

# Tianxiong Yu, Ph.D.

## Computational Biology | Genomics | Transposon Biology | Brain Mosaicism

Department of Genomics and Computational Biology

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## Education

- **Ph.D.** in Bioinformatics, Tongji University, China, 2014 – 2020
- **B.S.** in Bioinformatics, Tongji University, China, 2010 – 2014

## Research Experience

### - Postdoctoral Researcher | 2021 – present

University of Massachusetts Chan Medical School, USA

- Led studies of the evolution of transcriptional silencing of endogenous retroviruses in the koala germline using multi-omics approaches; published in *Cell* (Yu et al., 2025).
- Developed algorithms to detect transposon insertions from short- and long-read whole-genome sequencing data; published in *NAR* and under review at *GBP*.
- Revealed genome-wide transposition site selection patterns in *Drosophila*; published in *NAR*.
- Led single-cell genomic and transcriptomic analyses of human brain aging; published in *Nature* (Jeffries & Yu et al., 2025)
- Identified links between elevated 2bp deletions and Parkinson's disease pathology in human neurons; under review at *Neuron*.
- Led computational analyses in collaboration with experimental biologist to dissect the piRNA pathway functions in transposon silencing; results published and under review in peer-reviewed journals.

### - Ph.D. Student | 2014 – 2020

Tongji University, China

- Identified long-first-exon as a defining feature directing transcripts into the piRNA pathway; published in *Nat. Commun.*
- Annotated 83 human pachytene piRNA genes and revealed high divergence among modern humans; published in *Nat. Ecol. Evol.*

### - Visiting Scholar | 2017 – 2019

University of Massachusetts Chan Medical School, USA

- Led studies of post-transcriptional silencing of endogenous retroviruses in the koala germline; published in *Cell* (Yu et al., 2019).

## Publications

(\* co-first author; † corresponding author)

### - Representative publications

1. Yu T, Blyton M, Abajorga M, Koppetsch BS, Ho S, Xu B, Hu Z, Chappell K†, Luban J†, Weng Z†, Theurkauf WE†. Adaptive evolution of KoRV-A transcriptional silencing in wild koalas. *Cell*. 2025.
2. Jeffries AM\*, Yu T\*, Ziegenfuss JS, Tolles AK, Baer CE, Kim Y, Weng Z†, Lodato MA†. Single-cell transcriptomic and genomic changes in the aging human brain. *Nature*. 2025.
3. Cao J\*, Yu T\*†, Xu B, Hu Z, Zhang XO, Theurkauf WE, & Weng Z†. Epigenetic and chromosomal features drive transposon insertion in *Drosophila melanogaster*. *NAR*. 2023.

4. **Yu T\***, Biasini A\*, Cecchini K\*, Säflund M, Mou H,... Weng Z, Zamore PD† & Özata DM†. A-MYB/TCFL5 regulatory architecture ensures the production of pachytene piRNAs in placental mammals. **RNA**. 2023.
5. **Yu T**, Huang X, Dou S, Tang X, Luo S, Thuerkauf WE†, Lu J†, Weng Z†. A benchmark and an algorithm for detecting germline transposon insertions and measuring de novo transposon insertion frequencies. **NAR**. 2021.
6. **Yu T\***, Fan K\*, Ozata DM, Zhang G, Fu Y, Thuerkauf WE†, Zamore PD†, Weng Z†. Long first exons and epigenetic marks distinguish conserved pachytene piRNA clusters from other mammalian genes. **Nat. Commun.** 2021
7. Zhang G\*, **Yu T\***, Parhad SS, Ho S, Weng Z†, Theurkauf WE†. piRNA-independent transposon silencing by the Drosophila THO complex. **Dev. Cell**. 2021.
8. Ozata DM\*, **Yu T\***, Mou H, Gainetdinov I, Colpan C, Cecchini K, Kaymaz Y, Wu P, Fan K, Kucukural A, Weng Z†, Zamore PD†. Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. **Nat. Ecol. Evol.** 2020.
9. **Yu T\***, Koppetsch BS\*, Pagliarani S, Johnston S, Silverstein NJ, Luban J, Chappell K†, Weng Z†, Theurkauf WE†. The piRNA response to retroviral invasion of the koala genome. **Cell**. 2019

#### - Manuscripts under review / Preprints

1. **Yu T†**, Blyton M, Abajorga M, Koppetsch BS, Ho S, Xu B, Hu Z, Chappell K, Luban J, Theurkauf WE†, Weng Z†. The trajectory of KoRV-A evolution indicates initial integration into the koala germline genome near Coffs Harbour. *Under review*, **Genome Biol.** (Research Square preprint).
2. Ziegenfuss JS\*, **Yu T\***, Tolles AK, Jeffries AM, Nayak S, Ormsbee J, Weng Z†, Lodato MA†. Human neuron somatic mutations reflect misfolded protein aggregation in neurodegeneration. *Under review*, **Neuron**.
3. Hu Z\*, Bo X\*, Zhang X, Zhang X†, Weng Z†, **Yu T†**. LOCATE: using long-read to characterize all transposable elements. *Under review*, **GPB**. (bioRxiv preprint).
4. Säflund M\*, Askari M\*, Eghbali A\*, Abdi MM, Farrants AO, **Yu T†**, Ozata DM†. Transcriptional factor NFYA directs male meiotic entry by facilitating accessible chromatin at meiotic promoters in mice. *Under review*, **EMBO J.** (bioRxiv preprint).

#### - Other publications

1. Gustafsson HT, ..., **Yu T**, ..., Rando OJ. Deep sequencing of yeast and mouse tRNAs and tRNA fragments using OTTR. **eLife**. 2025.
2. Hoeve ALT, ..., **Yu T**, ..., Barragan A. Hypermigration of macrophages through the concerted action of GRA effectors on NF-κB/p38 signaling and host chromatin accessibility potentiates toxoplasma dissemination. **mBio**. 2024.
3. Cecchini K\*, Biasini A\*, **Yu T\***, ..., Zamore, PD† & Özata, DM†. The transcription factor TCFL5 responds to A-MYB to elaborate the male meiotic program in mice. **Reproduction**. 2023.
4. Mou H, ..., **Yu T**, ..., Beyaz S. CRISPR-induced exon skipping of β-catenin reveals tumorigenic mutants driving distinct subtypes of liver cancer. **J. Pathol.** 2023.
5. Smith JL, ..., **Yu T**, ..., Xue W. YAP1 withdrawal in hepatoblastoma drives therapeutic differentiation of tumor cells to functional hepatocyte-like cells. **Hepatology**. 2021.
6. Parhad SS, **Yu T**, ..., Weng Z†, Theurkauf WE†. Adaptive evolution targets a piRNA precursor transcription network. **Cell Rep**. 2020.
7. Wu P, ..., **Yu T**, ..., Weng Z†, Zamore PD †. An evolutionarily conserved piRNA-producing locus required for male mouse fertility. **Nat. Genet.** 2020.

8. Zhang G\*, Tu S\*, **Yu T**, ..., Weng Z†, Theurkauf WE†. Co-dependent assembly of drosophila piRNA precursor complexes and piRNA cluster heterochromatin. **Cell Rep.** 2020.

## Abstracts

### - Oral Presentations

1. The evolution of koala retrovirus and its transcriptional silencing in germline.  
*CSHL Retroviruses*. Coldspring Harbor, NY, USA. May 2025.
2. Epigenetic and chromosomal features drive transposon insertion in drosophila melanogaster.  
*Epigenetics Club Seminar*. Worcester, MA, USA. Dec 2022
3. The evolution of piRNA genes in mammals.  
*EMBO piRNA workshop*. Virtual. Apr 2022.
4. Lack of splicing distinguishes piRNA-producing transcripts from other RNAs in mammals.  
*8<sup>th</sup> Annual RNA Symposium*. Virtual. Mar 2022

### - Poster Presentations

1. Identifying transposon insertions using long-read.  
Mutation in Time and Space. Cambridge, MA. Apr 2025
2. The transition from innate to adaptive silencing of a retroviral genome invader in koalas.  
NHGRI annual trainee meeting. Salt Lake City, UT. Apr 2023

## Grants & Fellowships

- NIH Pathway to Independence Awards (K99/R00).  
Decoding transposon variations in human genomes: unveiling insights and implications.  
Submitted Jun 2024. Scored (40), not funded.

## Mentorship Experiences

- Jichuan Cao (M.S. student, 2020–2023). Supervised master's thesis on transposon insertion preferences; project resulted in a first-author publication in *NAR*. (2023).
- Zhongren Hu and Bo Xu (Ph.D. students, 2020–present). Mentored doctoral research on computational methods for transposon insertion detection; led to a first-author manuscript under review at *GPB*.
- Anisha Mhatre (Ph.D. student, 2024–present). Guiding research on transcription factor binding in transposons; project ongoing.
- Yuhe Wang (Junior Research Assistant, 2024). Supervised independent project on somatic mutations in muscle aging; provided training in genomic data analysis.

## Teaching Experience

- Advanced Topics in Bioinformatics (BBS741), *University of Massachusetts Chan Medical School* (Fall 2022). Developed teaching materials and assignments for non-negative matrix factorization.
- Transposon Silencing, *Tongji University* (Summer 2019). Developed teaching materials and assignments for the mechanisms of piRNA-mediated transposon silencing; guided student discussions on primary literature.

## Software & Resource

- **TEMP2**: Detecting transposon insertions using short-read DNA sequencing data.  
GitHub: <https://github.com/weng-lab/TEMP2>
- **LOCATE**: Detecting and characterizing transposon insertions using long-read DNA sequencing data.  
GitHub: <https://github.com/red-t/LOCATE>
- **piSet**: A pipeline for piRNA and general analysis of high-throughput sequencing data.

GitHub: <https://github.com/tianxiongbb/piSet>

- **SomaMut**: A resource website hosting somatic mutations, single-cell transcription levels and other data.  
Website: <https://publications.wenglab.org/SomaMut/>

## Academic & Community

- Peer reviewer for *Human Genetics and Genomics Advances*, *PCI Genomics*, *Scientific Reports*, and *Clinical Epigenetics*.
- Developed and maintained research software and pipelines for community use.

## REFERENCES

**Dr. Zhiping Weng** | Professor and Chair, Postdoctoral Advisor

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