

# Tianxiong Yu, Ph.D.

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## EDUCATION

<b>Ph.D. in Bioinformatics</b> , Tongji University, China	2014 – 2020
<b>B.S. in Bioinformatics</b> , Tongji University, China	2010 – 2014

## RESEARCH EXPERIENCE

<b>Postdoctoral Research</b>	2021 – present
University of Massachusetts Chan Medical School, USA	
<ul style="list-style-type: none"><li>Discovered the evolution of adaptive silencing of koala retrovirus invasion in the germline. (Yu et al., <b>Cell</b>, 2025)</li><li>Developed two software for detecting transposon insertion via DNA sequencing data. (Yu et al., <b>NAR</b>, 2021; Hu. ... Yu., Under Review)</li><li>Revealed the preference of transposon insertion sites in <i>Drosophila</i>. (Cao and Yu et al., <b>NAR</b>, 2023)</li><li>Studied the transcriptome and genome in single-cell level of human brain aging. (Jeffries and Yu et al., Under Minor Revision at <b>Nature</b>)</li><li>Uncovered the link between elevated somatic deletions and Parkinson's diseases in human neurons. (Ziegenfuss and Yu et al., in Preparation)</li><li>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., <b>RNA</b>, 2023; Zhang and Yu et al., <b>Dev. Cell</b>, 2021)</li></ul>	

<b>Ph.D. Student</b>	2014 – 2020
Tongji University, China	
<ul style="list-style-type: none"><li>Determined long-first-exon as the feature that differs pachytene piRNA genes from typical protein-coding genes and lincRNAs. (Yu et al., <b>Nat. Commun.</b>, 2021)</li><li>Annotated human pachytene piRNA genes and found they are highly divergent among modern humans. (Ozata and Yu et al., <b>Nat. Ecol. Evol.</b>, 2020)</li></ul>	

<b>Visiting Scholar</b>	2017 – 2019
University of Massachusetts Chan Medical School, USA	
<ul style="list-style-type: none"><li>Discovered the innate response of piRNA pathway to retroviral invasion in the koala germline. (Yu et al., <b>Cell</b>, 2019)</li></ul>	

## MENTORSHIP EXPERIENCE

Jichuan Cao, Ph.D. 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

## GRANT APPLICATION

## SOFTWARE

- **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>

## PUBLICATIONS

### Peer-reviewed Articles

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. 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.
3. **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.
4. Cecchini K\*, Biasini A\*, **Yu T\***, Säflund 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.
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. **Nucleic Acids Research**. 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. **Nature Communications**. 2021
7. Zhang G\*, **Yu T\***, Parhad SS, Ho S, Weng Z†, Theurkauf WE†. piRNA-independent transposon silencing by the *Drosophila* THO complex. **Developmental 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. **Nature Ecology & Evolution**. 2020.
9. Parhad SS, **Yu T**, Zhang G, Rice NP, Weng Z†, Theurkauf WE†. Adaptive Evolution Targets a piRNA Precursor Transcription Network. **Cell Reports**. 2020.
10. 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.
11. **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

### Preprints

1. 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. *Under Minor Revision at Nature*, **bioRxiv**.
2. **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**.

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

\* co-first authors

† corresponding authors

## ABSTRACTS

### **Oral Presentations**

1. The Evolution of piRNA Genes in Mammals.

EMBO piRNA workshop. Virtual. Apr 2022.

2. Lack of Splicing Distinguishes piRNA-producing Transcripts from other RNAs in Mammals.

8<sup>th</sup> Annual RNA Symposium. Virtual. Mar 2022

3. Epigenetic and Chromosomal Features Drive Transposon Insertion in *Drosophila Melanogaster*.

Epigenetics Club Seminar at University of Massachusetts Chan Medical School. Worcester, MA. Dec 2022

### **Poster Presentations**

1. The Transition from Innate to Adaptive Silencing of a Retroviral Genome invader in Koalas.

NHGRI annual trainee meeting. Salt Lake City, UT. Apr 2023

## ACADEMIC AND COMMUNITY SERVICE

Peer reviewers: Human Genetics and Genomics Advances, PCI Genomics.

Research software and pipelines development, maintenance, and support for community use.

## REFERENCES

### **Dr. Zhiping Weng**

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