Meta Gene 23 (2020) 100639

Contents lists available at ScienceDirect

Meta Gene

journal homepage: www.elsevier.com/locate/mgene

Metagenomic insights unveil the dominance of undescribed Actinobacteria in pond ecosystem of an Indian shrine

Radhakrishnan Manikkam[a,*,1], Madangchanok Imchen[b], Manigundan Kaari[a], Vignesh Angamuthu[a], Gopikrishnan Venugopal[c], Shanmugasundaram Thangavel[c], Jerrine Joseph[a], Balagurunathan Ramasamy[d], Ranjith Kumavath[b,*,1]

[a] Centre for Drug Discovery and Development, Sathyabama Institute of Science and Technology(Deemed to be University), Jeppiaar Nagar, Rajiv Gandhi Road, Chennai 600 119, Tamil Nadu, India
[b] Department of Genomic Science, School of Biological Sciences, Central University of Kerala, Padanakkad P.O., Kasaragod, Kerala 671314, India
[c] DRDO-BU Centre for Life Sciences, Bharathiar University Campus, Coimbatore 641 046, Tamil Nadu, India
[d] Department of Microbiology, Periyar University, Salem 636 011, Tamil Nadu, India

ARTICLE INFO

Keywords:
Metagenomics
Sediment
Rare Actinobacteria
Acidothermus
Novel secondary metabolites

ABSTRACT

Actinobacteria have been an excellent source of novel antibiotics for several decades. However, their community remains unexplored in the pond sediments. The metagenomic analysis holds immense potential for identifying rare and uncharacterized microorganisms from many ecological habitats. The present study was designed to delineate and understand the bacterial diversity with special focus on Actinobacteria in pond sediment collected from Sanjeeviraya Hanuman Temple, Tamil Nadu, India. The sediment had an average temperature (25.32%), pH (7.13), salinity (0.960 Mmhos/cm) and high organic content (10.7%) posing minimal stress on growth condition of the microbial community. Subsequent molecular manipulations, sequencing and metagenomics analysis of 16S rRNA confirmed the presence of 40 phyla, 100 classes, 223 orders, 319 families and 308 genera in the sediment sample dominated by Acidobacteria (18.14%), Proteobacteria (15.13%), Chloroflexi (12.34), Actinobacteria (10.84%), and, Cyanobacteria (5.58%). Within the Actinobacteria phylum, *Acidothermus* (29.68%) was the predominant genus followed by *Actinospica* (17.65%), *Streptomyces* (14.64%), *Nocardia* (4.55%) and *Sinomonas* (2.9%). At the species level, only 15.2% within the Actinobacterial phylum were assigned to cultured species. This study reveals the huge unexplored diversity of Actinobacterial community indicating that the microbial ecology of pond sediment is a neglected field which needs attention and also illustrates the highly enriched bioactivity with potential pharmaceutical and industrial significance.

1. Introduction

Emergences and global distribution of multidrug resistance have triggered the need for more potent antibiotics (Imchen et al., 2018; Reddy and Dubey, 2019). Actinobacteria are one of the largest phyla ubiquitous to both aquatic and terrestrial ecosystems having high G + C content (Ventura et al., 2007; Barka et al., 2016). They are overactive antibiotics producers producing over 10,000 known antibiotics (Radhakrishnan et al., 2017). However, the discovery of novel antibiotics are in decline since the last few decades. Understanding the diversity of rare Actinobacteria could shed some light on the isolation of rare Actinobacteria, which in turn could increase the likelihoods of discovering potentially novel bioactive compounds i.e. vancomycin was discovered from the rare Actinobacteria strain *Amycolatopsis orientalis* (Mahajan and Balachandran, 2012). Freshwater ecosystem, especially stagnant water bodies such as lakes have shown some promising results for rare Actinobacterial genus (Ningthoujam et al., 2011; Newton et al., 2011). However, it is estimated that only 1% of microbes in the natural environment are culturable under laboratory conditions (Vartoukian et al., 2010). More than 88% of culturable isolates belong to four phyla known as Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes (Ventura et al., 2007). Uncultivated bacteria possess a great diversity of enzymes adaptable to different environmental conditions, which could serve as a prolific source of novel bioactive compounds with industrial and pharmaceutical applications. Hence, several researchers have focused on the rare microbes in quest of novel antimicrobial metabolites

---

* Corresponding authors.
E-mail addresses: mrkactinos@gmail.com (R. Manikkam), RNKumavath@cukerala.edu.in (R. Kumavath).
[1] Equally contributed.

https://doi.org/10.1016/j.mgene.2019.100639
Received 8 August 2019; Received in revised form 15 November 2019; Accepted 17 November 2019