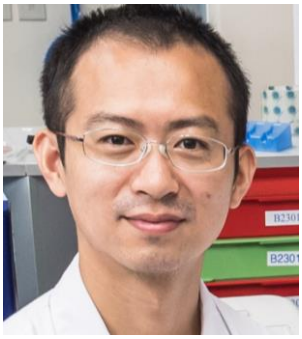
Hong Kong RNA Club

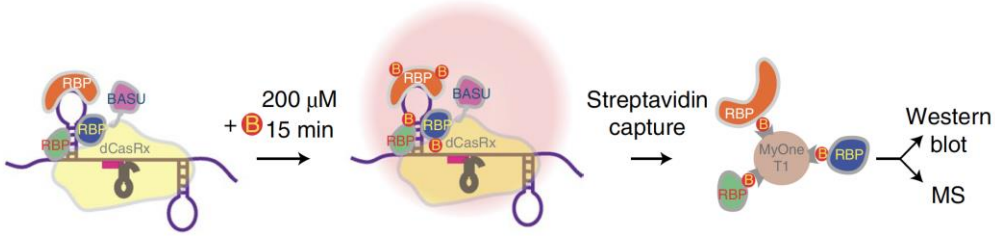
RNA Enthusiast Spotlight (Apr 2023)



Mr. Wenkai Yi is a Ph.D. student in Dr. Jian Yan's laboratory in the Department of Biomedical Sciences, Jockey Club College of Veterinary Medicine and Life Sciences, City University of Hong Kong. He could be reached at kaiyi2-c@my.cityu.edu.hk.

Wenkai's research focuses on elucidating the molecular mechanism of human endogenous retrovirus subfamily H (HERV-H) RNA-mediated 3D genome organization in human embryonic stem cells. To reach this goal, Wenkai has participated in establishing several practical approaches to study the roles of RNA in chromatin remodeling, including the invention of the CARPID method.

Wenkai has been involved in developing a CRISPR-assisted RNA-protein interaction detection method (CARPID), which leverages CRISPR/dCasRx-based RNA targeting and proximity labeling of biotin ligase BASU to identify binding proteins of RNA in the living cells. In this method, BASU-dCasRx fusion proteins and gRNA targeting specific RNA were first expressed in cells, then located near the given RNA after assembly. Second, by adding a high concentration of biotin in the medium for 15 min, the adjacent proteins of RNA targeted by CRISPR/BASU-dCasRx were effectively biotinylated for the following enrichment with streptavidin beads. At last, these biotinylated proteins associated with RNA were identified with Mass Spectrometry analysis and Western Blot. For specific RNA binding protein identification, CARPID has been successfully applied to several kinds of lncRNA with different localization and expression levels, like lncRNA XIST, MALAT1, and DANCR (Yi et al. *Nature Methods*, 2020).

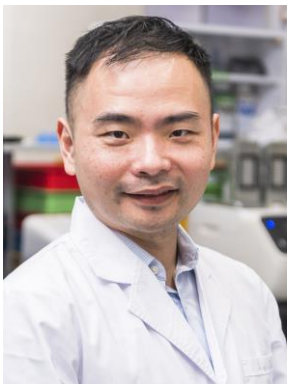


Recently, Wenkai continues developing CARPID 2.0 by employing the ribonucleoprotein (RNP)-based delivery strategy, which works well for difficult-to-transfect embryonic stem cell lines and cancer cell lines. For example, CARPID 2.0 method has been validated with high specificity and efficiency to identify the binding proteins of a given endogenous RNA in human embryonic stem cell line H9 and cancer cell lines MCF7 and U2OS. Finally, Wenkai and his supervisor Dr. Yan hope their newly developed method will be widely applied in the RNA community to foster the identification of RNA-binding proteins.

Recent representative publications

Yi, W., J. Li, X. Zhu, X. Wang, L. Fan, W. Sun, L. Liao, J. Zhang, X. Li, J. Ye, F. Chen, J. Taipale, K. M. Chan, L. Zhang and J. Yan (2020). "CRISPR-assisted detection of RNA-protein interactions in living cells." ***Nature Methods*** 17(7): 685-688.

Written by Mr. Wenkai Yi, edited by Kaixin Lyu (HKRNAClub Team)



Dr. Jian Yan is an assistant professor in the Department of Biomedical Sciences at City University of Hong Kong. In 2021, he received the university's prestigious prize of "Outstanding Research Award for Junior Faculty".

Dr. Yan's group at BMS CityU focuses on unraveling the molecular mechanism of how long noncoding RNAs (lncRNAs) affect cellular function and human health issues, using high throughput, state-of-the-art tools. He has invented several methods such as CARPID and Chrom-seq and applied them to delineate the molecular mechanism of lncRNAs in mammalian development and diseases. Dr. Yan is also interested in understanding the function of noncoding DNA/chromatin in regulating gene transcription and their impact on human/animal health. Please find more information on the website. http://www.cityu.edu.hk/bms/profile/jianyan.htm

Recent representative publications

J. Yan*,#, Y. Qiu*, A.M.R. dos Santos*, Y. Yin, Yang E. Li, N. Vinckier, N. Nariai, P. Benaglio, A. Raman, X. Li, S. Fan, J. Chiou, F. Chen, K.A. Frazer, K.J. Gaulton, M. Sander, J. Taipale#, B. Ren#, Systematic analysis of binding of transcription factors to noncoding variants, ***Nature*** (2021) 591:147–151

W. Yi*, J. Li*, X. Zhu*, X. Wang*, L. Fan, W. Sun, L. Liao, J. Zhang, X. Li, J. Ye, F. Chen, J. Taipale, K.M. Chan#, L. Zhang#, **J. Yan**#, CRISPR-assisted detection of RNA-protein interactions in living cells, ***Nature Methods*** (2020) 17(7):685–688

L. Fan*, T. Wang*, C. Hua*, W. Sun*, X. Li, L. Grunwald, J. Liu, N. Wu, X. Shao, Y. Yin, **J. Yan**#, X. Deng#, A compendium of DNA-binding specificities of transcription factors in Pseudomonas syringae, ***Nature Communications*** (2020) 11(1):4947

S. Fan*, W. Sun*, L. Fan*, N. Wu, W. Sun, H. Ma, S. Chen, Z. Li, Y. Li, J. Zhang, **J. Yan**#, The highly conserved RNA-binding specificity of nucleocapsid protein facilitates the identification of drugs with broad anti-coronavirus activity, ***Computational and Structural Biotechnology Journal*** 20 (2022) 5040-5044

Most human genome sequences are non-coding but not "non-function". These non-coding fractions are responsible for over 90% of the complex non-Mendelian genetic diseases, such as cancer, and cardiovascular and metabolic diseases. Dr. Yan has always believed that dissection of the function of the non-coding genome is one of the most pivotal steps towards understanding ourselves and provides the basis for developing solutions to many health issues.

"Where there is a will, there is a way", quoted from the *Book of the Later Han* (by Fan Ye). Being a mentor, Dr. Yan encourages his students and staff to be "persistent" in doing research and always accompanies them on the odysseys. He believes there's still a long journey to fully understand the function of non-coding RNAs and other non-coding elements in the human genome. But it deserves our passion to be devoted that will ultimately facilitate finding treatment for many critical diseases. Dr. Yan hopes that more and more passionate scientists can come to Hong Kong and join our RNA community.

Written by Dr. Jian Yan, edited by Kaixin Lyu (HKRNAClub Team)

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