

CURRICULUM VITAE

Xun Chen, Ph.D.

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PROFESSIONAL EXPERIENCE

Program-Specific Assistant Professor, Institute for the Advanced Study of Human Biology

Kyoto University, Kyoto, Japan 2021-2023

Program-Specific Researcher, Institute for the Advanced Study of Human Biology

Kyoto University, Kyoto, Japan 2020-2021

Postdoctoral Associate, Department of Microbiology and Molecular Genetics

University of Vermont, Vermont, United States 2014-2019

EDUCATION

Ph.D., Crop Genetics and Breeding, Huazhong Agricultural University, Wuhan 2008-2014

Research areas: Bioinformatics, Genomics, Epigenomics, Evolution

Minor, Computer Science, Huazhong University of Science and Technology, Wuhan 2005-2006

B.S., Agronomy, Huazhong Agricultural University, Wuhan 2004-2008

SELECTED HONORS & AWARDS

ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research 2017

2017 ACGA/The Association of Chinese Geneticists in America Trainee Awardees 2017

Graduate National Scholarship in China 2013

RESEARCH INTERESTS

My research interests are focused on developing and applying new computational methodologies to

study the evolution and functional roles of non-coding sequences and their involvement in various infectious diseases and cancers. Additionally, I am also interested in using the functional genomics approach to discover new oncoviruses and to systematically interpret the viral etiology in cancers. My ultimate research goal is to understand *what make humans human* and to cure human virus-related diseases using new technologies.

GRANTS

Japan Society for the Promotion of Science (JSPS) Grant-in-Aid for Early-Career Scientists (PI)

2021-2024, ¥ 4,680,000

Transposable elements shape the evolution of mammalian innate immunity against pathogens

Project Area Number: 21K15066

<https://kaken.nii.ac.jp/grant/KAKENHI-PROJECT-21K15066/>

ASHBi Fusion Research Grant (Lead PI)

2020-2022, ¥ 4,400,000

Deciphering evolutionary differences of germline transposable element dynamics

ASHBi Fusion Research Grant (Co-PI)

2022-2024, ¥ 4,400,000

Unraveling transcriptional regulatory mechanism of transposable elements across species

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

2019 - 2023

1. **Chen X**, Pacis A, Aracena A, Gona S, Kwan T, Groza C, Lin YL, Sindeaux R, Yotova V, Pramatarova A, Simon MM, Pastinen T, Barreiro L, Bourque G: **Transposable elements are associated with the variable response to influenza infection.** *Cell Genomics*. 2023 May;3(5):100292. PMID: 37228757 (We depicted major epigenetic shifts in transposable elements (TEs) in human macrophages upon influenza infection; more importantly, for the first time, we reported that TEs are an important source of regulatory variation between individuals)
2. Groza C, **Chen X**, Pacis A, Simon MM, Pramatarova A, Aracena K, Pastinen T, Barreiro L, Bourque G: Genome graphs detect human polymorphisms in active epigenomic states during influenza infection. *Cell Genomics*. 2023 May;3(5):100294. PMID: 37228750
3. **Chen X**[#], Bourque G, Goubert C[#]: Genotyping of transposable element insertions segregating in

- human populations using short-read re-alignments. *Methods Mol Biol.* 2023 Jan;2607:63-83. PMID: 36449158
4. Johnston M, Lee J, Hu B, Nikolic A, Baguette A, Paik S, Chen H, Kumar S, Chen C, Jessa S, Balin P, Fong V, Zwaig M, MichealRaj K, **Chen X**, et al: EPCO-38. Type B ultra long-range interactions in PFAS (TULIPS) are recurrent epigenomic features of PFA ependymoma. *Neuro-Oncology.* 2022 Nov;24. DOI: <https://doi.org/10.1093/neuonc/noac209.473>
 5. Mathkar PP, **Chen X**[#], Sulovari A, and Li D[#]: Characterization of hepatitis B virus integrations identified in hepatocellular carcinoma genomes. *Viruses.* 2021 Jan;13(2):245. PMID: 33557409
 6. **Chen X**, Li D: Sequencing facility and DNA source associated patterns of virus-mappable reads in whole-genome sequencing data. *Genomics.* 2021 Jan;113:1189-1198. PMID: 33301893
 7. **Chen X**, Li D: **ERVcaller: Identifying polymorphic endogenous retrovirus and other transposable element insertions using whole-genome sequencing data.** *Bioinformatics.* 2019 Oct;35(20):3913-3922. PMID: 30895294 (We developed a novel approach to accurately detect and genotype polymorphic TE insertions which may be associated with human diseases)
 8. Shi L, Song J, Guo C, Wang B, Yang P, **Chen X**, King GJ, Wang J, Liu K: A CACTA-like transposable element in upstream of *CYP78A9* acts as an enhancer to increase silique length and seed weight in rapeseed. *The Plant Journal.* 2019 Jan;98:524-539. PMID: 30664290
 9. **Chen X**, Kost J, Sulovari A, Wong N, Liang WS, Cao J, and Li D: **A virome-wide clonal integration analysis platform for discovering cancer viral etiologies.** *Genome Research.* 2019 May;29(5):819-830. PMID: 30872350 (We developed a virome-wide approach to detect clonal viral integration events in the human genome and found the involvement of several viruses in early stages of tumorigenesis in affected tumors; our results also suggested the regulatory roles of the integrated viral regulatory sequences to nearby oncogenes)
 10. **Chen X**, Kost J, Li D: **Comprehensive comparative analysis of methods and software for identifying viral integrations.** *Briefings in Bioinformatics.* 2019 Nov 27; 20(6):2088-2097. PMID: 30102374 (We systematically evaluated existing approaches for detecting viral integration events and for the first time proposed the “virome-wide” concept for viral integrations detection)

Before 2019

11. Yang S, Zhang B, Liu G, Hong B, Xu J, **Chen X**, Wang B, Wu Z, Hou F, Yue X *et al*: A comprehensive and precise set of intervarietal substitution lines to identify candidate genes and quantitative trait loci in oilseed rape (*Brassica napus* L.). *Theor Appl Genet.* 2018 Jul;1-13. PMID: 29998372

12. Wu Z, Wang B, Chen X, Wu J, King GJ, Xiao Y, Liu K: Evaluation of linkage disequilibrium pattern and association study on seed oil content in *Brassica napus* using ddRAD sequencing. *PLoS ONE*. 2016 Jan 5;11(1):e0146383. PMID: 26730738
13. Chen X, Ge X, Wang J, Tan C, King GJ, Liu K: Genome-wide DNA methylation profiling by modified reduced representation bisulfite sequencing in *Brassica rapa* suggests that epigenetic modifications play a key role in polyploid genome evolution. *Frontiers in Plant Science*. 2015 Oct;6:836. PMID: 26500672
14. Chen X, Li X, Zhang B, Xu J, Wu Z, Wang B, Li H, Younas M, Huang L, Luo Y *et al.*: Detection and genotyping of restriction fragment associated polymorphisms in polyploid crops with a pseudo-reference: a case study in allotetraploid *Brassica napus*. *BMC Genomics*. 2013 May;14:346. PMID: 23706002
15. Li H, Younas M, Wang X, Li X, Chen L, Zhao B, Chen X, Xu J, Hou F, Hong B *et al.*: Development of a core set of single-locus SSR markers for allotetraploid rapeseed (*Brassica napus* L.). *Theor Appl Genet*. 2013 Dec;126(4):937-947. PMID: 23238763
16. Tan C, Han Z, Yu H, Zhan W, Xie W, Chen X, Zhao H, Zhou F, Xing Y: QTL scanning for rice yield using a whole genome SNP array. *Journal of Genetics and Genomics*. 2013 Dec;40(12):629-638. PMID: 24377869
17. Li H, Chen X, Yang Y, Xu J, Gu J, Fu J, Qian X, Zhang S, Wu J, Liu K: Development and genetic mapping of microsatellite markers from whole genome shotgun sequences in *Brassica oleracea*. *Molecular Breeding*. 2011 Dec;28(4):585-596. PMID: 23033896
18. Zhou X, Li Q, Chen X, Liu J, Zhang Q, Liu Y, Liu K, Xu J: The Arabidopsis *RETARDED ROOT GROWTH* gene encodes a mitochondria-localized protein that is required for cell division in the root meristem. *Plant Physiology*. 2011 Oct;157(4):1793-1804. PMID: 21984726
19. Wang F, Wang X, Chen X, Xiao Y, Li H, Zhang S, Xu J, Fu J, Huang L, Liu C *et al.*: Abundance, marker development and genetic mapping of microsatellites from unigenes in *Brassica napus*. *Molecular Breeding*. 2011 Aug;30(4):1-14
20. Chen X, Wu J, Liu K: Genetic diversity comparison between spring and weak-winter *Brassica napus* cultivars using single-locus SSR markers. *Chinese Journal of Oil Crop Sciences*. 2010 Mar;32(1):6-13

BIOINFORMATICS SOFTWARE

1. **Vcaller**: a bioinformatics platform to study virome-wide viral sequences, clonal integration events, and fusion transcripts using high-throughput sequencing data

(<https://github.com/xunchen85/VIcaller>)

2. **ERVcaller**: detect and genotype polymorphic transposable element (TE) insertions using whole-genome sequencing data (<https://github.com/xunchen85/ERVcaller>)
3. **RFAPtools**: unambiguously discriminate between single nucleotide polymorphisms (SNPs) versus homoeologous sequences in polyploid crops (<https://github.com/xunchen85/RFAPtools>)
4. **VRscreen**: a bioinformatics platform designed for detecting uniquely mapped paired-end viral reads in high-throughput sequencing data (<https://github.com/xunchen85/VRscreen>)

CONTRIBUTED PRESENTATIONS

1. Transposable elements are associated with the variable response to influenza infection. *The 46th Annual Meeting of Molecular Biology Society of Japan*. Dec 1, 2022 (Talk)
2. Transposable elements are associated with the variable response to influenza infection. *The American Society of Human Genetics (ASHG) 2022*. Oct 25, 2022 (Poster)
3. Using MPRA to understand the functional cores of transposable element enhancer activity and evolution in primates. *The 8th Annual Canadian Conference on Epigenetics and IHEC Annual Meeting*. Oct 4, 2022 (Poster)
4. Transposable elements contribute to global chromatin remodeling in the human response to influenza infection. *The 45th Annual Meeting of Molecular Biology Society of Japan*. Dec 1, 2021 (Poster)
5. Transposable elements reveal inter-individual variability in the human response to influenza infection. *The 1st International Symposium of CCII*. Jan 15, 2021 (Talk)
6. A virome-wide clonal integration analysis platform for uncovering new cancer viral etiologies. *2018 UVM Cancer Center Clinical & Translational Research Symposium Cancer Control in A Rural Environment*. Apr 20, 2018 (Poster)
7. Identifying and characterizing novel virus integrations in hepatocellular carcinoma genomes by virome-wide analysis of whole-genome sequencing data. *UVM Graduate Student and Postdoctoral Trainee Research Showcase*. Nov 10, 2017 (Talk)
8. Identifying and characterizing novel virus integrations in hepatocellular carcinoma genomes by virome-wide analysis of whole-genome sequencing data. *The American Society of Human Genetics (ASHG) 2017*. Oct 17-21, 2017 (Talk)
9. Genome-scale DNA methylation profiling in *Brassica rapa* using modified RRBS method. *The*

19th Crucifer Genetic Workshop and Brassica 2014. Mar 30-Apr 4, 2014 (Talk)

10. Comparison of three methods for SNP discovery using modified ddRADseq sequencing data in allotetraploid *Brassica napus*. *Plant & Animal Genome Asia 2013*. Mar 19-21, 2013 (Poster)
11. Detection and genotyping of restriction fragment associated polymorphisms in polyploidy crops with a pseudo reference sequence: A case study in tetraploid *Brassica napus*. *Crop Genetic Improvement & Biology Seed Industry Doctoral Forum 2012*. Nov 2-4, 2012 (Talk)
12. Fine mapping and cloning of one gene controlling seed coat color in *Brassica napus*. *Third International Conference on Plant Molecular Breeding*. Sep 5-9, 2010 (Poster)

OTHER PROFESSIONAL ACTIVITIES

Editorial board, *Frontiers in Genetics*, 2023-present

Reviewer for peer-reviewed journals, including *Nature Communications*, *Briefings in Bioinformatics*, *Journal of Medical Virology*, *npj Genomic Medicine*, *Bioinformatics Advances*, *International Journal of Molecular Sciences*, *Viruses et al.*