *P. rubra*, ATCC 29570^T.

The genome of strain ATCC 29570^T was sequenced using Illumina Solexa technology (1). A 500-bp Illumina paired-end library produced 6,666,668 reads (read length, 90 bp) totaling 600 Mb, which represents 101 times the average genome coverage. Solexa paired-end reads were then assembled using SOAPdenovo, version 1.05 (12), resulting in 64 contigs (>500 bp). The protein-coding open reading frames (ORFs) were predicted using Glimmer, version 3.02 (4), and were annotated using the Swiss-Prot, NCBI nr, and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases (14). A comprehensive annotation and comparative genome analysis are under way.

The size of the *P. rubra* ATCC 29570^T genome is 5.97 Mb, larger than that of all other sequenced *Pseudoalteromonas* genomes except that of *P. luteoviolacea* 2ta16 (6.36 Mb) (https://moore.jcvi.org/moore/). The G+C content is 47.80%, higher than that of all other sequenced *Pseudoalteromonas* genomes.

The genome contains 5,195 protein-coding ORFs. A BLASTP search against the *pig* gene cluster in *H. chejuensisi* KCTC 2396 revealed a probable cycloprodigiosin biosynthetic gene cluster (13 ORFs) in the ATCC 29570^T genome. The first 11 ORFs encode proteins with high amino acid identity (43% to 60%) to their homologs in *H. chejuensisi* KCTC 2396. However, the amino acid sequence identities of the last two ORFs to their homologs were much lower (31% to 33%). This cluster represents the first reported biosynthetic cluster for cycloprodigiosin. In addition, the genome sequence of *P. rubra* ATCC 29570^T provides a good resource for the study of bioactive compounds produced by the *Pseudoalteromonas* genus.

Nucleotide sequence accession number. The data for the genome sequence of *P. rubra* ATCC 29570^T were deposited in GenBank under accession number AHCD00000000.

ACKNOWLEDGMENTS

The work was supported by the National Natural Science Foundation of China (grants 31025001, 31100367, and 41106161), the Hi-Tech Research and Development Program of China (grants 2006AA09Z414 and 2011AA09070303), the Foundation for Young Scientists in Shandong Province (grant BS2010SW015), the Specialized Research Fund for the Doctoral Program of Higher Education (grant 20100131120004), and Special Funds for Postdoctoral Innovative Projects of Shandong Province (grant 200901007).

REFERENCES

1. **Bennett S.** 2004. Solexa Ltd. Pharmacogenomics **5**:433–438.
2. **Bowman JP.** 2007. Bioactive compound synthetic capacity and ecological significance of marine bacterial genus *Pseudoalteromonas*. Mar. Drugs **5**:220–241.
3. **Coco EA, Narva KE, Feitelson JS.** 1991. New classes of *Streptomyces coelicolor* A3(2) mutants blocked in undecylprodigiosin (Red) biosynthesis. Mol. Gen. Genet. **227**:28–32.
4. **Delcher AL, Bratke KA, Powers EC, Salzberg SL.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23**:673–679.
5. **Feitelson JS, Hopwood DA.** 1983. Cloning of a *Streptomyces* gene for an O-methyltransferase involved in antibiotic biosynthesis. Mol. Gen. Genet. **190**:394–398.
6. **Feitelson JS, Malpartida F, Hopwood DA.** 1985. Genetic and biochemical characterization of the red gene cluster of *Streptomyces coelicolor* A3(2). J. Gen. Microbiol. **131**:2431–2441.
7. **Feitelson JS, Sinha AM, Coco EA.** 1986. Molecular genetics of Red biosynthesis in *Streptomyces*. J. Nat. Prod. **49**:988–994.
8. **Gerber NN, Gauthier MJ.** 1979. New prodigiosin-like pigment from *Alteromonas rubra*. Appl. Environ. Microbiol. **37**:1176–1179.
9. **Harris AK, et al.** 2004. The *Serratia* gene cluster encoding biosynthesis of

Received 29 December 2011 **Accepted** 9 January 2012

Address correspondence to Yu-Zhong Zhang, zhangyz@sdu.edu.cn.

doi:10.1128/JB.06822-11

the red antibiotic, prodigiosin, shows species- and strain-dependent genome context variation. Microbiology **150**:3547–3560.
10. **Jeong H, et al.** 2005. Genomic blueprint of *Hahella chejuensis*, a marine microbe producing an algicidal agent. Nucleic Acids Res. **33**:7066–7073.
11. **Kawauchi K, et al.** 1997. A possible immunosuppressant, cycloprodigiosin hydrochloride, obtained from *Pseudoalteromonas denitrificans*. Biochem. Biophys. Res. Commun. **237**:543–547.
12. **Li R, et al.** 2010. De novo assembly of human genomes with massively parallel short read sequencing. Genome Res. **20**:265–272.
13. **Malpartida F, Niemi J, Navarrete R, Hopwood DA.** 1990. Cloning and expression in a heterologous host of the complete set of genes for biosynthesis of the *Streptomyces coelicolor* antibiotic undecylprodigiosin. Gene **93**:91–99.
14. **Ogata H, et al.** 1999. KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Res. **27**:29–34.
15. **Rudd BA, Hopwood DA.** 1980. A pigmented mycelial antibiotic in *Streptomyces coelicolor*: control by a chromosomal gene cluster. J. Gen. Microbiol. **119**:333–340.
16. **Williamson NR, Fineran PC, Leeper FJ, Salmond GP.** 2006. The biosynthesis and regulation of bacterial prodiginines. Nat. Rev. Microbiol. **4**:887–899.
17. **Williamson NR, et al.** 2005. Biosynthesis of the red antibiotic, prodigiosin, in *Serratia*: identification of a novel 2-methyl-3-n-amyl-pyrrole (MAP) assembly pathway, definition of the terminal condensing enzyme, and implications for undecylprodigiosin biosynthesis in *Streptomyces*. Mol. Microbiol. **56**:971–989.