De-An Li

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Education

9/2019 - 6/2024 **PhD in Cell Biology, Interdisciplinary Research Center on Biology and Chemistry, Chinese Academy of Sciences, China**

'Development and Application of Computational Methods for Metabolite Modified Epitranscriptomics'

Supervisor: Professor Nan Liu

Planned dissertation submission: May, 2024

9/2015 - 6/2019 **B.S. in Biology, Jinan University, China**

Research Experience

Aging Fly Cell Landscape

- Provided the aging fly cell landscape, a single-nucleus transcriptomic map that characterizes changes in *Drosophila* across life span.
- Investigated age-related gene expression changes, alterations in cell compositions, and pathways that correlate with aging.

NAD-RNA Epitranscriptome Analysis of Normal Aging Cohort

- Proposed the first computational framework for the quantitative analysis of NAD-capped epitranscriptome, enONE, empowering the quantitative and comparative analysis of NAD-RNA-seq data (https://github.com/thereallda/enONE).
- Revealed the NAD-modified epitranscriptome from human peripheral blood and their age-related dynamics.
- Using machine learning strategies, developed an accurate age prediction model that combined epitranscriptomic and transcriptomic signatures.
- Developed an online platform, NADepot, for exploring and accessing NAD-RNA profiles across species (https://lida.shinyapps.io/NADepot/).

NAD-RNA Epitranscriptome Analysis of Aging Mouse

- Involved in the development of novel methods ONE-seq to specifically capture NAD-RNA, and developed a computational pipeline for NAD-RNA data analysis (https://github.com/thereallda/ONE-seq).
- Revealed NAD-RNA profiles in adult and aged mouse liver, as well as the changes in NAD capping during the aging process.

NAD-RNA Epitranscriptome Analysis of Beagle Dog

- Revealed the NAD-modified epitranscriptome in peripheral blood from beagle dogs, as well as the change of NAD capping upon mild NAD intermediate supplementation.
- Using machine learning strategies, identified a set of NAD-RNA biomarkers that can sensitize the mild NAD intermediate exposure from the peripheral blood of beagle dogs.

Epitranscriptome-wide Percentage Assessment of Metabolite-capped RNA

- Involved in the development of novel methods CompasSeq for the comprehensive assessment of metabolite-capped RNA, including NAD-, FAD-, and dpCoA-RNA.
- Developed a novel algorithm, CompassAnalyzer, for the quantitative assessment of the ratio between metabolite- and m^7G-capped forms of each transcript (https://github.com/thereallda/compassanalyzer).

Epitranscriptome-wide Profiling Strategy of dpCoA-capped RNA

- Developed novel methods dpCoA-RNA-seq to specifically capture dpCoA-capped RNA.
- Investigated the functional impacts of RNA 5' dpCoA-capping, including translation and stability.

Publications

1. **<u>Li, D.#</u>**, Ge, S.#, Liu, Y.#, Pan, Miao.#, Wang, X., Han, G., Zou S., Liu, R., Niu, K., Zhao, C., Liu, N., Qu, L. (2023). Epitranscriptome analysis of NAD-capped RNA by spike-in-based normalization and prediction of chronological age. *iScience,* 26(12), 108558. https://doi.org/10.1016/j.isci.2023.108558 **(#equal contribution)**

2. Niu, K#., Zhang, J.#, Ge, S.#, **<u>Li, D.#</u>**, Sun, K., You, Y., Qiu, J., Wang, K., Wang, X., Liu, R., Liu, Y., Li, B., Zhu, Z. J., Qu, L., Jiang, H., & Liu, N. (2023). ONE-seq: epitranscriptome and gene-specific profiling of NAD-capped RNA. *Nucleic Acids Research*, *51*(2), e12. https://doi.org/10.1093/nar/gkac1136 **(#equal contribution)**

3. Liu, Y.#, **<u>Li, D.#</u>**, Liu, N. CompasSeq: epitranscriptome-wide percentage assessment of metabolite-capped RNA at the transcript resolution. *Nucleic Acids Research* (*revision*) **(#equal contribution)**

4. Ni, J., Ren, Y., Su, T., Zhou, J., Fu, C., Lu, Y., **<u>Li, D.</u>**, Zhao, J., Li, Y., Zhang, Y., Fang, Y., Liu, N., Geng, Y., & Chen, Y. (2023). Loss of TDP−43 function underlies hippocampal and cortical synaptic deficits in TDP−43 proteinopathies. *Molecular Psychiatry*, 28, 931–945. https://doi.org/10.1038/s41380-021-01346-0

5. Ge, S., Wang, X., Niu, K., Wang, T., **<u>Li, D.</u>**, Liu, R., Zhao, C., Liu, N. (2023). Hidden features of NAD-RNA epitranscriptome in *Drosophila* life cycle. *iScience*

6. Li, J., Cao, Y., Niu, K., Qiu, J., Wang, H., You, Y., **<u>Li, D.</u>**, Luo, Y., Zhu, Z., Zhang, Y., & Liu, N. (2022). Quantitative Acetylomics Reveals Dynamics of Protein Lysine Acetylation in Mouse Livers During Aging and Upon the Treatment of Nicotinamide Mononucleotide. *Molecular & Cellular Proteomics*, 21. https://doi.org/10.1016/j.mcpro.2022.100276

7. Wu, X., Niu, K., Wang, X., Zhao, J., Wang, H., **<u>Li, D.</u>**, Wang, H., Miao, T., Yang, Y., Ma, H., Zhang, Y., Pan, L., Liu, R., Bai, H., & Liu, N. (2021). microRNA−252 and FoxO repress inflammaging by a dual inhibitory mechanism on dawdle-mediated TGF−β pathway in *drosophila*. *Genetics*, 220(3). https://doi.org/10.1093/genetics/iyab234

Conferences

1. China Aging and Anti-aging Conference (poster), China, 2023
2. Longevity Forum (poster), China, 2023

Awards

1. Scholarship for Graduate Excellence of the Interdisciplinary Research Center on Biology and Chemistry, 2023
2. Outstanding Student of the University of Chinese Academy of Sciences, 2021

Technical Skills

- **Computational**: R, Python, Linux, HTML, CSS, MySQL, server maintenance, website development, and database deployment.
  - Developed pipelines for scRNA-seq, bulk RNA-seq, ChIP-seq, RIP-seq, epitranscriptomic data, Nanopore sequencing data, DNA methylation sequencing data analysis.
  - Experience in machine learning and deep learning.
- **Experimental**: molecular cloning, cell and bacteria culture, CRISPR/Cas9, NAD-RNA and NCIN-RNA capture and sequencing.