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Genome sequence and genome mining of a bioactive deep-sea sediment isolated bacterium *Amycolatopsis* sp.WH001

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A deep-sea sediment derived actinobacteria *Amycolatopsis* sp.WH001 was identified as a broad-spectrum antibiotics producer and shared a 98% 16s ribosomal RNA (rRNA) sequence similarity with that of *Amycolatopsis lactamdurans*, which can produce cephamycin C. To further evaluate its biosynthetic potential and interesting or unusual features, the complete genome was sequenced with a size of 9,138,610-bp circular chromosome and a 67,043-bp dissociated plasmid. Genome analysis revealed 27 gene clusters potentially encoding secondary metabolite biosynthesis pathways including three polyketide synthases (PKSs), five non-ribosomal peptide synthetases (NRPSs), three hybrid NRPS-PKSs, four terpene, two lantipeptide and several other compounds biosynthetic gene clusters. One of the NRPS gene cluster, *nrps3*, shared a 57% nucleotide similarity with cephamycin C gene cluster, indicating the capacity of this organism to produce cephamycin C analogue. This study affirmatively identified *Amycolatopsis* sp.WH001 as a source of NRPS metabolites and highlighted genome mining of interested organism as a powerful tool for natural product discovery.

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