

Wee Wei Yee
Assistant Lecturer, School of Science
Monash University Malaysia

Education

PhD:

- Doctor of Philosophy (Bioinformatics)
- University of Malaya, Jalan Universiti, 50603 Kuala Lumpur, Malaysia
- 2013 – 2016 (3 years)

Degree:

- Bachelor of Science (Honours) Bioinformatics
- Multimedia University, Jalan Ayer Keroh Lama, Bukit Beruang, 75450 Melaka, Malaysia
- 2009 – 2012

Working Experience

Position	Address	Years
Internship	Genome Informatics Research Group, Level 1, High Impact Research (HIR) Building, University of Malaya, Lembah Pantai, 50603 Kuala Lumpur, Malaysia	March 2012 – June 2012
Research Assistant	Genome Informatics Research Group, Level 1, High Impact Research (HIR) Building, University of Malaya, Lembah Pantai, 50603 Kuala Lumpur, Malaysia	2012-2016
Bioinformatics Specialist	Genome Solution Sdn Bhd Suite 8, Innovation incubator UM, Level 5, Research Management & Innovation Complex, University of Malaya, 50603 Kuala Lumpur, Malaysia.	2014-2016
Research Fellow	Centre for Research in Biotechnology for Agriculture (CEBAR) Level 3, Research Management & Innovation Complex, University of Malaya	2016-2017
Assistant Lecturer	Monash University Malaysia Jalan Lagoon Selatan, Bandar Sunway, 47500 Subang Jaya, Selangor	2017 - Present

Research Experience

- Comparative whole genome analysis of *Mycobacterium abscessus*
 - First comparative whole-genome study of *Mycobacterium abscessus*
 - Performed *Mycobacterium abscessus* pan-genome analysis, phylogenetic tree analysis, functional genes comparison, prophage identification and comparative pathogenomics analysis.

- Whole genome analysis of Malayan Pangolin
 - Comparative study of pangolin genes
 - Gene expansion and contraction analysis on pangolin genes.
 - Positive selection study for pangolin

- Whole transcriptome analysis of Malayan Pangolin
 - First transcriptome study of Pangolin
 - Pangolin's gene structural and functional annotation.
 - Performed differential gene expression between Pangolin's organs.

- Involved in construction of bacteria genome databases
 - Provided bacteria whole genome sequences with functional annotation using Rapid Annotation using Subsystem Technology (RAST).
 - Integrated sequences data in the databases with bioinformatics tools to facilitate the genomic analysis

- Assembled bacteria genome and performed comparative genomic analysis on bacteria
 - Performed the first whole genome study of *Mycobacterium brisbanense*
 - Performed the first comparative genomic study of *Mycobacterium cosmeticum*
 - Performed comparative genomic study of *Actinomyces* genomes
 - Performed comparative genomic study of *Vibrio parahaemolyticus* genomes
 - Performed comparative genomic study of *Bartonella elizabethae* genomes
 - Performed the first comparative genomic study of *Mycobacterium cosmeticum*
 - Identification and genomic study of novel subspecies of *Fusobacterium nucleatum*
 - Identification and genomic study of novel Non-Tuberculous *Mycobacterium*

- Assembled fungal genome and performed comparative genomic analysis
 - Performed genome assembly and comparative genomic analysis of *Fusobacterium oxysporum*

- Metagenomic analysis on human oral samples
 - Performed metagenomic analysis on 9 human oral samples which comprised of diabetic and non-diabetic patients
 - Performed taxonomical analysis on the unmapped human region using MEGAN5 (MEta Genome ANalyser)

- Develop Bioinformatic pipelines such as:
 - Pairwise Genome Comparison (PGC) – Circular visualization tool of bacteria pairwise genome alignment
 - Pathogenomics Profiling Tools (PathoProT) – Tools to identify bacteria virulence gene and perform comparative pathogenomic analysis
 - Genome assembly pipeline – Pipeline which allow automated assembly of bacteria genome
 - Genome coverage and identity calculation tool – Calculate the genome coverage and similarity between 2 genomes

- HIV- transmission network analysis
 - Applied network approach to analyze global HIV transmission patterns through HIV transmission clusters with close genetic links and identify potential transmission partners.

- Human exome sequencing project
 - Identified SNP variants in human’s exome
 - Identified novel SNP variants by comparing to dbSNP and 1000 Genome Project database
 - Predicted the effects of the SNP variants

On-going Project

- Extracellular DNA as a Target for Oral Biofilm Control
- Comparative genomic analysis of *Pseudomonas nitroreducans*
- *De Novo* Sequencing and Assembly Analysis of the *Boesenbergia rotunda* Transcriptome

Scientific Publication:

Number of publication: 24

2017

Wee, W. Y., Dutta, A., & Choo, S. W. (2017). Comparative genome analyses of mycobacteria give better insights into their evolution. *PLoS one*, *12*(3), e0172831.

Mazumdar, P., Lau, S. E., Wee, W. Y., Singh, P., & Harikrishna, J. A. (2017). Genome-wide Analysis of the CCCH Zinc-Finger Gene Family in Banana (*Musa acuminata*): An Insight Into Motif and Gene Structure Arrangement, Evolution and Salt Stress Responses. *Tropical Plant Biology*, *10*(4), 177-193.

2016

Choo, S. W., Rayko, M., Tan, T. K., Hari, R., Komissarov, A., Wee, W. Y., ... & Wilson, R. K. (2016). Pangolin genomes and the evolution of mammalian scales and immunity. *Genome research*, 26(10), 1312-1322.

Ang, M. Y., Dutta, A., Wee, W. Y., Dymock, D., Paterson, I. C., & Choo, S. W. (2016). Comparative Genome Analysis of *Fusobacterium nucleatum*. *Genome biology and evolution*, 8(9), 2928-2938.

Wee, W. Y., Tan, T. K., Jakubovics, N. S., & Choo, S.W. (2016). Whole-genome sequencing and comparative analysis of *Mycobacterium brisbanense* reveals a possible soil origin and capability in fertiliser synthesis. *PLOS ONE*.

Choo, S.W., Dutta, A., Wong, G. J., Wee, W. W., Ang, M. Y., & Siow, C.C. (2016). Comparative genomic analysis reveals a possible novel Non-Tuberculous Mycobacterium species with high pathogenic potential. *PLOS ONE*.

Yusoff, A.M., Tan, T. K., Hari, R., Koepfli, K.P., Wee, W. Y., Antunes, A., Sitam, F.T., ... & Choo, S.W. (2016). De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. *Scientific Reports*.

2015

Tan, S. Y., Dutta, A., Jakubovics, N. S., Ang, M. Y., Siow, C. C., Mutha, N. V., Wee, W. Y.,...& Choo, S. W. (2015). YersiniaBase: a genomic resource and analysis platform for comparative analysis of *Yersinia*. *BMC bioinformatics*, 16(1), 1.

Teo, W. F. A., Wee, W. Y., Choo, S. W., & Tan, G. Y. A. (2015). Draft genome sequence of a marine actinobacteria *Sciscionella* strain SE31. *Marine genomics*, 20, 11-12.

Tan, M. F., Siow, C. C., Dutta, A., Mutha, N. V., Wee, W. Y., Heydari, H., ... & Choo, S. W. (2015). Development of ListeriaBase and comparative analysis of *Listeria monocytogenes*. *BMC genomics*, 16(1), 1.

Choo, S. W., Ang, M. Y., Dutta, A., Tan, S. Y., Siow, C. C., Heydari, H., Wee, W. Y., ... & Wong, G. J. (2015). MycoCAP-*Mycobacterium* Comparative Analysis Platform. *Scientific reports*, 5.

2014

Heydari, H., Siow, C. C., Tan, M. F., Jakubovics, N. S., Wee, W. Y., Mutha, N. V., ... & Choo, S. W. (2014). CoryneBase: *Corynebacterium* genomic resources and analysis tools at your fingertips. *PloS one*, 9(1), e86318.

Heydari, H., Mutha, N. V., Mahmud, M. I., Siow, C. C., Wee, W. Y., Wong, G. J., ... & Choo, S. W. (2014). StaphyloBase: a specialized genomic resource for the staphylococcal research community. *Database*, 2014, bau010.

Choo, S. W., Wee, W. Y., Ngeow, Y. F., Mitchell, W., Tan, J. L., Wong, G. J., ... & Xiao, J. (2014). Genomic reconnaissance of clinical isolates of emerging human pathogen *Mycobacterium abscessus* reveals high evolutionary potential. *Scientific reports*, 4.

Choo, S. W., Ang, M. Y., Fouladi, H., Tan, S. Y., Siow, C. C., Mutha, N. V., Wee, W. Y., ... & Rehvathy, V. (2014). HelicoBase: a Helicobacter genomic resource and analysis platform. *BMC genomic s*, 15(1), 1.

Ang, M. Y., Heydari, H., Jakubovics, N. S., Mahmud, M. I., Dutta, A., Wee, W. Y., ...& Choo, S. W. (2014). FusoBase: an online *Fusobacterium* comparative genomic analysis platform. *Database*, 2014, bau082.

Choo, S. W., Heydari, H., Tan, T. K., Siow, C. C., Beh, C. Y., Wee, W. Y., ... & Yazdi, A. H. (2014). VibrioBase: a model for next-generation genome and annotation database development. *The Scientific World Journal*, 2014.

Tan, J. L., Ngeow, Y. F., Wee, W. Y., Wong, G. J., Ng, H. F., & Choo, S. W. (2014). Comparative genomic analysis of *Mycobacterium iranicum* UM_TJL against representative mycobacterial species suggests its environmental origin. *Scientific reports*, 4.

2013

Khosravi, Y., Rehvathy, V., Wee, W. Y., Wang, S., Baybayan, P., Singh, S., ...& Choo, S. W. (2013). Comparing the genomes of *Helicobacter pylori* clinical strain UM032 and Mice-adapted derivatives. *Gut pathogens*, 5(1), 1.

Wee, W. Y., Heydari, H., Lokanathan, N., Hari, R., Yusoff, A. M., Beh, C. Y., ...& Choo, S. W. (2013). MabsBase: a *Mycobacterium abscessus* genome and annotation database. *PloS one*, 8(4), e62443.

Ngeow, Y. F., Leong, M. L., Wong, Y. L., Wong, G. J., Tan, J. L., Wee, W. Y., ... & Choo, S. W. (2013). Draft Genome Sequence of *Mycobacterium massiliense* Strain M159, Showing Phenotypic Resistance to β -Lactam and Tetracycline Antibiotics. *Genome announcements*, 1(4), e00669-13.

Tan, J. L., Ng, H. F., Wee, W. Y., Ang, M. Y., Wong, G. J., Ngeow, Y. F., & Choo, S. W. (2013). First whole-genome sequence of *Mycobacterium iranicum*, a newly reported mycobacterial species. *Genome announcements*, 1(5), e00732-13.

2012

Choo, S. W., Yusoff, A. M., Wong, Y. L., Wee, W. Y., Ong, C. S., Ng, K. P., & Ngeow, Y. F. (2012). Genome analysis of *Mycobacterium massiliense* strain M172, which contains a putative mycobacteriophage. *Journal of bacteriology*, 194(18), 5128-5128.

Ngeow, Y. F., Wee, W. Y., Wong, Y. L., Tan, J. L., Ongi, C. S., Ng, K. P., & Choo, S. W. (2012). Genomic analysis of *Mycobacterium abscessus* strain M139, which has an ambiguous subspecies taxonomic position. *Journal of bacteriology*, *194*(21), 6002-6003.

Attended conferences/training workshops

- UTAR National Postgraduate Fundamental and Applied Science Seminar 2013 (UTAR NPFASS 2013)
- Advanced Bioinformatics and Metagenomics Data Analysis 2014
- BGI' Tech Bioinformatics Workshop 2014