Editorial: A Focus on Actinobacteria: Diversity, Distribution, and Secondary Metabolites

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Actinobacteria are the most closely related prokaryotic microorganisms of significance to humans. Apart from their significant contribution to soil organic matter turnover (Crowther et al., 2019), they are critical as symbionts in plant-associated microbial communities (Barka et al., 2015), plant-promoting and biocontrol agents (Toumatia et al., 2016; Zahra et al., 2020), and prolific producers of useful natural compounds (Demain and Sanchez, 2009; Idris et al., 2017). As a result, an increasing number of studies have concentrated on the diversity and distribution of actinobacterial resources, as well as the application of novel technologies to explore these microorganisms (Qin et al., 2016). Actinobacteria are so intriguing and exciting that has led to considerable novel species, genera, and even higher taxa being proposed and their corresponding novel resources have been collected from diverse ecosystems in recent years (https://lpsn.dsmz.de/phylum/actinobacteria).

After more than a decade of focusing on the diversity of Actinobacteria in desert environments, we discovered that members of the family Geodermatophilaceae were ubiquitous in various micro-ecosystems in Tengger and Badain Jaran deserts, and that this group of microorganisms played a critical role in determining the bacterial community structure in deserts (Sun et al., 2015, 2018; Jiang et al., 2021). Based on these studies, we hypothesized that Geodermatophilaceae represent desert-specific microorganisms and may serve as model organisms for studying the Actinobacteria's resistance to multiple environmental pressures in extreme environments. Thus, we launched the topic “A Focus on Actinobacteria: Diversity, Distribution, and Secondary Metabolites” to bring together newly related research findings and ideas to demonstrate the diversity of Actinobacteria and their survival mechanisms in various ecosystems, and then to expound on useful Actinobacteria in detail.

We are indebted to all the authors for their contributions to this topic, which included one review and eight original research reports. These articles focused on the diversity, function, and biotechnology of Actinobacteria from desert, marine, gut, and nodule environments, as well as the application of gene manipulation technologies and metagenome analysis methods to other microorganisms.

Xie and Pathom-aree systematically reviewed recent advances on the technologies to the recovery of novel taxa, ecological functions, and the discovery of previously un-hitherto biotechnological properties of desert Actinobacteria.
(i) After comparing the efficiency of different actinobacterial isolation techniques, this review strongly recommended that Actinobacteria can be isolated from desert associated samples using the sprinkling technique. (ii) Whole-genome sequencing was not only effective at resolving taxonomic bottlenecks, but also provided a wealth of information about the ecology and biotechnology potential of desert species. (iii) The PLate Coverage Algorithm (PLCA), a culture-enriched metagenomic approach, may be used to improve the recovery of microbial diversity on any low-abundance microbial communities. This approach was also beneficial in elucidating the mechanisms by which microbial communities interact with their hosts. (iv) Advances in computational techniques and bioinformatics tools have resulted in an enormously richer understanding of Actinobacteria biology in desert environments.

Liu et al. further supported the preceding review. They described an investigation into the diversity, novelty, and pharmacological potential of actinobacterial strains isolated from the Taklamakan desert. A batch of newly isolates, representing novel taxa or exhibiting antagonistic activity against “ESKAPE” pathogens, merit further investigation and exploration. Multi-strategies, including high-throughput screening, small-scale fermentation using deep-plates, One Strain Many Compounds (OSMAC), and compound dereplication via UPLC-QToF-MS/MS, were proposed to thoroughly investigate the functional Actinobacteria.

Distinct from the desert environments, the deep-sea ecological environment has generally been regarded as another underexplored habitats for undiscovered, potentially pharmaceutical microbial resources. The orders Gaiellales and Rubrobacterales were discovered to be widespread in marine ecosystems, despite their difficulty in laboratory cultivation (Chen et al.). To obtain their pure cultures, Chen et al. optimized the growth conditions, and found that light, expanding culture time, and low nutrition could promote Rubrobacterales survival on media, and some marine factors are indispensable for their growth.

Guerrero-Garzón et al. investigated the antibiotic activity and comparative genomics of Streptomyces spp. isolated from marine sponges. The findings indicated that the dominant actinobacterial genus Streptomyces is not only a prolific producer of useful natural compounds, but also an ideal model for Synthetic Biology techniques to mine the selected biosynthesis gene clusters (BGCs).

Streptomyces spp. derived compounds have benefited humans for such a long time that it is becoming increasingly difficult to discover new compounds from Streptomyces continuously. As a result, it is critical to innovate perspectives, technologies, and strategies for conducting systematic investigations into Streptomyces’ potential to produce novel compounds. The endophytic Streptomyces strain YINM00001, has shown to be strong antimicrobial activity and multiple antibiotic resistances, was predicted as a promising candidate to discover valuable secondary metabolites by genome mining, and proven by using OSMAC approach (Liu et al.).

Besides above approaches, genetic manipulation was another popular strategy for enhancing Actinobacteria’s application potential. The genetic manipulation system for genome modification in the rare actinomycete Pseudonocardia alni Shahu was carried out, allowing for the delivery of the powerful CRISPR-Cas machinery into this bacterium via this approach (Li et al.). This work developed a toolkit to facilitate the development and improvement of strain P. alni Shahu, which served as a useful reference for the development of genetic manipulation methods in other rare actinomycetes.

Culture-independent techniques revealed that Actinobacteria dominated in nodule environment of Tunisia, with Frankia spp. most frequently being detected (Ghodhbane-Gtari et al.). Along a gradient of aridity ranging from humid to arid, Frankia’s absolute and relative prevalence decreased at semi-arid and arid sampling locations. Most abundant secondary metabolite biosynthetic gene clusters were predicted in genomes of Frankia sp. Therefore, as the niche builder of root nodules, the functional Frankia microsymbiont played a keystone role in the nodule environments, especially in shaping and maintaining the diversity and stability of nodule communities.

The core of research on actinobacterial resources is to discover new compounds to combat the growing spread of drug resistance. Mahilkar et al. developed a quantitative model to examine a population’s response to two temporal environmental cues and predicted variables that may be relevant for anticipatory regulatory response evolution. After approximately 850 generations of alternating rhamnose and paraquat environments while checking the experimental evolution of Escherichia coli, they concluded that pre-exposure to rhamnose resulted in increased fitness in paraquat environment. This anticipatory regulation is encoded by mutations in global regulators, as revealed by genome sequencing. This study advanced our understanding of how the environment shapes the topology of an organism’s regulatory networks.

The study by Mao et al. discovered a significantly altered microbial composition in Parkinson’s disease (PD) patients by examining the composition of the gut microbiome in PD patients using shotgun metagenomic sequencing. The Cluster of Orthologous Groups protein database, the KEGG Orthology database, and carbohydrate-active enzymes gene category analysis revealed that branched-chain amino acid–related proteins were significantly increased in the PD group, while GH43 was significantly decreased. Functional analysis of the metagenome confirmed differences in microbiome metabolism between the PD and non-PD groups, specifically in the metabolism of short-chain fatty acid precursors.

We are pleased to present this Research Topic in Frontiers in Microbiology. We sincerely hope that readers will find this Research Topic interesting. Surely, we will constantly contribute to the research on Actinobacteria and the journal Frontiers in Microbiology.

**AUTHOR CONTRIBUTIONS**

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.
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