

Curriculum Vitae



Name: Ben-Yang Liao, PhD Email: liaoby@nhri.org.tw
Tel: 886-37-246166 ext. 36118 Fax: 886-37-586-467
Address: Institute of Population Health Sciences,
National Health Research Institutes,
35, Keyan Road, Zhunan,
Miaoli County 350, Taiwan, R.O.C.

EDUCATION

Ph.D. in Ecology & Evolutionary Biology	University of Michigan, Ann Arbor, MI Advisor: Dr. Jianzhi George Zhang	2004-2008
M.S. in Zoology	National Taiwan University, Taipei, Taiwan	2000-2002
B.S. in Biology	National Taiwan Normal University, Taipei, Taiwan	1994-1998

PROFESSIONAL/ACADEMIC APPOINTMENT

<i>Investigator,</i>		(2018-present)
<i>Associate Investigator,</i>		(2013-2017)
<i>Assistant Investigator,</i> Institute of Population Health Sciences, National Health Research Institutes, Taiwan		(2008-2012),
<i>Rackham Predoctoral Fellow,</i> University of Michigan, Ann Arbor		(2007-2008)
<i>Graduate Student Research Assistant,</i> University of Michigan, Ann Arbor		(2006-2007)
<i>Graduate Student Instructor,</i> University of Michigan, Ann Arbor		(2005-2006)
<i>Research Assistant,</i> Institute of Biomed. Sci., Academia Sinica, Taiwan		(2002-2004)
<i>Teaching Assistant,</i> National Taiwan University, Taiwan		(2000-2002)

HONORS & AWARDS

<i>Junior Research Investigator Award,</i> Academia Sinica, ROC	(2018)
<i>Ta-You Wu Memorial Award,</i> Ministry of Science and Technology, ROC	(2015)
<i>Research Achievement Award for Junior Research Investigator,</i> N.H.R.I.	(2013)
<i>Rackham Predoctoral Fellowship,</i> University of Michigan	(2007-2008)
<i>Rackham Graduate School Travel Grant,</i> University of Michigan	(2007)
<i>Annual Symposium Travel Grant,</i> American Genetic Association	(2007)
<i>Dean's Award for Graduate Research,</i> College of Science, National Taiwan University	(2002)

EXTRAMURAL GRANT SUPPORT

§ Active support

2020-2023 P.I. Ministry of Science and Technology (MOST 109-2628-B-400-005-)
*On the evolutionary significance of "transcriptome-phenome comodularity": Bioinformatic investigations and application to the Nile grass rat (*Arvicanthis niloticus*) transcriptome project*

§ Previous support

- 2016-2020 P.I. Ministry of Science and Technology (MOST 105-2314-B-400-021-MY4)
Biological significance and molecular bases underlying alterations in gene expression following
- 2015-2018 P.I. Ministry of Science and Technology (MOST 104-2311-B-400-002-MY3)
Bioinformatic exploration of the Eukaryotic phenomes – evolutionary analyses and tool development
- 2012-2015 P.I. Ministry of Science and Technology (MOST 101-2311-B-400-001-MY3)
Exploring the significance of epigenetic factors to expression evolution of Eukaryotic genes
- 2011-2012 Co-P.I. (30%) National Science Council (NSC100-2319-B-400-001)
(P.I., I-Shou Chang, National Institute of Cancer Research, Natl. Health Res. Inst.)
Taiwan Bioinformatics Institute Core Facility Program project and Unit1: Statistical Genetics
- 2010-2012 P.I. National Science Council, Taiwan (NSC99-2311-B-400-003-MY2)
Regulatory evolution of eukaryotic genes: causes, consequences and mechanisms
- 2010-2011 Co-P.I. (20%) National Science Council (NSC99-2221-E-001-021)
(P.I., Chen-Hsiang Yeang, Institute of Statistical Science, Academia Sinica)
Analysis of the dependent evolution of biomolecular networks

ACADEMIC SERVICES**§ Editorship for Journals**

- Associate Editor, *BMC Ecology and Evolution* 2021-present
- Associate Editor, *Frontiers in Ecology and Evolution* 2021-present
Frontiers in Genetics
- Review Editor, *Frontiers in Ecology and Evolution* 2016-present
Frontiers in Genetics

§ Ad hoc Reviewer for Journals

Bioinformatics; BMC Complementary and Alternative Medicine; BMC Biology; BMC Evolutionary Biology; BMC Genomics; Briefings in Bioinformatics; Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics; Frontiers in Ecology and Evolution; Frontiers in Genetics ; Gene; Genome Biology; Genome Biology and Evolution; Genome Research; Molecular Biology and Evolution; Molecular Biology Reports; Molecular Ecology; Nature Communications; Nature Ecology & Evolution; Nucleic Acids Research; PLoS Computational Biology; PLoS Genetics; PLoS Neglected Tropical Diseases; PLoS ONE; Proceedings of the National Academy of Sciences of the United States of America; Proceedings of the Royal Society B; Scientific Reports

§ Reviewer for Book Chapters or Conference Proceedings

*IEEE International Conference on Bioinformatics and Bioengineering (BIBE 2009);
Handbook of Statistical Bioinformatics, Springer*

§ Reviewer for Awards

College Student Research Award, Ministry of Science and Technology, Taiwan, 2017

Taiwan Tech Trek (TTT) Award, Ministry of Science and Technology, Taiwan, 2016

§ Reviewer for Grant Proposal

Research Grant Proposals, Ministry of Science and Technology, Taiwan, 2019-present

National Science and Technology Development Fund, Executive Yuan, R.O.C., 2017

College Student Participation in Research Projects, Ministry of Science and Technology, Taiwan, 2016

The National Science Center (Narodowe Centrum Nauki), Poland, 2014; 2019

PROFESSIONAL SOCIETIES

American Society of Human Genetics (ASHG); Society for Molecular Biology and Evolution (SMBE);

International Society for Computational Biology (ISCB)

INVITED TALKS/SEMINARS/LECTURES

1. Invited Seminar, Inst. Genomics & Bioinformatics, Natl. Chung Hsing Univ., Taiwan, Nov 19, 2021
2. Invited Seminar, Dept. Life Sciences, National Central University, Taiwan, Oct 19, 2021
3. Invited Seminar, Inst. Ecology & Evol. Biology, National Taiwan University, Taiwan, April 30, 2021
4. Invited Seminar, TIGP-Bioinformatics Program., Academia Sinica, Taipei, Taiwan, Dec 3, 2020
5. Invited seminar, Dept Biotech. & Bioind. Sci., Natl. Cheng-Kung Univ., Tainan, Taiwan, March 30, 2020
6. Invited seminar, Dept of Life Science, Natl. Taiwan Univ., Taipei, Taiwan, March 13, 2020
7. Invited Talk, 中國統計學社社員大會暨統計學術研討會, Hsin-Chu, Taiwan, Dec 14, 2019
8. Invited Lecture, 生命科學院生物醫學講座, Natl. Yang-Ming Univ., Taipei, Taiwan, May 15, 2019
9. Invited Seminar, TIGP-Bioinformatics Program., Academia Sinica, Taipei, Taiwan, May 9, 2019
10. Invited Talk, Congress of Animal Behavior and Ecology, Taipei, Taiwan, Jan 21, 2019
11. Invited Lecture, Dept of Mol. Biol. & Human Genet., Tzu-Chi Univ., Taiwan, May 21, 2018
12. Invited Speaker, *International Symposium on Evolutionary Genomics and Bioinformatics (ISEGB 2017)*, Taiwan, November 2017.
13. Invited seminar, Dept of Life Science, Natl. Taiwan Normal Univ, Taiwan, Sept 30 2016
14. Invited Speaker, *The 1st Young Scientists' Forum in Evolutionary Genetics*, Kunming, China, July 2016
15. Invited Lecture, Kunming Institute of Zoology, Chinese Academy of Sciences, China, July 2016
16. Institute of Bioinformatics and Biosignal Transduction, Natl. Cheng-Kung Univ., Taiwan, April 2016
17. Invited speaker, *Taiwan Soc. Evol. & Comput. Biol. Mini-symposium*, Tainan, Taiwan, Jan 2016
18. Genomics Research Center, Academia Sinica, Taiwan, June 2015.
19. Taiwan International Graduate Program (TIGP), Academia Sinica, Taiwan, April 2014.

20. Institute of Systems Biology and Bioinformatics, National Central University, Taiwan, May 2013
21. Invited speaker, *The 6th Annual World Protein and Peptide Conference*, Suzhou, China, March 2013.
22. Invited speaker, *The 2nd Symp. on Evol. Genomics and Bioinformatics*, Taiwan, October 2012.
23. Institute of Statistical Science, Academia Sinica, Taiwan, January 2012.
24. Institute of Zoology, National Taiwan University, Taiwan, October 2011.
25. Guest Lecture on *Molecular Evolution*, National Yang-Ming University, Taiwan, November 2010.
26. Guest Lecture on *Molecular Evolution*, National Taiwan University, Taiwan, May 2010.
27. Institute of Biomedical Informatics, National Yang-Ming University, Taiwan, April 2010.
28. Taiwan International Graduate Program (TIGP), Academia Sinica, Taiwan, April 2009.
29. Division of Biostatistics & Bioinformatics, National Health Research Institute, Taiwan, December 2007.
30. *Michigan Symposium of Genomic Biology*, Ann Arbor, Michigan, USA, April 2007.
31. Department of Biostatistics, University of Michigan, Ann Arbor, USA, March 2006.

JOURNAL ARTICLES (*corresponding author)

1. Kuei-Yuan Lan, Ben-Yang Liao* (2022) Epigenomic signatures on paralogous genes reveal underappreciated universality of active histone codes adopted across animals. *Comput. Struct. Biotechnol. J.*, **in press**.
2. Ben-Yang Liao* (2021) Young duplicate genic DNA (News & Views). *Nature Ecol. Evol.*, **in press**.
3. Wei-Kai Wu, Suraphan Panyod, Po-Yu Liu, Chieh-Chang Chen, Hsien-Li Kao, Hsiao-Li Chuang, Ying-Hsien Chen, Hsin-Bai Zou, Han-Chun Kuo, Ching-Hua Kuo, Ben-Yang Liao, Tina Chiu, Ching-Hu Chung, Angela Y. Lin, Yi-Chia Lee, Sen-Lin Tang, Jin-Town Wang, Yu-Wei Wu, Cheng-Chih Hsu, Lee-Yan Sheen, Alexander N. Orekhov, Ming-Shiang Wu*. (2020) Characterization of TMAO productivity from carnitine challenge facilitates personalized nutrition and microbiome signatures discovery. *Microbiome* **8**: 162.
4. Andrew Y. Chang and Ben-Yang Liao*. (2020) Reduced translational efficiency of Eukaryotic genes after duplication Events. *Mol Biol Evol.* **37**: 1452-1461.
5. Min R. Lu, Cheng-Kuo Lai, Ben-Yang Liao, Isheng J. Tsai*. (2020) Comparative transcriptomics across Nematode life cycles reveal gene expression conservation and correlated evolution in adjacent developmental stages. *Genome Biol. Evol.* **12**: 1019-1030.
6. Chia-Yin Chiang, Yung-Hao Ching, Ting-Yan Chang, Liang-Shuan Hu, Yee Siang Yong, Pei Ying Keak, Ivana Mustika, Ming-Der Lin*, Ben-Yang Liao*. 2020. Novel eye genes systematically discovered through an integrated analysis of mouse transcriptomes and phenome. *Comput. Struct. Biotechnol. J.* **18**: 73-82

7. Wei-Kai Wu, Chieh-Chang Chen, Po-Yu Liu, Suraphan Panyod, Ben-Yang Liao, Pei-Chen Chen, Hsien-Li Kao, Han-Chun Kuo, Ching-Hua Kuo, Tina Chiu, Rou-An Chen, Hsiao-Li Chuang, Yen-Te Huang, Hsin-Bai Zou, Cheng-Chih Hsu, Ting-Yan Chang, Chin-Lon Lin, Chi-Tang Ho, Hon-Tsen Yu, Lee-Yan Sheen, Ming-Shiang Wu*. 2019. Identification of TMAO-producer phenotype and host–diet–gut dysbiosis by carnitine challenge test in human and germ-free mice. *Gut* **68**: 1439-1449
8. Tze-Ho Chen, Gwo-Chin Ma, Wen-Hsiang Lin, Dong-Jay Lee, Sheng-Hai Wu, Ben-Yang Liao, Ming Chen*, Liang-Kong Lin* (2019, Mar). Genome-wide microarray analysis suggests transcriptomic response may not play a major role in high- to low-altitude acclimation in harvest mouse (*Micromys minutus*). *Animals (Basel)* **9**: 92.
9. Yu-Ting Lai, Carol K. L. Yeung, Kevin E. Omland, Er-Li Pang, Yu Hao, Ben-Yang Liao, Hui-Fen Cao, Bo-Wen Zhang, Chia-Fen Yeh, Chih-Ming Hung, Hsin-Yi Hung, Ming-Yu Yang, Wei Liang, Yu-Cheng Hsu, Cheng-Te Yao, Lu Dong, Kui Lin, and Shou-Hsien Li*. 2019. Standing genetic variation as the predominant source for adaptation of a songbird. *Proc. Natl. Acad. Sci. USA* **116**: 2152-2157.
10. Andrew Y.-F. Chang and Ben-Yang Liao*. 2017. Recruitment of histone modifications to assist mRNA dosage maintenance after degeneration of cytosine DNA methylation during animal evolution. *Genome Res.* **27**: 1513-1524.
11. Meng-Pin Weng and Ben-Yang Liao*. 2017. *modPhEA*: model organism phenotype enrichment analysis on eukaryotic gene sets. *Bioinformatics* **33**: 3505-3507.
12. Chia-Hsin Hsu, Austin Chiang, Ming-Jing Hwang* and Ben-Yang Liao*. 2016. Proteins with highly evolvable domain architectures are nonessential but highly retained. *Mol. Biol. Evol.* **33**: 1219-1230.
13. Ben-Yang Liao* and Meng-Pin Weng. 2016. Functionalities of expressed mRNAs revealed from mutant phenotypes. *Wiley Interdiscip. Rev. RNA* **7**: 416-427
14. Kuei-Han Lin[†], Ben-Yang Liao[†], Hao-Wei Chang[†], Shiao-Wei Huang, Ting-Yan Chang, Cheng-Yu Yang, Yu-Bin Wang, Kirk Yu-The Lin, Sen-Lin Tang*, Hon-Tsen Yu*. 2015. Metabolic characteristics of dominant microbes and key rare species from an acidic hot spring in Taiwan revealed by metagenomics. *BMC Genomics* **16**: 1029. ([†]co-first author)
15. Ben-Yang Liao* and Meng-Pin Weng. 2015. Unraveling the association between mRNA expressions and mutant phenotypes in a genome-wide assessment of mice. *Proc. Natl. Acad. Sci. USA* **112**: 4707-4712.
16. Ben-Yang Liao* and Andrew Y.-F. Chang. 2014. Accumulation of CTCF binding sites in between drives expression divergence of tandemly duplicated genes in the human genome. *BMC Genomics* **15** (Suppl 1): S8.

17. Ting-Yan Chang and Ben-Yang Liao*. 2013. Flagellated algae protein evolution suggests the prevalence of lineage-specific rules governing evolutionary rates of eukaryotic proteins. *Genome Biol. Evol.* **5**: 913-922.
18. De-Hua Chen, Andrew Y.-F. Chang, Ben-Yang Liao and Chen-Hsiang Yeang*. 2013. Functional characterization of motif sequences under purifying selection. *Nucleic Acids Res.* **41**: 2105-2120.
19. Ben-Yang Liao* and Meng-Pin Weng. 2012. Natural selection drives rapid evolution of mouse embryonic heart enhancers. *BMC Systems Biol.* **6** (Suppl 2): S1.
20. Feng-Chi Chen*, Ben-Yang Liao*, Chia-Lin Pan, Hsuan-Yu Lin, Andrew Y.-F. Chang. 2012. Assessing evolutionary rate determinants of mammalian exons. *Mol. Biol. Evol.* **29**: 3121-3129.
21. Meng-Shin Shiao[†], Andrew Y.-F. Chang[†], Ben-Yang Liao, Yung-Hao Ching, Wen-Hsiung Li*. 2012. Transcriptomes of mouse olfactory epithelium reveal sexual differences in odorant detection. *Genome Biol. Evol.* **4**: 703-712.
22. Jian-Rong Yang, Ben-Yang Liao, Shi-Mei Zhuang and Jianzhi Zhang*. 2012. Protein misinteraction avoidance causes highly expressed proteins to evolve slowly. *Proc. Natl. Acad. Sci. USA* **109**: e831-840
23. Andrew Y.-F. Chang and Ben-Yang Liao*. 2012. DNA methylation rebalances gene dosage after mammalian gene duplications. *Mol. Biol. Evol.* **29**: 133-144.
24. Ben-Yang Liao* and Andrew Y.-F. Chang. 2012. Mammalian genes preferentially co-retained in radiation hybrid panels tend to avoid co-expression. *PLoS ONE* **7**: e32284.
25. Meng-Pin Weng and Ben-Yang Liao*. 2011. DroPhEA: *Drosophila* phenotype enrichment analysis for insect functional genomics. *Bioinformatics* **27**: 3218-3219.
26. Chun-Hsi Chen, Ben-Yang Liao* and Feng-Chi Chen*. 2011. Exploring the selective constraint on the sizes of insertions and deletions in 5' untranslated regions in mammals. *BMC Evol. Biol.* **11**: 192.
27. Zhi Wang, Ben-Yang Liao and Jianzhi Zhang*. 2010. Genomic patterns of pleiotropy and the evolution of complexity. *Proc. Natl. Acad. Sci. USA* **107**: 18034-18039.
28. Wenfeng Qian[†], Ben-Yang Liao[†], Andrew Y.-F. Chang and Jianzhi Zhang*. 2010. Maintenance of duplicate genes and their functional redundancy by reduced expression. *Trends Genet.* **26**: 425-430. (†co-first author)
29. Meng-Pin Weng and Ben-Yang Liao*. 2010. MamPhEA: a web tool for mammalian phenotype enrichment analysis. *Bioinformatics* **26**: 2212-2213.
30. Ben-Yang Liao*, Meng-Pin Weng and Jianzhi Zhang*. 2010. Contrasting genetic paths to morphological and physiological evolution. *Proc. Natl. Acad. Sci. USA* **107**: 7353-7358.

31. Ben-Yang Liao*, Meng-Pin Weng and Jianzhi Zhang. 2010. Impact of extracellularity on the evolutionary rate of mammalian proteins. *Genome Biol. Evol.* **2**: 39-43.
32. Chun-Hsi Chen, Trees-Juen Chuang, Ben-Yang Liao and Feng-Chi Chen*. 2009. Scanning for the signatures of positive selection for human-specific insertions and deletions. *Genome Biol. Evol.* **1**: 415-419.
33. Ben-Yang Liao and Jianzhi Zhang*. 2008. Coexpression of linked genes in mammalian genomes is generally disadvantageous. *Mol. Biol. Evol.* **25**: 1555-1565.
34. Ben-Yang Liao and Jianzhi Zhang*. 2008. Null mutations in human and mouse orthologs frequently result in different phenotypes. *Proc. Natl. Acad. Sci. USA* **105**: 6987-6992.
35. Meng-Shin Shiao, Ben-Yang Liao, Manyuan Long* and Hon-Tsen Yu. 2008. Adaptive evolution of the insulin two-gene system in mouse. *Genetics* **178**: 1683-1691.
36. Ben-Yang Liao and Jianzhi Zhang*. 2007. Mouse duplicate genes are as essential as singleton genes. *Trends Genet.* **23**: 378-381.
37. Ben-Yang Liao, Nicole M. Scott and Jianzhi Zhang*. 2006. Impacts of gene essentiality, expression pattern, and gene compactness on the evolutionary rate of mammalian proteins. *Mol. Biol. Evol.* **23**: 2072-2080.
38. Ben-Yang Liao and Jianzhi Zhang*. 2006. Low rates of expression-profile divergence in highly-expressed genes and tissue-specific genes during mammalian evolution. *Mol. Biol. Evol.* **23**: 1119-1128.
39. Ben-Yang Liao and Jianzhi Zhang*. 2006. Evolutionary conservation of expression profiles between human and mouse orthologous genes. *Mol. Biol. Evol.* **23**: 530-540.
40. Ben-Yang Liao, Yu-Jung Chang, Jan-Ming Ho and Ming-Jing Hwang*. 2004. The UniMarker (UM) method for synteny mapping of large genomes. *Bioinformatics* **20**: 3156-3165.