Science of the Total Environment 743 (2020) 140699

Contents lists available at ScienceDirect

Science of the Total Environment

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

16s rRNA metagenomic analysis reveals predominance of *Crtl* and *CruF* genes in Arabian Sea coast of India

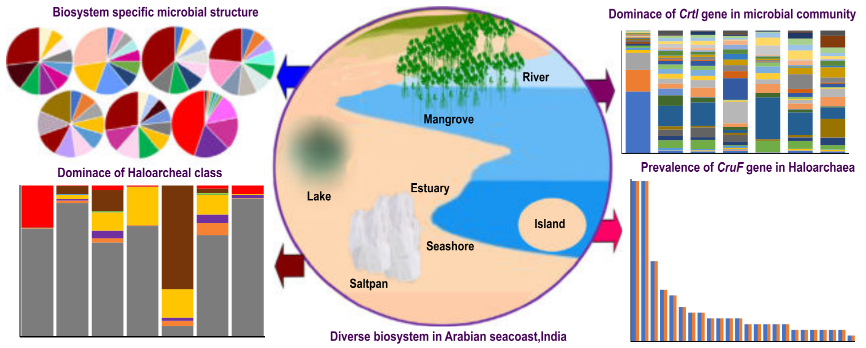
Jamseel Moopantakath [a], Madangchanok Imchen [a], Busi Siddhardha [b], Ranjith Kumavath [a],*

[a] *Department of Genomic Science, Central University of Kerala, Tejaswini Hills, Periya, Kasaragod 671320, Kerala, India*
[b] *Department of Microbiology, School of Life Sciences, Pondicherry University, Puducherry 605014, India*

HIGHLIGHTS

- Haloarchaea dominated the Archaeal domain in biosystems irrespective of salinity.
- Haloarchaeal spp. were detected in freshwater as well as saline sediments.
- High abundance of *Crtl* and *CruF* encoding genera were detected in all biosystems.
- *CruF* gene was detected in every species within the Haloarchaeal genus.

GRAPHICAL ABSTRACT



ARTICLE INFO

Article history:
Received 3 May 2020
Received in revised form 25 June 2020
Accepted 1 July 2020
Available online 8 July 2020

Editor: Ewa Korzeniewska

Keywords:
16s RNA metagenomic
CruF gene
Microbial ecology
Haloarchaea
Carotenoid
Bacterioruberin

ABSTRACT

Microbial communities perform crucial biogeochemical cycles in distinct ecosystems. Halophilic microbial communities are enriched in the saline areas. Hence, haloarchaea have been primarily studied in salterns and marine biosystems with the aim to harness haloarcheal carotenoids biosynthesis. In this study, sediment from several distinct biosystems (mangrove, seashore, estuary, river, lake, salt pan and island) across the Arabian coastal region of India were collected and analyzed though 16s rRNA metagenomic and whole genome approach to elucidated the dominant representative genre, haloarcheal diversity, and the prevalence of *Crtl* and *CruF* genes. We found that the microbial diversity in mangrove sediment (794 OTUs) was highest and lowest in lake and river (558–560 OTUs). Moreover, the bacterial domain dominated in all biosystems (96.00–99.45%). Top 10 abundant genera were involved in biochemical cycles such as sulfur, methane, ammonia, hydrocarbon degradation, and antibiotics production. The Archaea was mainly composed of Haloarchaea, Methanobacteria, Methanococci, Methanomicrobia and Crenarchaeota. Carotenoid gene, *Crtl*, was observed in a major portion (abundance 60%; diversity 45%) of microbial community. Interestingly, we found that all species under haloarcheal class that were represented in fresh as well as marine biosystems encodes *CruF* gene (bacterioruberin carotenoid). Our study demonstrates the high microbial diversity in various ecosystems, enrichment of *Crtl* gene, and also shows that *Crtl* and *CruF* genes are highly abundant in haloarcheal genera. The finding of ecosystems specific *Crtl* and *CruF* encoding genera opens up a promising area in bioprospecting the carotenoid derivatives from the wide range of natural biosystems.

1. Introduction

Marine ecosystems are the principle bionetwork on earth covering about 70–75% of earth's total surface area and play a significant role in

---

* Corresponding author.
E-mail address: RNKumavath@gmail.com (R. Kumavath).

https://doi.org/10.1016/j.scitotenv.2020.140699
0048-9697/