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Microbial communities in mangrove ecosystem differs by intertidal location and microhabitat of pneumatophores

Varsha Bohra & Fred Wang-Fat Lee*

School of science and Technology, Hong Kong Metropolitan University, Hong Kong, SAR China

INTRODUCTION

- Mangrove ecosystem supports rich prokaryotic diversity (solely comprising more than 95% of the total microbial biomass) which remains yet to be explored
- The high abundance of prokaryotes is associated with their role in various biogeochemical processes operating in mangrove ecology.
- Mangroves are characterized by periodic tidal cycles which induce wide variation in environmental conditions across small spatiotemporal scales.
- This leads to the formation of characteristic microbial zones with variable community structure and function.

SAMPLING PLAN AND METHODOLOGY

- ➢ Ting Kok mangrove was divided into three different zones: mudflat (TK_MF), mangrove (TK_M) and pneumatophore associated sediments (TK_PSAM).
- ➢ The metagenomic DNA was extracted for library preparation and sequencing using Illumina platform DNBSEQ- G400
- ➢ Taxonomic and functional classification of the metadata was performed using BLASTX against the RefSeq and KEGG database on MG-RAST server

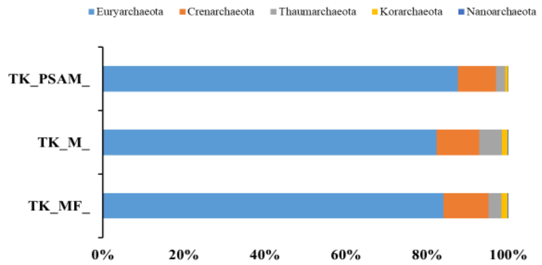
CONCLUSION

- ✓ Proteobacteria was the most dominant phyla in all the microhabitats with Bacteroidetes, the second most, Firmicutes (TK_MF_ and TK_M_) and cyanobacteria (TK_PSAM) were the third abundant phyla.
- ✓ Archaeal distribution with the most abundant Thaumarchaeota remained uniform in all the three habitats.
- ✓ Genes associated with CO_2 to methane production pathway of methanogenesis was dominant in all three zones, with relatively high proportion in TK_MF_ and TK_M_.
- ✓ The relative abundance of nitrate reduction pathway of nitrogen metabolism was high in TK_PSAM_ whereas nitrogen fixation and the denitrification pathway were high in TK_MF_ and TK_M_ samples.
- ✓ This is the first attempt to unveil prokaryotic zonation in mangrove ecology using NGS sequencing.

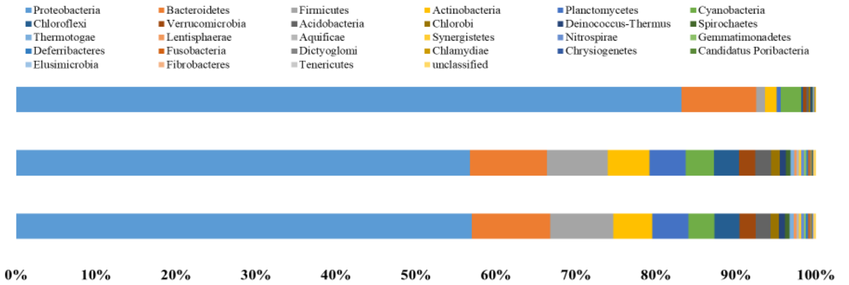
RESULTS

TAXONOMIC

Microbial distribution at domain level
Inside to outside: TK_MF_, TK_M_ and TK_PSAM



Archaeal distribution at phylum level



Bacterial distribution at phylum level

FUNCTIONAL

Pathway	Enzymes	TK_MF_	TK_M_	TK_PSAM_
Carbon Dioxide Methane Production Pathway	Formylmethanofuran dehydrogenase (A-E, G) [EC:1.2.99.5]	1.69	1.64	0.27
	Formylmethanofuran tetrahydromethanopterin-N-formyltransferase [EC:2.3.1.101]	0.40	0.35	0.11
	Methenyltetrahydromethanopterin cyclohydrolase [EC:3.5.4.27]	0.34	0.32	0.07
	Tetrahydromethanopterin S-methyltransferase (A,H) [EC:2.1.1.86]	0.25	0.33	0.00
	Heterodisulfide reductase subunit (A-D) [EC:1.8.98.1]	34.89	33.61	2.09
	5,10-Methylenetetrahydromethanopterin reductase [EC 1.5.98.2]	0.00	0.00	0.00
	Methylenetetrahydromethanopterin dehydrogenase [EC 1.5.98.1]	0.00	0.00	0.00
	5,10-Methenyltetrahydromethanopterin hydrogenase [EC 1.12.98.2]	0.00	0.00	0.00
	Methyl coenzyme M reductase [EC 2.8.4.1]	0.00	0.00	0.00
Acetate to Methane Production Pathway	Tetrahydromethanopterin S-methyltransferase (A,H) [EC:2.1.1.86]	0.25	0.33	0.00
	Heterodisulfide reductase subunit (A-D) [EC:1.8.98.1]	34.89	33.61	2.09
	acetate kinase [EC 2.7.2.1]	0.00	0.00	0.00
	phosphate acetyltransferase [EC 2.3.1.8]	0.00	0.00	0.00
	acetyl-CoA synthetase [EC 6.2.1.1]	0.00	0.00	0.00
	acetyl-CoA decarboxylase [EC 2.3.1.−]	0.00	0.00	0.00
	methyl coenzyme M reductase [EC 2.8.4.1]	0.00	0.00	0.00

Methane metabolism

Pathway	Enzymes	TK_MF_	TK_M_	TK_PSAM_
N- fixation pathway	Nitrogenase (D, H, K) [EC:1.18.6.1]	12.74	13.22	3.91
Assimilatory Nitrate Reduction Pathway	Nitrite reductase (NAD(P)H) (B,D) [EC:1.7.1.4]	7.76	9.01	24.45
Dissimilatory Nitrate Reduction Pathway	Nitrate reductase [EC:1.7.99.4]	21.21	20.14	15.12
	Nitrite reductase (NAD(P)H) (B,D) [EC:1.7.1.4]	7.76	9.01	24.45
	Nitrite reductase (Cytochrome ammonia forming) [EC 1.7.2.2]	0.00	0.00	0.00
Denitrification Pathway	Nitrate reductase [EC:1.7.99.4]	21.21	20.14	15.12
	Nitrite reductase (NO-forming) [EC:1.7.2.1]	2.81	3.70	0.83
	Nitrous-oxide reductase [EC:1.7.2.4]	6.75	7.85	1.40
	Nitric oxide reductase [EC 1.7.2.5]	0.00	0.00	0.00

Nitrogen metabolism

REFRENCE

- Basak, P., Majumder, N.S., Nag, S., Bhattacharyya, A., Roy, D., Chakraborty, A., SenGupta, S., Roy, A., Mukherjee, A., Pattanayak, R. 2015. Spatiotemporal analysis of bacterial diversity in sediments of Sundarbans using parallel 16S rRNA gene tag sequencing. *Microbial ecology*, **69**, 500-511.
- Bohra, V., Dafale, N.A., Purohit, H.J. 2019b. Understanding the alteration in rumen microbiome and CAZymes profile with diet and host through comparative metagenomic approach. *Archives of Microbiology*, **201**, 1385-1397
- Dafforn, K.A., Baird, D.J., Chariton, A.A., Sun, M.Y., Brown, M.V., Simpson, S.L., Kelaher, B.P., Johnston, E.L. 2014. Faster, higher and stronger? The pros and cons of molecular faunal data for assessing ecosystem condition. in: *Advances in Ecological Research*, Vol. 51, Elsevier, pp. 1-40.
- Sanka Loganathachetti, D., Sadaiappan, B., Poosakkannu, A., Muthuraman, S. 2016. Pyrosequencing-based seasonal observation of prokaryotic diversity in pneumatophore-associated soil of Avicennia marina. *Current microbiology*, **72**, 68-74.

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