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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

- Discovered the evolution of adaptive silencing of koala retrovirus invasion in the germline. (Yu et al., **Cell** 2025)
- Developed two software for detecting transposon insertion via DNA sequencing data. (Yu et al., **NAR** 2021; Hu. ... Yu., Under Review)
- Revealed the preference of transposon insertion sites in *Drosophila*. (Cao & Yu et al., **NAR** 2023)
- Bridged genomic and transcriptomic changes in single-cell level during human brain aging. (Jeffries & Yu et al., **Nature** Accepted)
- Uncovered the link between elevated somatic deletions and Parkinson's diseases in human neurons. (Ziegenfuss & Yu et al., in Preparation)
- Collaborated with experimental biologist on multiple projects, including studying the functions of piRNA pathways, as well as identifying ELAVL2 as a novel genetic modifier of neurodegeneration in C9ORF72-FTD/ALS. (Yu et al., **RNA**, 2023; Zhang & Yu et al., **Dev. Cell**, 2021)

- Ph.D. Student

2014 – 2020

Tongji University, China

- Determined long-first-exon as the feature that differs pachytene piRNA genes from typical protein-coding genes and lincRNAs. (Yu et al., **Nat. Commun.**, 2021)
- Annotated human pachytene piRNA genes and found they are highly divergent among modern humans. (Ozata & Yu et al., **Nat. Ecol. Evol.**, 2020)

- Visiting Scholar

2017 – 2019

University of Massachusetts Chan Medical School, USA

- Discovered the innate response of piRNA pathway to retroviral invasion in the koala germline. (Yu et al., **Cell**, 2019)

PUBLICATIONS

(* Authors contributed equally; † corresponding authors)

- 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**, accepted.
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*. **Nucleic Acids Research**, 2023.

4. **Yu T***, Biasini A*, Cecchini K*, Sjöflund 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. Cecchini K*, Biasini A*, **Yu T***, Sjöflund M, Mou H, Arif A, Eghbali A, Colpan C, Gainetdinov I, de Rooij DG, Weng Z, Zamore, PD† & Özata, DM†. The transcription factor TCFL5 responds to A-MYB to elaborate the male meiotic program in mice. **Reproduction**. 2023.
6. **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. **Nucleic Acids Research**. 2021.
7. **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. **Nature Communications**. 2021
8. Zhang G*, **Yu T***, Parhad SS, Ho S, Weng Z†, Theurkauf WE†. piRNA-independent transposon silencing by the Drosophila THO complex. **Developmental Cell**. 2021.
9. 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. **Nature Ecology & Evolution**. 2020.
10. **Yu T***, Koppetsch BS*, Pagliarini 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

- 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. *Research Square*.
2. Hu Z*, Bo X*, Zhang X, Zhang X†, Weng Z†, **Yu T†**. LOCATE: using Long-read to Characterize All Transposable Elements. *bioRxiv*.
3. Sjöflund 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. *bioRxiv*.

- Contributing co-author publications

1. Gustafsson HT, Ferguson L, Galan C, **Yu T**, Upton H, Kaymak E, Weng Z, Collins K, 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. Mou H, ..., **Yu T**, ..., Beyaz S. CRISPR-induced Exon Skipping of β-catenin Reveals Tumorigenic Mutants Driving Distinct Subtypes of Liver Cancer. **The Journal of pathology**. 2023.
4. Smith JL, ..., **Yu T**, ..., Xue W. YAP1 Withdrawal in Hepatoblastoma Drives Therapeutic Differentiation of Tumor Cells to Functional Hepatocyte-like Cells. **Hepatology**. 2021.
5. Parhad SS, **Yu T**, Zhang G, Rice NP, Weng Z†, Theurkauf WE†. Adaptive Evolution Targets a piRNA Precursor Transcription Network. **Cell Reports**. 2020.
6. Wu P, Fu Y, Cecchini K, Ozata DM, Arif A, **Yu T**, Colpan C, Gainetdinov I, Weng Z†, Zamore PD †. An Evolutionarily Conserved piRNA-producing Locus Required for Male Mouse Fertility. **Nature Genetics**. 2020.

7. Zhang G*, Tu S*, **Yu T**, Zhang XO, Parhad SS, Weng Z†, Theurkauf WE†. Co-dependent Assembly of Drosophila piRNA Precursor Complexes and piRNA Cluster Heterochromatin. **Cell Reports**. 2020.

ABSTRACTS

- Oral Presentations

1. The Evolution of Koala Retrovirus and Its Transcriptional Silencing in Germline. CSH Retroviruses. Coldspring Harbor. May 2025.
2. Epigenetic and Chromosomal Features Drive Transposon Insertion in Drosophila Melanogaster. Epigenetics Club Seminar at University of Massachusetts Chan Medical School. Worcester, MA. 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. 8th 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

GRANT APPLICATION

NIH Pathway to Independence Awards (K99)	Score: 40
Decoding Transposon Variations in Human Genomes: Unveiling Insights and Implications	
NIH Exploratory/Developmental Grants (R21) (Co-Investigator)	Under Review
Investigate the Effect of Transposon Insertions to Quantitative Traits Using the TOPMed CARDIA Datasets	

MENTORSHIP EXPERIENCE

Jichuan Cao, M.S. student	transposon insertion preference	2020 – 2023
Zhongren Hu and Bo Xu, Ph.D. students	transposon insertion detection	2020 – present
Anisha Mhatre, Ph.D. student	TF binding in transposons	2024
Yuhe Wang, Junior Research Assistant	somatic mutation in muscle aging	2024

TEACHING EXPERIENCE

Participation of teaching Advanced Topics in Bioinformatics (BBS741) at UMMS	2022 Fall
Participation of teaching Transposon Silencing at Tongji University	2019 Summer

SOFTWARE AND 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 AND COMMUNITY SERVICE

Peer reviewers: Human Genetics and Genomics Advances; PCI Genomics; Scientific Reports.
Research software and pipelines development, maintenance, and support for community use.

REFERENCES

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