#### **CURRICULUM VITAE**

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## **Research Interests**

I'm interested in the theoretical population genetics and specialized in computational biology and mathematical modelling. My research focuses on exploring how mutation, selection, genetic drift, and migration to affect evolutionary dynamics, including tumor evolution (tumorigenesis, cancer metastasis, tumor heterogeneity), aging, and viral evolution. In addition, I'm interested in theoretical aspects of traditional evolutionary processes, including the evolution of sex, how recombination and beneficial mutations affect the fitness dynamics of a population, rigorous characterization of Hill-Robertson effect.

Recently, I'm paying much attention to the project on evolution of SARS-CoV-2, including the origin, cross-species transmission, intra- and inter-host evolution, spread dynamics of variants of concerns (VOCs). This project mainly focuses on the spatiotemporal distribution of new SARS-CoV-2 variants and the evolutionary dynamics of these variants. This project will systematically track the dynamic changes of the viral variants from three levels: intra-individual, inter-individual and global, including exploring the intra-host genetic diversity, estimating the size of the transmission bottleneck between individuals, comparing the relative importance of evolutionary driving forces such as natural selection and random genetic drift in each evolutionary stage. Based on these analyses, we will systematically summarize the adaptive evolution patterns and theory of SARS-CoV-2 at different levels. This project could provide theoretical support and decision-making basis for the scientific prevention and control of COVID-19 pandemic and the blocking of other emergent infectious public events.

#### **Education**

Year/Period	Degree	Thesis	Institution
09/2015 - 08/2020	Ph.D. in Biochemistry	Theoretical Study on	School of Life Sciences,
	and Molecular Biology	Evolution of Mutation Rate in	Sun Yat-sen University
		Soma and Germline Cell	Mentor: Prof. Chung-I Wu
09/2011 07/2015	B.S. in Biotechnology	Heat shock impact on the	School of Life Sciences
09/2011 - 07/2013	B.S. III Diotectinology	development of dcr-1 <sup>RNAi</sup>	· · · · · · · · · · · · · · · · · · ·
		Drosophila Melanogaster	= === = = = = = = = = = = = = = = = =

## **Professional History**

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

#### **Awards and Other Honors**

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 14th China Post-Graduate Mathematical Contest in Modeling
08/2012	Outstanding student scholarship, Sun Yat-sen University

#### **Grants**

Year/Period	Project
2021 - 2023	The origin tracing of SARS-CoV-2 and evaluation of epidemic prevention and control
	strategies based on adaptive evolution theory, National Postdoctoral Innovative Talents
	Supporting Program (博士后创新人才支持计划), 630K RMB

# **Publications** 1-10

- (1) **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. *Mol. Biol. Evol.* **39**, doi:10.1093/molbev/msac046 (2022).
- (2) **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).
- (3) **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? *Natl. Sci. Rev.* **8**, nwaa246, doi:10.1093/nsr/nwaa246 (2021).
- (4) **Ruan Y**, Wen H, He X & Wu C I. A theoretical exploration of the origin and early evolution of a pandemic. *Sci Bull (Beijing)* **66**, 1022-1029, doi:10.1016/j.scib.2020.12.020 (2021).
- (5) **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. *Natl. Sci. Rev.*, doi:10.1093/nsr/nwab223 (2021).
- (6) 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. *Sci China Life Sci* 64, 1560-1563, doi:10.1007/s11427-021-1972-1 (2021).
- (7) 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. *J. Med. Genet.*, jmedgenet-2021-107886, doi:10.1136/jmedgenet-2021-107886 (2021).
- (8) 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. *Sci. Bull.* **65**, 2130-2140, doi:10.1016/j.scib.2020.08.011 (2020).
- (9) **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. *Mol. Biol. Evol.* **37**, 1007-1019, doi:10.1093/molbev/msz283 (2020).

(10) **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**

- 2019-7-22 <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.
- 2018-07-11 Yongsen Ruan, Ao Lan, Chung-I Wu. Different types of cell migration during tumor growing process lead to spatial patterns of genetic variation. Poster (POB-086) presentation at the Annual Meeting of the Society for Molecular Biology and Evolution, Pacifico Yokohama, Yokohama, Japan.