

Lei Li

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Date of Birth: 8th July, 1987

Scientific Education

■ Postdoc in Computational Biology, 11/2013 ~ Present
Institute for Molecular Infection Biology, University of Würzburg, Germany
Advisor: Prof. Jörg Vogel

■ PhD in Biology, 08/2009 ~ 10/2013
The Chinese University of Hong Kong, Hong Kong SAR. China
Advisor: Prof. Hoi Shan Kwan

■ Internship, 07/2008 ~ 05/2009
CAS-MPG Partner Institute for Computational Biology of Chinese Academy of sciences, Shanghai, China
Advisor: Prof. Shuhua Xu

■ B.S, 09/2005 ~ 06/2009
Bioengineering, School of Life Sciences, Nanchang University, China

Bioinformatics Skills

- Expertise in Python, R, Perl, SQL, Unix
- Population genomics and genetics analysis
- Comparative microbial genomics and evolution analysis
- RNA deep sequencing data analysis (Single cell RNA-Seq, CLIP-Seq, Ribosome profiling, Degradome sequencing, dRNA-Seq)
- Mass Spectrometry data analysis
- Machine-learning

Main conferences attended

- From Functional Genomics to Systematic Biology. Nov 8-11th, 2014. EMBL Heidelberg, Germany
- 3rd Mol Micro Meeting, May 7-9th, 2014. Würzburg, Germany
- Cell Symposia on Functional RNAs, December 2-4th, 2012. Sitges, Spain.
- The 6th International Conference on Genomics, November 12-15th, 2011. Shenzhen, China
- Bio-IT APAC Conference & Expo 2011, July 4-7th, 2011. Shenzhen, China

- Health Research Symposium 2010, September 11th, 2010. Hong Kong

Awards

- 2008.9 National Computer Rank Examination Grade 4 (highest rank)

Teaching experience

- 2009-2013 Teaching Assistant (Labs in General Microbiology and Genetics), The Chinese University of Hong Kong.

Personal character

Integrity; Responsible and good teamwork spirits; Hard-working, Excellent communication skills; Diligent and love of scientific research;

Publications

Published

13. Erik Holmqvist, Patrick Wright, **Lei Li**, Thorsten Bischler, Lars Barquist, Richard Reinhardt, Rolf Backofen, Jörg Vogel. Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking in vivo. *The EMBO Journal*, 2016. embj.201593360.
12. Xiang Xinjie, Li Chuan, **Li Lei**, Bian Yinbing, Kwan Hoishan, Nong Wenyang, Cheung Mankit, Xiao Yang, Genetic diversity and population structure of Chinese *Lentinula edodes* revealed by InDel and SSR markers, *Mycological Progress*, 2016. doi: 10.1007/s11557-016-1183-y.
11. Gong, WB, **Lei Li**, Zhou, Y., Bian, Y. B., Kwan, H. S., Cheung, M. K., & Xiao, Y. (2016). Genetic dissection of fruiting body-related traits using quantitative trait loci mapping in *Lentinula edodes*. *Applied Microbiology and Biotechnology*, 1-16.
10. Fan, B., **Lei Li**, Chao, Y., Förstner, K., Vogel, J., Borriss, R., & Wu, X. Q. (2015). dRNA-Seq Reveals Genomewide TSSs and Noncoding RNAs of Plant Beneficial Rhizobacterium *Bacillus amyloliquefaciens* FZB42. *PloS one*, 10(11), e0142002.
9. **Lei Li**, Hin-chung Wong, Wenyan Nong, Man Kit Cheung, Patrick Tik Wan Law, Kai Man Kam and Hoi Shan Kwan. Comparative genomic analysis of clinical and environmental strains provides insight into the pathogenicity and evolution of *Vibrio parahaemolyticus*. *BMC Genomics* 2014, 15:1135.
8. **Lei Li**, Hoi Shan Kwan. A novel computational approach for genome-wide prediction of small RNAs in bacteria. *Biorxiv*.
<http://dx.doi.org/10.1101/011668>.

7. Dagmar Krysciak, Jessica Grote, Mariita Rodriguez Orbegoso, Christian Utpatel, Konrad U. Förstner, **Lei Li**, Christel Schmeisser, Hari B. Krishnan, Wolfgang R. Streit. RNA-seq in the broad host range strain *Sinorhizobium fredii* NGR234 identifies a large set of genes linked to quorum sensing-dependent regulation in the background of a *traI* and *nglI* deletion mutant. *Applied and Environmental Microbiology*. 2014. 2014. doi: 10.1128/AEM.01835-14.
6. Qianli Huang, Jinhui Chang, Man Kit Cheung, Wenyan Nong, **Lei Li**, Ming-Tsung Lee, and Hoi Shan Kwan. Human proteins with target sites of multiple post-translational modification types are more prone to be involved in disease. *Journal of Proteome Research*. 2014. vol. 13 (6). 2735-2748.
5. Chi Keung Cheng, Chun Hang Au, **Lei Li**, Wenyan Nong, Patrick Tik Wan Law, William Man Wai Cheung, Julia Mei Lun Ling, Hoi Shan Kwan. Genome sequences of *Salmonella* enterica serotype Typhimurium blood clinical isolate ST4848/06 and stool isolate ST1489/06. *Genome announcements*. 2013. vol. 1 no. 5 e00823-13.
4. **Lei Li**, Dandan Huang, Man Kit Cheung, Wenyan Nong, Qianli Huang, Hoi Shan Kwan. BSRD: a repository for bacterial small regulatory RNA. *Nucleic Acids Research*. 2013. vol. 41. D233-238.
3. **Lei Li**, Chi Keung Cheng, Man Kit Cheung, Patrick Tik Wan Law, Julia Mei Lun Ling, Kai Man Kam, William Man Wai Cheung, Hoi Shan Kwan. Draft Genome Sequence of *Salmonella* enterica Serovar Typhimurium ST1660/06, a Multidrug-Resistant Clinical Strain Isolated from a Diarrheic Patient. *Journal of bacteriology*. 2012. vol. 194. 6319-6320.
2. Jingwei Jiang, Jun Li, Hoi Shan Kwan, Chun Hang Au, Patrick Tik Wan Law, **Lei Li**, Kai Man Kam, Julia Mei Lun Ling, Frederick C Leung. A cost-effective and universal strategy for complete prokaryotic genomic sequencing proposed by computer simulation. *BMC Research Notes*. 2012. 5:80. (Highly accessed)
1. Man Kit Cheung, **Lei Li**, Wenyan Nong, Hoi Shan Kwan. 2011 German *Escherichia coli* O104:H4 outbreak: whole-genome phylogeny without alignment. *BMC Research Notes*. 2011. 4:533. (Highly accessed)