BIOGRAPHICAL SKETCH

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NAME: Leping Li

eRA COMMONS USER NAME (credential, e.g., agency login): leping001

POSITION TITLE: Senior Investigator

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

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
2009-2018	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

1. Xu, Q, Li, Y, Gao, X, Kang, K, Williams, JG, Ji, M, Deterding, LJ, Locasale, JW, **Li, L**, Shats, I, and Li, X. HNF4α confers sensitivity to methionine restriction through regulation of sulfur amino acid metabolism in human hepatocellular carcinoma. *Nat Commun* 11, 3978 (2020). https://doi.org/10.1038/s41467-020-17818-w.
2. Teresa Gagliano, Kalpit Shah, Sofia Gargani Liyan Lao, Mansour Alsaleem, Jianing Chen, Vasileios Ntafis, Penghan Huang, Angeliki Ditsiou, Viviana Vella, Kritika Yadav, Kamila Bienkowska, Giulia Bresciani, Kai Kang, **Leping Li**, Philip Carter, Graeme Benstead-Hum, Timothy O'Hanlon, Michael Dean, Frances M.G. Pearl, Soo-Chin Lee, Emad A Rakha, Andrew R Green, Dimitris L. Kontoyiannis, Erwei Song, Justin Stebbing and Georgios Giamas. PIK3Cδ expression by fibroblasts promotes triple-negative breast cancer progression. *J Clin Invest*. 2020 Mar 3. pii: 128313. doi: 10.1172/JCI128313.
3. Chelsea M. Clinton, James R. Bain, Michael J. Muehlbauer, YuanYuan Li, **Leping Li**, Sara K. O'Neal, Brenna L. Hughes, David E. Cantonwine, Thomas F. McElrath, Kelly K. Ferguson. Non-targeted urinary metabolomics in pregnancy and associations with fetal growth restriction. *Sci Rep. 2020 Mar 24;10(1):5307. doi: 10.1038/s41598-020-62131-7.*
4. Shats, I., Williams, J.G., Liu, J., Deterding, L.J., Lim, C., Xu, X., Randall, T.A., Lee, E., Li, W., Fan, W., Li, J.-L., Sokolsky, M., Kabanov, A.V., **Li, L.**, Locasale, J.W. and Li, X. Bacteria boost mammalian host NAD metabolism by engaging the deamidated biosynthesis pathway. *Cell Metab. 2020 Mar 3;31(3):564-579.e7*
5. Kang K, Meng Q, Shats I, Umbach DM, Li M, Li Y, Li, X. and **Li, L**. CDSeq: A novel complete deconvolution method for dissecting heterogeneous samples using gene expression data. *PLoS Comput Biol*., 2019, 15(12): e1007510.
6. Li, Y., Bingham, A., Umbach, D.M., Li, Q.-J., Zhuang, Y., and **Li, L**. Putative biomarkers for tumor sample purity prediction based on gene expression data. *BMC Genomics*. 2019 Dec 27;20(1):1021. doi: 10.1186/s12864-019-6412-8.
7. Li, Y, Li M, Shats, I, Krahn, JM, Flake, GP, Umbach, D1, Li, X, **Li, L**. Glypican 6 is a putative biomarker for metastatic progression of cutaneous melanoma. *PLoS One*. 2019 Jun 14;14(6):e0218067. doi: 10.1371/journal.pone.0218067.
8. Nguyen, T.-A., Grimm, S.A., Bushel, P.R., Li, J., Li, Y., Bennett, B.D., Lavender, C.A., Ward, J.M., Fargo, D.C., Anderson, C.W., **Li, L.**, Resnick, M.A., Menendez, D. Revealing a human p53 universe. *Nucleic Acids Research*, gky720, https://doi.org/10.1093/nar/gky720.
9. Ungewitter EK, Rotgers E, Kang HS, Lichti-Kaiser K, **Li, L**, Grimm SA, Jetten AM, Yao HH. Loss of Glis3 causes dysregulation of retrotransposon silencing and germ cell demise in fetal mouse testis. *Sci Rep*. 2018 Jun 25;8(1):9662. doi: 10.1038/s41598-018-27843-x.
10. Miao, Y.-L., Gambini, A., Zhang, Y., Jefferson, W.N., Padilla-Banks, E., Bernhardt, M.L., Huang, W., **Li**, **L.**, and Williams, C.J. Mediator complex component MED13 regulates the mouse oocyte-to-embryo transition and is required for postimplantation development. *Biol Reprod.* 2018 Jan 9. doi: 10.1093/biolre/ioy004. [Epub ahead of print]
11. Roy, S., Moore, A.J., Love, C., Reddy, A., Rajagopalan, D., Dave, S., **Li, L.**, Murre, C., and Zhuang, Y. Id proteins suppress E2A-driven innate-like T cell development prior to TCR selection. *Front Immunol*. 2018 Jan 24;9:42.
12. Li, Y, Umbach, D.M., and **Li**, **L**. Putative genomic characteristics of BRAF V600K versus V600E cutaneous melanoma. *Melanoma Res. 2017 Dec;27(6):527-535.*
13. Fan, Z., Ahn, M., Roth, H.L., **Li, L**., and Vaugh, B.V. Sleep Apnea and Hypoventilation in Patients with Down Syndrome: Analysis of 144 Polysomnogram Studies. *Children (Basel).* 2017 Jun 30;4(7). pii: E55. doi: 10.3390/children4070055.
14. 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.* 2017 Jul 3;18(1):508. doi: 10.1186/s12864-017-3906-0.
15. 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, 27(4), 483–494.
16. 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.
17. 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 tristetraprolin family member ZFP36L3

identifies likely mRNA targets and an unexpected link to placental iron metabolism. *Development*, 2016, 143, 1424-1433.

18. 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 Nov 23. [Epub ahead of print].
19. Xu, Z., Niu, L., **Li**, **L**.* and Taylor, J.A.* ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. *Nucleic Acids Research*, 2015, doi: 10.1093/nar/gkv907. (**co-corresponding authors**)
20. 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, 28, 453-63.
21. 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 Blackshear1, P.J. Post-transcriptional regulation of transcript abundance by a conserved member of the tristetraprolin family in *Candida albicans*. *Mol*. *Microbiol*. 2015, 95, 1036-1053.
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https://www.ncbi.nlm.nih.gov/myncbi/leping.li.1/bibliography/public/

C. Research Support

NIH Intramural Research Support

Sources:	NIEHS Division of Intramural Research (NIH Z01 ES101765)
Title:	Bioinformatics
Role:	Principal Investigator
Dates:	05/01/2003-current