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Investigator

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Education

- 1998
B.S. in Biology,
National Taiwan Normal University, Taiwan
- 2002
M.A. in Zoology,
National Taiwan University, U.S.A.
- 2008
Ph.D. in Ecology and Evolutionary Biology,
University of Michigan, Ann Arbor, U.S.A.

Professional Experiences

- 2018/01-present
Institute of Population Health Sciences, National Health Research
Institutes, Taiwan
Investigator
- 2013/01-2017/12
Institute of Population Health Sciences, National Health Research
Institutes, Taiwan
Associate Investigator
- 2008/9-2012/12
Institute of Population Health Sciences, National Health Research
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Assistant Investigator
- 2007/09-2008/08
University of Michigan, Ann Arbor, U.S.A.
Rackham Predoctoral Fellow

Research Interests

Bioinformatics; Comparative genomics and transcriptomics; Epigenomics;
Molecular evolution; Mammalian genetics; Functional genomics of model
organisms; Metagenomics

Recent Publications

The Full List of Publications at NHRI:

<http://ir.nhri.org.tw/handle/3990099045/3729>

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.*,
in press. doi: 10.1101/gr.221739.117.

Meng-Pin Weng and **Ben-Yang Liao***. 2017. modPhEA: model organism
phenotype enrichment analysis on eukaryotic gene sets.
Bioinformatics, in press. doi: 10.1093/bioinformatics/btx426.

Chia-Hsin Hsu, Austin Chiang, Ming-Jing Hwang* and **Ben-Yang Liao***. 2015. Proteins with highly evolvable domain architectures are non-essential but highly retained. *Mol. Biol. Evol.* 33:1219-30.

Ben-Yang Liao* and Meng-Pin Weng. 2015. Functionalities of expressed mRNAs revealed from mutant phenotypes. *Wiley Interdiscip Rev RNA* 7:416-27

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)

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.

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.

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.

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.

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.

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.

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.

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

Andrew Y.-F. Chang and **Ben-Yang Liao***. 2012. DNA methylation rebalances gene dosage after mammalian gene duplications. *Mol.*

Biol. Evol. 29: 133-144.

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.