# CURRICULUM VITAE

## PERSONAL INFORMATION:

**Name:** Ms. Chalita Phutthasimma

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**Current Status:** Master's degree student (Bioinformatics and Systems Biology Program), School of Bioresources and Technology and School of Information Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

## EDUCATIONAL PROFILE:

**2016-Present:** Master student (Bioinformatics and Systems Biology Program), School of Bioresources and Technology and School of Information Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

**2012-2016:** Bachelor of Science (Microbiology and Parasitology) Naresuan University (NU), Phitsanulok, Thailand, 2016

**2009-2012:** Witthayanukulnaree school, Phetchabun, Thailand

## RESEARCH & EXPERIENCES:

**Master's degree thesis** "*Exploring Functional Relationships of Photosynthetic Genes in Cyanobacteria through Gene Neighborhood and Transcriptomic Data Analyses*"

**Short description:** Functional annotation of photosynthetic genes in cyanobacteria by

integrating information from gene neighborhood relationships, orthologous relationships and transcriptomic data. My work aims at identifying novel photosynthetic genes in cyanobacteria.

**Bachelor's senior projects** "*Microbial Diversity of Phenol Degradation in Wastewaters Systems"*

**Short description:** Isolating microorganism from wastewater treatment using mature vetiver root system. The wastewater was contaminated by illegal dumping of phenol from factories in Nong Nea subdistrict, Chacherngsao province, Thailand. The result shows that there are 27 strains of microorganisms consist of bacteria, fungi, and yeast. Furthermore, there are only 9 strains, which can grow in Minimal salt medium containing 400 ppm of phenol and *Acinetobacter* spp. These have ability of phenol degraded to 383.94 ppm in 72 hr.

**Bachelor's internship projects** "*Evaluating of Recombinant Strains with High DGLA Accumulation"*

**Organization:** National Center for Genetic Engineering and Biotechnology (BIOTEC), Bangkok, Thailand

**Short description:** Selection transformants strain of *Aspergillus* sp. that contain high DGLA content in cell by fluorescence microscope and PCR. Extraction lipid to evaluate and analysis fatty acid profiling.

### Mini-project

1. Gene Expression profile to clustering Recurrence of Colorectal Cancer
2. Microbiome in patient with Alzheimer's disease
3. Re-annotation of *Arthrospira platensis* C1 genome
4. Qualitative Genome-Scale Metabolic Network Reconstruction of Cassava and Topology Analysis Underlying Root Development Condition
5. Operon Prediction in *Synechocystis* sp. pcc 6803

## COMPUTATIONAL SKILLS:

**Computational Languages:** R, Unix command line and Python

**Bioinformatics Tools:** Sequence alignment and clustering (BLAST), Network analysis (Cytoscape, MCODE), Next-generation sequencing (fastqc,Bowtie2, Cufflinks), Molecular modelling (Modeller, Zdock, Rosetta tools, Pymol), Metagenomics analysis (mothur), Database construction (MySQL), etc.

**Language Skills:** English, Thai (Mother tongue)

## LABORATORY SKILLS:

1. Basic biological techniques (e.g. cell culture, DNA extraction, Protein extraction)
2. Basic molecular biology techniques (e.g. PCR, RT-PCR, gene cloning, transformation, Western blot).

## SCHOLARSHIP:

**Received a Master's degree Scholarship** from Bioinformatics and Systems Biology Program, School of Bioresources and Technology and School of Information Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand. (For 2 years)

## RECENT TRAINING & WORKSHOP ATTENDED:

**Gene expression networks reveal co-expression in metabolic pathway in Cholangiocarcinoma cancer**, Institute of Cancer and Genomic Sciences, University of Birmingham, United Kingdom (May 1$^{st}$ – July 9$^{th}$, 2019)

**Biological Data Analysis Using R Programming** (as participant), King Mongkut's University of Technology Thonburi, Bangkok, Thailand (March 5$^{th}$, 2016).

**Biological Data Analysis Using Perl Programming** (as participant), King Mongkut's University of Technology Thonburi, Bangkok, Thailand (April 23th, 2016).

**Metagenomics Analysis Workshop** (as participant), King Mongkut's University of Technology Thonburi (Bang Khun Thian), Bangkok, Thailand (November 23-25, 2016)

**NGS for Food Safety and Health Workshop** (as organizer), KMUTT Knowledge Exchange for Innovation Center (KX), Bangkok, Thailand, (February 28th, 2017)

**Microbiome and Functional Metagenomics Analysis Workshop** (as organizer), KMUTT Knowledge Exchange for Innovation Center (KX), Bangkok, Thailand, (July 17th, 2017**)**

## PUBLICATIONS:

### Proceeding

Phutthasimma, C., Laomettachit, T., Ruengjitchatchawalya, M. and Sutheeworapong, S. (2018). Exploring Functional Relationships of Photosynthetic Genes in Cyanobacteria through Gene Neighborhood and Transcriptomic Data Analyses. pp., 970-981. In The 30th Annua Meeting of the Thai Society for Biotechnology and International Conference TSB 2018, 22-23 November, 2018, Bangkok, Thailand

## ACADEMIC REFERENCES:

**Asst. Prof. Dr. Teeraphan Laomettachit,**

Lecturer, Bioinformatics and Systems Biology Program, School of Bioresources and Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok 10150, Thailand.

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Bioresources and Technology, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok 10150, Thailand.

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**Master's degree thesis** "Exploring Functional Relationships of Photosynthetic Genes in Cyanobacteria through Gene Neighborhood and Transcriptomic Data Analyses"

## Description

For generating the structure of genome neighborhood network (GNN) in cyanobacteria use the 2 side of data.

The first is the position of start and stop genes in whole genome. We have retrieved data form Cyanobase. In this case, some of them could not order the position of gene. To get the scaffold of in each genome, it should be rearranged order of gene and separated the stand of DNA in to plus and minus stand. After that we will get the set of neighborhood gene, and cut off them by using the criteria less than equal 250 base pairs.

The second is whole protein of cyanobacteria genome, we have retrieved the data from Cyanobase. In this side, we BLASTP against all of them to find the orthologous gene. For this data, we used the criteria less than equal 1e-10 for cut off. Finally, when use the output of the 2 side of data to visualize in Cytoscape program.

And the important one is the transcriptomics data that we will mapped into the GNN. Some of the data should be normalization. After that preprocess data to find the gene which are

represent probes. Moreover, we also concern about the condition between of them to prepare data. Finally, it will be mapped the transcriptomics data into the GNN.

For the analysis network, we can get the pattern to interesting both of the networks analysis and statistical analysis.

## Expected output

- Functional relationships between photosynthetic and related genes under different light condition.
- Identification of new photosynthetic genes & their function.
- Proposed modifications/manipulation of gene clusters that increase photosynthetic efficiency.