Name: Ling-Hui Li
Gender: Female
Date of Birth: 01/25/1969
Nationality: Taiwan
Address: N520, Institute of Biomedical Science, 128, Sec.2, Academia Rd. Taipei 115, Taiwan
Telephone: 886-2-27899078
Fax: 886-2-27824066
e-mail: lli@ibms.sinica.edu.tw

Present position

2012-present Associate Research Scientist, Institute of Biomedical Science, Academia Sinica
2005-present Assistant Director, National Center for Genome Medicine at Academia Sinica
2005-2011 Assistant Research Scientist, Institute of Biomedical Science, Academia Sinica

Education and Training

Education / Training:			
Institution and Location	Degree	Year	Field of study
Graduate program of Molecular and Cellular Biology, SUNY at Stony Brook, USA	Ph.D.	1993-1999	Developmental Biology
Institute of Genetics, National Yang-Ming University, Taiwan	Post-doctoral fellow	1999-2000	Cancer Genetics
Division of Molecular and Genomic Medicine, National Health Research Institutes, Taiwan	Post-doctoral fellow	2001-2005	Cancer Genomics
Institute of Biomedical Science Academic Sinica, Taiwan	Post-doctoral fellow	2005	Human Molecular Genetics

Specialty: Molecular biology, Human molecular genetics, Cancer genomics

Research Description

Our lab is primarily focusing on using Affymetrix SNP genotyping platform to investigate genomic variants in general population and psychological diseases, and chromosomal aberrations in patients with congenital malformation syndromes and cancers. We have constructed a copy number variation (CNV) map for the Han Chinese population, which is an important reference for identifying pathogenic or susceptible CNV in disease groups. We have identified *de novo* CNVs which could be responsible for the phenotypes in several patients with congenital malformation syndromes. In addition, we integrate chromosomal aberrations and differential expression of microRNA and protein-coding genes to identify cancer-related genes. Currently we are working on colorectal cancer. We have identified and validated several candidate tumor-related genes by integrative analysis. In the future, we will investigate the underlying mechanisms of these genes contributing to tumorigenesis. We will also evaluate whether the candidate genes can serve as biomarkers for diagnosis and/or disease monitoring.

Research Grant:

08/01/2007-07/31/2009 (PI) Construction of genome-wide copy number variation map in Han Chinese and its application in disease gene identification. (Grant #: NSC 96-2320-B-001-023-MY2, supported by National Science Council)

01/01/2009-12/31/2010 (PI) Identification and characterization of oncogenic miRNAs and genes involved in initiation and progression of colorectal cancer by genome-wide SNP scan. (A sub-project of an IBMS New Project Grant; supported by Institute of Biomedical Sciences, Academia Sinica)

08/01/2011-07/31/2014 (Co-PI) Study population genomics and human disease genomics using genome-wide single nucleotide polymorphism arrays, gene expression arrays and deep sequencing data. (Grant #: 100-2314-B-001-005-MY3, supported by National Science Council)

01/01/2016-12/31/2016 (PI) Identification of Genes and Oncogenic miRNAs Involved in Colorectal Cancer Susceptibility and Progression (I). (Grant #: VTA105-A-1-1, supported by Taichung Veteran Hospital and Academia Sinica)

01/01/2017-12/31/2017 (PI) Identification of Genes and Oncogenic miRNAs Involved in Colorectal Cancer Susceptibility and Progression (II). (Grant #: VTA106-A-1-1, supported by Taichung Veteran Hospital and Academia Sinica)

01/01/2018-12/31/2018 (co-PI) Developing a gut microbiota-based platform for guiding colorectal cancer screening and treatment-from animal study to pre-clinical trial (supported by Ministry of Science and Technology)

01/01/2019-12/31/2019 (co-PI) Developing a gut microbiota-based platform for guiding colorectal cancer screening and treatment-from animal study to pre-clinical trial (supported by Ministry of Science and Technology)

National Core Grant:

05/01/2012-04/30/2013 (Co-PI) National Center for Genome Medicine (II). (Grant #: NSC101-2319-B-001-001, supported by National Science Council)

05/01/2013-04/30/2014 (Co-PI) National Center for Genome Medicine (III). (Grant #: NSC102-2319-B-001-001, supported by National Science Council)

05/01/2014-04/30/2015 (Co-PI) National Center for Genome Medicine (IV). (Grant #: NSC103-2319-B-001-001, supported by National Science Council)

05/01/2015-04/30/2016 (Co-PI) National Center for Genome Medicine (I). (Grant #: MOST 104-2319-B-001-002, supported by Ministry of Science and Technology)

05/01/2016-04/30/2017 (Co-PI) National Center for Genome Medicine (II). (Grant #: MOST 105-2319-B-001-001, supported by Ministry of Science and Technology)

05/01/2017-04/30/2018 (Co-PI) National Center for Genome Medicine (II). (Grant #: MOST 106-2319-B-001-001, supported by Ministry of Science and Technology)

05/01/2018-04/30/2019 (Co-PI) National Center for Genome Medicine (II). (Grant #: MOST 107-2319-B-001-001, supported by Ministry of Science and Technology)

Academic Service

2012-2018 Committee Member of Institutional Review Board at Academia Sinica

2016-2018 Chief Executive Officer of Institutional Review Board at Academia Sinica

Publications

1. Chen, C. H., Chen, H. I., Chien, W. H., Li, L. H., Wu, Y. Y., Chiu, Y. N., Tsai, W. C., Gau, S. S. (2017) High resolution analysis of rare copy number variants in patients with autism spectrum disorder from Taiwan. Scientific Reports, 7:11919.
2. Chuang, T.P., Wang, J.Y., Jao, S.W., Wu, C.C., Chen, J.H., Hsiao, K.H., Lin, C.Y., Chen, S.H., Su, S.Y., Chen, Y.J., Chen, Y.T., Wu, D.C.*, Li, L.H.* Over-expression of AURKA, SKA3 and DSN1 contributes to colorectal adenoma to carcinoma progression. Oncotarget 2016; 7(29):45803-45818. (Co-corresponding author)
3. Lin, Y.-F., Li, L.-H., Lin, C.-H., Tsou, M.-H., Chuang, M.-T.K., Wu, K.-M., Liao, T.-L., Li, J.-C., Wang, W.-J., Tomita, A., Tomita, B., Huang, S.-F., and Tsai, S.-F. (2016). Selective Retention of an Inactive Allele of the DKK2 Tumor Suppressor Gene in Hepatocellular Carcinoma. PLoS Genetics 12, e1006051
4. Yin, C.-L.[#], Chen, H.-I.[#], Li, L.-H.[#], Chien, Y.-L., Liao, H.-M., Chou, M.C., Chou, W.-J., Tsai, W.-C., Chiu, Y.-N., Wu, Y.-Y., Lo, C.-Z., Wu, J.-Y., Chen, Y.-T., and Gau, S.S.-F. (2016). Genome-wide analysis of copy number variations identifies PARK2 as a candidate gene for autism spectrum disorder. Molecular Autism 7, 23. (Co-first authors)
5. Huang, M.-C., Chuang, T.-P., Chen, C.-H., Wu, J.-Y., Chen, Y.-T., Li, L.-H.*, and Yang, H.-C*. (2016). An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays. BMC Genomics 17, 266. (Co-corresponding authors)
6. Lin, D.S., Chuang, T.P., Chiang, M.F., Ho, C.S., Hsiao, C.D., Huang, Y.W., Wu, T.Y., Wu, J.Y., Chen, Y.T., Chen, T.C., and Li, L.H.* (2014). De novo MECP2 duplication derived from paternal germ line result in dysmorphism and developmental delay. Gene 533, 78-85.
7. Chiu, L.-Y., Kishnani, P.S., Chuang, T.-P., Tang, C.-Y., Liu, C.-Y., Bali, D., Koeberl, D., Austin, S., Boyette, K., Weinstein, D.A., Murphy, E., Yao, A., Chen, Y.-T., and Li, L.-H.* (2014). Identification of differentially expressed microRNAs in human hepatocellular adenoma associated with type I glycogen storage disease: a potential utility as biomarkers. Journal of gastroenterology 49, 1274-1284.
8. Lin, Y.C., Lee, Y.C., Li, L.H., Cheng, C.J., and Yang, R.B. (2013). Tumor suppressor SCUBE2 inhibits breast-cancer cell migration and invasion through the reversal of epithelial-mesenchymal transition. Journal of cell science.
9. Yang, H.C., Lin, H.C., Kang, M., Chen, C.H., Lin, C.W., Li, L.H., Wu, J.Y., Chen, Y.T., and Pan, W.H. (2011). SAQC: SNP Array Quality Control. BMC Bioinformatics 12, 100.
10. Lin, C.H., Lin, J.K., Chang, S.C., Chang, Y.H., Chang, H.M., Liu, J.H., Li, L.H., Chen, Y.T., Tsai, S.F., and Chen, W.S. (2011). Molecular profile and copy number analysis of sporadic colorectal cancer in Taiwan. Journal of biomedical science 18, 36.
11. Yang, H.C., Lin, H.C., Huang, M.C., Li, L.H., Pan, W.H., Wu, J.Y., and Chen, Y.T. (2010). A new analysis tool for individual-level allele frequency for genomic studies. BMC Genomics

11, 415.

12. Wu, I.C., Wu, D.C., Huang, C.C., Lin, H.S., Chen, Y.K., Tsai, H.J., Lu, C.Y., Chou, S.H., Chou, Y.P., Li, L.H., Tai, S.Y., and Wu, M.T. (2010). Plasma decorin predicts the presence of esophageal squamous cell carcinoma. Int J Cancer 127, 2138-2146.
13. Shiao, Y.M., Lee, C.C., Hsu, Y.H., Huang, S.F., Lin, C.Y., Li, L.H., Fann, C.S., Tsai, C.Y., Tsai, S.F., and Chiu, H.C. (2010). Ectopic and high CXCL13 chemokine expression in myasthenia gravis with thymic lymphoid hyperplasia. J Neuroimmunol 221, 101-106.
14. Chien, S.C., Li, Y.C., Li, L.H., Wu, J.Y., Hsu, P.C., Shi, S.L., Tsai, F.J., and Lin, C.C. (2010). A new familial insertion, ins(18;9)(q12.2;q33.1q31.1) with a 9q31.1-9q33.1 deletion in a girl with a cleft lip and palate. Am J Med Genet A 152A, 1862-1867.
15. Chen, Y.K., Chang, W.S., Wu, I.C., Li, L.H., Yang, S.F., Chen, J.Y., Hsu, M.C., Chen, S.H., Wu, D.C., Lee, J.M., Huang, C.H., Goan, Y.G., Chou, S.H., Huang, C.T., and Wu, M.T. (2010). Molecular characterization of invasive subpopulations from an esophageal squamous cell carcinoma cell line. Anticancer Res 30, 727-736.
16. Chang, C.F., Li, L.H., Wang, C.H., Tsai, F.J., Chen, T.C., Wu, J.Y., Chen, Y.T., and Tsai, A.C. (2010). Identification of a submicroscopic 3.2 Mb chromosomal 16q12.2-13 deletion in a child with short stature, mild developmental delay, and craniofacial anomalies, by high-density oligonucleotide array-a recognizable syndrome. Am J Med Genet A 152A, 2365-2371.
17. Wu, K.M., Li, L.H., Yan, J.J., Tsao, N., Liao, T.L., Tsai, H.C., Fung, C.P., Chen, H.J., Liu, Y.M., Wang, J.T., Fang, C.T., Chang, S.C., Shu, H.Y., Liu, T.T., Chen, Y.T., Shiau, Y.R., Lauderdale, T.L., Su, I.J., Kirby, R., and Tsai, S.F. (2009). Genome sequencing and comparative analysis of Klebsiella pneumoniae NTUH-K2044, a strain causing liver abscess and meningitis. J Bacteriol 191, 4492-4501.
18. Kishnani, P.S., Chuang, T.P., Bali, D., Koeberl, D., Austin, S., Weinstein, D.A., Murphy, E., Chen, Y.T., Boyette, K., Liu, C.H., Chen, Y.T., and Li, L.H.* (2009). Chromosomal and genetic alterations in human hepatocellular adenomas associated with type Ia glycogen storage disease. Hum Mol Genet 18, 4781-4790.
19. Yang, H.C., Huang, M.C., Li, L.H., Lin, C.H., Yu, A.L., Diccianni, M.B., Wu, J.Y., Chen, Y.T., and Fann, C.S. (2008). MPDA: microarray pooled DNA analyzer. BMC Bioinformatics 9, 196.
20. Lin, C.H., Li, L.H., Ho, S.F., Chuang, T.P., Wu, J.Y., Chen, Y.T., and Fann, C.S. (2008). A large-scale survey of genetic copy number variations among Han Chinese residing in Taiwan. BMC Genet 9, 92.
21. Lin, C.H., Huang, M.C., Li, L.H., Wu, J.Y., Chen, Y.T., and Fann, C.S. (2008). Genome-wide copy number analysis using copy number inferring tool (CNIT) and DNA pooling. Hum Mutat 29, 1055-1062.
22. Huggins, R., Li, L.H., Lin, Y.C., Yu, A.L., and Yang, H.C. (2008). Nonparametric estimation of LOH using Affymetrix SNP genotyping arrays for unpaired samples. J Hum Genet 53, 983-990.
23. Yang, H.C., Liang, Y.J., Huang, M.C., Li, L.H., Lin, C.H., Wu, J.Y., Chen, Y.T., and Fann, C.S. (2006). A genome-wide study of preferential amplification/hybridization in

microarray-based pooled DNA experiments. Nucleic Acids Res 34, e106.

24. Li, L.H., Ho, S.F., Chen, C.H., Wei, C.Y., Wong, W.C., Li, L.Y., Hung, S.I., Chung, W.H., Pan, W.H., Lee, M.T., Tsai, F.J., Chang, C.F., Wu, J.Y., and Chen, Y.T. (2006). Long contiguous stretches of homozygosity in the human genome. Hum Mutat 27, 1115-1121.
25. Chen, Y.T., Shu, H.Y., Li, L.H., Liao, T.L., Wu, K.M., Shiau, Y.R., Yan, J.J., Su, I.J., Tsai, S.F., and Lauderdale, T.L. (2006). Complete Nucleotide Sequence of pK245, a 98-Kilobase Plasmid Conferring Quinolone Resistance and Extended-Spectrum-{beta}-Lactamase Activity in a Clinical Klebsiella pneumoniae Isolate. Antimicrob Agents Chemother 50, 3861-3866.
26. Liu, Y.F., Chen, W.M., Lin, Y.F., Yang, R.C., Lin, M.W., Li, L.H., Chang, Y.H., Jou, Y.S., Lin, P.Y., Su, J.S., Huang, S.F., Hsiao, K.J., Fann, C.S., Hwang, H.W., Chen, Y.T., and Tsai, S.F. (2005). Type II collagen gene variants and inherited osteonecrosis of the femoral head. N Engl J Med 352, 2294-2301.
27. Chou, T.Y., Chiu, C.H., Li, L.H., Hsiao, C.Y., Tzen, C.Y., Chang, K.T., Chen, Y.M., Perng, R.P., Tsai, S.F., and Tsai, C.M. (2005). Mutation in the tyrosine kinase domain of epidermal growth factor receptor is a predictive and prognostic factor for gefitinib treatment in patients with non-small cell lung cancer. Clin Cancer Res 11, 3750-3757.
28. Li, L.H., Li, J.C., Lin, Y.F., Lin, C.Y., Chen, C.Y., and Tsai, S.F. (2004). Genomic shotgun array: a procedure linking large-scale DNA sequencing with regional transcript mapping. Nucleic Acids Res 32, e27.
29. Jong, Y.J., Li, L.H., Tsou, M.H., Chen, Y.J., Cheng, S.H., Wang-Wuu, S., Tsai, S.F., Chen, C.M., Huang, A.T., Hsu, M.T., and Lin, C.H. (2004). Chromosomal comparative genomic hybridization abnormalities in early- and late-onset human breast cancers: correlation with disease progression and TP53 mutations. Cancer Genet Cytogenet 148, 55-65.
30. Huang, S.F., Liu, H.P., Li, L.H., Ku, Y.C., Fu, Y.N., Tsai, H.Y., Chen, Y.T., Lin, Y.F., Chang, W.C., Kuo, H.P., Wu, Y.C., Chen, Y.R., and Tsai, S.F. (2004). High frequency of epidermal growth factor receptor mutations with complex patterns in non-small cell lung cancers related to gefitinib responsiveness in Taiwan. Clin Cancer Res 10, 8195-8203.
31. Chang, Y.T., Shiao, Y.M., Chin, P.J., Liu, Y.L., Chou, F.C., Wu, S., Lin, Y.F., Li, L.H., Lin, M.W., Liu, H.N., and Tsai, S.F. (2004). Genetic polymorphisms of the HCR gene and a genomic segment in close proximity to HLA-C are associated with patients with psoriasis in Taiwan. Br J Dermatol 150, 1104-1111.
32. Vander Zwan, C.J., Wheeler, J.C., Li, L.H., Tracey, W.D., and Gergen, J.P. (2003). A DNA-binding-independent pathway of repression by the Drosophila Runt protein. Blood Cells Mol Dis 30, 207-222.
33. Li, L.H., and Gergen, J.P. (1999). Differential interactions between Brother proteins and Runt domain proteins in the Drosophila embryo and eye. Development 126, 3313-3322.
34. Aimes, R.T., Li, L.H., Weaver, B., Hawkes, S., Hahn-Dantona, E.A., and Quigley, J.P. (1998). Cloning, expression, and characterization of chicken tissue inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed chicken embryo fibroblasts. J Cell Physiol 174, 342-352.
35. Golling, G., Li, L., Pepling, M., Stebbins, M., and Gergen, J.P. (1996). Drosophila homologs of

the proto-oncogene product PEBP2/CBF beta regulate the DNA-binding properties of Runt. Mol Cell Biol 16, 932-942.