
NAME: Leping Li

POSITION TITLE: Senior Investigator

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Fudan University (formerly Shanghai Medical University), China	B.A	07/1982	Medicinal Chemistry
University of North Carolina at Chapel Hill, NC	Ph.D.	05/1994	Medicinal Chemistry
University of North Carolina at Chapel Hill, NC	Postdoc	07/1996	Computational chemistry
National Institute of Environmental Health Sciences, NIH, NC	Postdoc	07/1998	Computational Biology

A. Positions and Honors

Positions

2013-present	Senior Investigator with tenure, National Institute of Environmental Health Sciences, National Institute of Health, Research Triangle Park, NC
2003-2012	Tenure-track Investigator, National Institute of Environmental Health Sciences, National Institute of Health, Research Triangle Park, NC
2000-2003	Research Fellow, National Institute of Environmental Health Sciences, National Institute of Health, Research Triangle Park, NC
1998-2000	Staff Scientist, National Institute for Occupational Safety and Health, Center for Disease Control, WV

Honors and Professional Activities

2014	NIH Award of Merit
2010-present	Editorial Board, Journal of Biometrics & Biostatistics
2009-present	Editorial Board, The Indian Society of Agricultural Statistics
2003	NIH Award of Merit
1987	Rong-Lin distinguished student award, Shanghai Medical University, Shanghai, China
1984	Distinguished student of the Higher Education Bureau of Shanghai Metropolitan Schools, Shanghai, China

B. Contribution to Science

Advances in technologies such as next-gen sequencing make it possible to study genome-wide gene expression and protein binding in a single experiment. These studies provide a global view on the functional roles of proteins involved in the regulation of gene transcription (e.g., using ChIP-seq) and on transcriptome changes (e.g., using mRNA-seq) during development or in response to environmental exposures. Making sense of the huge amount of data remains a challenge. My group has been focused on developing statistical and computational methods for mining high-dimensional data to facilitate new discovery and hypothesis generation. Bioinformatics is an integral part of modern biology. We work closely with bench scientists; together we can have a substantial impact on environmental health sciences research.

Selected peer-reviewed publications

- Li, Y., Kang, K., Krahn, J.M., Croutwater, N., Lee, K., David M. Umbach, D.M. and Li, L. A comprehensive genomic pan-cancer classification using The Cancer Genome Atlas gene expression data. BMC Genomics, in press.
- Ren, NSX, Ji, M, Tokar, EJ, Busch, EL, Xu, X, Lewis, D, Li, X, Jin, A., Zhang, Y., Wu, WKK, Huang, W, Li, L, Fargo, D, Keku, T, Sandler, RS and Li X. Haploinsufficiency of SIRT1 enhances glutamine metabolism and promotes cancer development. Curr. Biol., 2017, Volume 27, Issue 4, p483–494, 20.

3. Lowe, J.M., Nguyen, T-A, Resnick, M.A., Grimm, S., Gabor, K.A, Peddada, S.D., Li, L., Anderson, C.W., Menendez, D., Fessler, M.B. The novel p53 target TNFAIP8 variant 2 is increased in cancer and offsets p53-dependent tumor suppression. *Cell Death and Differentiation*, 2017 Jan;24(1):181-191.
4. Stumpo, D.J., Trempus, C.S., Tucker, C.J., Huang, W., Li, L., Kluckman, K., Bortner, D.M. and Blackshear, P.J. Deficiency of the placenta- and yolk sac-specific tristetruprolin family member ZFP36L3 identifies likely mRNA targets and an unexpected link to placental iron metabolism. *Development*, 2016, 143, 1424-1433.
5. Dong J, Wyss A, Yang J, Price TR, Nicolas A, Nalls M, Tranah G, Franceschini N, Xu Z, Schulte C, Alonso A, Cummings SR, Fornage M, Zaykin D, Li L, Huang X, Kritchevsky S, Liu Y, Gasser T, Wilson RS, De Jager PL, Singleton AB, Pinto JM, Harris T, Mosley TH Jr, Bennett DA, London S, Yu L, and Chen H. Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. *Mol Neurobiol* (2016). doi:10.1007/s12035-016-0282-8
6. Xu, Z., Niu, L., Li, L. and Taylor, J.A. ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. *Nucleic Acids Research. Nucl. Acids Res.*, 2015, doi: 10.1093/nar/gkv907.
7. Li, Y., Umbach, D.M., Krahn, J.M., Flake, G. and Li, L. Towards predicting metastatic progression of melanoma based on gene expression data. *Pigment Cell Melanoma Res.*, 2015.
8. Wells, M.L., Washington, O.L., Hicks, S.N., Nobile, C.J., Hartooni, N., Wilson, G.M., Zucconi, B.E., Huang, W., Li, L., Fargo, D.C., and Blackshear, P.J. Post-transcriptional regulation of transcript abundance by a conserved member of the tristetruprolin family in *Candida albicans*. *Mol. Microbiol.* 2015, 95, 1036-1053.
9. Choi, Y.-J., Lai, W.S., Fedic, R., Stumpo, D.J, Huang, W., Li, L., Perera, L., Brewer, B.Y., Brewer, B.Y., Wilson, G.M., Mason, J.M., and Blackshear, P.J. The Drosophila Tis11 protein and its effects on mRNA expression in flies. *J. Biol. Chem.*, 2014, 289(51):35042-60.
10. Niu, L., Huang, W., Umbach, D.M. and Li, L. IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. *BMC Genomics*, 2014, 15:862.
11. Zhang, X., Li, B., Ma, L., Li, L., Zheng, D., Li W., Chu, M., Mailman, R.B., Archer, T.K., and Wang, Y. Transcriptional repression by specific SWI/SNF components affects pluripotency of human embryonic stem cells. *Stem Cell Report*, 2014, 3, 460-474.
12. Hewitt, S.C., Li, L., Grimm, S.A., Winuthayanon, W., Hamilton, K.J., Pockette, B., Rubel, CA., Pedersen, L.C., Fargo, D., Lanz, R.B., DeMayo, F.J., Schütz, G., Korach, K.S. Novel DNA motif binding activity observed in vivo with an estrogen receptor α mutant mouse. *Mol. Endocrinol.* 2014, 28(6):899-911.
13. Li, Y., Umbach, D.M. and Li, L. T-KDE: A method for analyzing genome-wide protein binding patterns from ChIP-seq data. *BMC Genomics*, 2014, 15:27.
14. Li, Y., Hamilton, K.J., Lai, A.Y., Burns, K.A., Li, L., Wade, P.A. and Korach, K.S. Diethylstilbestrol (DES)-stimulated hormonal toxicity is mediated by ER α alteration of target gene methylation patterns and epigenetic modifiers (DNMT3A, MBD2, and HDAC2) in the mouse seminal vesicle. *Environ. Health Perspect.*, 2014, 122(3):262-8.
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21. Hewitt, S.C., Li, L., Grimm, S.A. Chen, Y., Liu, L., Li, Y., Bushel, P.R., Fargo, D., and Korach, K.S. Research Resource: Whole-Genome Estrogen Receptor α Binding in Mouse Uterine Tissue Revealed by ChIP-Seq. *Mol. Endocrinol.* , 2012, 26(5):887-898.
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