

Dang Liu

+33-1-4061-3979
28 Rue du Docteur Roux, 75015 Paris, France

dang.liu@pasteur.fr
dangliu.github.io

EDUCATION

PhD in Biology (Molecular Anthropology) 2018-2021

International Max Planck Research School "The Leipzig School of Human Origins",
Leipzig University and Max Planck Institute for Evolutionary Anthropology, Leipzig,
Germany

Thesis: Human population genetic history of Mainland Southeast Asia

Advisor: Prof. Dr. Mark Stoneking

MSc in Biology (Evolutionary Genomics) 2015-2017

Genome and Systems Biology Degree Program, National Taiwan University and
Academia Sinica, Taipei, Taiwan

Thesis: Comparative genomics of *Caenorhabditis* species

Advisor: Dr. Isheng Jason Tsai

BSc in Biology 2011-2015

Department of Life Sciences, National Cheng Kung University, Tainan, Taiwan

RESEARCH EXPERIENCE

Postdoc 2022-present

Topic: Demographic and adaptive history of Polynesians

Advisors: Prof. Dr. Lluís Quintana-Murci & Dr. Etienne Patin

Pasteur Institute, Paris, France

Postdoc 2021-2022

Topic: Human genetic history and the relationships with cultural variation in Southeast
Asia and Oceania

Advisor: Prof. Dr. Mark Stoneking

Max Planck Institute for Evolutionary Anthropology, Leipzig, 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, Taichung, Taiwan

PUBLICATIONS

*Equal contribution / #correspondence

- 1 **Liu, D.*#**, Ko, A. M. S.*, & Stoneking, M.# (2023). The genomic diversity of Taiwanese Austronesian groups: implications for the "Into and Out of Taiwan" models. **PNAS Nexus**, 2(5). doi:10.1093/pnasnexus/pgad122
- 2 Stoneking, M.*, Arias, L.*, **Liu, D.***, Oliveira, S.*, Pugach, I.*, & Rodriguez, J. J. R. B.* (2023). Genomic perspectives on human dispersals during the Holocene. **PNAS**, 120(4), e2209475119. doi:10.1073/pnas.2209475119

- 3 **Liu, D.**, Peter, B. M., Schiefenhover, W., Kayser, M., & Stoneking, M. (2022). Assessing Human Genome-wide Variation in the Massim Region of Papua New Guinea and Implications for the Kula Trading Tradition. **Mol Biol Evol**, 39(8). doi:10.1093/molbev/msac165
- 4 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. **Mol Biol Evol**, 38(8), 3459-3477. doi:10.1093/molbev/msab124
- 5 **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. **Mol Biol Evol**, 37(9), 2503-2519. doi:10.1093/molbev/msaa099
- 6 Srithawong, S., Muisuk, K., Srikumool, M., Kampuansai, J., Pittayaporn, P., Ruangchai, S., **Liu, D.**, Kutanan, W. (2021). Close genetic relationship between central Thai and Mon people in Thailand revealed by autosomal microsatellites. **International Journal of Legal Medicine**, 135(2), 445-448. doi:10.1007/s00414-020-02290-4
- 7 Kanzaki, N.*, Tsai, I. J.*, Tanaka, R.*, Hunt, V. L.*, **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*. **Nat Commun**, 9(1), 3216. doi:10.1038/s41467-018-05712-5
- 8 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**, 200(15). doi:10.1128/JB.00001-18
- 9 **Liu, D.**, Hunt, M., & Tsai, I. J. (2018). Inferring synteny between genome assemblies: a systematic evaluation. **BMC Bioinformatics**, 19. doi: 10.1186/s12859-018-2026-4
- 10 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 genomic landscape of *Phellinus noxius*: A hypervariable fungus causing root rot in trees. **Mol Ecol**, 26(22), 6301-6316. doi:10.1111/mec.14359

PRESENTATIONS AND CONFERENCES

Oral presentations

- 2022 **EMBO | EMBL Symposium - Reconstructing the human past: using ancient and modern genomics**, Heidelberg, Germany. Title: The genomic diversity of Taiwanese Austronesian groups: implications for the 'Into and Out of Taiwan' models
- 2021 **Human Evolution - From Fossils to Ancient and Modern Genomes (Welcome Genome Campus)**, virtual Conference. Title: Assessing human genome-wide variation in the Massim region of Papua New Guinea and implications for the Kula trading tradition
- 2016 **International Symposium on Evolutionary Genomics and Bioinformatics**, Kaohsiung, Taiwan. Title: The genome sequence of *Caenorhabditis sp. 34*: a true sister species of *C. elegans* advancing model species biology

Poster presentations

- 2023 **Annual Meeting of the American Society of Human Genetics**, Washington, DC, USA. Title: Dissecting the genetic and evolutionary sources of phenotypic variation in East Polynesians
- 2021 **Cold Spring Harbor Laboratory meeting - Biology of Genomes**, virtual conference. Title: Assessing human genome-wide variation in the Massim region of Papua New Guinea and implications for the Kula trading tradition

- 2021 **EMBO Virtual Course on Population Genomics**. Title: Reconstructing the human genetic history of mainland Southeast Asia: insights from genome-wide data from Thailand and Laos
- 2019 **Human Evolution - From Fossils to Ancient and Modern Genomes (Welcome Genome Campus)**, Cambridge, UK. Title: Extensive ethnolinguistic diversity in Vietnam reflects multiple sources of genetic diversity

TEACHING EXPERIENCE

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

HONORS

Pasteur-Roux-Cantarini Postdoctoral Fellowships 2023-2025

Semi-Finalist for the Trainee Awards for Excellence in Human Genetics Research for the Annual Meeting of the American Society of Human Genetics 2023

Reviewers' Choice Award (top 10% poster abstracts) for the Annual Meeting of the American Society of Human Genetics 2023

Government Scholarship to Study Abroad from Taiwan Ministry of Education 2020-2022

Semi-Finalist Award for Best Student Oral Presentation on International Symposium on Evolutionary Genomics and Bioinformatics, Kaohsiung, Taiwan 2016

The Award of Outstanding Student for the Academic Achievement, Department of Life Sciences, National Cheng Kung University, Tainan, Taiwan 2012,2013

SKILLS

- Proficiency in programming language such as Python and R
- Familiar with Linux environment and Bash scripting
- 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

Contribution to a cover art selected for the journal of Molecular Biology and Evolution 2021

Internal PhD representative at Dept. of Evolutionary Genetics, MPI-EVA 2019-2020

Player on National Taiwan University Football Team 2015-2017

- Assistant coach in 2015/2016 season of University Football Association

Player on National Cheng Kung University Football Team 2011-2015

- Captain in 2013/2014 season of University Football Association

Poetry Exhibition in National Cheng Kung University 2013,2015

REFERENCES

Postdoc advisor

Lluís Quintana-Murci, Ph.D.

Director of the Human Evolutionary Genetics Unit, Institut Pasteur and Professor at the Collège de France, Chair of Human Genomics and Evolution

Unit Human Evolutionary Genetics, 25-28 Rue du Docteur Roux, 75015 Paris, France

Tel: +33-1-40-61-34-43

lluis.quintana-murci@pasteur.fr

PhD advisor

Mark Stoneking, Ph.D.

Visiting Professor, CNRS Laboratory for Biometry and Evolutionary Biology

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

Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, 04103 Leipzig, Germany /

UMR CNRS 5558 Biométrie et Biologie Évolutive Université Claude Bernard – Bât Mendel – 43 bd du 11 novembre 1918, 69622 Villeurbanne, France

Tel: N.A.

stoneking@eva.mpg.de / mark.stoneking@univ-lyon1.fr

MSc advisor

Isheng Jason Tsai, Ph.D.

Associate Research Fellow of Biodiversity Research Center, Academia Sinica

Biodiversity Research Center, Academia Sinica, 128 Academia Road Sec. 2, Nankang Taipei 115 Taiwan, Room B303

Tel: +886-2-2787-2230

ijtsai@gate.sinica.edu.tw