

YAN WEI LIM

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Highlights

- Hands-on experience with all next generation sequencing (NGS) technologies and workflows, from sample processing to data analysis
- Ability to design workflows and protocols to process complex environmental and clinical samples
- Set up NGS facility in SDSU and trained others in NGS workflow
- Understand the importance of NGS applications in clinical settings (see Lim *et al.* 2014 JCM)
- Work well in collaborative environments

Education

- 2015
(Expected) **Ph.D., Cell and Molecular Biology**, University of California, San Diego, CA
- Joint doctoral program with San Diego State University. The title of my dissertation is “Association of microbial metabolisms and the progression of Cystic Fibrosis pulmonary disease”
- 2006 **B.Sc (Hons) Biomedical Sciences**, University of Sunderland, United Kingdom
- Developed a real-time quantitative gene expression assay by using the RT-PCR standard curve method to investigate NDST-2 gene expression in HMEC-1 cell line
Grade: First-class honor (4.0 GPA equivalent)

Experience

- 2012 – 2015 **Doctoral Research**, San Diego State University, San Diego, CA
- Designed and developed a workflow to process complex host-associated samples for NGS and metabolomics studies of viral and microbial communities
 - Developed an *in vitro* model to study the role of anaerobes in plugged airways
 - Performed DNA- and RNA-seq experiments using NGS to identify molecular markers of microbial metabolisms causing exacerbation events in Cystic Fibrosis patients
 - Presented work at more than 10 conferences and received 4 awards for research
 - Authored and co-authored 20 publications, many related to the application of NGS in research and clinical settings
- 2014 – 2015 **Scientific Consultant**, Portable Genomics, San Diego, CA
- Developed a mobile application to aggregate and visualize clinical, genomics, research, and life style information for Cystic Fibrosis patients
- 2011 – 2015 **Teaching Assistant**, San Diego State University, San Diego, CA
- Taught classes including Biochemistry and Molecular Biology, Microbiology, and Ecological Metagenomics
- 2009 – 2011 **Research Assistant**, Global Viral Forecasting Initiative Inc., San Francisco, CA
- Characterized viral communities in human nasopharyngeal swab samples from patients with flu-like symptoms but tested negative with known viruses
 - Set up and facilitated Roche 454-GSFLX sequencing in SDSU

2006 – 2009 **Research Assistant**, Genome Institute of Singapore, Singapore

- Performed metagenomic studies of mosquito-associated viruses using high-throughput sequencing
- Studied the bacterial flora in health and disease through gastric and oral samples from patients with and without gastric pathology and characterized microbial flora in pre-term birth using 16S rRNA sequence analysis
- Performed genome sequencing of highly virulent *Burkholderia pseudomallei* isolate, *Streptococcus pneumoniae*, and *Neisseria* spp using Paired-End diTagging (gPET) technique
- Managed laboratory risk as a member of the Risk Assessment committee, responsible in risk assessment of the various projects performed within the group

Selected Awards

- 2015 Cystic Fibrosis Research Inc. (CFRI) research fellow grant
- 2014 Inamori Fellowship recipient
- 2012 The CSUPERB student travel award
- 2012 The International Symposium on Microbial Ecology (ISME) travel grant award
- 2011 Mabel Myers Memorial Scholarship, San Diego State University
- 2006 The President's Prize, Institute of Biomedical Science, United Kingdom
- 2006 North East Region Symposium Prize, University of Sunderland, United Kingdom

List of References

Professor Forest Rohwer
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Professor Robert Edwards
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Dr. Douglas J. Conrad
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Relationship: Ph.D. adviser

List of Publications

1. **Lim Y.W.**, Haynes M., Furlan M., Robertson C.E., Harris J.K., Rohwer F. (2014) Purifying the impure: Sequencing metagenomes and metatranscriptomes from complex animal-associated samples. *Journal of Visualized Experiment*
2. **Lim Y.W.**, Cuevas DA, Silva GGZ, Aguinaldo K, Dinsdale EA, Haas AF, Hatay M, Sanchez SE, Wegley-Kelly L, Dutilh BE, Harkins TT, Lee CC, Tom W, Sandin SA, Smith JE, Zgliczynski B, Vermeij MJA, Rohwer F, Edwards RA. (2014) Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. *PeerJ*
3. **Lim Y.W.**, Evangelista J.S III, Schmieder R., Bailey B., Haynes M.R., Furlan M., Maughan H., Edwards R., Rohwer F., Conrad D. (2014) Clinical Insights from Metagenomic Analysis of Sputum Samples from Patients with Cystic Fibrosis. *Journal of Clinical Microbiology*
4. **Lim Y.W.**, Schmieder R., Haynes M.R., Furlan M., Matthews T. D., Whiteson K., Poole S. J., Hayes C. S., Low D. A., Maughan H., Edwards R., Conrad D., Rohwer F. (2013) Mechanistic model of *Rothia mucilaginosa* adaptation toward persistence in the CF lung, based on a genome reconstructed from metagenomic data. *PLoS ONE*
5. **Lim Y.W.**, Schmieder R., Haynes M.R., Willner D., Furlan M., Youle M., Abbott K., Edwards R., Evangelista J., Conrad D., Rohwer F. (2012) Metagenomics and metatranscriptomics: Windows on CF-associated viral and microbial communities. *Journal of Cystic Fibrosis* <http://dx.doi.org/10.1016/j.jcf.2012.07.009>
6. Haas, A.F., Knowles, B., **Lim, Y.W.**, McDole Somera, T., Kelly, L.W., Hatay, M., et al. (2014) Unraveling the Unseen Players in the Ocean - A Field Guide to Water Chemistry and Marine Microbiology. *Journal of Visualized Experiment*
7. Grasis J.A., Lachnit T., Anton-Erxleben F.A., **Lim Y.W.**, Schmieder R., Fraune S., et al. (2014) Species-specific viromes in the ancestral holobiont Hydra. *PLoS ONE*
8. Kelly L.W., Williams G.J., Barott K.L., Carlson C.A., Dinsdale E.A., Edwards R.A., Haas A.F., Haynes M., **Lim Y.W.**, McDole T., Nelson C.E., Sala E., Sandin S.A., Smith J.E., Vermeij M.J.A., Youle M., Rohwer F. (2014) Local genomic adaptation of coral reef-associated microbiomes to gradients of natural variability and anthropogenic stressors. *PNAS*
9. Whiteson K.L., Bailey B., Bergkessel M., Conrad D., Delhaes L., Felts B., Harris J.K., Hunter R., **Lim Y.W.**, Maughan H., Quinn R., Salamon P., Sullivan J., Wagner B., Rainey P. (2014) The upper respiratory tract as a microbial source for pulmonary infections in Cystic Fibrosis: Parallels from Island Biogeography. *American Journal of Respiratory and Critical Care Medicine*.
10. Garg N., Kapono C., **Lim Y.W.**, Koyama N., Vermeij M.J.A., Conrad D., Rohwer F., Dorrestein P. (2014) Mass spectral similarity for untargeted metabolomics data analysis of complex mixtures. *International Journal of Mass Spectrometry*
11. Quinn R., **Lim Y.W.**, Maughan H., Rohwer F., Whiteson K.L. (2014) Biogeochemical Forces Shape the Composition and Physiology of Polymicrobial Communities in the Cystic Fibrosis Lung. *MBIO*
12. Whiteson K.L., Meinardi S., **Lim Y.W.**, Schmieder R., Maughan H., Quinn R., Blake D., Conrad D., Rohwer F. (2014) Breath gas metabolites and bacterial metagenomes from cystic fibrosis airways indicate active pH neutral 2,3-butanedione fermentation. *ISME Journal*
13. Mokili J.L., Dutilh B.E., **Lim Y.W.**, Schneider B.S., Taylor T, et al. (2013) Identification of a Novel Human Papillomavirus by Metagenomic Analysis of Samples from Patients with Febrile Respiratory Illness. *PLoS ONE* 8(3): e58404. doi:10.1371/journal.pone.0058404
14. Schmieder R., **Lim Y.W.**, Edwards R. (2011) Identification and removal of ribosomal RNA sequences from metatranscriptomes *Bioinformatics* doi: 10.1093/bioinformatics/btr669
15. Willner D., Haynes M.R., Furlan M., Hanson N., Kirby B., **Lim Y.W.**, Rainey P.B., Schmieder R., Youle M., Conrad D., Rohwer F. (2011) Case studies of the spatial heterogeneity of DNA viruses in the cystic fibrosis lung. *American Journal of Respiratory Cell and Molecular Biology*. rcm.2011-0253OC
16. Willner D., Haynes M.R., Furlan M., Schmieder R., **Lim Y.W.**, Rainey P.B., Rohwer F., Conrad D. (2011) Spatial distribution of microbial communities in the cystic fibrosis lung. *ISMEJ*. 2011.104
17. Ng T.F.F., Willner D., **Lim Y.W.**, Schmieder R., Chau B., Nilsson C., Anthony S., Ruan Y., Rohwer F., Breitbart M. (2011) Broad surveys of DNA viral diversity obtained through viral metagenomics of mosquitoes. *PLoS ONE* 6(6): e20579.
18. Schmieder R., **Lim Y.W.**, Rohwer F. and Edwards R. (2010) TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. *BMC Bioinformatics*, 11(1), 341.
19. Ng T.F.F., Willner D., Nilsson C., **Lim Y.W.**, Schmieder R., Chau B., Ruan Y., Rohwer F., Breitbart M. (2010) Vector-based metagenomics for animal virus surveillance. *International Journal of Infectious Diseases*, DOI:10.1016/j.ijid.2010.02.461.
20. Rosario K., Nilsson C., **Lim Y.W.**, Ruan Y., Breitbart M. (2009) Metagenomic analysis of viruses in reclaimed water. *Environmental Microbiology*, 1462-2920