



## ORIGINAL RESEARCH ARTICLE

## Relationship between bacteria and nitrogen dynamics in wastewater treatment oxidation ponds

S. Saneha<sup>1</sup>, T. Pattamapitoon<sup>1\*</sup>, S. Bualert<sup>1</sup>, O. Phewnil<sup>1</sup>, W. Wararam<sup>1</sup>, N. Semvimol<sup>1</sup>, K. Chunkao<sup>2</sup>, C. Tudsanaton<sup>1</sup>, M. Srichomphu<sup>1</sup>, U. Nachaiboon<sup>2</sup>, O. Wongsrikaew<sup>2</sup>, P. Wichittrakarn<sup>2</sup>, C. Chanthasoon<sup>2</sup><sup>1</sup> Department of Environmental Science, Environmental Faculty, Kasetsart University, Bangkok, Thailand<sup>2</sup> The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand

## ARTICLE INFO

## Article History:

Received 16 November 2022

Revised 23 February 2023

Accepted 28 March 2023

## Keywords:

Bacterial communities

Nitrogen dynamics

Oxidation Ponds

Total kjeldahl nitrogen (TKN)

Wastewater treatment

## ABSTRACT

**BACKGROUND AND OBJECTIVES:** The bacterial community plays a crucial role in the nitrogen cycle. Oxidation ponds act as a natural treatment system for wastewater and are designed to promote the growth and activity of certain bacterial species that remove contaminants from the water. The nitrogen cycle in these ponds involves the conversion of nitrogen compounds through biological processes by bacteria. The presence or absence of certain bacterial species can greatly influence the efficiency of the nitrogen cycle in these ponds. This research investigates the relationship between bacteria and nitrogen dynamics, the key components of wastewater treatment, in oxidation ponds. This work aims to identify the bacterial community composition in oxidation ponds, investigate the role of bacteria in the transformation and removal of nitrogen compounds from wastewater in oxidation ponds, and evaluate the impact of environmental factors on the microbial communities and nitrogen dynamics in oxidation ponds. This study was carried out in the oxidation wastewater treatment at the King's Royally Initiated Laem Phak Bia Environmental Research and Development or LERD Project, in Phetchaburi, Thailand.

**METHODS:** Wastewater samples were collected from the 1st–5th oxidation ponds at a depth of 30 centimeter from the water surface and analyzed for various quality parameters including temperature, dissolved oxygen, potential of hydrogen, biochemical oxygen demand, nitrates, ammonia, and total kjeldahl nitrogen. Next-generation sequencing by Illumina Miseq was used to examine the 16S ribosomal ribonucleic acid of bacteria in the collected samples. Correlation test was used for statistical analysis.

**FINDINGS:** The temperature, potential of hydrogen (1<sup>st</sup> to 5th ponds), and dissolved oxygen (2nd to 5th ponds) in the oxidation ponds were within the standard value. Fifteen bacterial phyla were identified in the five oxidation ponds, with phylum Proteobacteria accounting for the highest population comprising 47.56% of the total bacterial population.

**CONCLUSION:** Genera *Novosphingobium* (phylum Proteobacteria), *Ammonia-11* (phylum *Verrucomicrobiota*), and *Vicinamibacteraceae* (phylum *Acidobacteriota*) have the strongest relationships with ammonia, nitrate, and total kjeldahl nitrogen ( $R^2 = 0.9710, 0.986, 0.8124$ ). The bacterial population is a crucial factor in nitrogen nutrient and water quality. *Novosphingobium* is involved in the removal of ammonia from wastewater, *Verrucomicrobiota* act as denitrifiers, and *Vicinamibacteraceae* increases the total kjeldahl nitrogen levels.

DOI: [10.22035/gjesm.2023.04.04](https://doi.org/10.22035/gjesm.2023.04.04)This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

NUMBER OF REFERENCES

54



NUMBER OF FIGURES

5



NUMBER OF TABLES

2

\*Corresponding Author:

Email: [thanit.pa@ku.th](mailto:thanit.pa@ku.th)

Phone: +668 0455 4242

ORCID: [0009-0005-1664-450X](https://orcid.org/0009-0005-1664-450X)

Note: Discussion period for this manuscript open until January 1, 2024 on GJESM website at the "Show Article".

## INTRODUCTION

Increasing urbanization and rapid population growth has intensified the generation of waste, including human excretion, e-waste, garbage food, fat oil and wastewater (Bajsa et al., 2003). Domestic wastewater is a complex mixture of suspended and dissolved materials with extremely high concentrations of nutrients and organic content, including nitrogen in the form of ammonia ( $\text{NH}_3$ ), nitrates ( $\text{NO}_3^-$ ), and total kjeldahl nitrogen (TKN) (Latrach et al., 2015; Vlyssides et al., 2002). These nutrients can remarkably affect water quality (Quiros, 2003; Camargo et al., 2006). When untreated, wastewater is discharged directly into water bodies, causing contamination and water quality issues (Wedyan et al., 2016; Noophan et al., 2018; Kumar et al., 2020). Excess nitrogen can harm aquatic ecosystems, causing the eutrophication of amphibian systems and the depletion of dissolved oxygen (DO) and leading to the death of fish and other marine organisms (Ahmed et al., 2022). In addition, nitrate leaching from soil can contaminate groundwater, which could cause methemoglobinemia in infants under 3 months upon ingestion (Ward et al., 2018). Wastewater treatment is essential to maintain the quality of the environment and protect public health. Oxidation ponds are a low-cost and widely used wastewater treatment system that includes five consecutive ponds and involves interactions with sunlight, wind, bacteria, and algae: the first one is for sedimentation (2.43 m in depth with 5 days of retention time), the second to fourth are for oxidation (2.23, 1.93, and 1.64 m in depth with 12, 15, and 15 days of retention time, respectively), and the fifth is for polishing (1.42 m in depth with 16 days of retention time) (Pattamapitoon et al., 2013; Jinjaruk et al., 2018; Nimitim et al., 2020). Biological treatment using aerobic and facultative heterotrophic bacteria is an environmentally friendly alternative method for treating domestic wastewater. This approach involves using oxygen from a thermosiphon process (Noikondee et al., 2019) and photosynthesis from *Cyanobacteria*, such as *Cylindrospermopsis* genus (Sukchinda et al., 2019), to consume biodegradable soluble organic contaminants, such as sugars, fats, and organic short-chain carbon molecules. This process oxidizes the organic matter and nutrients in the wastewater (Posadas et al., 2013; Bestawy et al., 2014; Zurano et al., 2021). Biological nitrogen

removal is preferred over biochemical process because the former can convert nitrogen compounds to nitrogen gas ( $\text{N}_2$ ). Particulate organic nitrogen is hydrolyzed to soluble organic nitrogen by aerobic and facultative heterotrophic bacteria (Sun et al., 2010). In particular, nitrifying bacteria play a crucial role in wastewater treatment oxidation ponds by converting ammonia to nitrite and then to nitrate. This process is known as nitrification and is essential for breaking down harmful waste products in the water. Meanwhile, denitrifying bacteria are responsible for converting nitrate to  $\text{N}_2$ , which is then released into the atmosphere. They help reduce nitrogen levels in the water. Both types of bacteria work together to provide an effective method of wastewater treatment in oxidation ponds. However, the relationship between bacteria and nitrogen dynamics in oxidation ponds is still not fully understood. This study aims to determine the relationship between bacteria and nitrogen dynamics in wastewater treatment oxidation ponds by investigating the microbial communities present in these systems and how they affect the transformation and removal of nitrogen compounds. The objectives are to identify the bacterial community composition in wastewater treatment oxidation ponds, investigate the role of bacteria in the transformation and removal of nitrogen compounds from wastewater in oxidation ponds, and evaluate the impact of environmental factors, such as temperature and DO levels, on the microbial communities and nitrogen dynamics in oxidation ponds. The results will be useful in the development and management of water quality at the LERD project in the future. This study was carried out in the oxidation wastewater treatment at the LERD project, Phetchaburi, Thailand during the dry period in 2022.

## MATERIALS AND METHODS

### Study area

The study area is the LERD project (Fig. 1), which aims to treat community wastewater from Phetchaburi municipal. The project has five ponds for treating community wastewater, namely, the 1st pond (sedimentation pond), 2<sup>nd</sup> to 4<sup>th</sup> ponds (oxidation pond), and 5<sup>th</sup> pond (polishing pond). The project area is located at latitude 130 02'40" to 130 03'20" N and longitude 1000 05'10" to 100 06'05" E, close to the mangrove forest and Phetchaburi coastal area.

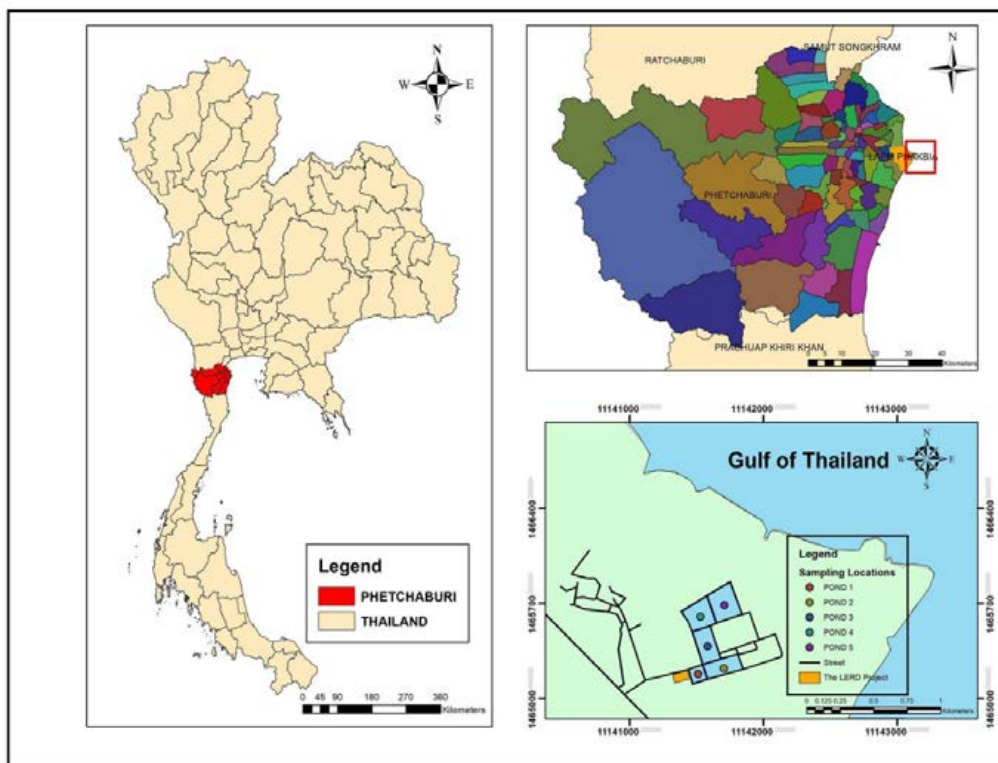


Fig. 1: Geographic location of the study area in the LERD project, Phetchaburi province, Thailand

#### Wastewater sampling and bacteria analysis

For wastewater collection, 1 liter polyethylene (PE) bottles were used. Samples were collected down to 30 centimeter (cm) from water surface in oxidation ponds (1<sup>st</sup> to 5<sup>th</sup> ponds) of the LERD project during the dry period in February 2022 because of the high nutrient concentration throughout this season. Compared with the dry period, the wet period features heavier rainfall and rain flowing into the pond that affect the performance of the wastewater treatment (Makuwa *et al.*, 2022). The increased temperature in the dry period increases biological activity, respiration of organisms, and rate of organic matter decomposition (Kamarudin *et al.*, 2020). The wastewater samples were kept at 4 °C during transfer to the laboratory and then centrifuged at 8,000 rpm to separate the sludge. The lower sediment was collected in a centrifuge tube for high-efficiency sequencing. For bacterial analysis using next generation sequencing (NGS) technique, deoxyribonucleic acid (DNA) was extracted and sequenced using Illumina Miseq. The generated data were assembled, annotated, and

compared with other genomes.

#### Wastewater quality analysis

On-site measurements of the following three parameters were conducted to determine wastewater quality: temperature, DO, and potential of hydrogen (pH). Four parameters of nutrient concentrations were measured in the laboratory, namely, biochemical oxygen demand (BOD), nitrate ( $\text{NO}_3^-$ ), ammonia ( $\text{NH}_3$ ), and TKN. Nutrient concentrations were measured using the standard methods for the examination of water and wastewater (APHA, 2017).

#### Statistical analysis

A correlation test was used to describe the relationship between bacterial population and nutrients ( $\text{NO}_3^-$ ,  $\text{NH}_4^+$ , and TKN) in an oxidation pond. Coefficients of determination are considered a measure of the degree of linear relationship between two variables. They express the extent to which two variables vary together in the same or opposite direction. They also reveal the magnitude

and direction of these relationships. A correlation coefficient can have a value ranging from -1 to 1. Values close to the absolute value of 1 indicate a strong positive linear relationship between the variables, and values close to 0 indicate no linear relationship between the variables (Khambete and Christian, 2014).

## RESULTS AND DISCUSSION

### Bacterial population diversity

The bacterial populations in the oxidation ponds (1<sup>st</sup> to 5<sup>th</sup> ponds) consisted of normal flora bacteria. (Fig. 2) Fifteen bacterial phyla, namely, Proteobacteria, Actinobacteriota, Cyanobacteria, Planctomycetota, Verrucomicrobiota, Firmicutes, Bacteroidota, Chloroflexi, Desulfobacterota, Patescibacteria, Acidobacteriota, SAR324\_clade (Marine\_group\_B), Fusobacteriota, Campilobacterota, and Nitrospinota, were found in the five oxidation ponds. To our knowledge, most studies on heterotrophic nitrification and aerobic denitrification have focused on phyla Proteobacteria, Actinobacteria, and Firmicutes (Huang *et al.*, 2013; Srivastava *et al.*, 2016; Zhou *et al.*, 2017; Wang *et al.*, 2019). Proteobacteria were mainly found in the nitrification and denitrification systems and belonged to denitrifying bacteria; its large amount allowed for the effective removal of nitrate nitrogen (Bruckner *et al.*, 2012). This finding is consistent with previous studies, indicating that Proteobacteria are widely spread in wastewater treatment (Wu *et al.*, 2019). Verrucomicrobiota are mostly free-living bacteria and can be found in freshwater, marine water, soil, and seawater (Zwart

*et al.*, 1998).

Proteobacteria have the highest population, accounting for 47.56% of total bacterial population. Its population decreased from the 1<sup>st</sup> pond to the 5<sup>th</sup> pond (6.21%). Proteobacteria are one of the most dominant bacterial groups found in wastewater. Table 1 shows that under aerobic conditions, Proteobacteria use oxygen as an electron acceptor in the respiratory chain. As a result, the presence of DO is essential for their survival and growth. However, too high DO concentration can lead to the complete oxidation of organic matter, causing a decrease in the food base for Proteobacteria. This phenomenon can cause a reduction in their population. Meanwhile, the populations of phyla Actinobacteriota, Cyanobacteria, Planctomycetota, Firmicutes, Chloroflexi, Patescibacteria, Acidobacteriota, SAR324\_clade (Marine\_group\_B), and Nitrospinota increased from the 1<sup>st</sup> pond to the 5<sup>th</sup> pond (27.74%, 22.43%, 20.12%, 6.54%, 2.53%, 0.83%, 0.91%, 0.65%, and 0.07%, respectively). Under aerobic conditions, bacteria use oxygen as an electron acceptor in the respiratory chain. As a result, the presence of DO is essential for their survival and growth. An increase in DO concentration results in an increase in the abundance of bacteria in wastewater. In addition, the BOD values in Table 1 indicated that the presence of organic matter and nutrients stimulates the growth of bacteria, which break down the organic matter and release carbon dioxide and other byproducts. The amount of BOD in the wastewater is directly related to the amount of organic matter present and hence the rate at which it is being broken down by bacteria.

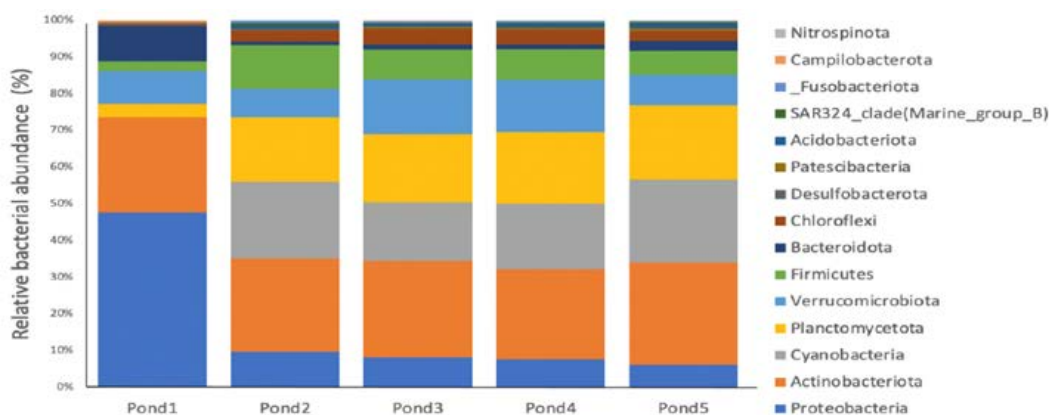


Fig. 2: Bacterial communities (phylum) at the LERD project, Phetchaburi province, Thailand

SAR324\_clade is a marine bacterium species that was most commonly found in the 2nd pond (0.71%) because this pond was nearest to a mangrove forest. The population of Cyanobacteria was the highest in the 5th pond (22.43%), causing their rapid bloom. Some Cyanobacteria species can produce toxins (Sukchinda *et al.*, 2019; Rastogi *et al.*, 2015; Zhang *et al.*, 2022; Huang *et al.*, 2018; Flanzenbaum *et al.*, 2022), leading to fish death during winter season (Srichomphu *et al.*, 2015).

#### Wastewater quality

The temperature and pH of the wastewater were within the standard values (23 °C–32 °C and 5.5–9.0, respectively). The average temperatures in the 1st to 5th ponds were 27.4 °C, 27 °C, 26.7 °C, 26.8 °C, and 26.9 °C, respectively, and their pH values were 8.05, 8.92, 9.13, 9.06, and 9.21, respectively. The average DO levels in the 2nd to 5th ponds met the standard value (>3 mg/L), but that in the 1st pond failed to meet the standard (2.97 mg/L). The highest concentrations of NO<sub>3</sub><sup>-</sup> and TKN were observed in the 2nd pond, and the lowest concentrations were found in the 5th pond. The highest concentrations of NH<sub>4</sub><sup>+</sup> were observed in pond 1<sup>st</sup>. The concentration of NH<sub>4</sub><sup>+</sup> decreased from the 1st pond to the 5th pond due to bacterial decomposition, resulting in a decrease in NH<sub>3</sub> (Table 1). DO levels increased from the 1st pond to the 5th pond due to photosynthesis activity from Cyanobacteria during daytime, resulting in high DO levels. BOD levels decreased because aerobic bacteria use a large amount of oxygen during degradation (Sukchinda *et al.*, 2019; Annisa *et al.*, 2021; Boyd, 2018; Irfan, 2016). Nutrient concentrations in oxidation ponds tend to increase because Cyanobacteria can fix nitrogen gas from the atmosphere and convert it into ammonia and nitrate (Abbaszadeh *et al.*, 2022; Purwono *et al.*, 2017; Mahmud *et al.*, 2021).

#### Bacterial communities and nutrient

Bacterial communities and nitrogen compounds such as NH<sub>3</sub>, NO<sub>3</sub><sup>-</sup>, and TKN were analyzed to determine their relationship with each other. As shown in Fig. 3, phyla Proteobacteria, Planctomycetota, Bacteroidota, Chloroflexi, Desulfobacterota, Patescibacteria, Acidobacteriota, Campilobacterota, and Nitrospinota were highly related to NH<sub>3</sub> in the oxidation ponds with R<sup>2</sup> values of 0.81, 0.84, 0.79, 0.98, 0.82, 0.81, 0.68, 0.79, and 0.75, respectively. Chhimwal *et al.* (2022) investigated the treatment efficiency of domestic wastewater using an oxidation pond and found a decrease in wastewater quality, including nitrate, phosphate, COD, and BOD, after treatment, indicating that the oxidation pond was effective in reducing nutrient concentrations. In addition, they found that the dominant bacterial phylum was Proteobacteria using 16S ribosomal ribonucleic acid (rRNA) gene sequencing. Studies of Hwang *et al.* (2005), Chen *et al.* (2014), Lawson *et al.* (2017), and Suto *et al.* (2017) on heterotrophic bacteria, such as Proteobacteria, Chloroflexi, Bacteroidetes, and Acidobacteria, revealed that these bacteria convert NH<sub>3</sub> to N<sub>2</sub> and play a role in adapting to environmental changes (Egli *et al.* 2001; Isaka *et al.* 2007; Jin *et al.* 2012). Nitrification mostly occurs under aerobic and anaerobic conditions. NH<sub>4</sub><sup>+</sup> oxidation can also occur, mediated by a limited number of bacteria within Planctomycetota (Strous *et al.*, 1999). This phylum has a unique metabolic ability to oxidize NH<sub>4</sub><sup>+</sup> with NO<sub>2</sub><sup>-</sup> as electron acceptor to produce N<sub>2</sub> and a small amount of NO<sub>3</sub><sup>-</sup> under anoxic conditions without requiring an organic carbon source (Date *et al.*, 2008; Kuenen, 2008).

Fig. 4 shows that phyla Verrucomicrobiota, Firmicutes, Chloroflexi, Fusobacteriota Bacteroidota and Nitrospinota had a high correlation with a NO<sub>3</sub><sup>-</sup> in the oxidation ponds (R<sup>2</sup> =0.88, 0.84, 0.64, 0.80, 0.73, 0.86). This finding is consistent with a previous study

Table 1: Water quality in oxidation pond at the LERD project during dry period in February 2022

Parameters	Domestic wastewater	Oxidation pond					Wastewater standard
		1 <sup>st</sup> pond	2 <sup>nd</sup> pond	3 <sup>rd</sup> pond	4 <sup>th</sup> pond	5 <sup>th</sup> pond	
Temp. (°C)	28.5	27.4	27	26.7	26.8	26.9	23-32 <sup>2</sup>
DO (mg/L)	0.264	2.97	7.45	8.92	7.7	8.31	>3 <sup>2</sup>
pH	7.25	8.05	8.92	9.13	9.06	9.21	5.5-9.0 <sup>1</sup>
BOD (mg/L)	64.3	21	23.1	21.3	15.8	9	< 20 <sup>1</sup>
NO <sub>3</sub> <sup>-</sup> (mg/L)	0.726	0.549	2.246	0.947	0.763	0.616	-
NH <sub>3</sub> (mg/L)	2.728	1.842	1.553	1.165	0.591	0.282	-
TKN (mg/L)	7.0	4.8	6.2	4.8	4.2	3.9	-

<sup>1</sup> Ministry of Natural Resources and Environment, Thailand.

<sup>2</sup> Department of Fisheries, Thailand.

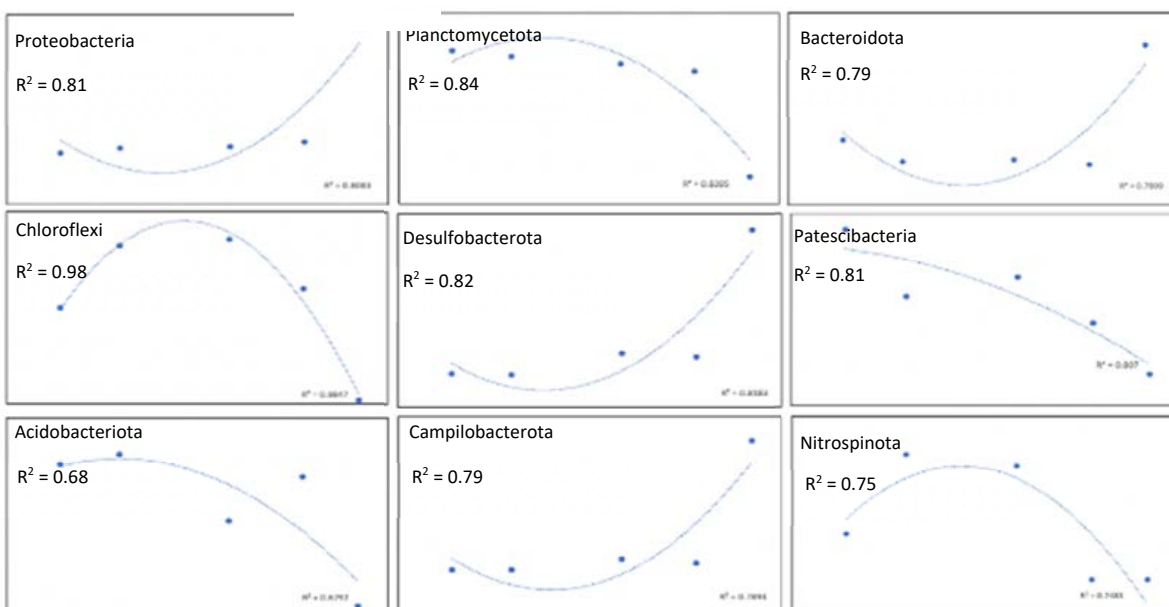


Fig. 3: Correlation between ammonia (NH<sub>3</sub>) and bacterial communities (phylum)

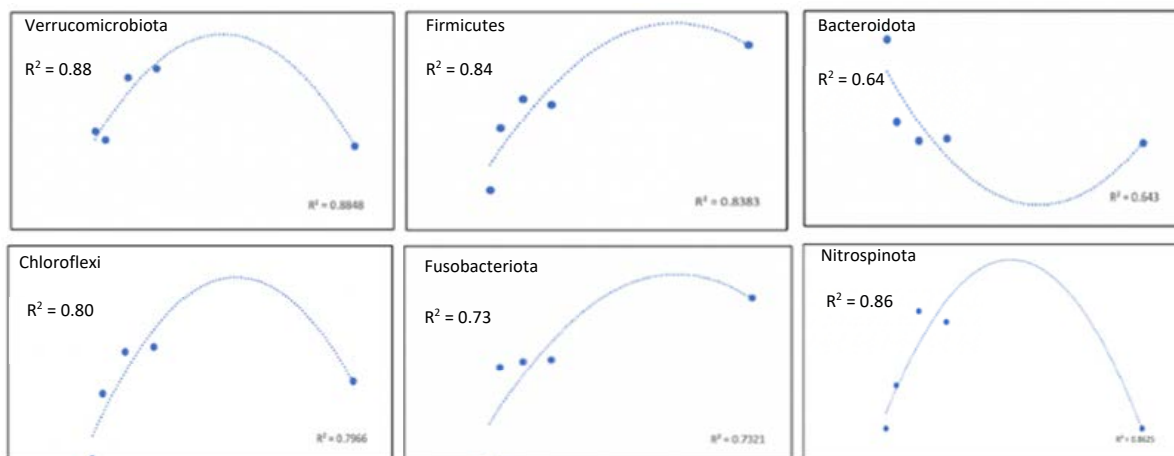


Fig. 4: Correlation between Nitrate (NO<sub>3</sub><sup>-</sup>) and bacterial population (phylum)

that reported a positive correlation between NO<sub>3</sub><sup>-</sup> and the abundance of Chloroflexi and Bacteroidota (Zhang *et al.*, 2018). However, Verrucomicrobiota do not appear to reduce NO<sub>3</sub><sup>-</sup> or other nitrogenous compounds, but rather take up and use NH<sub>3</sub> (Shaomi *et al.*, 2017).

Fig. 5 shows that phyla Cyanobacteria, SAR324\_ clade, and Acidobacteriota had a high correlation with TKN in the oxidation ponds (R<sup>2</sup>= 0.60, 0.77, 0.63).

Chaffin and Bridgeman (2014) studied the utilization of organic and inorganic nitrogen by Cyanobacteria and found that this phylum has preference for NH<sub>3</sub> but can assimilate other forms of nitrogen in the presence of ammonium. These results suggest that Cyanobacterial blooms assimilate multiple forms of nitrogen to support their growth. Genomic information indicated that SAR324\_ clade has a flexible metabolism that includes sulfur oxidation, carbon fixation, hydrocarbon

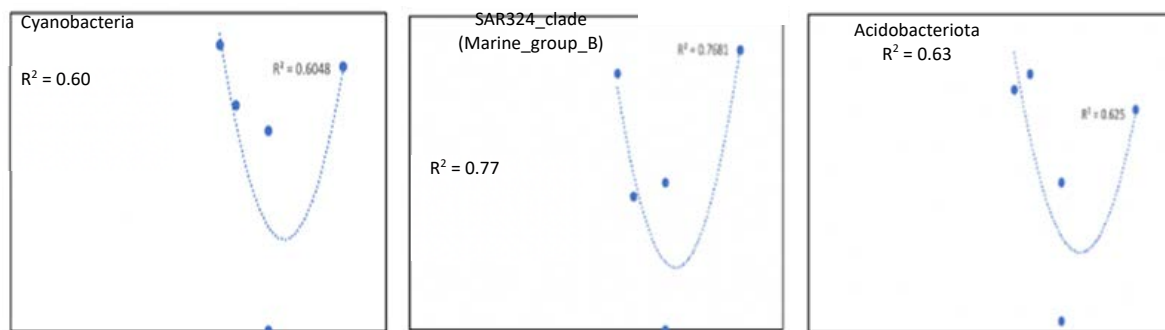


Fig. 5: Correlation between TKN and bacterial population (phylum)

Table 2: Correlation analysis between bacterial communities at the genus level and nutrient ( $\text{NH}_3$ ,  $\text{NO}_3^-$ , and TKN) in oxidation ponds

Nutrient	Phylum	Genus	R <sup>2</sup>	
$\text{NH}_3$	Proteobacteria	<i>Novosphingobium</i>	0.8944	
		<i>Methylocystis</i>	0.8731	
		<i>Polynucleobacter</i>	0.8409	
		<i>Alsobacter</i>	0.8364	
		<i>Methyloparacoccus</i>	0.8253	
		<i>C39</i>	0.7837	
	Planctomycetota	<i>Roseimaritima</i>	0.7863	
		<i>CL500-3</i>	0.7120	
	Bacteroidota	<i>Blastopirellula</i>	0.6096	
		<i>Fluviicola</i>	0.8909	
		<i>Flavobacterium</i>	0.8056	
		<i>Kapabacteriales</i>	0.7843	
		<i>Chloroflexi</i>	<i>JG30-KF-CM45</i>	0.9551
			<i>1-20</i>	0.8872
	<i>Desulfobacterota</i>	<i>Desulfomonile</i>	0.8022	
	<i>Patescibacteria</i>	<i>TM7a</i>	0.8707	
	<i>Acidobacteriota</i>	<i>Luteitalea</i>	0.9120	
	<i>Campilobacterota</i>	<i>Sulfurospirillum</i>	0.7837	
<i>Nitrospinta</i>	<i>P9X2b3D02</i>	0.8199		
$\text{NO}_3^-$	Verrucomicrobiota	<i>NH3-11</i>	0.9886	
		<i>LD29</i>	0.8992	
	Firmicutes	<i>Luteolibacter</i>	0.6767	
		<i>Akkermansia</i>	0.6141	
		<i>Romboutsia</i>	0.9565	
	Chloroflexi	<i>Clostridium_sensu_stricto_1</i>	0.9261	
		<i>G30-KF-CM45</i>	0.8631	
		<i>RBG-13-54-9</i>	0.8420	
		<i>Fusobacteriota</i>	<i>Cetobacterium</i>	0.7321
		<i>Bacteroidota</i>	<i>Fluviicola</i>	0.7336
<i>Nitrospinta</i>	<i>P9X2b3D02</i>	0.7789		
TKN	<i>SAR324_clade</i>	<i>SAR324_clade</i>	0.7681	
	<i>Acidobacteriota</i>	<i>Vicinamibacteraceae</i>	0.8124	

utilization, and heterotrophy (Sheik *et al.*, 2014).

Table 2 shows the bacterial populations at the genus level. Six genera (*Methylocystis*, *C39*, *Methyloparacoccus*, *Alsobacter*, *Novosphingobium*, and *Polynucleobacter*) in phylum Proteobacteria, three genera (*Roseimaritima*, *Blastopirellula*, and

*CL500-3*) in phylum Planctomycetota, three genera (*Flavobacterium*, *Kapabacteriales*, and *Fluviicola*) in phylum Bacteroidota, two genera (*JG30-KF-CM45* and *1\_20*) in phylum Chloroflexi, one genus (*Desulfomonile*) in phylum *Desulfobacterota*, one genus (*TM7a*) in phylum Patescibacteria, one genus (*Luteitalea*) in

phylum Acidobacteriota, one genus (*Sulfurospirillum*) in phylum Campilobacterota, and one genus (*P9X2b3D02*) in phylum Nitrospinta had a high correlation with  $\text{NH}_3$  in the oxidation ponds. Meanwhile, genera *LD29*<sup>3</sup>, *Akkermansia*, *Luteolibacter*, and *NH3-11* in phylum Verrucomicrobiota, two genera (*Clostridium\_sensu\_stricto\_1* and *Romboutsia*) in phylum Firmicutes, and one genus (*G30-KF-CM45*, *RBG-13-54-9*, *Cetobacterium*, *Fluviicola*, and *P9X2b3D02*) each in phylum Chloroflexi, Fusobacteriota, Bacteroidota, and Nitrospinta had a high correlation with  $\text{NO}_3^-$  in the oxidation ponds. Finally, genera *SAR324\_clade*<sup>3</sup> and *Vicinamibacteraceae* in phylum SAR324\_clade and Acidobacteriota, respectively, had a high correlation with TKN in the oxidation ponds (Fig. 5).

## CONCLUSION

On the basis of the results of this research, oxidation ponds exhibit water quality that meets the standard value. Fifteen different types of bacterial communities were identified in the oxidation ponds. Among these communities, phylum Proteobacteria had the highest population, accounting for 45.7%. Bacterial communities showed a strong relationship with  $\text{NH}_3$  in the oxidation ponds, and genus *Novosphingobium* in Proteobacteria phylum showed a significant correlation with  $\text{NH}_3$  ( $R^2 = 0.8944$ ). *Novosphingobium* is a genus of bacteria that is capable of metabolizing a wide range of chemicals, including ammonia. These bacteria can be found in various environments, such as soil, water, and plant surfaces, and they play important roles in nutrient cycling and biodegradation. *Novosphingobium* can use ammonia as a nitrogen source for growth and metabolism. They can convert ammonia into other nitrogen-containing compounds such as amino acids, nucleotides, and proteins. Some strains of *Novosphingobium* are involved in the removal of ammonia from wastewater and other contaminated environments. They can actively take up ammonia from the surrounding environment and transform it into less harmful forms. Overall, *Novosphingobium* is an important player in the nitrogen cycle and has versatile abilities to adapt to different environmental conditions, including in the presence of ammonia. Genus *NH3-11* in phylum Verrucomicrobiota had a high relationship with  $\text{NO}_3^-$  ( $R^2 = 0.9886$ ). *Verrucomicrobiota* are a phylum of bacteria that play a role in the nitrogen cycle, including in the conversion of nitrate to other forms of nitrogen. Some

species of Verrucomicrobiota are capable of reducing nitrate to nitrite or even further to nitrogen gas. This process is important in the biogeochemical cycling of nitrogen and can have implications for the availability of nutrients in ecosystems. Some studies suggested that Verrucomicrobiota play a role in the treatment of nitrate-polluted wastewater by acting as denitrifiers. Overall, the relationship between Verrucomicrobiota and nitrate is complex and not fully understood. Research suggested that these bacteria may play an important role in nitrogen cycling and environmental remediation. Genus *Vicinamibacteraceae* in phylum Acidobacteriota had a high relationship with a TKN ( $R^2 = 0.8124$ ) *Vicinamibacteraceae* includes bacterial strains that are capable of degrading complex nitrogen compounds, including proteins and amino acids. As a result, the presence of these bacteria in a sample can impact the levels of TKN, a measurement of the amount of nitrogen in a sample that can be converted into ammonia. In particular, the presence of *Vicinamibacteraceae* can increase TKN levels because they break down nitrogen-containing compounds into ammonia, which contributes to the TKN content. The presence of *Vicinamibacteraceae* can be an important factor to consider when analyzing TKN levels in a particular sample. Therefore, the management of bacterial communities is a key factor for nitrogen removal in oxidation ponds.

## AUTHOR CONTRIBUTIONS

S. Sanaha designed the experiment, conducted field study, bacteria population and water quality analyses in the laboratory, contributed in the data analysis, interpreted the results, and prepared the manuscript. T. Pattamapitoon, the corresponding author, designed the experiment, contributed in the data analysis, interpreted the results, and examined the manuscript. S. bualert designed the experiment and contributed in the data analysis. O. Phewnil designed the experiment, contributed in the data analysis, and interpreted the results. W. Wararam designed the water quality experiment and contributed in the data analysis. N. Semvimol designed the water quality experiment and contributed in the data analysis. K. Chunkao designed the water quality experiment and interpreted the results. C. Tudsanaton contributed in bacteria population analysis in the laboratory. M. Srichomphu contributed in the water quality analysis in the laboratory. U. Nachaiboon collected wastewater and contributed in the water



quality analysis in the field. O. Wongsrikaew contributed in the water quality analysis in the field. P. Wichittrakarn designed the field experiment and collected wastewater in the field. C. Chanthasoon designed the field experiment and collected wastewater in the field.

#### ACKNOWLEDGEMENT

This study was funded by the King's royally initiated Laem Phak Bia Environmental Research and Development Project, Phetchaburi, Thailand. The study fund number is [LERD\_RD 4/2562].

#### CONFLICT OF INTEREST

The author declares no conflict of interests regarding the publication of this manuscript. Ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been completely observed by the authors.

#### OPEN ACCESS

©2023 The author(s). This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third-party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit: <http://creativecommons.org/licenses/by/4.0/>

#### PUBLISHER'S NOTE

GJESM Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

#### ABBREVIATIONS

%	Percent
°C	Degree Celsius
1_20	Genus in the Phylum <i>Bacteroidota</i>

APHA	American Public Health Association
BOD	Biochemical oxygen demand
C39	Genus in the Phylum Proteobacteria
CL500-3	Genus in the Phylum Proteobacteria
cm	Centimeter
DNA	Deoxyribonucleic acid
DO	Dissolved oxygen
et. al.	And others
Fig.	Figure
G30-KF-CM45	Genus in the phylum <i>Chloroflexi</i>
JG30-KF-CM45	Genus in the phylum <i>Bacteroidota</i>
m	Meter
mg/L	Milligrams per liter
NH <sub>3</sub>	Ammonia
NH3-11	Genus in the phylum <i>Verrucomicrobiota</i>
NGS	Next generation sequencing
NO <sub>2</sub>	Nitrogen dioxide
NO <sub>3</sub> <sup>-</sup>	Nitrates
PE	Polyethylene
pH	Potential of hydrogen
P9X2b3D02	Genus in the phylum <i>Nitrospinta</i>
R <sup>2</sup>	Coefficient of determination
RBG-13-54-9	Genus in phylum <i>bacteroidota</i>
RNA	Ribonucleic acid
rRNA	Ribosomal ribonucleic acid
Rpm	Revolutions per minute
SAR324_clade	Bacteria phylum
TKN	Total Kjeldahl nitrogen
The LERD project	the King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Phetchaburi, Thailand
TM7a	Genus in phylum <i>patescibacteria</i>
WPCF	Water Pollution Control Federation

## REFERENCES

- Abbaszadeh, L.; Koutra, E.; Tsigkou, K.; Gaspari, M.; Kougias, P.G.; Kornaros, M., (2022). Nitrification upon nitrogen starvation and recovery: Effect of stress period, substrate concentration and pH on ammonia oxidizers' performance. *Fermentation*, 8: 1-12 (12 pages).
- Annisa, K.; Sutarno; Santosa, S., (2021). Azolla microphylla and Pseudomonas aeruginosa for bioremediation of bioethanol wastewater. *Biodiversitas*. 22: 1799-1805 (7 pages).
- APHA, (2017). Standard Methods for the Examination of Water and Wastewater, 20<sup>th</sup>. American Public Health Association. AWWA; WPCF.
- Bajsa, O.P.; Nair, P.J.; Mathew P.K.; Ho, P.G.E., (2003). Vermiculture as a tool for Domestic Wastewater management. *Water Sci. Technol.*, 48: 125-132 (8 pages).
- Bestawy, E.; Hejin, A.A.; Amer, R.; Kashmeri, R.A., (2014). Decontamination of Domestic Wastewater Using Suspended Individual and Mixed Bacteria in Batch System. *J. Bioremed. Biodegrad.*, 5: 1-8 (8 pages).
- Boyd, C.E., (2008). Calculating the feed oxygen demand (FOD) of aquafeeds. *Kasetsart Univers. Fish. Res. Bull.*, 32: 26-31 (6 pages).
- Camargo, J; Alonso, A., (2006). Ecological and toxicological effects of inorganic nitrogen pollution in aquatic ecosystems: A global assessment. *Environ. Int.*, 32: 831-849 (19 pages).
- Chaffin, J.D; Bridgeman, T.B., (2014). Organic and inorganic nitrogen utilization by nitrogen-stressed Cyanobacteria during bloom conditions. *J. Appl. Phychol.*, 26: 299-309 (11 pages).
- Chen, M.; Wang, W.; Feng, Y.; Zhu, X.; Zhou, H.; Tan, Z.; Li, X., (2014). Impact resistance of different factors on ammonia removal by heterotrophic nitrification-aerobic denitrification bacterium *Aeromonas* sp. HN-02. *Bioresour. Technol.*, 167: 456-461 (6 pages).
- Chhimwal, M.; Srivastava, R.K.; Mudgal, A.; Khan, S., (2022). Metagenomic decoding and oxidation pond-based treatment of domestic wastewater using 16 s V3-V4 rRNA sequencing tool. *Int. J. Environ. Sci. Technol.*, 19: 1-12 (12 pages).
- Date, Y.; Isaka, K.; Ikuta, H.; Sumino, T.; Kaneko, N.; Yoshie, S.; Tsuneda, S.; Inamori, Y., (2009). Microbial diversity of anammox bacteria enriched from different types of seed sludge in an anaerobic continuous-feeding cultivation reactor. *J. Biosci. Bioeng.*, 107: 281-286 (6 pages).
- Egli, K.; Fanger, U.; Alvarez, P.J.J.; Siegrist, H.; van der Meer, J.R.; Zehnder, A.J.B., (2001). Enrichment and characterization of an anammox bacterium from a rotating biological contactor treating ammonium-rich leachate. *Arch. Microbiol.*, 175: 198-207 (9 pages).
- Flanzenbaum, J.M.; Jankowiak, J.G.; Goleski, J.A.; Gorney, R.M.; Gobler, C.J., (2022). Nitrogen Limitation of Intense and Toxic Cyanobacteria Blooms in Lakes within Two of the Most Visited Parks in the USA: The Lake in Central Park and Prospect Park Lake. *Toxin*. 14: 1-21 (21 pages).
- Huang, X.; Li, W.; Zhang, D.; Qin, W., (2013). Ammonium removal by a novel oligotrophic *Acinetobacter* sp. Y16 capable of heterotrophic nitrification-aerobic denitrification at low temperature. *Bioresour Technol.*, 146: 44-50 (7 pages).
- Huang, Y.Q.; Cai, D.S.; Li, M.Q.; Wu, T.H.; Wu, P.G.; Li, L., (2018). Influence of changes in dissolved oxygen content on fish behavioral trajectories during water eutrophication. *Appl. Ecol. Environ. Res.*, 17: 653-666 (14 pages).
- Hwang, I.S.; Min, K.S.; Choi, E.; Yun, Z., (2005). Nitrogen removal from piggery waste using the combined SHARON and ANAMOX process. *Water Sci. Technol.*, 52: 487 (1 page).
- Irfan, S., (2016). Role of nutrient and oxygen demand in the aquatic system. *J. Environ. Sci. Toxicol. Food Technol.*, 10: 49-54 (6 pages).
- Isaka, K.; Sumino, T.; Tsuneda, S., (2007). High nitrogen removal performance at moderately low temperature utilizing anaerobic ammonium oxidation reactions. *J. Biosci. Bioeng.*, 10: 486-490 (5 pages).
- Jin, R.C.; Yang, G.F.; Yu, J.J.; Zheng, P., (2012). The inhibition of the Anammox process: A review. *J. Chem. Eng.*, 197: 67-79 (13 pages).
- Jinjaruk, T.; Chunkao, K.; Pongput, K.; Choeihom, C.; Pattamapitton, T.; Wararam, W.; Thaipakdee, S.; Srichomphu, M.; Maskulrath, P., (2018). HDPE Pipeline Length for Conditioning Anaerobic Process to Decrease BOD in Municipal Wastewater. *Environ. Asia.*, 11: 31-44 (14 pages).
- Kamarudin, M.K.A.; Wahab, N.A.; Bati, S.N.A.M.; Toriman, M.A.; Saudi, A.S.M.; Umar, R.; Sunardi. (2020). Seasonal Variation on Dissolved Oxygen, Biochemical Oxygen Demand and Chemical Oxygen Demand in Terengganu River Basin, Malaysia. *J. Environ. Manage.*, 23: 1-7 (7 pages).
- Khambete, A.K.; Christian, R.A., (2014). Statistical analysis to identify the main parameters to effecting WWQI of sewage treatment plant and predicting BOD. *IJRET.*, 3: 186-195 (10 pages).
- Kumar, S.; Pratap, B.; Dubey, D.; Dutta, V., (2020). Removal of nutrients from domestic wastewater using constructed wetlands: assessment of suitable environmental and operational conditions. *Environ. Sustainability*. 3: 341-352 (12 pages).
- Kunen, J.G., (2008). Anammox bacteria: From discovery to application. *Nat. Rev. Microbiol.*, 6: 320-326 (7 pages).
- Latrach, L.; Masunaga, T.; Ouazzani, N.; Hejjaj, A.; Mahi, M.; Mandi, L., (2015). Removal of bacterial indicators and pathogens from domestic wastewater by the multi-soil-layering (MSL) system. *Soil Sci. Plant Nutr.*, 61: 337-346 (10 pages).
- Lawson, C.E.; Wu, S.; Bhattacharjee, A.S.; Hamilton, J.J.; McMahon, K.D.; Goel, R.; Noguera, D.R., (2017). Metabolic network analysis reveals microbial community interactions in anammox granules. *Nat. Commun.*, 8: 15416-15423 (8 pages).
- Mahmud, K.; Pandey, D.; Mergoum, A.; Missaoui, A., (2021). Nitrogen losses and potential mitigation strategies for a sustainable agroecosystem. *Sustainability*. 13: 1-23 (23 pages).
- Makuwa, S.; Tlou, M.; Kankeu, E.F.; Green, E., (2022). The effects of dry versus wet season on the performance of a wastewater treatment plant in North West Province, South Africa. *Water SA*. 48: 40-49 (10 pages).
- Nimtim, M.; Chaichana, R.; Woo, T.S., (2020). Role of freshwater bryozoans in wastewater treatment ponds at Laem Phak Bia Environmental Research and Development Project site, Phetchaburi province Thailand. *Agric. Nat. Resour.*, 54: 649-656 (8 pages).
- Noikondee, R.; Chunkao, K.; Bualert, S.; Pattamapitton, T., (2019). Evaluation of dissolve oxygen stratification in an oxidation pond for community wastewater treatment through king's royally initiated "nature by nature" process. *Environ. Asia.*, 12: 169-177 (9 pages).
- Noophan, P.; Rodpho, R.; Sonmee, P.; Hahn, M.; Sirivitayaphakorn, S., (2018). Nutrient Removal Performance on Domestic Wastewater Treatment Plants (Full Scale System) between Tropical Humid and Cold Climates. *Appl. Environ. Res.*, 40: 32-39 (8 pages).
- Pattamapitton, T.; Sirirote, P.; Pakkong, P.; Chankaew, K., (2013). H.M. The King's Royally Initiated LERD Project on Community wastewater treatment at H.M. The LERD Project site in Phetchaburi province, Thailand. *Modern Appl. Sci.*, 7: 26-41 (15 pages).
- Posadas, E.; Garcia-Encina, P.A.; Soltan, A.; Dominguez, A.; Diaz, I.; Munoz, R., (2013). Carbon and nutrient removal from centrates and domestic wastewater using algal-bacterial biofilm bioreactors. *Bioresour. Technol.*, 139: 50-58 (9 pages).
- Purwono; Rezagama, A.; Hibbaan, M.; Budihardjo, M.A., (2017). Ammonia-nitrogen (NH<sub>3</sub>-N) and ammonium-nitrogen (NH<sub>4</sub><sup>+</sup>-N) equilibrium on the process of removing nitrogen by using tubular plastic media. *J. Mater. Environ. Sci.*, 8: 4915-4922 (8 pages).
- Quirós, R., (2003). The relationship between nitrate and ammonia concentrations in the pelagic zone of lakes. *Limnetica*. 22: 37-50 (14 pages).
- Rastogi, R.P.; Madamwar, D.; Incharoensakdi, A., (2015). Bloom dynamics of Cyanobacteria and their toxins: environmental health impacts and mitigation strategies. *Front. Microbiol.*, 6: 1-22 (22 pages).
- Shaomi, H.; Sarah, L.; Stevens, R.; Katherine, D., (2017). Ecophysiology of freshwater Verrucomicrobia inferred from Metagenome-Assembled Genomes. *mSphere*. 2: 1-17. (17 pages).

- Sheik, C.S.; Jain, S.; Dick G.J., (2014). Metabolic flexibility of enigmatic SAR324 revealed through metagenomics and metatranscriptomics. *Environ. Microbiol.*, 16: 304-317 (14 pages).
- Srichomphu, M.; Boonprakong, T.; Chunkao, K.; Pattamapitooon, T.; Semvimol, N., (2015). Effects of *Microcystis aeruginosa* blooming on community wastewater quality in pond technology system. *KKU Sci. J.*, 43: 126-136 (11 pages).
- Srivastana, M.; Kaushik, M.S.; Singh, A.; Singh, D.; Mishra, A.k., (2016). Molecular phylogeny of heterotrophic nitrifiers and aerobic denitrifiers and their potential role in ammonium removal. *J. Basic Microbiol.*, 56: 907-921 (15 pages).
- Strous, M.; Heijnen, J.J.; Kuenen, J.G.; Jetten, M.S.M., (1998). The sequencing batch reactor as a powerful tool for the study of slowly growing anaerobic ammonium-oxidizing microorganisms. *Appl. Microbiol. Biotechnol.*, 50: 589-596 (8 pages).
- Sukchinda, S.; Bualert, S.; Phewnil, O.; Pattamapitooon, T.; Srichomphu, M., (2019). Effect of solar radiation on Cyanobacteria bloom in oxidation ponds community wastewater treatment at the King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Phetchaburi, Thailand. *Environ. Asia*. 12: 54-61 (8 pages).
- Sun, S.P.; Nacher, C.P.; Merkey, B.; Zhou, Q.; Xia, S.Q.; Yang, D.H.; Sun, J.H.; Smets, B.F., (2010). Effective Biological Nitrogen Removal Treatment Processes for Domestic Wastewaters with Low C=N Ratios: A Review. *Environ. Eng. Sci.*, 27: 111-127 (17 pages).
- Suto, R.; Ishimoto, C.; Chikyu, M.; Aihara, Y.; Matsumoto, T.; Uenishi, H.; Yasuda, T.; Fukumoto, Y.; Waki, M., (2017). Anammox biofilm in activated sludge swine wastewater treatment plants. *Chemosphere*. 167: 300-307 (8 pages).
- Vlyssides, A.G.; Karlis, P.K.; Rori, N.; Zorpas, A.A., (2002). Electrochemical treatment in relation to pH of domestic wastewater using Ti/Pt electrodes. *J. Hazard. Mater.*, 95: 215-226 (12 pages).
- Wang, H.Y.; Wang, T.; Yang, S.Y.; Liu, X.Q.; Kou, L.Q.; Huang, T.L.; Wen, G., (2019). Nitrogen removal in oligotrophic reservoir water by a mixed aerobic denitrifying consortium: influencing factors and immobilization effects. *Int. J. Environ. Res. Public Health*. 16: 1-15 (15 pages).
- Ward, M.H.; Jones, R.R.; Brender, J.D.; De Kok, T.M.; Weyer, P.J.; Nolan, B.T.; Villanueva, C.M.; Van Breda, S.G., (2018). Drinking Water Nitrate and Human Health: An Updated Review. *Int. J. Environ. Res. Public Health*. 15: 1-31 (31 pages).
- Wedyan, M.; Harahsheh, A.A.; Qnaish, E., (2016). Determination of the Fate of Dissolved Organic Nitrogen in the Three Wastewater Treatment Plants, Jordan. *Int. J. Environ. Sci. Educ.*, 11: 767-777 (11 pages).
- Wu, L.; Ning, D.; Zhang, B.; Li, Y.; Zhang, P.; Shan, X.; Zhang, Q.; Brown, M.; Li, Z.; Van Nostrand, J.D., (2019). Global diversity and biogeography of bacterial communities in wastewater treatment plants. *Nat. Microbiol.*, 4: 1183-1195 (13 pages).
- Zhang, H.H.; Wang, Y.; Chen, S.N.; Zhao, Z.F.; Feng, J.; Zhang, Z.H.; Lu, K.Y.; Jia, J.Y., (2018). Water bacterial and fungal community compositions associated with urban lakes, Xi'an, China. *Int. J. Environ. Res. Public Health*, 15: 1-18 (18 pages).
- Zhang, W.; Liu, J.; Xiao, Y.; Zhang, Y.; Yu, Y.; Zheng, Z.; Liu, Y., (2022). The Impact of Cyanobacteria Blooms on the Aquatic Environment and Human Health. *Toxin*. 14: 1-10 (10 pages).
- Zhao, J.Q.; Wu, J.N.; Li, X.L.; Wang, S.; Hu, B.; Ding, X.Q., (2017). The denitrification characteristics and microbial community in the cathode of an MFC with aerobic denitrification at high temperatures. *Front. Microbiol.*, 8: 1-11 (11 pages).
- Zhou, S.; Huang, T.; Ngo, H.H.; Zhang, H.; Liu, F.; Zeng, M.; Shi, J.; Qiu, X., (2016). Nitrogen removal characteristics of indigenous aerobic denitrifiers and change in microbial community of reservoir enclosure system via in situ oxygen enhancement using water lifting and aeration technology. *Bioresour. Technol.*, 214: 63-73 (11 pages).
- Zurano, A.S.; Rodriguez-Miranda, E.; Guzman, J.L.; Acien-Fernandez, F.G.; Fernandez-Sevilla, J.M.; Grima, E.M., (2021). ABACO: A New Model of Microalgae-Bacteria Consortia for Biological Treatment of Wastewaters. *Appl. Sci.*, 11: 1-23 (23 pages).
- Zwart, G.; Hiorns, W.D.; Methé, B.A.; Van Agterveld, M.P.; Huis-Mans, R.; Nold, S.C.; Zehr, J.P.; Laanbroek, H.J., (1998). Nearly identical 16S rRNA sequences recovered from lakes in North America and Europe indicate the existence of clades of globally distributed freshwater bacteria. *Syst. Appl. Microbiol.*, 21: 546-556 (7 pages).

#### AUTHOR (S) BIOSKETCHES

**Saneha, S.**, Ph.D. Candidate, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

▪ Email: [sathapatsaneha@gmail.com](mailto:sathapatsaneha@gmail.com)

▪ ORCID: 0000-0003-0689-5987

▪ Web of Science ResearcherID: NA

▪ Scopus Author ID: NA

▪ Homepage: <https://envi.ku.ac.th/en/>

**Pattamapitooon, T.**, Ph.D., Assistant Professor, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

▪ Email: [thanit.pa@ku.th](mailto:thanit.pa@ku.th)

▪ ORCID: 0009-0005-1664-450X

▪ Web of Science ResearcherID: NA

▪ Scopus Author ID: 55822416300

▪ Homepage: <https://envi.ku.ac.th/en/>

**Bualert, S.**, Ph.D., Assistant Professor, Dean of Environmental Faculty, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

▪ Email: [ecsr@ku.ac.th](mailto:ecsr@ku.ac.th)

▪ ORCID: 0000-0003-1385-792X

▪ Web of Science ResearcherID: NA

▪ Scopus Author ID: 6504138469

▪ Homepage: <https://envi.ku.ac.th/en/>

**Phewnil, O.**, Ph.D., Assistant Professor, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

▪ Email: [fgraonp@ku.ac.th](mailto:fgraonp@ku.ac.th)

▪ ORCID: 0000-0001-9616-551X

▪ Web of Science ResearcherID: NA

▪ Scopus Author ID: 56252364600

▪ Homepage: <https://envi.ku.ac.th/en/>

**AUTHOR (S) BIOSKETCHES (Continued):**

**Wararam, W.**, Ph.D., Assistant Professor, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

- Email: [watcharapong.warar@ku.th](mailto:watcharapong.warar@ku.th)
- ORCID: 0009-0000-1487-4284
- Web of Science ResearcherID: NA
- Scopus Author ID: 57096032600
- Homepage: <https://envi.ku.ac.th/en/>

**Semvimol, N.**, Ph.D., Assistant Professor, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

- Email: [noppawan.sem@ku.th](mailto:noppawan.sem@ku.th)
- ORCID: 0000-0002-9581-1986
- Web of Science ResearcherID: NA
- Scopus Author ID: 57096067300
- Homepage: <https://envi.ku.ac.th/en/>

**Chunkao, K.**, Ph.D., Professor, The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand.

- Email: [prof.kasemc@gmail.com](mailto:prof.kasemc@gmail.com)
- ORCID: 0009-0002-8035-4732
- Web of Science ResearcherID: NA
- Scopus Author ID: 54683551800
- Homepage: <https://www.chaipat.or.th/eng/>

**Tudsanaton, C.**, Ph.D. Candidate, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

- Email: [Chalisa.tu@ku.th](mailto:Chalisa.tu@ku.th)
- ORCID: 0009-0004-8738-2263
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: <https://envi.ku.ac.th/en/>

**Srichomphu, M.**, Ph.D. Candidate, Department of Environmental Science, Environmental Faculty, Kasetsart university, Bangkok, Thailand.

- Email: [manlikasri@gmail.com](mailto:manlikasri@gmail.com)
- ORCID: 0009-0004-4965-5769
- Web of Science ResearcherID: NA
- Scopus Author ID: 57202059256
- Homepage: <https://envi.ku.ac.th/en/>

**Nachai boon, U.** MSc., The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand.

- Email: [utchara.lerd@gmail.com](mailto:utchara.lerd@gmail.com)
- ORCID: 0009-0006-1086-5368
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: <https://www.chaipat.or.th/eng/>

**Wongsrikaew, O.** MSc., The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand.

- Email: [oraphannoot@gmail.com](mailto:oraphannoot@gmail.com)
- ORCID: 0009-0007-9219-2810
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: <https://www.chaipat.or.th/eng/>

**Wichittrakarn, P.** MSc., The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand.

- Email: [pavin32398@gmail.com](mailto:pavin32398@gmail.com)
- ORCID: 0009-0008-8834-2158
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: <https://www.chaipat.or.th/eng/>

**Chanthasoorn, C.**, Ph.D., The King's Royally Initiated Laem Phak Bia Environmental Research and Development Project, Ban Laem District, Phetchaburi Province, Thailand.

- Email: [Chulabuut@gmail.com](mailto:Chulabuut@gmail.com)
- ORCID: 0009-0004-2568-0687
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: <https://www.chaipat.or.th/eng/>

**HOW TO CITE THIS ARTICLE**

Saneha, S.; Pattamapitoon, T.; Bualert, S.; Phewnil, O.; Wararam, W.; Semvimol, N.; Chunkao, K.; Tudsanaton, C.; Srichomphu, M.; Nachai boon, U.; Wongsrikaew, O.; Wichittrakarn, P.; Chanthasoorn, C., (2023). Relationship between bacteria and nitrogen dynamics in wastewater treatment oxidation ponds *Global J. Environ. Sci. Manage.*, 9(4): 707-718.

DOI: 10.22035/gjesm.2023.04.04

URL: [https://www.gjesm.net/article\\_703868.html](https://www.gjesm.net/article_703868.html)

