CURRICULUM VITAE

PERSONAL INFORMATION:

Name: Mr.Apiwat Sangphukieo

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Current Status: PhD student (year 5) (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.

GPA: 4.0

EDUCATIONAL PROFILE:

2019-2019 (10 months): Internship at Cyanolab, Institute of Biology III, University of Freiburg, Germany.

2018-2018 (15 days): Short-term Study at Saitama University, Japan.

2014-Present: PhD student (Bioinformatics and Systems Biology Program), King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

2014-2014 (46 days**):** Short-term Study at Osaka University, Japan.

2011-2014: Master's Student (Bioinformatics and Systems Biology Program), King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

2007-2011: Bachelor of Science (Biology), Mahidol University, Thailand.

RESEARCH & EXPERIENCES:

PhD thesis "*Exploring new functional photosynthetic genes in photosynthetic prokaryote by gene neighborhood analysis*"

Short description: Photosynthetic proteins, especially auxiliary factors, are difficult to identify in wet lab and by common computational approaches. In this work, I developed a new approach using genome neighborhood feature and machine learning approach for identifying photosynthetic proteins and their function (http://bicep.kmutt.ac.th/photomod). Also, a new method to visualize genome neighborhood, called photomodGNN is developed.

Internship project 1 (**at University of Freiburg**) "Identification of small regulatory RNA (sRNA) in *Synechocystis* sp. PCC 6803"

Short description: Many regulatory sRNAs were identified using several conditions of RNA-sequencing, but the function of these sRNA remains to be elucidated. In this work, I integrate computational tools e.g. GLASSgo (sRNA homolog prediction tool) and CopraRNA (sRNA function prediction tool) as a pipeline. Then, I applied the pipeline to automatically identify sRNA function by using the input sequence from transcriptome data of *Synechocystis* sp. PCC 6803.

Internship project 2 (**at University of Freiburg**) "Bioinformatics analysis of SR1 dual-function RNA from *Bacillus subtilis*"

Short description: SR1 is a regulatory sRNA from the *Bacillus subtilis* which the function remains to be elucidated. In this work, I identified the distribution of SR1 sRNA among Bacterial domain, and also analyzed the diversity of protein-coding sequence, the conservation of gene synteny and potential gene target of SR1. I showed that SR1 is conserved in 12 genera and the function is involved in sporulation and reproduction.

Master's thesis "*Computational design of new peptides based on cyclotide scaffold as HIV-1 gp120 competitive inhibitor*"

Short description: Gp120 is an HIV envelope glycoprotein that use for initiating replication cycle. Current gp120-targeting drug is inefficient due to structural barrier of gp120. Cyclotide is a natural

peptide that holds anti-HIV feature. In this work, I constructed a new computational method to automatically modify cyclotide molecule to bind to gp120 protein to increase anti-HIV feature. The method consists of many molecular modelling tools (e.g. 3D modelling, docking and binding scoring) connected as a pipeline which is optimized by genetic algorithm.

Bachelor's senior projects "*The role of gadd45β in stress response of cholangiocarcinoma cells*"

Short description: Growth arrest and DNA-damage-inducible, beta, also known as *gadd45β* is involved in the regulation of growth and apoptosis. Its role in cancer cell line, especially the common cancer in Thailand cholangiocarcinoma, remains unclear. In this study, I observed the expression of gadd45β in the level of transcription (RT-PCR) and translation (Western blot assay) in response to drugs of cholangiocarcinoma cell line.

Mini-project

1. Construction of dynamic model of starch accumulation pathway in cassava root
2. Identification of potential secondary metabolites in bloom-forming cyanobacteria via comparative genomic analysis
3. Identification of core conserved coding genes in photosynthetic prokaryotes genome (154 genomes)
4. Building web-based application of miRNA (http://bicep.kmutt.ac.th/HeteroMirPred) and non-coding RNA (http://bicep.kmutt.ac.th/HLRF) predictions using Flask environments and python programing
5. Building web site for BiCEP research group (http://bicep.kmutt.ac.th/)

6. Building web site for Science and Industrial Park (SAI) King Mongkut's University of Technology Thonburi (KMUTT) (http://www.sai.kmutt.ac.th)

COMPUTATIONAL SKILLS:

Computational Languages: Python, R and Unix command line

Bioinformatics Tools: Sequence alignment and clustering (BLAST, clustalW, MCL) phylogenetic reconstruction (MEKA, BioPhython.Phylo), Network analysis (Cytoscape), Comparative genomic analysis (CMGbiotools), Next-generation sequencing (Bowtie2, Cufflinks), Molecular modelling

(Modeller, Zdock, Rosetta tools, Pymol), Machine learning (Weka, Meka), Database construction (SQlite), 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, Western blot, MTT assay).

SCHOLARSHIP:

Received a Short-term Study Scholarship from Japan-Asia Youth Exchange Program in Science for short-term study in Saitama University (1-15 March 2018)

Received a PhD Scholarship from Petchra Pra Jom Klao Research Scholarship, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand. (For 3 years)

Received a Short-term Study Scholarship from Japan Student Services Organization (JASSO) for short-term study in Osaka University (12 Sep 2014 - 27 Oct 2014)

Received a Masters 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:

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

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

Biological Data Analysis Using R Programming (as organizer), King Mongkut's University of Technology Thonburi, Bangkok, Thailand (March 5, 2016).

Comparative Microbial Genomics Analysis Workshop (as participant and organizer)**,** King Mongkut's University of Technology Thonburi, Bangkok, Thailand (November 30 - December 4, 2015).

Bioinformatics and Drug Design (as lecturer and organizer), King Mongkut's University of Technology Thonburi, Bangkok, Thailand (November 1, 2014).

PUBLICATIONS:

Proceeding

Sangphukieo, A., Nawae, W., Laomettachit, T., Supasitthimethee, U., & Ruengjitchatchawalya, M. (2015). A new computationally designed cyclotide as a potential HIV-1 gp120 inhibitor. 10th International Symposium of the Protein Society of Thailand. Chulabhorn Research Institute, Don Muang, Bangkok, Thailand.

Journal

Sangphukieo, A., Nawae, W., Laomettachit, T., Supasitthimethee, U., & Ruengjitchatchawalya, M. (2015). Computational design of hypothetical new peptides based on a cyclotide scaffold as HIV gp120 inhibitor. PloS one, 10(10), e0139562.

REPOSITORIES:

Github: https://github.com/asangphukieo

Dockerhub: https://hub.docker.com/u/asangphukieo

ACADEMIC REFERENCES:

Asst. Prof. Dr. Marasri Ruengjitchatchawalya,

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