**OE3C 2024 - Abstract for a TALK**

Tittle: "Exploring noncoding transcriptomes from organelle genomes by using long-read data"

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Mitochondria and chloroplasts are information processing hubs with genomes inherited from prokaryotic ancestors. Despite billions of years of reductive evolution (via Endosymbiotic Gene Transfer), organelle genomes exhibit a remarkable diversity in size, content, and structure. Just as convoluted, organelle transcriptomes can be seen as hybrid system - a prokaryotic relic entombed in a eukaryotic vessel. By using publicly available RNA-Seq data, I have demonstrated that organelle genomes are pervasively transcribed. The essence of these transcriptomes was hard to dissect because of the nature of short Illumina reads. As public repositories (such as NCBI SRA) are finally teeming with high-quality 3rd-generation RNA-Seq data (e.g., ONT and PacBio), I can investigate organelle transcriptomes in a detail not possible before. I have first (re)annotated the noncoding portion of ~ 36K organelle genomes and found hundreds of potential ncRNA genes of various sizes. I am now tapping onto long RNA data to identify these ncRNAs and sORFs with putative functions. Given the plethora of ncRNAS and micropeptides found elsewhere in the cell(s), I hypothesize that organelle genomes and transcriptomes are a treasure trove of regulatory elements.