

Dang Liu

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EDUCATION

National Taiwan University (NTU) and Academia Sinica

2015-2017

MSc, Genome and Systems Biology Degree Program, Taiwan.
(Overall GPA: 4.09/4.3; Ranking: 2/5)

National Cheng Kung University (NCKU)

2011-2015

BSc, Department of Life Sciences, Taiwan.
(Overall GPA: 3.91/4; Ranking: 1/49)

RESEARCH EXPERIENCE

PhD Student

2018-present

Topic: Genome-wide investigation of human population diversity and history in Southeast Asia and Oceania

Supervisor: Prof. Dr. Mark Stoneking

Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Germany

Substitutive Military Service

2017-2018

Topic: Core collection of tomato populations through NGS technology

Director: Dr. Ien-Chie Wen

Plant Germplasm Division, Taiwan Agricultural Research Institute, Taiwan

MSc Student

2015-2017

Topic: Comparative genomics of *Caenorhabditis* species

Advisor: Dr. Isheng Jason Tsai

Biodiversity Research Center, Academia Sinica, Taiwan

PUBLICATIONS

- 1 Kutanan, W.*, **Liu, D.***, Kampuansai, J., Srikumool, M., Srithawong, S., Shoocongdej, R., Sangkhano, S., Ruangchai, S., Pittayaporn, P., Arias, L., Stoneking, M. (2021). Reconstructing the human genetic history of mainland Southeast Asia: insights from genome-wide data from Thailand and Laos. *Molecular Biology and Evolution*. (*: contributed equally as first authors).
- 2 **Liu, D.**, Duong, N. T., Ton, N. D., Van Phong, N., Pakendorf, B., Van Hai, N., & Stoneking, M. (2020). Extensive ethnolinguistic diversity in Vietnam reflects multiple sources of genetic diversity. *Molecular Biology and Evolution*.
- 3 Srithawong, S., Muisuk, K., Srikumool, M., Kampuansai, J., Pittayaporn, P., Ruangchai, S., **Liu, D.**, Kutanan, W. (2020). Close genetic relationship between central Thai and Mon people in Thailand revealed by autosomal microsatellites. *International Journal of Legal Medicine*.
- 4 Kanzaki, N.*, Tsai, I. J.*, Tanaka, R.*, Hunt, L. V.*, **Liu, D.**, Tsuyama, K., Maeda, Y., Namai, S., Kumagai, R., Tracey, A., Holroyd, N., Doyle, R. S., Woodruff, C. G., Murase, K., Kitazume, H., Chai, C., Akagi, A., Panda, O., Ke, H. M., Schroeder, C. F., Wang, J., Berriman, M., Sternberg, P. W., Sugimoto, A., & Kikuchi, T. (2018). Biology and genome of a newly discovered sibling species of *Caenorhabditis elegans*. *Nature Communications*. (*: contributed equally as first authors).

- 5 Ke, H. M., **Liu, D.**, Ogura, Y., Hayashi, T., Urbanczyk, H., & Tsai, I. J. (2018). Tracing genomic divergence of *Vibrio* bacteria in the Harveyi clade. *Journal of bacteriology*.
- 6 **Liu, D.**, Hunt, M., & Tsai, I. J. (2018). Inferring synteny between genome assemblies: a systematic evaluation. *BMC Bioinformatics*.
- 7 Chung, C. L., Lee, T. J., Akiba, M., Lee, H. H., Kuo, T. H., **Liu, D.**, Ke, H. M., Yokoi, T., Roa, B. M., Lu, J. M., Chang, Y. Y., Ann, P. J., Tsai, J. N., Chen, C. Y., Tzean, S. S., Ota, Y., Hattori, T., Sahashi, N., Liou, R. F., Kikuchi, T., & Tsai, I. J. (2017). Comparative and population genomics landscape of *Phellinus noxius*: a hypervariable fungus causing root rot in trees. *Molecular Ecology*.

PRESENTATIONS AND CONFERENCES

- 1 **Liu, D.**, Ensing, J., Schiefenhövel, W., Kayser, M., Stoneking, M. (2021). Assessing human genome-wide variation in the Massim region of Papua New Guinea and implications for the *Kula* trading tradition. Poster presentation, *CSHL Biology of Genomes 2021 virtual meeting*.
- 2 Kutanan, W.*, **Liu, D.***, Kampuansai, J., Srikumool, M., Srithawong, S., Shoocongdej, R., Sangkhano, S., Ruangchai, S., Pittayaporn, P., Arias, L., Stoneking, M. (2021). Reconstructing the human genetic history of mainland Southeast Asia: insights from genome-wide data from Thailand and Laos. Poster presentation, *EMBO Virtual Course on Population Genomics*. (*: contributed equally as first authors).
- 3 **Liu, D.**, Duong, N. T., Ton, N. D., Van Phong, N., Pakendorf, B., Van Hai, N., & Stoneking, M. (2019). Extensive ethnolinguistic diversity in Vietnam reflects multiple sources of genetic diversity. Poster presentation, *Human Evolution 2019 at Welcome Genome Campus, UK*.
- 4 **Liu, D.**, Kanzaki, N., Tanaka, R., Woodruff, G., Maeda, Y., Sternberg, P. W., Tsai, I. J., Sugimoto, A., & Kikuchi, T. (2016). The genome sequence of *Caenorhabditis* sp. 34: a true sister species of *C. elegans* advancing model species biology. Oral presentation, *International Symposium on Evolutionary Genomics and Bioinformatics*.

TEACHING EXPERIENCE

Seminar mentor at the Molecular Anthropology course, University Leipzig	2021
Seminar mentor at the Molecular Anthropology course, University Leipzig	2020

HONORS

Government Scholarship to Study Abroad from Taiwan Ministry of Education	2020
Semi-Finalist Award for Best Student Oral Presentation on International Symposium on Evolutionary Genomics and Bioinformatics	2016
The Award of Outstanding Student for the Academic Achievement	2011-2012 2012-2013

SKILLS

- Proficiency in programming language such as Python and R
- Familiar with Linux environment
- Familiar with Adobe Illustrator
- Experience in NGS data analysis such as assembly, annotation, comparative genomics and population genomics
- Molecular and genetics techniques such as DNA/RNA extraction, cloning and cell culture

LANGUAGE ABILITIES

- Mandarin (native speaker)
- English (fluent)
- German (basic)

EXTRACURRICULAR ACTIVITIES

Internal PhD representative at Dept. of Evolutionary Genetic, MPI-EVA	2019-2020
Player on National Taiwan University Football Team	2015-2017
<ul style="list-style-type: none">• Assistant coach in 2015/2016 season of University Football Association• Championship in 2015/2016 season of University Football Association	
Player on National Cheng Kung University Football Team	2011-2015
<ul style="list-style-type: none">• Captain in 2013/2014 season of University Football Association	
Poetry Exhibition in National Cheng Kung University	2013 2015

REFERENCES

Mark Stoneking, Ph.D.

Group Leader of Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, and Honorary Professor of Biological Anthropology, University of Leipzig.

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Isheng Jason Tsai, Ph.D.

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