

❖ **EDUCATION****Nanjing University, School of Life Science**

Nanjing, China

China's Top-Notch Undergraduate Training Program, which is an honor program designed for the students with outstanding academic records (top 30 out of 120 students)Bachelor of Science in Biology, **GPA: 3.82/4.0, Ranking: 2/23**

Sep.2012–Jul.2016

Awards: First-class People's Scholarship (twice, 2014&2015); Outstanding graduate with honor (2016)

GRE: V154+Q170; TOEFL: 107(R29+L29+S23+W26)

University of Melbourne, Exchange Student in Science, Melbourne, Australia Feb.2015–Jun.2015❖ **PUBLICATIONS**

- Zhu-Qing Shao, Jia-Yu Xue, Ping Wu, Yan-Mei Zhang, **Yue Wu**, Yue-Yu Hang, Bin Wang, and Jian-Qun Chen. 2016. Large-scale analyses of angiosperm nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes reveal three anciently diverged classes with distinct evolutionary patterns. *Plant Physiology* 170: 2095-2109.
- Ping Wu, **Yue Wu**, Cheng-Chen Liu, Li-Wei Liu, Fang-Fang Ma, Xiao-Yi Wu, Mian Wu, Yue-Yu Hang, Jian-Qun Chen, Zhu-Qing Shao, and Bin Wang. 2016. Identification of Arbuscular Mycorrhiza (AM)-Responsive microRNAs in Tomato. *Front. Plant Sci* 7:429.
- **Yue Wu** and Zhu-Qing Shao. Distribution of tRNA in Archaea and analysis of corresponding evolution causes. (Under Revision)

❖ **RESEARCH EXPERIENCES**

- **Computational Systems Biology (CSBL) Lab in the University of Georgia**
Internship, Advisor: Prof. Ying Xu and Dr. Chi Zhang Jul. 2016-Aug. 2017
 - **A computational method for mitochondria counting in expression level analysis**
Jul. 2016-present (for the first four project)
 - Estimating mitochondria number based on genes in stable co-expression network for different tissues and conditions. Testing the method in several cell lines and tissues.
 - Trying to find other markers for mitochondria number in cell.
 - **A computational method for pH estimation in subcellular compartments**
 - Estimating the optimum working pH by expression data and enzyme optimum pH from BRENDA. Testing this method in different cell lines, different condition, and different subcellular compartments.
 - Using metabolic pathway methods and expression data to estimate pH variation.
 - **Roles of respiratory chain related mutation in process of cancer**
 - Spotting frequent mutation of proteins in respiratory chain in different tumors. Predicting influences on complex structure and efficiency of electron transportation.
 - Trying to find corresponding supports in expression variation and ROS level.
 - **Roles of microenvironment in metastasis**
 - Using expression data to find links between tissue environment and metastasis tendency.
 - Exploring its relationship with cardiovascular system and lymphatic system.
 - **A system method for downloading and analyzing TCGA data.** Jul. 2016-Aug. 2016
 - Github: https://github.com/mikeaalv/TCGA_download
 - Gave a systemic presentation of structure and statistics of data in new TCGA Portal. Constructed a program for downloading and classifying TCGA data for most categories.
- **Chen Lab in Nanjing University** Feb. 2013-Jul. 2016
Research Assistant, Advisor: Prof. Jian-Qun Chen, Dr. Bin Wang, and Dr. Zhu-Qing Shao
 - **Roles of miRNA and PhasiRNA in symbiosis in *Solanum lycopersicum* and *Phaseolus vulgaris*** Jul.2015–Mar. 2016
 - Predicted miRNA from sRNA sequencing data of tomato and common bean from both plants and microbes, including mapping, quality control, and structure prediction. Found symbiosis related novel and known miRNAs, especially miR171.

Email: yuewu_mike@163.com

Phone number: 706-542-9779(work)

- Applied statistic methods on PhasiRNA loci prediction and drawn of corresponding distribution figures. Found probable functional links between miRNAs (ex: miR482, miR6026) and PhasiRNA loci (DCL2, CNL).

The program could be found on <https://github.com/mikeaalv/phase>

- Responsible for writing and reviewing of related parts of paper.

▪ **Fine mapping of gene for resistance to Soybean Mosaic Virus (SC6-N and SC7-N) in Suweon 97**
Leader of the team on National training programs of innovation for undergraduates

Advisor: Prof. Jianqun Chen

2014 - 2016

- Identified the region (BARCSOYSSR_13_1114-BARCSOYSSR_13_1115) for SC7 resistance on chromosome 13 in Suweon 97 by crossing experiments, and analysis on both phenotypes and genetic markers.

▪ **Analysis of tRNA distribution in Archaea and corresponding evolutionary causes**

Nominee for excellent thesis among graduates in Jiangsu, China

Dec. 2015-present

- Constructed phylogenetic tree of 167 Archaea complete genomes by ML methods using ortholog proteins, which is persuasive and more informative.
- Analyzed tRNA distribution patterns in different Archaea clades. Detailed Records of both tRNA absence (intensely in Methanococcales and Methanobacteriales) and gaining. Display of codon usage in these genomes and discovering definite codon composition in Methanococcales and Methanobacteriales.
- Analyzed corresponding evolutionary causes for the tRNA composition changes, including correlation among genome size, GC contents, and codon composition. Analyzed the role of adaptive evolution and enzyme efficiency in this absence process. The manuscript is under revision.

➤ **Other projects**

▪ **Quantitative detection and degradation of the toxins in the environment by *E.coli***

Assistant Leader, Nanjing-China iGEM Team, Nanjing University Nov. 2013 – Nov. 2014**Silver Medal**, iGEM (International Genetically Engineered Machine) competitionWebsite: <http://2014.igem.org/Team:Nanjing-China>

Advisor: Dr. Wei Wei and Prof. Jing Zhao

- Designed the system for detection, timer, positive feedback, and degradation.
- Predicted genetic circuit efficiency, molecular distribution, and riboswitches function, through ODE and PDE modeling, by MATLAB and RNAstructure.
- Implemented experiments on plasmid construction and function verification.
- Participated in team websites construction and made poster presentation.

▪ **Analysis of Hi-C interaction and sequence distances between genes** Mar. 2016-present

- Using existing Hi-C data for genome interaction prediction and sequence distance profiling in a phylogenetic way. Analyze the function of corresponding interaction genes and variation of interactions in evolution process for both 3D distances and sequence distances.

▪ ***Drosophila* research about *Wolbachia* influence**

June 2015

Member, cesar, University of Melbourne, Advisor: Prof. Ary Hoffman

❖ **EXTRACURRICULAR ACTIVITIES**

- iGEM club, publicity of iGEM and synthetic biology

Oct. 2014–Jul.2016

Member, one of **Founders**, Nanjing University

- Volunteered to care for children with autism

Jul. 2012–Aug. 2012

Member, Xinger Guardian program, Nanjing University & Nanjing Mingxin Children's intelligence training Center

❖ **PERSONAL SKILLS**

- Mastered in programing by C, R, and Perl, and phylogenetic analyzing.
- Familiar with Transcriptome, Public databases, Circuit modeling, ODE sets solving, databases API usage, mapping, RNA structure prediction, and protein modeling.
- Proficient in conducting molecular experiments and fly experiments.
- Familiar with phylogenetic methods, statistics, and population genetics.