Department seminar

日時：5 月 15 日（木）、16:30-17:30

場所：工学部 3 号館 8B04 講義室

演者：Ru-Juan LIU
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Decoding the Complexity of tRNA Gene Expression in Mammalian Cells

Transfer RNAs (tRNAs) are indispensable for translating 61 codons into 20 amino acids, the universal building blocks of proteins. Despite this seemingly straightforward decoding requirement, mammalian genomes encode over 500 nuclear tRNA genes, organized into approximately 45 isoacceptor families. Each family includes multiple isodecoders that share the same anticodon but differ in body sequences, raising questions about the functional necessity and regulation of this extensive tRNA gene repertoire. Mutations in tRNA modification enzymes, despite tRNAs' universal importance, predominantly lead to specific human diseases such as neurodevelopmental disorders, metabolic syndromes, and cancers. This paradox highlights major gaps in understanding how tRNA biology contributes to tissue-specific regulation and pathology. Progress has been limited by the lack of sensitive methods for profiling tRNA expression at high resolution with minimal input. Here, we introduce an ultra-low input sequencing approach that simultaneously detects full-length tRNAs and tRNA-derived fragments (tdRs) using as few as five cells. Applying this strategy across 26 mouse hematopoietic cell types, we reveal dynamic remodeling of tRNA and tdR expression during lineage commitment and differentiation. We identify over 50 tRNA isodecoders with strong cell type-specific expression patterns, suggesting specialized regulatory roles during hematopoiesis. These findings provide new insights into the diversity and functional specificity of the tRNA pool in mammalian development.

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