

For full publication list, please see <https://goo.gl/MqOkfK>

(* Works included in dissertation, [§]Contributed equally, shared senior author)

1. Selection of publications:

- [1] **Li CX**, Wheelock CE, Sköld CM, **Wheelock ÅM** (2018) Integration of multi-omics datasets enables molecular classification of COPD. *European Respiratory Journal*. *Eur Respir J* **51**(5). (Time Cited 12. **IF:10.6**, **PMID: 29545283**)

My contributions: conception and design; analysis and interpretation and drafting of manuscript. This is the most important pilot work supporting our research hypothesis.

- [2] [§]Xu, J., **C. X. Li**, Y. S. Li, J. Y. Lv, Y. Ma, T. T. Shao, L. D. Xu, Y. Y. Wang, L. Du, Y. P. Zhang, W. Jiang, C. Q. Li, Y. Xiao, and X. Li, MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. *Nucleic Acids Res*, 2011. 39(3): p. 825-36, (**Times Cited 227**, **JIF 10.16**).

Equally contributed author. *My contributions: conception and design; analysis and interpretation and drafting of manuscript. In this work, we were the first group to investigate miRNA-miRNA synergies from a network perspective. It supported multi-omics integration for disease prediction.*

- [3] [§]Xu, J., **C. X. Li**, J. Y. Lv, Y. S. Li, Y. Xiao, T. T. Shao, X. Huo, X. Li, Y. Zou, Q. L. Han, X. Li, L. H. Wang, and H. Ren, Prioritizing candidate disease miRNAs by topological features in the miRNA target-dysregulated network: case study of prostate cancer. *Mol Cancer Ther*, 2011. 10(10): p. 1857-66, (**Times Cited 5109**, **JIF 5.76**).

Equally contributed author. *My contributions: conception and design; analysis and interpretation and drafting of manuscript. We further predict disease-related miRNA based on their synergistic network property, to prioritize prostate cancer disease-risk miRNA based on network topology features. Method will be applied in this project.*

- [4] Xu, J., Y. Li, X. Li, **C. Li**, T. Shao, J. Bai, H. Chen, and X. Li, Dissection of the potential characteristic of miRNA-miRNA functional synergistic regulations. *Mol Biosyst*, 2013. 9(2): p. 217-24, (**Times cited 21**, **JIF 2.78**).

My contributions: conception and design. We further dissect the potential characteristic of miRNA-miRNA synergistic regulations and applied in disease miRNA prediction. Method will be applied.

- [5] [§]Sun, J., M. Zhou, Z. T. Mao, D. P. Hao, Z. Z. Wang, and **C. X. Li**, Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. *FEBS Lett*, 2013. 587(7): p. 976-82, (**Times Cited 14**, **JIF 3.62**).

Senior Author. *My contributions: conception and design and revision of manuscript.*

- [6] [§]**Li, C.**, G. Zhang, X. Li, S. Rao, B. Gong, W. Jiang, D. Hao, P. Wu, C. Wu, L. Du, Y. Xiao and Y. Wang, A systematic method for mapping multiple loci: an application to construct a genetic network for rheumatoid arthritis. *Gene*, 2008. 408(1-2): p. 104-11, (**Times Cited 17**, **JIF 2.42**).

My contributions: conception and design; analysis and interpretation and drafting of manuscript. From the view of system medicine, we aim to identify risk genes for complex disease using the network-based method and predict robust module-based biomarkers. The GWAs analysis and machine learning methods will be applied.

- [7] [§]Li, C., Y. Li, J. Xu, J. Lv, Y. Ma, T. Shao, B. Gong, R. Tan, Y. Xiao and X. Li, Disease-driven detection of differential inherited SNP modules from SNP network. *Gene*, 2011. 489(2): p. 119-29, **(Times Cited 8, JIF 2.42)**.

My contributions: conception and design; analysis and interpretation and drafting of manuscript. We developed new algorithms to identify Single Nucleotide Polymorphism (SNP) collaborations and modules in complex disease, and disease candidate miRNA-miRNA and miRNA-mRNA modules.

- [8] [§]Hao, D., C. Ren, and C. Li, Revisiting the variation of clustering coefficient of biological networks suggests new modular structure. *BMC Syst Biol*, 2012. 6: p. 34, **(Times Cited 30, JIF 2.3)**.

Senior Author. *My contributions: conception and design and revision of manuscript. We identified new modular structures in biological networks. The methods in computational network biology will be applied.*

- [9] Hao, D., C. Li, S. Zhang, J. Lu, Y. Jiang, S. Wang, and M. Zhou, Network-based analysis of genotype-phenotype correlations between different inheritance modes. *Bioinformatics*, 2014, **(Times Cited 5, JIF 7.31)**.

My contributions: analysis and drafting of manuscript. We investigate genotype-phenotype correlations between different inheritance modes based on network-based analysis, and provide new insight into human "diseasome". The "diseasome" view is the fundamental hypothesis to link COPD and asthma.

- [10] Hao, D. and C. Li, The dichotomy in degree correlation of biological networks. *PLoS One*, 2011. 6(12): p. e28322, **(Times Cited 34, JIF 2.81)**.

My contributions: analysis and drafting of manuscript. We systematically analyze the modularity structure and dichotomy property in degree correlation of biological networks. Its computational network biology methods will be applied.

2. Total number of publications: 20

Peer-reviewed original articles

(* Works included in dissertation, [§]Contributed equally, shared senior author)

- [1] Li CX, Wheelock CE, Sköld CM, **Wheelock AM** (2018) Integration of multi-omics datasets enables molecular classification of COPD. *European Respiratory Journal*. In press. www.ncbi.nlm.nih.gov/pubmed/29545283 **(IF:10.6, PMID: 29545283)**
- [2] Hao, D., G. Wang, Z. Yin, C. Li, Y. Cui, and M. Zhou, Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human diseasome. *Eur J Hum Genet*, 2014. 22(11): p. 1260-7, www.ncbi.nlm.nih.gov/pubmed/24448549 **(IF: 7.31)**
- [3] Hao, D., C. Li, S. Zhang, J. Lu, Y. Jiang, S. Wang, and M. Zhou, Network-based analysis of genotype-phenotype correlations between different inheritance modes. *Bioinformatics*, 2014, www.ncbi.nlm.nih.gov/pubmed/25078399 **(IF: 4.29)**
- [4] Lu, J., D. Wu, C. Li, M. Zhou, and D. Hao, Correlation between gene expression and mutator phenotype predicts homologous recombination deficiency and outcome in ovarian cancer. *J Mol Med (Berl)*, 2014, www.ncbi.nlm.nih.gov/pubmed/25062964 **(IF: 4.69)**
- [5] Wu, Y., N. Jin, H. Zhu, C. Li, N. Liu, Y. Huang, Z. Miao, X. Bi, D. Wu, X. Chen, Y. Xiao, D. Hao, C. Li, B. Gong, S. Zhang, L. Zhuang, K. Li, and D. Wang, Global gene expression distribution in non-cancerous complex diseases. *Mol Biosyst*, 2014. 10(4): p. 728-31, www.ncbi.nlm.nih.gov/pubmed/24488172 **(IF: 2.78)**

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- [6] [§]Sun, J., M. Zhou, Z. T. Mao, D. P. Hao, Z. Z. Wang, and **C. X. Li**, Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. *FEBS Lett*, 2013. 587(7): p. 976-82, www.ncbi.nlm.nih.gov/pubmed/23454638 (IF: 3.62)
- [7] Xu, J., Y. Li, X. **Li**, **C. Li**, T. Shao, J. Bai, H. Chen, and X. Li, Dissection of the potential characteristic of miRNA-miRNA functional synergistic regulations. *Mol Biosyst*, 2013. 9(2): p. 217-24, www.ncbi.nlm.nih.gov/pubmed/23154827 (IF: 2.78)
- [8] Sun, J., M. Zhou, Z. Mao, and **C. Li**, Characterization and evolution of microRNA genes derived from repetitive elements and duplication events in plants. *PLoS One*, 2012. 7(4): p. e34092, www.ncbi.nlm.nih.gov/pubmed/22523544 (IF: 2.81)
- [9] [§]Hao, D., C. Ren, and **C. Li**, Revisiting the variation of clustering coefficient of biological networks suggests new modular structure. *BMC Syst Biol*, 2012. 6: p. 34, WWW.NCBI.NLM.NIH.GOV/PUBMED/22548803 (IF: 2.3)
- [10] [§]Xu, J., **C. X. Li**, J. Y. Lv, Y. S. Li, Y. Xiao, T. T. Shao, X. Huo, X. Li, Y. Zou, Q. L. Han, X. Li, L. H. Wang, and H. Ren, Prioritizing candidate disease miRNAs by topological features in the miRNA target-dysregulated network: case study of prostate cancer. *Mol Cancer Ther*, 2011. 10(10): p. 1857-66, www.ncbi.nlm.nih.gov/pubmed/21768329 (IF: 10.16)
- [11] [§]Xu, J., **C. X. Li**, Y. S. Li, J. Y. Lv, Y. Ma, T. T. Shao, L. D. Xu, Y. Y. Wang, L. Du, Y. P. Zhang, W. Jiang, C. Q. Li, Y. Xiao, and X. Li, MiRNA-miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. *Nucleic Acids Res*, 2011. 39(3): p. 825-36, www.ncbi.nlm.nih.gov/pubmed/20929877 (IF: 5.76)
- [12] [§]**Li, C.**, Y. Li, J. Xu, J. Lv, Y. Ma, T. Shao, B. Gong, R. Tan, Y. Xiao, and X. Li, Disease-driven detection of differential inherited SNP modules from SNP network. *Gene*, 2011. 489(2): p. 119-29, www.ncbi.nlm.nih.gov/pubmed/21920414 (IF: 2.42)
- [13] Hao, D. and **C. Li**, The dichotomy in degree correlation of biological networks. *PLoS One*, 2011. 6(12): p. e28322, www.ncbi.nlm.nih.gov/pubmed/22164269 (IF: 2.81)
- [14] [§]**Li, C.**, G. Zhang, X. Li, S. Rao, B. Gong, W. Jiang, D. Hao, P. Wu, C. Wu, L. Du, Y. Xiao, and Y. Wang, A systematic method for mapping multiple loci: an application to construct a genetic network for rheumatoid arthritis. *Gene*, 2008. 408(1-2): p. 104-11, www.ncbi.nlm.nih.gov/pubmed/18082339 (IF: 2.42)
- [15] Jiang, W., X. Li, S. Rao, L. Wang, L. Du, **C. Li**, **C. Wu**, H. Wang, Y. Wang, and B. Yang, Constructing disease-specific gene networks using pair-wise relevance metric: application to colon cancer identifies interleukin 8, desmin and enolase 1 as the central elements. *BMC Syst Biol*, 2008. 2: p. 72, www.ncbi.nlm.nih.gov/pubmed/18691435 (IF: 2.3)
- [16] Li, X., S. Rao, W. Jiang, **C. Li**, Y. Xiao, Z. Guo, Q. Zhang, L. Wang, L. Du, J. Li, L. Li, T. Zhang, and Q. K. Wang, Discovery of Time-Delayed Gene Regulatory Networks based on temporal gene expression profiling. *BMC Bioinformatics*, 2006. 7: p. 26, www.ncbi.nlm.nih.gov/pubmed/16420705 (IF: 2.45)
- [17] [§]**Li, C. X.**, L. Du, X. Li, B. S. Gong, J. Zhang, and S. Q. Rao, Novel strategies to identify relevant molecular signatures for complex human diseases based on data of identical-by-decent profiles and genomic context. *Beijing Da Xue Xue Bao*, 2006. 38(1): p. 74-7, www.ncbi.nlm.nih.gov/pubmed/16415972
- [18] [§]**Li, C. X.**, X. Li, Z. Guo, B. S. Gong, and K. Tu, [Analysis of the mRNA expression similarity of genes in the same gene expression regulatory

pathway]. Yi Chuan, 2004. 26(6): p. 929-33,
www.ncbi.nlm.nih.gov/pubmed/15640129

Peer-reviewed conference contributions

- [1] Bertrand De Meulder, Romain Tching Chi Yen, **Chuan-Xing Li**, Asa Wheelock, et.al. U-BIOPRED accessible handprint: combining omics platforms to identify stable asthma subphenotypes. *European Respiratory Journal* 2018 52: OA3578.
- [2] AM Wheelock, V Lagani, **C-X Li**, Multi-Omics Integration at the Pathway-and Network Level Improves the Power to Identify Subgroups and Disease Pathways in COPD A28. *ADVANCES IN COPD AND ASTHMA*, 2018
- [3] Åsa M Wheelock and **Chuan-xing Li**, Multi-Compartment, Multi-Omics Integration Affords Power To Facilitate Detection Of Molecular COPD Sub-Phenotypes In Small Cohorts. Vol. A75. *BIG AND BIGGER (DATA): OMICS AND BIOMARKERS OF LUNG DISEASES*. 2017: American Thoracic Society.
- [4] **Chuan-Xing Li**, Shama Naz, Bettina Levänen, Maria Eldh, Susanne Gabrielsson, David J. Erle, Craig E. Wheelock, C. Magnus Sköld, Åsa M. Wheelock.(2016) Prediction of COPD- and smoking status by network-based multi-omics data fusion analysis. *Lung Science Conference*, Estoril, Portugal.
- [5] **Li, C. X.**, Bheda-Malge, A., Gelinas, R., Isfort, R. J., & Bascom, C. C. (2015). A probabilistic Boolean network model for retinoic acid-regulated responses in skin. Paper presented at the 23rd World Congress of Dermatology.

Peer-reviewed books and book chapters

Binsheng Gong, **Chuan-xing Li**, Dapeng Hao, Functional genomics and gene expression analysis, *Bioinformatics Theory and Medical Practice*, People's Health Publishing House, China, 2013, ISBN: 9787117162777
This book is the first textbook for bioinformatics in Medical Universities of China.

Invited speaker or chair

- How to make sense of your data: Clustering and multi-omics integration. **European Respiratory Society Workshop: Translational Research data handling and analysis, Berlin, Oct 2017**
- Multi-omics analysis for stratification of chronic inflammatory lung diseases. **Symposium on Computational Integration of Multi-Omics data**, 17-18 June 2019, ZMB Kiel.
- Lung Science Conference, Poster session chairs: Prof. Peter Sterk and Dr. Chuan-Xing Li, European Respiratory Society, Estoril, March 2016