

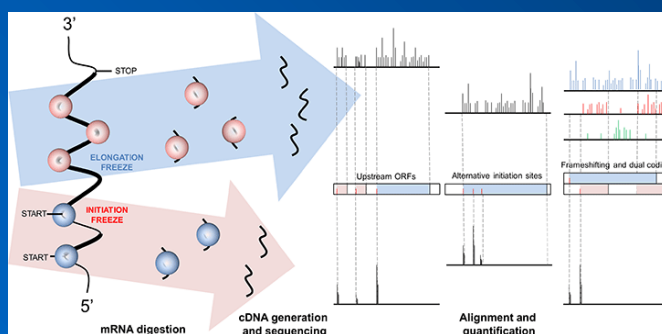
Diversity of human RNA decoding

Parvel Baranov
Professor
University College Cork
Ireland

Host: Dr. Katsura Asano
Professor, Specially Appointed
Laboratory of Translational
Control Study
Graduate School of Integrated
Sciences for Life
Hiroshima University

《Summary》

Proteins play diverse functions in our cells as enzymes, scaffolds for our cell structure, molecular motors, membrane channels, receptors, etc. Cells spend most of their energy on the biosynthesis of proteins. Therefore, it is important to understand the full repertoire of proteins encoded by the human genome. Recent evidence suggests the existence of numerous proteins and proteoforms encoded outside of currently annotated genomic regions. To help identification of these proteoforms we established several computational tools (GWIPS-viz and Trips-Viz) for the evaluation of processed publicly available high-throughput data (RNA-seq, ribosome profiling, mass spec proteomics, etc). The evaluation of these data in combination with orthogonal approaches for studying expression of individual genes suggests that the plurality of translation initiation sites (enabled by leaky scanning and reinitiation) is the main contributor to the observable decoding diversity together with hitherto poorly characterized heterogeneity of RNA transcripts.



本セミナーは、統合生命科学研究科セミナーとして、プログラム共同セミナーの対象です

開催日時: 令和4年 6月 28日(火) 16:00-17:00

Zoomによるwebセミナー
ミーティングID: 853 7102 0570
パスコード: 415199

お問い合わせ先 広島大学大学院統合生命科学研究科
HiHA事務局 (healthy-aging@hiroshima-u.ac.jp)