CURRICULUM VITAE

WEN-YA KO PhD (可文亞)

Associate Professor
Department of Life Sciences and Institute of Genome Sciences,
National Yang Ming Chiao Tung University
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EDUCATION

Ph.D.	Biology (Molecular Evolutionary Biology option), Pennsylvania State University, 2007 Advisor: Dr. Hiroshi Akashi Thesis title: Molecular phylogeny and evolution in the *Drosophila melanogaster* species subgroup
M.S.	Biology, Tunghai University, Taiwan, Advisors: Drs. Paul S. Alexander and Liang-Kong Lin Thesis title: Reproductive cycle of the house bat, *Pipistrellus abramus*, in south Taiwan
B.S.	Biology, Tunghai University, Taiwan

AWARDS AND HONORS

Japan Society for the Promotion of Science (JSPS) Postdoctoral Fellowship for Foreign Researchers, 2013-2015

Trainee Research Semifinalist Award for the 60th annual meeting of the American Society of Human Genetics (ASHG), Washington DC, USA, November 2 - 6 2010

Postdoctoral Research Travel Award for the Society of Molecular Biology and Evolution (SMBE), Lyon, France, July 4 - 8 2010

Burroughs Wellcome Travel Scholarship for Ecology and Evolution of Infectious Diseases (EEID) Meeting, Atlantic City, New Jersey March 22-25, 2010

Biology Graduate Student Research Excellence Awards, Pennsylvania State University, 2006

TECHNICAL SKILLS AND PROFICIENCIES

Computational skills: programming in Perl, and R languages.

Analytical skills: allele frequency spectrum-based analysis, LD analysis, within- and between-species sequence analysis using high-throughput and next-generation genomic data, whole-genome genotyping data analysis, phylogenetic analysis, coalescent-based simulation on modeling DNA sequence evolution

Laboratory skills: restriction enzyme digestion of DNA, DNA ligation, real-time PCR, and dye-terminator sequencing, fluorescent labeling for protein, western-blotting, animal cell culture.

PROFESSIONAL EXPERIENCE:

Associate Professor, Department of Life Sciences and Institute of Genome Sciences, National Yang Ming Chiao Tung University, Taiwan Aug 2021 – present

Assistant Professor, Department of Life Sciences and Institute of Genome Sciences, National Yang-Ming University, Taiwan Aug 2014 – July 2021

JSPS Research Fellow, Center of Genomic Medicine, Graduate School of Medicine, Kyoto University, Japan Sep 2013 – July 2014

Auxiliary Researcher, Research Center of Biodiversity and Genetic Resources (CIBIO) Campus Agrário de Vairão, University of Porto Dec 2012 – Sep 2013

Postdoctoral Researcher, Dept. of Genetics at the School of Medicine, University of Pennsylvania Jun 2007 – Nov 2012

Teaching Assistant, Department of Biology, Pennsylvania State University

- Population Genetics
- Molecular Evolution
- Genetics
- Biology of Molecules and Cell

Research Assistant, Section of Integrative Biology, University of Texas at Austin Jul 1999 – May 2000

- Molecular phylogeny of fireflies in North America

Research Assistant, Department of Biology, Tunghai University, Taiwan Jan 1999 - Jun 1999

- Species investigation of bats in Taiwan
- Dynamics of species compositions of small mammals in Ta-Ta-Jia,Yushan National Park, Taiwan

Research Assistant, Molecular Oncology Laboratory, Department of Education and Research, Taichung Veterans General Hospital, Taichung, Taiwan 1997 - 1998

- Apoptosis in neuroblastoma cells induced by hydrogen peroxide

COURSES TAUGHT

- Principles and Practice of Biostatistics (3 credits)
- Molecular Population Genetics and Genomic Data Analysis (In English) (3 credits)
- Introductory Ecology and Evolutionary Biology (In English) (3 credits)
- Genetics (population genetics part) (3 credits)
- General Biology (evolution part) (4 credits)
- Methods in phylogenetic analysis (workshop)
- Seminar in Molecular Biology (2 credits)

GRANTS

- Identifying genomic signatures of natural selection and its implication on disease susceptibility - funded by Ministry of Science and Technology of Taiwan (2015-2016: $ 1,980,000)
- Genetic origins and adaptation of Taiwanese people - funded by Ministry of Science and Technology of Taiwan (2016-2019: $5,045,000)
- Conservation status of the flying fox population on the Gueishan Island - funded by Council of Agriculture Executive Yuan of Taiwan (2018-2019: $ 900,000)
- Conservation genetics of the Formosan flying fox and its sister subspecies on the Ryukyu Islands - funded by Ministry of Science and Technology of Taiwan (2018-2019: $1000,000)
- Identifying genetic variants that affect evolutionary fitness in the Taiwanese Han people - funded by Ministry of Science and Technology of Taiwan (2020-2023: $ 4,110,000)

PUBLICATIONS

Book Chapter/Reviews

Ko, W.-Y., Gomez, F., and S. A. Tishkoff., 2012 Evolution of human erythrocyte-specific genes involved in malaria susceptibility, a chapter in "Evolution In The Fast Lane: Rapidly Evolving Genes and Genetic Systems. Singh R. S., Xu J. and Kulathinal R. J. Ed. Oxford University Press, Oxford.

Gomez, F., **W.-Y. Ko**, A. Davis, and S. A. Tishkoff. 2013 Impact of Natural Selection due to Malarial Disease on Human Genetic Variation. In J.F. Brinkworth and K. Pechenkina (eds) "Primates, Pathogens and Evolution. Developments in Primatology: Progress and Prospects" **38**:117-160 Springer publishing, New York.

Tishkoff, S. A., M. Campbell, and J. Hirbo, J. Jarvis, **W.-Y. Ko** et al., 2010 Genomic variation and adaptation in Africa: Implications for human evolutionary history and disease. Genome Biology 11 (Suppl 1): 120.

Original research papers

K-P Lin, S-M Chaw, Y-H Lo, T Kinjo, C-Y Tung, H-C Cheng, Q Liu, Y Satta, M Izawa, S-F Chen, and **Wen-Ya Ko**. Genetic differentiation and demographic trajectory of the insular Formosan and Orii's flying foxes. J. Hered. **112**(2): 192 (major corresponding author)(IF: 2.809, ranking: Q1 in Biotechnology).

Y-H Lo, H-C Cheng, H-Y Wang, C-W Peng, C-Y Chen, K-P Lin, M-L Kang, C-N Hsiung, C-H Chen, H-W Chu, C-Y Shen, C-F Lin, M-H Lee, Q. Liu, Y. Satta, C-J Lin, M. Lin, S-M Chaw, J-H Loo, **Wen-Ya Ko**. 2020. Detecting genetic ancestry and adaptation in the Taiwanese Han people. Mol. Biol. Evol. (Ahead of print; IF=16.24) (major corresponding author).

S.-F. Chen, C.-H. Juan, S. J. Rossiter, T. Kinjo, D. Fukui, K. Kawai, S. M. Tsang, M. J. Veluz, H. Sakurai, H.-C. Lin, N.-H. Jang-Liaw, K. Osawa, **W.-Y. Ko**, and M. Izawa. Population Genetic Structure of the Insular Ryukyu Flying Fox Pteropus dasymallus. 2021. Biotropica **53**(2):548-559. (impact factor = 2.09; ranking: Q1 in Ecology, Evolution, Behavior and Systematics) (co-corresponding author)

Y-H Huang, S-F Liao, S-S Khor, Y-J Lin, H-Y Chen, Y-H Chang, Y-H Huang, S-N Lu, H-W Lee, **W-Y Ko**, C H, P-C Liu, Y-J Chen, P-F Wu, H-W Chu, P-E Wu, K Tokunaga, C-Y Shen, M-H Lee. 2020. Large-scale genome-wide association study identifies HLAclass II variants associated with chronic HBV infection: a study from Taiwan Biobank. Aliment Pharmacol Ther. 52(4):682-691.

Laura B. Scheinfeldt, Sameer Soi, Charla Lambert, **Wen-Ya Ko**, et al. 2019. Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. 2019. Proc Natl Acad Sci U S A, 116 (10) 4166-4175.

Fumihiko M., Higasa K., Miyake N., Yoshimura J., Okamura K., Niihori T., Saitsu H., Doi K., Shimizu M, Nakabayashi K, Aoki Y, Tsurusaki Y, Morishita S, Kawaguchi T., Migita O., Nakayama K., Nakashima M., Mitsui J., Narahara M, Hayashi K., Funayama R., Yamaguchi D, Ishiura H., **Ko W.-Y.**, et al. 2016. Human Genetic Variation Database (HGVD), a reference database of genetic variations in the Japanese population. J Hum Genet. **61**: 547-553.

Ranciaro A., Campbell M. C., Hirbo J. B., **Ko, W.-Y.**, et al. 2014 Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. Am J Hum Genet **94**: 496-510 (IF: 11.2).

Ko, W.-Y., P. Rajan, F. Gomez, et al., 2013 Darwinian selection acting on different human *APOL1* variants among diverse African populations. Am J Hum Genet **93**: 90-102 (IF: 11.2).

Gomez F., Tomas G., **Ko, W.-Y.** et al. 2013. Patterns of Nucleotide and Haplotype Diversity at ICAM-1 Across Global Human Populations with Varying Levels of Malaria Exposure. Human Genetics 132: 987-999 (IF: 5.07).

Ko, W.-Y., K. Kaercher, E. Giombini et al., 2011 Effects of gene conversion and natural selection on the evolution of human glycophorins coding for MNS polymorphism in malaria endemic African populations. Am J Hum Genet **88**: 741-754 (selected as a featured article)(IF: 11.2).

Iida, K., D. L. Cox-Foster, X. Yang, **W.-Y. Ko**, D. R. Cavener, 2007 Expansion and evolution of insect GMC oxidoreductases. BMC Evolutionary Biology 7:75. (IF: 3.52).

Ko, W.-Y., S. Piao, and H. Akashi., 2006 Strong regional heterogeneity in base composition evolution on the Drosophila X chromosome. Genetics 174:349-362. (IF: 4.24).

Akashi, H., **W.-Y. Ko,** S. Piao, A. John, P. Goel, C. F. Lin, and A. Vitins, 2006 Molecular evolution in the *Drosophila melanogaster* species subgroup: Frequent parameter fluctuations on the time-scale of molecular divergence. Genetics 172: 1711-1726. (IF: 4.24).

Ko, W.-Y., R. David, and H. Akashi, 2003 Molecular phylogeny of the *Drosophila melanogaster* species subgroup. J. Mol. Evol. 57: 562-573. (IF: 3.78).

Ko, W.-Y., 1997 A Note on the Playing-Dead Behavior of *Pipistrellus abramus*. Notes of Wildlifers and Newsletter of Wildlifers, 4(2): 10 (in Chinese).

Ko, W.-Y., 1995 Reproductive cycle of the house bat, *Pipistrellus abramus*, in South Taiwan. Master's thesis, Tunghai University Department of Biology, Taichung, Taiwan (in English).

International CONFERENCE PRESENTATIONS

Yun-Hua Lo, Han-Yu, Wang, Chia-Wei Peng, Chun-Yu Chen, Hsueh-Chien Cheng, Shu-Miaw Chaw, Marie Lin and **Wen-Ya Ko***. Distinct patterns of genetic ancestry and adaptation in the islanders of Taiwan. 2019 annual meeting of the American Society of Human Genetics (ASHG), Houston TX, Oct 15 - 19, 2019 (*Corresponding author)
*Poster presentation

Wen-Ya Ko*, Koichiro Higasa, Han-Yu Wang, Yun-Hwa Lo, Maiko Narahara, Kaori Iida, Fumihiko Matsuda, and Ryo Yamada. Genetic origins and admixed ancestry characterization of Japanese people. International Symposium on Integrated Anthropology From Genetics to Ecology, Biodiversity – conservation of organisms, Cultures, and Ethnicities. SOKENDAI, Hayama, Japan. Feb.1, 2019 (*Invited talk)

Wen-Ya Ko***,** Koichiro Higasa, Han-Yu Wang, Yun-Hwa Lo, Maiko Narahara, Kaori Iida, Fumihiko Matsuda, and Ryo Yamada. Genetic origins and admixed ancestry characterization of Japanese people. The 16th Korea-Japan-China Bioinformatics Symposium Aug 29-31 2018 (*Invited talk)

Symposium on Evolutionary Genetics and Omics. National Institute of Genetics, Mishima, Japan, July 13-14 2018
*Oral presentation (x 2)

1. **Wen-Ya Ko*****,** Koichiro Higasa, Han-Yu Wang, Yun-Hwa Lo, Maiko Narahara, Kaori Iida, Fumihiko Matsuda, and Ryo Yamada. Genetic origins and admixed ancestry characterization of Japanese people. (*1st author and Corresponding author)
2. Yun-Hua Lo, Han-Yu, Wang, Chia-Wei Peng, Chun-Yu Chen, Hsueh-Chien Cheng, Shu-Miaw Chaw, Marie Lin and **Wen-Ya Ko***. Genetic adaptation and ancestry inference of Taiwanese people. (*Corresponding author)

The annual meeting of the Society for Molecular Biology and Evolution (SMBE), Pacifico Yokohama, Japan, July 8- 12, 2018
*Poster presentation (x 3)

1. **Wen-Ya Ko*****,** Koichiro Higasa, Han-Yu Wang, Yun-Hwa Lo, Maiko Narahara, Kaori Iida, Fumihiko Matsuda, and Ryo Yamada. Genetic origins and admixed ancestry characterization of Japanese people. (*1st author and Corresponding author)
2. Yun-Hua Lo, Han-Yu, Wang, Chia-Wei Peng, Chun-Yu Chen, Hsueh-Chien Cheng, Shu-Miaw Chaw, Marie Lin and **Wen-Ya Ko***. Genetic adaptation and ancestry inference of Taiwanese people. (*Corresponding author)
3. Kung-Ping Lin, Yun-Hwa Lo, Shiang-Fan Chen, Masako Izawa, **Wen-Ya Ko***. Uncovering the demographic history of the endangered Formosan fruit bats (*Pteropus dasymallus formosus*) in Taiwan. (*Corresponding author)

Ko W.-Y., K. Higasa, M. Narahara, F. Matsuda, and R. Yamada,. Genetic origins and admixed ancestry characterization of Japanese people. The 65th annual meeting of the American Society of Human Genetics (ASHG), Baltimore MD, Nov 6 - 10, 2015
*Poster presentation

Ko, W.-Y., P. Rajan, F. Gomez, et al., 2014 Identifying Darwinian selection acting on different human *APOL1* variants among diverse African populations. SMBE Satellite Meeting/NIG International Symposium, Mishima, Japan, Mar 14-17 2014
*Poster presentation

Ko, W.-Y., P. Rajan, F. Gomez, et al., 2013 Identifying Darwinian selection acting on different human *APOL1* variants among diverse African populations. International Symposium on Evolutionary Genomics and Bioinformatics (ISEGB), Taichung, Taiwan, Nov 8-9 2013
*Invited talk

Ko, W.-Y., P. Rajan, F. Gomez, et al., 2013 Darwinian selection acting on different human *APOL1* variants among diverse African populations. Congress of the European Society for Evolution Biology (ESEB), Lisbon, Portugal, Aug 19-24 2013
*Platform presentation

Ko, W.-Y., F. Gomez, and S. A. Tishkoff, Spatially heterogeneous selection on human ApoL1 variants among diverse African populations in trypanosomiasis endemic areas. The annual meeting of the Society for Molecular Biology and Evolution (SMBE), Kyoto, Japan, July 26-30 2011
*Platform presentation

Ko, W.-Y. and S. A. Tishkoff, Effects of gene conversion and natural selection on the evolution of human glycophorins coding for MNS polymorphism in malaria endemic African populations. Young Researchers Conference On Evolutionary Genomics, Tokyo, Japan, August 1-2 2011
*Invited talk

Ko, W.-Y., K. Kaercher, and S. A. Tishkoff, Adaptive evolution of human glycophorin loci in malaria endemic African populations. The 60th annual meeting of the American Society of Human Genetics (ASHG), Washington DC, Nov 2 - 6, 2010
*Platform presentation with trainee research award
*Invitation for a press briefing session at the meeting on the latest advances in evolutionary and population genetics research.

Ko, W.-Y., K. Kaercher, and S. A. Tishkoff, Adaptive evolution of human glycophorin loci in malaria endemic African populations. The annual meeting of the Society for Molecular Biology and Evolution (SMBE), Lyon, France, July 4 - 8 2010
*Platform presentation with travel award

Ko, W.-Y., F. Gomez, and S. A. Tishkoff, An evolutionary and population genetic approach to malaria susceptibility in Africa. The 79th annual meeting of the American Association of Physical Anthropologists (AAPA), Albuquerque, New Mexico, Apr 14 - 17 2010
*Invited talk

Ko, W.-Y., K. Kaercher, and S. A. Tishkoff, Population genetic analysis of erythrocyte surface glycoproteins in malaria-endemic human populations of Africa.
Poster presentations at:

- 58th Annual meeting of the American Society of Human Genetics, Philadelphia, Pennsylvania, Nov 11 - 15, 2008
- Poster presentation at Ecology and Evolution of Infectious Disease PI Meeting, Albuquerque, New Mexico, Dec 02 - 05 2007

Ko, W.-Y., S. Piao, and H. Akashi, Strong regional heterogeneity in base composition evolution on the Drosophila X chromosome.
Poster presentations at:

- Evolution 2006, the join annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN) at Stony Brook University, Stony Brook, NY, June 23 - 27 2006
- Genomes, Evolution, and Bioinformatics, the annual meeting for the Society for Molecular Biology and Evolution at Arizona State University, Tempe, AZ, May 24 - 28 2006
- 47th Annual Drosophila Research Conference, Houston, TX, March 29 - April 2 2006
- The Comparative and Functional Genomics of Summer Symposium at Pennsylvania State University, University Park, PA, July 20 - 23 2005

Oral presentations at:

- Northeast Ecology and Evolution Conference (NEEC) at Pennsylvania State University, University Park, PA, March 18 - 20 2005

Ko, W.-Y., R. David, J. Anoop, C.-F. Lin, S. Piao, and H. Akashi, Lineage-specific molecular evolution in the *Drosophila melanogaster* species subgroup. Poster presentation at

Genome and Evolution conference for the Society for Molecular Biology and Evolution (SMBE) at Pennsylvania State University, University Park, PA, June 17 - 20 2004

Ko, W.-Y., R. David, and H. Akashi, Molecular phylogeny of the *Drosophila melanogaster* species subgroup.
Poster presentations at:

- Eastern Great Lake Molecular Evolution Meeting (EGLME VIII) at Cornell University, Ithaca, NY, April 24 2004
- The annual conference for the Society of Molecular Biology and Evolution (SMBE), Newport Beach, CA, June 26 - 29 2003

ACADEMIC SERVICE:

Moderator in the 60th annual meeting of the American Society of Human Genetics (ASHG) for the session of Evolutionary and Population Genetics, Washington DC, USA, November 2 - 6 2010

External reviewing panel of grant application for the Swiss National Science Foundation 2013

Manuscripts reviewed:

- BMC Evolutionary Biology
- BMC Source Code for Biology and Medicine
- G3 – Genes | Genomes | Genetics
- GENE
- Journal of Molecular Evolution
- Molecular Biology and Evolution
- PLoS Genetics

PROFESSIONAL AFFILIATIONS:

- The European Society for Evolutionary Biology
- Genetics Society of America
- American Society of Human Genetics
- Society for Molecular Biology and Evolution
- Society for the Study of Evolution

SERVICE TO COMMUNITIES:

- Graduate Affairs Committee of Biology Department, Pennsylvania State University, 2006
- Institutional Review Board for Research on Human subjects, 2014 - present
- Committee of Faculty Housing and Residential Affairs (Chairman), 2017 - present