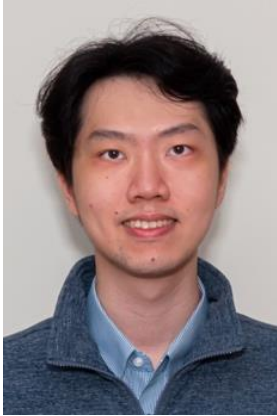




# Hong Kong RNA Club

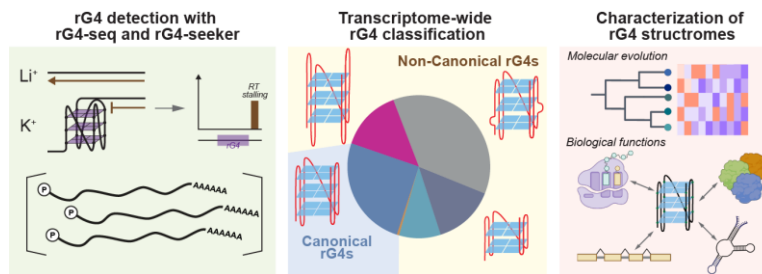


## RNA Enthusiast Spotlight (Mar 2023)



**Mr. Eugene Yui-Ching Chow** is a Ph.D. student in Dr. Ting-Fung Chan's lab at the Chinese University of Hong Kong. He received the Hong Kong Ph.D. Fellowship in 2016. He was selected young scientist participant for the interdisciplinary 70th Lindau Nobel Laureate Meeting in 2021. He can be reached at [eugenechow823@gmail.com](mailto:eugenechow823@gmail.com).

Eugene's work focused on studying the RNA G-quadruplex (rG4) structures from an RNomics and bioinformatics approach. Collaborating with Dr. Chun-Kit Kwok's lab at the City University of Hong Kong, he established a bioinformatic pipeline *rG4-seeker* that improved the outcomes of experimental, transcriptome-wide rG4 detection by incorporating a novel background noise model. The work laid the foundation for further studies that revealed the prevalence and significance of the non-canonical species of rG4s in humans, plasmodium, and other model organisms. His ongoing work involves characterizing rG4s from functional and evolutionary perspectives.



### Recent Representative Publications

Zhao J<sup>†</sup>, **Chow EY<sup>†</sup>**, Yeung PY, Zhang QC, Chan TF, Kwok CK. (2022). Enhanced transcriptome-wide RNA G-quadruplex sequencing for low RNA input samples with rG4-seq 2.0. *BMC Biol*, 20(1), 257.

Dumetz F<sup>†</sup>, **Chow EY<sup>†</sup>**, Harris LM, Umar MI, Jensen A, Chung B, Chan TF, Merrick CJ, Kwok CK. (2021) G-quadruplex RNA motifs influence gene expression in the malaria parasite *Plasmodium falciparum*. *Nucleic Acids Res*. 49 (21), 12486-12501.

Lyu K<sup>†</sup>, **Chow EY<sup>†</sup>**, Mou X<sup>†</sup>, Chan TF, Kwok CK. (2021) RNA G-quadruplexes (rG4s): genomics and biological functions. *Nucleic Acids Res*. 49 (10), 5426-5450.

**Chow EY**, Lyu K, Kwok CK, Chan TF. (2020). rG4-seeker enables high-confidence identification of novel and non-canonical rG4 motifs from rG4-seq experiments. *RNA biology*, 17(7), 903-917.

(<sup>†</sup> denotes joint first authors)

Eugene is interested in an interdisciplinary research theme combining data science, bioinformatics, and RNA biology. He believes that the increasing number and diversity of RNomics datasets generated by the community will enable more refined metanalysis to elucidate deep RNA sequences and structures, reveal the crosstalks between different elements, and predict associated phenotypic changes.

Written by Eugene Yui-Ching Chow, edited by Kaixin Lyu and Hill Lam Lau (HKRNAclub Team)



**Dr. Ting-Fung Chan** is an associate professor in the School of Life Sciences at the Chinese University of Hong Kong. He is the co-director of the Hong Kong Bioinformatics Center and an investigator in the State Key Laboratory for Agrobiotechnology, CUHK. He can be reached at [tf.chan@cuhk.edu.hk](mailto:tf.chan@cuhk.edu.hk).

Dr. Chan's group applies RNomics and bioinformatics to study the genotype-phenotype relationships of RNAs in biological processes. His team focuses on experimentally identifying regulatory transcripts and computationally characterizing RNA regulatory elements in model organisms, employing cutting-edge high-throughput methods, including Nanopore and single-cell sequencing. His group's findings contribute to understanding novel RNA players in cellular mechanisms and their influence on normal and diseased pathways. Dr. Chan's group is also interested in developing technologies and algorithms to generate and integrate RNomics and other multi-omics datasets to explore novel biological questions. Please find more information on the website: <http://goo.gl/vl4tf>; and Twitter: @TFChan5.

### **Recent Representative Publications**

Zhang J, Lin X, Chen Y, Li TH, Lee AC, Chow EY, Cho WC, **Chan TF\***. (2022) LAFITE reveals the complexity of transcript isoforms in subcellular fractions. *Adv Sci (Weinh)*. 2022 Dec 3:e2203480.

Chen Y, Wang Y, Chen Y, Cheng Y, Wei Y, Li Y, Wang J, Wei YY, **Chan TF\***, Li Y\*. (2022) Deep autoencoder for interpretable tissue-adaptive deconvolution and cell-type-specific gene analysis. *Nat Commun* 13 (1), 1-17.

Dumetz F, Chow EY, Harris LM, Umar MI, Jensen A, Chung B, **Chan TF\***, Merrick CJ\*, Kwok CK\*. (2021) G-quadruplex RNA motifs influence gene expression in the malaria parasite *Plasmodium falciparum*. *Nucleic Acids Res*. 49 (21), 12486-12501.

Lyu K, Chow EY, Mou X, **Chan TF\***, Kwok CK\*. (2021) RNA G-quadruplexes (rG4s): genomics and biological functions. *Nucleic Acids Res*. 49 (10), 5426-5450.

Lin X, Lin W, Ku YS, Wong FL, Li MW, Lam HM\*, Ngai SM\*, **Chan TF\*** (2020) Analysis of soybean long non-coding RNAs reveals a subset of novel small peptide-coding transcripts. *Plant Physiol* 182(3):1359-74.

(\* denotes corresponding authors)



Dr. Chan is fascinated by the elegance and versatility of RNA-driven regulatory mechanisms that underlie living organisms' adaptivity to changes. He believes that the non-coding information on transcripts could be translated into a chain of functional motifs, structures, and modified bases, whereby profiling and deciphering these elements would be the key to understanding the RNome.

Written by Dr. Ting-Fung Chan, edited by Kaixin Lyu and Hill Lam Lau (HKRNAclub Team)

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