

Bacterial diversity and culturable actinomycetes antimicrobial activity in tidal flats of southern China

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Tidal flats are globally distributed coastal ecosystems that occur at the interface between land and sea. They support biodiversity and maintain the ecosystem by offering services including storm protection, shoreline stabilization, and food production. Although marine ecosystems have become hotspots in recent decades, little attention was given to the microbial diversity and resources of coastal tidal flats. Using high-throughput sequencing of 16S rRNA gene, this study examined the bacterial diversity and community structure of tidal flats in southern China with coastlines exceeding 10,000 kilometers. Combining the co-occurrence network analysis, was used culturomics approach to acquire tidal flat bacterial resources, especially for actinomycetes, to discover more antibiotics that held medical and industrial potential. The research suggested that bacterial communities varied with distinct latitude and longitude, as well as the texture of tidal flats. Pseudomonadota, Chloroflexota, Acidobacteriota, and Bacteroidota were the dominating bacterial phyla, at the genus level, unassigned operational taxonomic units were most prevalent. Additionally, network analysis indicated that the top 20 percent of core taxa were all uncultured bacteria, which might be keystone taxa during tidal flat microbial community construction. Microbial functions predicted based on phylogenetic investigation of communities by reconstruction of unobserved states (PICRUSt2) demonstrated that terpenoids and polyketide metabolism genes were abundant. To get more antibiotic producing bacteria, 15 types of isolate media were used, and a total of 629 actinomycete strains belonging to 35 genera, including Micromonospora, Streptomyces, Agromyces, Rhodococcus, and Micrococcus, were isolated, of which 45 novel species candidates were discovered. 56 isolates were found to contain at least one of the three biosynthetic gene clusters (PKS-I, PKS-II, and NRPS), taking into account their biosynthetic potential. Furthermore, six human opportunistic pathogens (*Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Aeromonas veronii*, and *Aeromonas hydrophila*) were used to assay their antimicrobial activity. Out of the 56 strains, 31 exhibited positive resistance against at least one of the six test pathogens. All our preliminary results highlight the diversity and composition of the microbiome in underexplored habitats such as tidal flats. In addition, this work also advanced the understanding of tidal flats as a treasury of antibacterial compounds that may be with uncommon resistance mechanisms for human pathogens.