

## 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> <sup>RNAi</sup> <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 <sup>th</sup> 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)

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### Published:

- (1) Hou M<sup>#</sup>, Shi J<sup>#</sup>, 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**<sup>#</sup>, Hou M<sup>#</sup>, Tang X<sup>#</sup>, 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<sup>#</sup>, Wu X<sup>#</sup>, **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<sup>#</sup>, Qin Z<sup>#</sup>, 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<sup>#</sup>, Lu G-A<sup>#</sup>, 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<sup>#</sup>, Tai J-H<sup>#</sup>, Lin H-F<sup>#</sup>, 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**<sup>#</sup>, Hou M<sup>#</sup>, Li J<sup>#</sup>, Song Y<sup>#</sup>, 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 | <b><u>Yongsen Ruan</u></b> . “The paradox of genetic drift and the solution by the Haldane model based on the branching process”. <b>Poster presentation</b> at the SMBE regional meeting, Shanghai, China.   |
| 07/2019 | <b><u>Yongsen Ruan</u></b> , Chung-I Wu. “Mutations beget more mutations – The evolution of mutation rate and the runaway accumulation”. <b>Oral presentation</b> (OR-051) at the Annual Meeting of the Society for Molecular Biology and Evolution, Manchester, England.   |
| 07/2018 | <b><u>Yongsen Ruan</u></b> , Ao Lan, Chung-I Wu. “Different types of cell migration during tumor growing process lead to spatial patterns of genetic variation”. <b>Poster presentation</b> (POB-086) at the Annual Meeting of the Society for Molecular Biology and Evolution, Pacifico Yokohama, Yokohama, Japan. |

## Professional Services

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*Ad-hoc* Reviewers for journals:

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