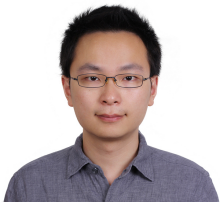
CURRICULUM VITAE

Sep 2016

Yingxiang LI



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EDUCATION

2005 - 2008 The First Middle School of Changsha, Changsha, Hunan, P.R. China.
High school student in the key class of science.

2008 - 2012 Tongji University, Shanghai, P.R. China.
Bachelor's Degree in Bioinformatics.

2012 - 2013 Tongji University, Shanghai, P.R. China.
PhD candidate in Bioinformatics.
Advisor: Cheng Li*.
Related Advisors: Xiaole Shirley Liu*, Yong Zhang*.

2013 - 2017 Tongji University, Shanghai, P.R. China.
PhD candidate in Bioinformatics.
Advisor: Zhiping Weng*.
Related Advisors: Wen Xue*, Cheng Li*, Xiaole Shirley Liu*, Yong Zhang*.

2015 – 2016 University of Massachusetts Medical School, Worcester, MA, United States.
Joint-PhD under China Scholarship Council.
Advisor: Wen Xue*, Zhiping Weng*.
Related Advisors: Guangping Gao*, Daniel G. Anderson.

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Cheng Li: Principal investigator. School of Life Sciences, Peking University. P.R. China.
Xiaole Shirley Liu: Professor. Biostatistics and Computational Biology, Dana-Farber and Harvard. United States.
Yong Zhang: Professor. School of Life Science, Tongji University. P.R. China.
Zhiping Weng: Director, Professor. Program in Bioinformatics and Integrative Biology, University of Massachusetts Medical School. United States.
Wen Xue: Assistant Professor. Program in Molecular Medicine, University of Massachusetts Medical School. United States.
Guangping Gao: Professor. Microbiology and Physiological Systems, University of Massachusetts Medical School. United States.

Daniel G Anderson: Associate Professor, Chemical Engineering and Institute for Medical Engineering and Science, Massachusetts Institute of Technology. United States.

PUBLICATIONS (#: co-first author)

1. Fulciniti, M., **Li, Y.**, … Munshi, N. (2012) Integrating Gene and Mir Expression Profiles and Regulatory Network Structures to Define Aberrent Feed Forward Loops with Functional and Clinical Implications in Myeloma. ***BLOOD*** (Conference Poster).
   IF: 10.5 *https://ash.confex.com/ash/2012/webprogram/Paper54063.html*
   Published in November 2012 in BLOOD annual meeting of AMER SOC HEMATOLOGY. I helped the cooperator on data collection and analysis, which focused on regular network structure and feed forward loops of multiple myeloma.

2. **Li, Y.**#, … Li, C. (2013). Classify hyperdiploidy status of multiple myeloma patients using gene expression profiles. ***PloS One***, *8*(3), e58809.
   IF: 3.2 *http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0058809*
   Published in March 2013 during my first year as a PhD candidate. We designed and realized the classification of multiple myeloma into hyperdiploidy and non-hyperdiploidy status by gene expression profiling.

3. Wang, X., Yan, Z., Fulciniti, M., **Li, Y.**, … Li, C. (2014). Transcription factor-pathway coexpression analysis reveals cooperation between SP1 and ESR1 on dysregulating cell cycle arrest in non-hyperdiploid multiple myeloma. ***Leukemia***, *28*(4), 894–903.
   IF: 10.4 *http://www.nature.com/leu/journal/v28/n4/full/leu2013233a.html*
   This work was published in Augest 2013 after I helped my elder mate with his topic. It's about co-expression analysis that effect transcription factor pathway in multiple myeloma and focus on SP1/ESR1.

4. **Li, Y.**#, … Xue, W. (2015). A versatile reporter system for CRISPR-mediated chromosomal rearrangements. ***Genome Biology***, *16*(1).
   IF: 10.8 *http://genomebiology.biomedcentral.com/articles/10.1186/s13059-015-0680-7*
   This work was published in May 2015. It was the first co-operation with the CRISPR/Cas9 experiment lab. I designed part of the study and worked on the bioinformatics section.

5. Wang, D., Mou, H., Li, S., **Li, Y.**, … Xue, W. (2015). Adenovirus-mediated somatic genome editing of Pten by CRISPR/Cas9 in mouse liver in spite of Cas9-specific immune responses. ***Human Gene Therapy***, *26*(7), 432–442.
   IF: 3.8 *http://online.liebertpub.com/doi/abs/10.1089/hum.2015.087*
   This work was published in July 2015. I mainly worked on the bioinformatics part to calculate the indel frequency created by CRISPR/Cas9.

6. Yin, H., Song, C.-Q., Dorkin, J.R., Zhu, L.J., **Li, Y**., …Anderson, G.D. (2016). Therapeutic genome editing by combined viral and non-viral delivery of CRISPR system components in vivo. ***Nat. Biotechnol***. 34, 328–333.
   IF: 41.5 *http://www.nature.com/nbt/journal/v34/n3/full/nbt.3471.html*
   This work was published in Feb 2016. I mainly supported the bioinformatic analysis and plot the indel frequency created by CRISPR.

RESEARCH EXPERIENCE

2009 - 2011 **The character and biological effect of transmission module of gene relationship**
It was Students Innovation Training Program in Tongji University. This project was about an investigation of genes in one orthologous group. We measured the linear distance between genes from basic organisms to complex ones. This program was supervised by Haiyun Wang (Tongji University).

2011 - 2012 **Integrating gene and Mir expression profiles and regulatory network structures to define aberrant feed forward loops with functional and clinical implications in myeloma**"
We have here developed and defined multi-gene transcriptional and post-transcriptional feed-forward loop (FFL). These conceptual FFLs consist of a master TF which regulates a miR and together with it controls a set of specific common gene/s. We have developed a comprehensive novel integrative analysis method, dChip-GemiNI (Gene and miRNA Network-based Integration), which combines gene and miR expression profiles, and also incorporates regulatory network structure in the form of computationally identified TF–miRNA FFLs. This work was exhibited as conference poster in 54th ASH Annual Meeting and Exposition held by ***Blood***. This program was supervised by Cheng Li and Nikhil C. Munshi (DFCI, Harvard Medical School).

2011 - 2013 **Classify hyperdiploidy status of multiple myeloma patients using gene expression profiles**
Multiple myeloma (MM) frequently harbors alterations in DNA and chromosome copy numbers, and can be divided into two major subtypes, hyperdiploid (HMM) and non-hyperdiploid multiple myeloma (NHMM). The two subtypes have different survival prognosis, possibly due to different but converging paths to oncogenesis. Using five MM expression datasets that have HMM status measured by FISH and copy number microarrays, we have developed and validated a K-nearest-neighbor method to classify MM into HMM and NHMM based on gene expression profiles. We published our result in ***PLOS ONE***. This program was supervised by Cheng Li.

2012- 2014 **Transcription factor-pathway coexpression analysis reveals cooperation between SP1 and ESR1 on dysregulating cell cycle arrest in non-hyperdiploid multiple myeloma**
Transcription factors (TrFs) have been implicated in myeloma oncogenesis, but their dysregulation in myeloma subtypes are less studied. Here, we developed a TrF-pathway coexpression analysis to identify altered coexpression between two sample types. We find that TrFs MYC, nuclear factor-kB and HOXA9 have significantly lower coexpression with cell cycle arrest in HMM, co-occurring with their overactivation in HMM. In contrast, TrFs ESR1 (estrogen receptor 1), SP1 and E2F1 have significantly lower coexpression with cell cycle arrest in NHMM. This work was published in ***Leukemia***. This program was supervised by Cheng Li.

2013 – 2014 **Cell cycle genes and related miR expression analysis**
This program is under the cooperation with Dana-Farber Cancer Institute and Harvard Medical School. We are analyzing the relation between miR and mRNA in cell cycle pathway. This program was supervised by Cheng Li and Peter Sicinski (Harvard University).

2013 – 2014 **Squamous cell lung carcinoma related analysis**
This program is under the cooperation with Shanghai Chinese Academy of Sciences. We are analyzing the SCC's pathogenesis and related gene expression/copy number/gene mutation. This program was supervised by Cheng Li and Hongbin Ji (Shanghai Institutes for Biological Sciences).

2013 – Present **Bi-state gene in cancer**
We hypothesized that there're genes that could show different subtypes of cancer which we called them bi-state genes. We wanted to find out the genes that have such potential, and they could be regarded as key genes for determining subtypes of cancers. We combined the TCGA (The Cancer Genome Atlas) data and statistic method. This program was supervised by Zhiping Weng.

2013 – Present **Role of X gene** (trade secret of Novartis)
We are interested in one gene and we are researching its role in all kinds of regulation in cells. ChIP-Seq and ChIP-MS experiments have been performed on this gene. We have a deep cooperation with Novartis in Shanghai. This program was supervised by Zhiping Weng and Bin Xiang (Novartis International).

2014 – Present **Studying protein P function in regulating protein B transcription activity** (trade secret of Novartis)
We are under an ongoing drug discovery project. Multiple ChIP-Seq data are designed for search of their relationship. This project is also a cooperation with Novartis in Shanghai. It was supervised by Zhiping Weng and Bin Xiang.

2014 – 2015 **Identification of LncRNA in lung cancer**
We collected lncRNA information of various types of cancers. At the same time, we gathered mutation data from different papers or public database. Then we hope to explore the mutation effect on lncRNA function only in the non-coding region, and try to find their influence on cancers. This program was supervised by Zhiping Weng.

2014 – 2015 **A versatile reporter system for CRISPR-mediated chromosomal rearrangements**
We have developed a direct and quantifiable method that can measure CRISPR-mediated DNA inversion and deletion in cultured human and mouse cells as well as in mouse liver. Thus our CRISPR-based method can provide a platform for studying chromosomal rearrangements in cancers. Finally, we published our result in ***Genome Biology***. This program was supervised by Zhiping Weng and Wen Xue.

2014 – Present **Integrated analysis of human hepatic carcinoma**
We have made multiple experiments including ChIP-Seq, exome methylation, HBV integration sites, small RNA, transcriptome lincRNA, SNP and other high-through sequencing. All these data were integrated for a comprehensive analysis of human hepatic carcinoma. We hope to combine all these result to figure out a overall knowledge of liver cancer. This project is also an cooperation with Novartis in Shanghai. This program was supervised by Zhiping Weng and Tianlun Zhou (Novartis International).

2014 – 2015 **Adenovirus-mediated somatic genome editing of Pten by CRISPR/Cas9 in mouse liver in spite of Cas9-specific immune responses**
We used adenovirus (Ad) vector to deliver a Streptococcus pyogenes-derived Cas9 system (SpCas9) targeting Pten, a gene involved in NASH and a negative regulator of the PI3K-AKT pathway, in mouse liver. Our findings provide a strategy to model human

liver diseases in mice and highlight the importance considering Cas9-specific immune responses in future translational studies involving in vivo delivery of CRISPR/Cas9. Finally, we published our result in ***Human gene therapy***. This program was supervised by Zhiping Weng, Wen Xue and Guangping Gao (Massachusetts Institute of Technology).

2015 – 2016 **Combined viral and nonviral delivery of CRISPR components corrects liver disease in adult rodents**

The ability to correct defective genes in vivo has broad potential utility for both therapy and the study of genetics. By combining viral and nonviral nucleic acid delivery we report the first therapeutically relevant formulations capable of inducing repair of a disease gene in an adult animal. This treatment fully rescued body weight loss, alleviated liver damage-associated serum markers and generated Fah-positive hepatocytes. Our study indicates that systemic CRISPR-mediated genome editing is possible in vivo, and provides proof-of-principle for therapeutic correction of genetic diseases in adult animals. It was published in ***Nature biotechnology***. This program was supervised by Zhiping Weng, Wen Xue and Daniel G. Anderson (Massachusetts Institute of Technology).

2015 – Present **Genome-wide CRISPR screen identifies MAPK regulators as key tumor suppressors in liver**

Using a CRISPR-based genetic screen, we identify candidate liver tumor suppressors, including NF1-a negative regulator of Ras mutated in neurofibromatosis. CRISPR-mediated knockout of Nf1 accelerates liver tumor formation in mice, and loss of Nf1 or activation of Ras upregulates the liver progenitor cell markers Hmga2 and Sox9. In human liver cancer patients, low NF1 or high HMGA2 mRNA levels predict poor survival. Treatment of human liver cancer cells with RAS pathway inhibitors including sorafenib suppresses HMGA2 and SOX9 expression, and knockdown of Hmga2 delays tumorigenesis driven by oncogenic RAS. We are submitting the project to the journal. This program was supervised by Zhiping Weng, Wen Xue, supported by China Scholar Council (CSC).

HONORS AND AWARDS

2009 Outstanding student scholarship of Tongji University, second class

2009 The 20th Qingnian Cup inter-college debate competition of Tongji University, second place (a member of the college team)

2010 Outstanding student of Tongji University

2010 The Tongbo Cup football match of Tongji University, first place (a member of the college team)

2011 Excellent league member of Tongji University

2011 Learning scholarship of Tongji University, third class

2013 National scholarship for graduate students, master

2015 Joint-PhD supported by China Scholarship Council, one year

2015 National scholarship for graduate students, PhD

EXTRACURRICULAR EXPERIENCES

2008 - 2009	The monitor. Process the routines of the class. School of life science and technology, Tongji University.
2009	The member of college debate team and won the second place.
2009 - 2010	The vice president of college student union. Help the college with common routines.
2010	A forward in our college soccer team and finally won the champion.
2010 - 2011	The president of college student union. Manage the students' routines of our college, and arranged a graduate ceremony as the director.
2011	A volunteer in the Tongji-Novartis Cancer and Epigenetics Symposium. Help with the meeting affairs.
2012	A teaching assistant: Statistical Model by Prof. Li Cheng.

SOCIAL WORK EXPERIENCES

2009	A volunteer of the Red Cross. Help to advertise the knowledge of AIDS and help the school hospital with medical affair. Tongji University.
2009	The team leader of an internship about advertisement of the CBA. Help to investigate the market of sportswear. Shanghai.

LANGUAGE PROFICIENCY

CET 6 540. TOEFL 90.

SKILLS

bioinformatics, biology, cancer research, non-invasive prenatal diagnosis, genetics, Dota2, sequencing analysis, programme, big data, data mining, R, python, shell, Cytoscape, Office Suit and so on.