

Geographical Distribution and Seasonal Dynamics of Polyphosphate Accumulating Organisms and Glycogen Accumulating Organisms in Sewage Treatment Plants

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* Background

PAOs – bacteria that accumulate excess phosphorus from wastewater in Enhanced biological phosphorus removal (EBPR).

Candidatus Accumulibacter phosphatis (referred to Accumulibacter), *Tetrasphaera* sp.,
Candidatus Halomonas phosphatis, *Gemmatimonas aurantiaca*.

GAOs – compete for organic carbon sources with PAOs but not contribute to P removal.

Candidatus Competibacter phosphatis (referred to Competibacter),
Defluvicoccus-related tetrad-forming organisms (referred to TFOs)

Research gap:

The **geographical distribution** of PAOs and GAOs within STPs across a **global scale** has not been fully uncovered, and their **temporal dynamics** is still inconclusive.

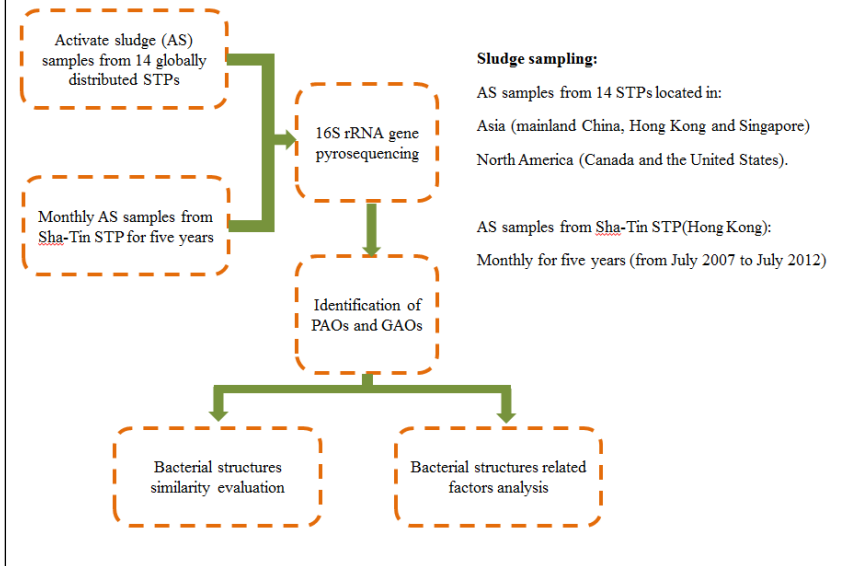
Target:

The **geographical distribution** of PAOs and GAOs among 14 full-scale STPs of Asia and North America;

The **monthly microbial variations** of PAOs and GAOs in AS samples of a STP

In this study, we investigated the geographical distribution of EBPR (Enhanced biological phosphorus removal) among 14 full-scale STPs, and their monthly microbial variations in AS samples of a Sewage Treatment Plant (STP).

* Materials and methods



Activate sludge (AS) samples were collected from 14 STPs located in Asia and North America.

AS samples from Sha-Tin STP (Hong Kong) have been taken monthly for five years.

* Materials and methods

16S rRNA gene pyrosequencing and identification of PAOs and GAOs:

Pyrosequencing reads assigned as PAO-like or GAO-like: 97% similarity
 16S rRNA genes in V4 region with 200bp alignment length cutoff.:
 Identify the bacterial community in the 14 STPs
 16S rRNA genes in V3 and V4 regions with 400bp alignment length cutoff.:
 Identify the bacterial community in Sha-Tin STP.

Statistic analysis:

Principle component analysis (PCA):

To evaluate the similarity of the EBPR-related bacterial structures in AS samples.

Canonical corresponding analysis (CCA):

To reveal the relationship between the EBPR-related bacterial structure to geographic conditions, operational parameters and water characteristics.

The overall profile of bacterial communities has been revealed by assigning 16S rRNA gene pyrosequencing reads to well-defined databases.

* Results and discussion

	CN-NJ-SJ	CN-JD-TD	CN-HR-UN	CN-SH-HH	CN-BJ-BX	CN-WH-LW	CN-GZ-DT	SG-SG-UP	US-CO-CO	US-OR-PC	CA-GP-GP	CN-HK-SJT1	CN-HK-SJT2	CN-HK-SH	CN-HK-SL
Competibacter subgroup 1	0.0	2.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Competibacter subgroup 2	0.1	0.4	0.0	0.1	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Competibacter subgroup 3	0.0	0.8	0.1	0.1	0.4	0.0	0.0	0.4	0.0	0.1	0.0	0.1	0.0	0.0	0.0
Competibacter subgroup 4	0.2	2.3	0.4	0.9	0.4	0.2	0.1	0.1	0.0	0.0	0.0	0.2	0.1	0.2	0.0
Competibacter subgroup 5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Competibacter subgroup 6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.6	0.0	0.0	0.0	0.0	0.0	0.1	0.0
Competibacter subgroup 7	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Defluviococcus-related TFO cluster I	1.1	0.7	0.7	1.4	0.8	1.1	0.6	0.8	0.5	0.4	1.3	0.9	1.5	0.5	0.0
Defluviococcus-related TFO cluster II	0.0	0.1	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Defluviococcus-related TFO cluster III	0.0	0.0	0.5	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0
Defluviococcus-related TFO cluster IV	0.0	1.2	0.3	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Accumulibacter clade I	0.1	0.4	0.3	0.1	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0
Accumulibacter clade IIA	0.4	0.0	0.1	0.1	0.2	0.4	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Accumulibacter clade IIB	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Accumulibacter clade IIC&IID	0.5	0.7	0.2	0.3	1.0	0.7	1.1	1.5	0.4	1.5	0.0	0.2	0.0	0.3	0.6
Candidatus Halomonas phosphatis	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.7	0.2	0.1	0.0	0.0	0.0	0.0	0.0
Gemmatimonas aurantiaca	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.1	0.1	0.0	0.0	0.1	0.0
Tetrasphaera cluster I	0.1	0.1	0.2	0.1	0.1	0.0	0.0	0.4	0.1	0.1	3.4	0.3	0.3	0.4	0.0
Tetrasphaera cluster II	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0	3.8	0.0	0.0	0.4	0.0
Tetrasphaera cluster III	0.3	0.2	0.1	0.1	0.1	0.0	0.2	0.0	0.3	0.1	0.0	0.8	0.0	0.0	0.0

Figure 1. Relative abundances (%) of EBPR-related microorganisms in AS samples from 14 STPs.

Accumulibacter and Tetrasphaera were most popular PAOs in most STPs. Tetrasphaera clusters were evenly distributed and GAOs presented in almost all full-scale STPs.

* Results and discussion

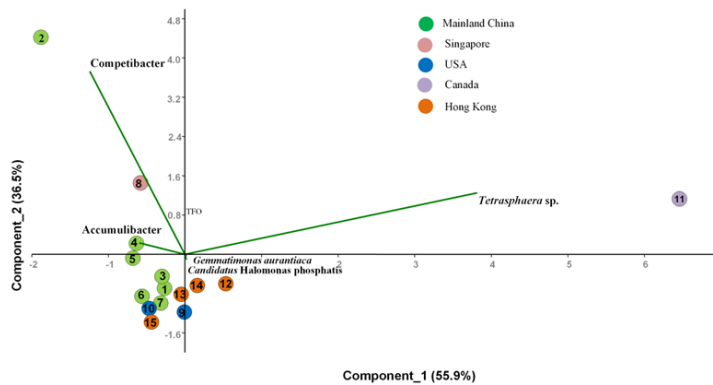


Figure 2. PCA of sludge samples extracted from 14 STPs based on the relative abundances of putative PAOs and GAOs.

No significant geographical difference was found between sludge samples from Asia and North America.

* Results and discussion

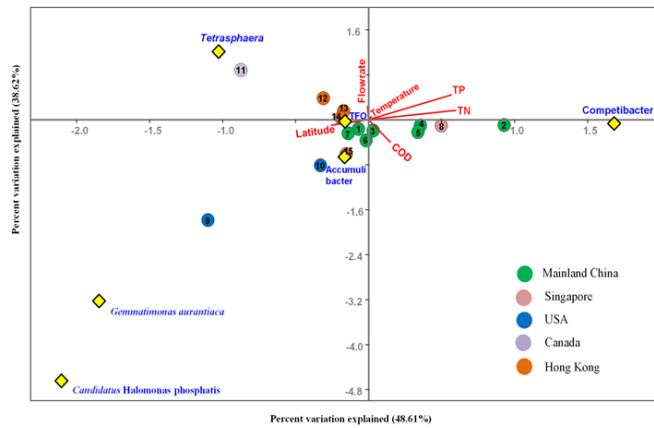


Figure 3. the variations of relative abundances of PAOs and GAOs with respect to the variable geographic conditions and wastewater characteristics in 14 STPs.

Most AS samples in Asia distributed either along or very close to the TP, TN and COD lines (or their extension lines).

* Results and discussion

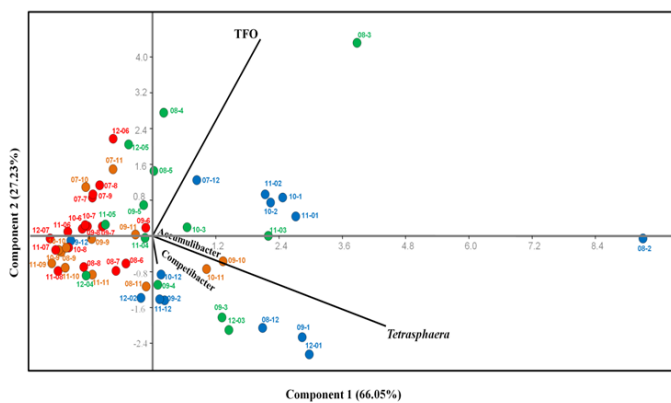


Figure 4. PCA of time series AS samples extracted from the Sha-Tin STP in regarding to the relative abundances of putative PAOs and GAOs.

A seasonal variation pattern was observed among abundances of the identified PAO and GAO populations.