

CURRICULUM VITAE

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Research Interests

My research focuses on integrating approaches from evolutionary genomics, mathematical statistics, machine learning and computational biology to understand various evolutionary processes. I am particularly interested in investigating the relative contributions of stochastic and deterministic forces to evolutionary phenomena across three major research directions:

1. **Adaptive evolution of viruses.** I explore viruses such as SARS-CoV-2, IBV, and PEDV to understand their adaptive evolution, including factors such as origin, cross-species transmission, intra- and inter-host evolution, and spread dynamics of emerging variants. This research direction contributes to my understanding of viral evolution and its implications for public health.
2. **Theoretical aspects of traditional evolutionary processes.** I delve into theoretical aspects of traditional evolutionary processes by combining evolutionary approaches with mathematical modeling, machine learning, and computational simulation. By analyzing publicly available data, I aim to understand various aspects of evolution, including mutation rate, individual-based genetic drift, epistasis, fitness landscapes, and Hill-Robertson effect. This interdisciplinary approach helps me uncover fundamental principles underlying evolutionary dynamics.
3. **Cancer evolutionary dynamics.** I focus on understanding the evolutionary dynamics of cancer, including tumorigenesis, heterogeneity, and metastasis. By applying population genetics theory, I aim to elucidate how mutation, selection, genetic drift, and migration drive tumor evolution, leveraging insights from cancer genomics. This research has implications for cancer diagnosis, prognosis, and treatment strategies.

Education

Year/Period	Degree	Thesis	Institution
09/2015 – 08/2020	Ph.D. in Biochemistry and Molecular Biology	Theoretical Study on Evolution of Mutation Rate in Soma and Germline Cell	School of Life Sciences, Sun Yat-sen University Mentor: Prof. Chung-I Wu
09/2011 – 07/2015	B.S. in Biotechnology	Heat shock impact on the development of <i>dcr-1</i> ^{RNAi} <i>Drosophila Melanogaster</i>	School of Life Sciences, Sun Yat-sen University

Employment

Year/Period	Position	Institution
11/2020 – 10/2022	Postdoctoral Research Fellow	School of Life Science, Sun Yat-sen University
11/2022 – date	Research Associate	School of Life Science, Sun Yat-sen University

Honors and Awards

11/2022	Beijing Science and Technology Award - Science and Technology Progress Award, Second Prize (北京市科学技术进步奖二等奖)
05/2021	National Postdoctoral Innovative Talents Supporting Program (博士后创新人才支持计划)
12/2017	Third prize of the 14 th China Post-Graduate Mathematical Contest in Modeling
08/2012	Outstanding student scholarship, Sun Yat-sen University

Funding

Year/Period	Project title, Grant number, Funding agency, Award amount, Role
01/2023 – 12/2024	A theoretical study on adaptive evolution of SARS-CoV-2 variants within and among individuals, 32200493, National Natural Science Foundation of China, 200,000 RMB, PI (主持)
07/2021 – 02/2023	The origin tracing of SARS-CoV-2 and evaluation of epidemic prevention and control strategies based on adaptive evolution theory, BX2021395, National Postdoctoral Innovative Talents Supporting Program (博士后创新人才支持计划), 630,000 RMB, PI (主持)
01/2022 – 12/2024	Domestication of mammalian cells and evolution between unicellular and multicellular organisms, 32150006, National Natural Science Foundation of China, 2,980,000 RMB, Participant (参与)

Publications (# co-first authors, * corresponding authors)

Published:

- (1) Hou M[#], Shi J[#], Gong Z, Wen H, Lan Y, Deng X, Fan Q, Li J, Jiang M, Tang X*, Wu C I*, Li F* & **Ruan Y***. Intra- vs. Interhost Evolution of SARS-CoV-2 Driven by Uncorrelated Selection-The Evolution Thwarted. *Mol. Biol. Evol.* 40, doi: 10.1093/molbev/msad204 (2023).
- (2) **Ruan Y**, Wen H, Hou M, Zhai W, Xu S & Lu X. On the epicenter of COVID-19 and the origin of the pandemic strain. *Natl. Sci. Rev.* 10, nwac286, doi: 10.1093/nsr/nwac286 (2023).
- (3) **Ruan Y**[#], Hou M[#], Tang X[#], He X, Lu X, Lu J*, Wu C I* & Wen H*. The Runaway Evolution of SARS-CoV-2 Leading to the Highly Evolved Delta Strain. *Molecular Biology and Evolution* 39, msac046, doi:10.1093/molbev/msac046 (2022).
- (4) **Ruan Y**, Wen H, Hou M, He Z, Lu X, Xue Y, He X, Zhang Y P* & Wu C I*. The twin-beginnings of COVID-19 in Asia and Europe-one prevails quickly. *National Science Review* 9, nwab223, doi:10.1093/nsr/nwab223 (2022).
- (5) **Ruan Y**, Luo Z, Tang X, Li G, Wen H, He X, Lu X, Lu J* & Wu C I*. On the founder effect in COVID-19 outbreaks: how many infected travelers may have started them all? *National Science Review* 8, nwaa246, doi:10.1093/nsr/nwaa246 (2021).
- (6) **Ruan Y**, Wen H, He X & Wu C I*. A theoretical exploration of the origin and early evolution of a pandemic. *Science Bulletin* 66, 1022-1029, doi:10.1016/j.scib.2020.12.020 (2021).
- (7) **Ruan Y**, Wang H, Chen B, Wen H* & Wu C I*. Mutations Beget More Mutations-Rapid Evolution of Mutation Rate in Response to the Risk of Runaway Accumulation. *Molecular Biology and Evolution* 37, 1007-1019, doi:10.1093/molbev/msz283 (2020).
- (8) Wu C I*, Wen H, Lu J, Su X D, Hughes A C, Zhai W, Chen C, Chen H, Li M, Song S, Qian Z, Wang Q, Chen B, Guo Z, **Ruan Y**, Lu X, Wei F, Jin L, Kang L, Xue Y, Zhao G & Zhang Y P. On the origin of SARS-CoV-2-The blind watchmaker argument. *Science China Life Sciences* 64, 1560-1563, doi:10.1007/s11427-021-1972-1 (2021).
- (9) Chen B[#], Wu X[#], **Ruan Y**, Zhang Y, Cai Q, Zapata L, Wu C I*, Lan P* & Wen H*. Very large hidden genetic diversity in one single tumor: evidence for tumors-in-tumor. *National Science Review* 9, nwac250, doi:10.1093/nsr/nwac250 (2022).
- (10) Zhang L[#], Qin Z[#], Huang T, Tam B, **Ruan Y**, Guo M, Wu X, Li J, Zhao B, Chian J S, Wang X, Wang L & Wang S M*. Prevalence and spectrum of DNA mismatch repair gene variation in the general Chinese population. *Journal of Medical Genetics*, jmedgenet-2021-107886, doi:10.1136/jmedgenet-2021-107886 (2021).
- (11) Ma F[#], Lu G-A[#], Chen Q, **Ruan Y**, Li X, Lu X* & Li C*. Dynamic global analysis of transcription reveals the role of miRNAs in synergistic stabilization of gene expression. *Science Bulletin* 65, 2130-2140, doi:10.1016/j.scib.2020.08.011 (2020).

Preprint:

- (1) **Ruan Y**, Wang X, Hou M, Diao W, Xu S, Wen H & Wu C-I. Resolving Paradoxes in Molecular Evolution: The Integrated WF-Haldane (WFH) Model of Genetic Drift. *bioRxiv*, 2024.2002.2019.581083, doi: 10.1101/2024.02.19.581083 (2024).
- (2) Lee D-C[#], Tai J-H[#], Lin H-F[#], Chao T-L, **Ruan Y**, Cheng Y-W, Chou Y-C, Lin Y-Y, Chang S-Y,

- Chen P-J, Yeh S-H* & Wang H-Y*. Antagonistic pleiotropy plays an important role in governing the evolution and genetic diversity of SARS-CoV-2. *bioRxiv*, 2023.2002.2010.527437, doi:10.1101/2023.02.10.527437 (2023).
- (3) **Ruan Y**[#], Hou M[#], Li J[#], Song Y[#], Wang H-Y I, He X, Zeng H, Lu J, Wen H*, Chen C* & Wu C-I*. One viral sequence for each host? – The neglected within-host diversity as the main stage of SARS-CoV-2 evolution. *bioRxiv*, 2021.2006.2021.449205, doi:10.1101/2021.06.21.449205 (2021).
- (4) **Ruan Y**, Wang H, Zhang L, Wen H* & Wu C-I*. Sex, fitness decline and recombination – Muller’s ratchet vs. Ohta’s ratchet. *bioRxiv*, 2020.2008.2006.240713, doi:10.1101/2020.08.06.240713 (2020).

Academic Presentations

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| 10/2023 | <u>Yongsen Ruan</u> . “The paradox of genetic drift and the solution by the Haldane model based on the branching process”. Poster Presentation at the SMBE regional meeting, Shanghai, China. |
| 04/2023 | <u>Yongsen Ruan</u> . “The study on the adaptive evolution of SARS-CoV-2”. Invited Seminar , Wuhan Institute of Virology, Wuhan, China |
| 07/2019 | <u>Yongsen Ruan</u> , Chung-I Wu. “Mutations beget more mutations – The evolution of mutation rate and the runaway accumulation”. Oral Presentation (OR-051) at the Annual Meeting of the Society for Molecular Biology and Evolution, Manchester, England. |
| 07/2018 | <u>Yongsen Ruan</u> , Ao Lan, Chung-I Wu. “Different types of cell migration during tumor growing process lead to spatial patterns of genetic variation”. Poster Presentation (POB-086) at the Annual Meeting of the Society for Molecular Biology and Evolution, Pacifico Yokohama, Yokohama, Japan. |

Professional Services

Ad-hoc Reviewers for journals:

- *Nature Communications*
- *National Science Review*
- *Molecular Biology and Evolution*
- *Journal of Medical Virology*
- *Virologica Sinica*
- *BMC Cancer*