

The search for novel natural products is not an easy task. It is imperative to find new strategies that will streamline the discovery of new compounds to save time, effort, and resources. The work by the Piel group showcases the use of bioinformatics to pinpoint a bacterial source that has potential to produce novel compounds based on biosynthetic genes. Their efforts lead to the discovery of several compounds of different classes with distinct structures and bioactivity. It is my hope that I will be able to apply this knowledge to my own study.

### **Genome-Based Identification of a Plant-Associated Marine Bacterium as a Rich Natural Product Source**

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#### **Abstract**

The large number of sequenced bacterial genomes provides the opportunity to bioinformatically identify rich natural product sources among previously neglected microbial groups. Testing this discovery strategy, unusually high biosynthetic potential was suggested for the *Oceanospirillales* member *Gyneuella sunshinyii*, a Gram-negative marine bacterium from the rhizosphere of the halophilic plant *Carex scabrifolia*. Its genome contains numerous unusual biosynthetic gene clusters for diverse types of metabolites. Genome-guided isolation yielded representatives of four different natural product classes, of which only alteramide A was known. Cytotoxic lacunalides were identified as products of a giant trans-acyltransferase polyketide synthase gene cluster, one of six present in this strain. Cytological profiling against HeLa cells suggested that lacunalide A disrupts CDK signaling in the cell cycle. In addition, chemical studies on model compounds were conducted, suggesting the structurally unusual ergoynes as products of a conjugated diyne–thiourea cyclization reaction.