

1. CURRICULUM VITAE

Jian Lu, Ph.D.

Professor (with tenure)

The Yangtze River Scholar Professor
School of Life Sciences, Peking University
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EDUCATION

Year/Period	Degree	Institution
9/2002-3/2008	Ph.D. in Evolutionary Biology	The University of Chicago, USA Mentor: Dr. Chung-I Wu
9/1999-7/2002	M.S. in Genetics	Peking University, China Mentor: Prof. Zuhua Dai
9/1995-7/1999	B.S. in Cellular Biology & Genetics	Peking University, China

PROFESSIONAL APPOINTMENTS

Year/Period	Position	Institution
1/2022-present	The Yangtze River Scholar Professor	Ministry of Education, the People's Republic of China
1/2022-present	Professor	School of Life Sciences, Peking University
8/2020-2021/12	Tenured Associate Professor	School of Life Sciences, Peking University
5/2013-present	Principal Investigator	School of Life Sciences, Peking University
1/2013-4/2013	Postdoc Associate	Cornell University Mentor: Dr. Zhenglong Gu
6/2008-12/2012	Postdoc Associate	Cornell University Mentor: Dr. Andrew Clark
4/2008-5/2008	Postdoc Associate	The University of Chicago Mentor: Dr. Chung-I Wu

HONORS AND AWARDS

2018	Peking University Excellent Class Advisor Award
2017	Boya Young Scholar in Peking University
2013	Thousand Talent Program for Young Outstanding Scientists
2008	Honorable Mention for Best Dissertation of Division of Biological Sciences, the University of Chicago
2007	Chinese Government Award for Outstanding Self-financed Students Abroad
2000	Guangcai Scholarship of Peking University

RESEARCH GRANTS

Year/Period	Project title, Grant number, Funding agency, Award amount (to JL), Role
2021-2024	Construction of a retrospective and evolutionary platform for pathogenic variation and its cross-species transmission, 19,230,000 RMB, PI
2021-2022	Monitoring and Functional Impact Analysis of SARS-CoV-2 variants, MOST, 1,200,000 RMB, participating
2020-2022	Development of the research platform for studying the variation of the SARS-CoV-2 genomes, MOST, 800,000 RMB, participating
2021-2024	The genetic mechanism and evolutionary studies of <i>Drosophila</i> 's adaptation to the environment, National Natural Science Foundation of China, 580,000 RMB, PI

2021-2023	The evolutionary history and environmental adaptation of the fruit fly to the Tibetan Plateau, Beijing Natural Science Foundation, 200,000 RMB, PI
2020-2023	Evolution and function of Drosophila A-to-I editing, The National Natural Science Foundation of China (NSFC) and Israel Science Foundation (ISF) cooperation project, 2,000,000 RMB, PI
2018-2021	Function and evolution of A-to-I RNA editing in <i>Drosophila</i> , 31771411, National Natural Science Foundation of China, 610,000 RMB, PI
2018-2020	Genomic mechanisms of speciation with gene flow, 91731301, National Natural Science Foundation of China, 2,000,000 RMB, Multiple PI
2017-2020	Function and mechanisms of the interactions between non-coding RNAs and proteins in plants, 2016YFA0500800, Ministry of Science and Technology of China, 2,300,000 RMB, Multiple PI
2016-2019	Molecular mechanism and evolutionary principles of mammalian microRNA regulatory networks, 31571333, National Natural Science Foundation of China, 600,000 RMB, PI
2015-2017	Genomic conflicts between transposable elements and piRNAs and the implication in speciation, 91431101, National Natural Science Foundation of China, 1,200,000 RMB, PI
2014-2016	Function and evolution of small RNA regulation, Thousand Talent Program for Young Outstanding Scientists, 3,000,000 RMB, PI

SERVICES AND PROFESSIONAL ACTIVITIES

1) PROFESSIONAL SOCIETY AFFILIATIONS

Year/Period	Society affiliations
2019-present	Society for Molecular Biology & Evolution (SMBE)
2018-present	The RNA Society
2018-present	Chinese Society for Cell Biology
2016-2017	American Association for the Advancement of Science

2) EDITORIAL ACTIVITIES

Year/Period	Position	Journals
2018-present	Associate Editor	<i>Science Bulletin</i> (English Version)
2016-present	Editorial Board Member	<i>Non-coding RNA Research</i>
2015-present	Editorial Board Member	<i>Hereditas</i>

3) GRANT & JOURNAL REVIEW

Ad hoc grant reviewer for the National Natural Science Foundation of China (Major Program, Key Program, and Excellent Young Scholar Program), Ministry of Science and Technology of China (Budget evaluation), China Postdoctoral Science Foundation, and U.S.-Israel Binational Science Foundation

Ad hoc reviewer for the journals *Molecular Biology and Evolution* (>20 times), *Genome Research*, *PLOS Biology*, *PNAS*, *Nature Communications*, *Nature Protocols*, *Nucleic Acids Research*, *National Science Review*, *PLOS Genetics*, *Genome Biology and Evolution*, *Journal of Molecular Evolution*, *PLOS Computational Biology*, *Genetics*, *Molecular Genetics and Genomics*, *Gene*, *Communications Biology*, *Current Genomics*, and *Genomics, Proteomics & Bioinformatics*

4) MEETING ORGANIZATION RESPONSIBILITIES

November 2021	Session Chair, The 6 th National <i>Drosophila</i> Conference of China, Guangzhou, China
July 2021	Session Chair, SMBE 2021
August 2019	Session Chair, The 5th National <i>Drosophila</i> Conference of China, Dalian, China

August 2019	Organization Committee & Session Chair, The 14th International Bioinformatics Workshop (IBW), Beijing, China
April 2018	Session Chair, The 1st AsiaEvo Conference, Shenzhen, China
December 2017	Organizer, 2017 Beijing Area Fly Meeting, Beijing, China
June 2017	Session Chair, Beijing Normal University Symposium of Ecology and Evolutionary Biology, Beijing, China
April 2017	Organizer, Symposium of Ecology and Evolution at Peking-Taiwan University Day, Beijing, China

5) Invited Talks (Conferences)

2021-11-12	Session Chair, The 6 th National <i>Drosophila</i> Conference of China, Guangzhou, China
2019-08-18	The 5th National <i>Drosophila</i> Conference of China, Dalian, China
2019-04-17	Keystone Symposia on Molecular and Cellular Biology: Small Regulatory RNAs, Daejeon, South Korea
2019-02-21	The Gordon Research Conference: Translation Machinery in Health and Disease, Galveston, United States
2018-12-23	Chinese Biological Investigators Society 12th Biennial Conference, Shenzhen, China
2018-11-26	The 12th International Conference and Expo on Proteomics and Molecular Medicine, Dublin, Ireland
2018-11-06	The 2nd Jiujiang International <i>Drosophila</i> Conference, Jiujiang, China
2018-11-01	Cold Spring Harbor Asia Conference: RNA Biology, Suzhou, China
2018-10-23	The 8th National Conference on Bioinformatics and Systems Biology of China, Macau, China
2018-10-15	The 4th National Academic Conference for Developmental Biology, Kunming, China
2018-10-13	The 7th Young Bioinformatics PI workshop, Guiyang, China
2018-10-10	Cold Spring Harbor Asia Conference: Systems Biology of Gene Regulation & Genome Editing, Suzhou, China
2018-09-27	The 22nd Evolutionary Biology Meeting at Marseilles, Marseilles, France
2018-09-26	The 27th tRNA Conference (tRNA2018), Strasbourg, France
2018-07-13	Symposium on Evolutionary Genetics and Omics at National Institute of Genetics, Mishima, Japan
2018-05-31	The Molecular Tree of Life: From Coalescence to Comparative Genomics, Xuzhou, China
2018-04-21	The Chinese Society of Biochemistry and Molecular Biology Medical Biochemistry Branch "Youth Forum" III, Shenzhen, China
2018-04-20	The 1st AsiaEvo Conference, Shenzhen, China
2018-04-14	Chinese Society of Biotechnology Young Scientists Forum III, Tianjin, China
2018-01-16	Annual Meeting for the Key Program of "Mechanisms of Multiple-gene Interactions in the Micro-evolutionary Process", Zhoushan, China
2017-11-13	Cold Spring Harbor Asia Conference: RNA Modifications and Epitranscriptomics, Suzhou, China
2017-10-22	The 4th National <i>Drosophila</i> congress of China, Shanghai, China
2017-09-17	High-end RNA Biology Symposium of China, Beijing, China
2017-06-24	Beijing Normal University Symposium of Ecology and Evolutionary Biology, Beijing, China
2017-04-24	Symposium of Ecology and Evolution at Peking-Taiwan University Day, Beijing, China
2016-12-06	Annual Meeting for the Key Program of "Mechanisms of Multiple-gene Interactions in the Micro-evolutionary Process", Guangzhou, China
2016-08-11	The 1st Jiujiang International <i>Drosophila</i> Conference, Jiujiang, China
2016-07-15	The 1st Symposium for Young Evolutionary Biologists, Kunming, China
2015-09-13	RNAi China 2015 Programme, Kunshan, China

2014-10-12	Cold Spring Harbor Asia Conference: Evolutionary Genetics & Genomics, Suzhou, China
2013-10-19	The 2nd Young Bioinformatics PI workshop, Beijing, China
2013-07-11	Society for Molecular Biology and Evolution Annual Conference, Chicago, United States

6. Departmental seminars

2019-09-11	Institute of Biochemistry and Molecular Biology, University of Hamburg, Hamburg, Germany
2019-04-19	Korea Research Institute of Bioscience & Biotechnology, Daejeon, South Korea
2019-04-02	Department of Molecular Biology and Genetics, Cornell University, Ithaca, United States
2019-03-01	Institute of Zoology, Chinese Academy of Science, Beijing, China
2018-11-23	School of Biosciences, University of Birmingham, Birmingham, United Kingdom
2018-11-13	National Institute of Biological Sciences, Beijing (NIBS, Beijing), Beijing, China
2018-10-05	Department of Animal and Plant Sciences, the University of Sheffield, Sheffield, United Kingdom
2018-10-03	Institut Curie, Paris, France
2018-09-21	Laboratoire de Biométrie et Biologie Evolutive, UMR 5558, CNRS, Université Lyon 1, Villeurbanne, France
2018-08-17	Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China
2018-08-08	College of Marine Life Sciences, Ocean University of China, Qingdao, China
2018-06-20	Institute of Biophysics, Chinese Academy of Sciences, Beijing, China
2018-06-08	School of Life Sciences, Nanjing University, Nanjing, China
2015-11-30	School of Life Sciences, Sun Yat-Sen University, Guangzhou, China
2015-09-16	School of Life Sciences, Shandong University, Jinan, China
2014-04-24	Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China

FULL LIST OF PUBLICATIONS (# equal contribution, * corresponding author)

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1. Qian Z*, Li P, Tang X, Lu J* (2022) Evolutionary dynamics of the severe acute respiratory syndrome coronavirus 2 genomes. *Medical Review*. DOI: 10.1515/mr-2021-0035 .
 2. Ruan Y#, Hou M#, Tang X#, He X, Lu X, Lu J*, Wu CI*, Wen H* (2022) The runaway evolution of SARS-CoV-2 leading to the highly evolved Delta strain. *Molecular Biology and Evolution*. msac046. DOI: 10.1093/molbev/msac046 .
 3. Sun Q#, Shu C#, Shi W, Luo Y, Fan G, Nie J, Bi Yu, Wang Q, Qi J, Lu J, Zhou Y, Shen Z, Meng Z, Zhang X, Yu Z, Gao S*, Wu L*, Ma J*, Hu S* (2022) VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. *Nucleic Acids Research*. **50**(D1): D888–D897. DOI: 10.1093/nar/gkab921 .
 4. Duan Y, Tang X, **Lu J*** (2022) Evolutionary driving forces of A-to-I editing in metazoans. *WIREs RNA*. **13**: e1666.
 5. Zhang H, Wang Y, Wu X, Tang X, Wu C, **Lu J*** (2021) Determinants of genome-wide

distribution and evolution of uORFs in eukaryotes. *Nature Communications*. 12: 1076.

6. Zhang H[#], Wang Y[#], Tang X, Dou S, Sun Y, Zhang Q, **Lu J*** (2021) Combinatorial regulation of gene expression by uORFs and microRNAs in Drosophila. *Science Bulletin*. 66(3): 225–228.
7. Duan Y, Dou S, Porath HT, Huang J, Eisenberg E*, **Lu J*** (2021) A-to-I RNA editing in honeybees shows signals of adaptation and convergent evolution. *iScience* 24(1): 101983.
8. Ruan Y, Luo Z, Tang X, Li G, Wen H, He X, Lu X*, **Lu J***, Wu CI* (2021) On the founder effect in COVID-19 outbreaks: how many infected travelers may have started them all?. *National Science Review* 8(1): nwaa246.
9. Tang X[#], Ying R[#], Yao X[#], Li G, Wu C, Tang Y, Li Z, Kuang B, Wu F, Chi C, Du X, Qin Y, Gao S, Hu S, Ma J, Liu T, Pang X, Wang J, Zhao G, Tan W*, Zhang Y*, Lu X*, **Lu J*** (2021) Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. *Science Bulletin*. 66(22): 2297-2311.
10. Hu B[#], Liu R[#], Tang X[#], Pan Y[#], Wang M[#], Tong Y[#], Ye G[#], Shen G[#], Ying R[#], Fu A, Li D, Zhao W, Peng J, Guo J, Men D, Yao X, Wang Y, Zhang H, Feng Z, Yu J, Chen L, Deng Z, Lu X, Zhang YP*, Li Y*, Liu B*, Yu L*, Li Y*, **Lu J***, Liu T* (2021) The concordance between the evolutionary trend and the clinical manifestation of the two SARS-CoV-2 variants. *National Science Review* 8(8): nwab073.
11. Wu CI*, Wen H, **Lu J**, Su X, Hughes AC, 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 YP (2021) On the origin of SARS-CoV-2—The blind watchmaker argument. *Science China Life Sciences* 64: 1560–1563.
12. Wu Z, Jin Q, Wu G, **Lu J**, Li M, Guo D, Lan K, Feng L, Qian Z, Ren L, Tan W, Xu W, Yang W, Wang J*, Wang C (2021) SARS-CoV-2's origin should be investigated worldwide for pandemic prevention. *The Lancet* 398(10308): 1299-1303.
13. Sun Q, Shu C, Shi W, Luo Y, Fan G, Nie J, Bi Yu, Wang Q, Qi J, **Lu J**, Zhou Y, Shen Z, Meng Z, Zhang X, Yu Z, Gao S*, Wu L*, Ma J*, Hu S* (2021) VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. *Nucleic Acids Research* gkab921.
14. Peng MS^{#*}, Li JB[#], Cai ZF[#], Liu H[#], Tang X[#], Ying R, Zhang JN, Tao JJ, Yin TT, Zhang T, Hu JY, Wu RN, Zhou ZY, Zhang ZG, Yu L, Yao YG, Shi ZL, Lu XM, **Lu J***, Zhang YP* (2021) The high diversity of SARS-CoV-2-related coronaviruses in pangolins alerts potential ecological risks. *Zoological Research*. 42(6): 833–843.
15. Yu T, Huang X, Dou S, Tang X, Luo S, Theurkauf WE*, **Lu J***, Weng Z* (2021) A benchmark and an algorithm for detecting germline transposon insertions and measuring de novo transposon insertion frequencies. *Nucleic Acids Research* 49(8): e44.
16. Feng Y[#], Xu H[#], Liu J[#], Xie N, Gao L, He Y, Yao Y, Lv F, Zhang Y, **Lu J**, Zhang W, Li CY, Hu X*, Yang Z*, Xiao RP (2021) Functional and adaptive significance of promoter mutations that

affect divergent myocardial expressions of *TRIM72* in primates. *Molecular Biology and Evolution*. 38(7): 2930–2945.

14. Tang X[#], Wu C[#], Li X[#], Song Y[#], Yao X, Wu X, Duan Y, Zhang H, Wang Y, Qian Z, Cui J*, **Lu J*** (2020) On the origin and continuing evolution of SARS-CoV-2. *National Science Review*. 7(6): 1012–1023.
15. Li T[#], Tang X[#], Wu C, Yao X, Wang Y, Lu X*, **Lu J*** (2020) The use of SARS-CoV-2-related coronaviruses from bats and pangolins to polarize mutations in SARS-CoV-2. *Science China Life Sciences*. 63(10): 1608–1611.
16. Luo S[#], Zhang H[#], Duan Y[#], Yao X, Clark AG*, **Lu J*** (2020) The Evolutionary Arms Race between Transposable Elements and piRNAs in *Drosophila melanogaster*. *BMC Evolutionary Biology*. 20: 14.
17. Wang Y[#], Zhang H[#], **Lu J*** (2020). Recent advances in ribosome profiling for deciphering translational regulation. *Methods* 176: 46–54 (Invited Review, 被 Faculty of 1000 推荐).
18. Zhang H[#], Wang Y[#], **Lu J*** (2019). Function and evolution of upstream ORFs in eukaryotes. *Trends in Biochemical Sciences* 44(9): 782–794 (Invited Review).
19. Dou S[#], Wang Y[#], **Lu J*** (2019). Metazoan tsRNAs: biogenesis, evolution and regulatory functions. *Non-Coding RNA* 5(1): 18 (Invited Review).
20. Wu C, **Lu J*** (2019). Diversification of transposable elements in arthropods and its impact on genome evolution. *Genes* 10(5).
21. Zhang H[#], Wang Y[#], Li J, Chen H, He X, Zhang H, Liang H*, **Lu J*** (2018). Biosynthetic energy cost for amino acids decreases in cancer evolution. *Nature Communications* 9(1): 4124.
22. Zhang H[#], Dou S[#], He F, Luo J, Wei L, and **Lu J*** (2018). Genome-wide maps of ribosomal occupancy provide insights into adaptive evolution and regulatory roles of uORFs during *Drosophila* development. *PLOS Biology* 16(7): e2003903.
23. Luo S[#], He F[#], Luo J[#], Dou S[#], Wang Y[#], Guo A, **Lu J*** (2018). *Drosophila* tsRNAs preferentially suppress general translation machinery via antisense pairing and participate in cellular starvation response. *Nucleic Acids Research* 46(10): 5250–5268.
24. Luo J[#], Wang Y[#], Yuan J[#], Zhao Z, **Lu J*** (2018). MicroRNA duplication accelerates the recruitment of new targets during vertebrate evolution. *RNA* 24(6): 787–802.
25. Duan Y[#], Dou S[#], Zhang H[#], Wu C, Wu M, **Lu J*** (2018). Linkage of A-to-I RNA editing in metazoans and the impact on genome evolution. *Molecular Biology and Evolution* 35(1): 132–148.
26. Duan Y[#], Dou S[#], Luo S[#], Zhang H, **Lu J*** (2017). Adaptation of A-to-I RNA editing in *Drosophila*. *PLOS Genetics* 13(3): e1006648.
27. Luo S, **Lu J*** (2017). Silencing of transposable elements by piRNAs in *Drosophila*: an evolutionary perspective. *Genomics, Proteomics & Bioinformatics* 15(3): 164–176.
28. Wang Y, Luo J, Zhang H, and **Lu J*** (2016). MicroRNAs in the same clusters evolve to coordinately regulate functionally related genes. *Molecular Biology and Evolution* 33(9): 2232–2247; author reply in 10.1093/molbev/msz121.
29. Yin S, Fan Y, Zhang H, Zhao Z, Hao Y, Li J, Sun C, Yang J, Yang Z, Yang X, **Lu J**, Xi JJ*. (2016). Differential TGFβ pathway targeting by miR-122 in humans and mice affects liver cancer

metastasis. *Nature Communications* 7: 11012.

30. Zhang XY, Zhu Y, Liu XD, Hong XY, Xu Y, Zhu P, Shen Y, Ji YS, Wen X, Zhang C, Zhao Q, Wang YC, **Lu J**, Guo HW*. (2015). Suppression of endogenous gene silencing by degradation of normal cytoplasmic RNA in Arabidopsis. *Science* 348(6230): 120–123.
31. Yu FL[#], **Lu J**[#], Liu XM[#], Gazave E, Chang D, Raj S, Hunter-Zinck H, Blekhman R, Arbiza L, Hout C, Morrison A, Johnson AD, Bis J, Cupples LA, Psaty BM, Muzny D, Yu J, Gibbs RA, Keinan A, Clark G, Boerwinkle E* (2015). Population genomics analyses of 962 whole genomes of humans reveal natural selection in non-coding regions. *PLOS One* 10(3): e0121644.
32. Ye KX, **Lu J**, Ma F, Keinan A, Gu ZL* (2014). Extensive Pathogenicity of Mitochondrial Heteroplasmy in Healthy Human Individuals. *Proceedings of the National Academy of Sciences of the United States of America* 111(29): 10654–10659.
33. Ye KX*, **Lu J**, Raj SM, Gu ZL* (2013). Human expression QTLs are enriched in signals of environmental adaptation. *Genome Biology and Evolution* 5(9): 1689–1701.
34. **Lu J***, Clark AG* (2012). Impact of microRNA regulation on variation in human gene expression. *Genome Research* 22(7): 1243–1254.
35. Zhou RC[#], Ling SP[#], Zhao WM[#], Osada N, Chen SF, Zhang M, He ZW, Bao H, Zhong CR, Zhang B, Lu XM, Turissini D, Duke NC, **Lu J***, Shi SH*, Wu CI* (2011). Population genetics in non-model organisms: II. Natural selection in marginal habitats revealed by deep sequencing on dual platforms. *Molecular Biology and Evolution* 28(10): 2833–2842.
36. Tang T[#], Kumar S[#], Shen Y, **Lu J**, Wu ML, Shi S, Li WH, Wu CI* (2010). Adverse interactions between micro-RNAs and target genes from different species. *Proceedings of the National Academy of Sciences of the United States of America* 107: 12935–12940.
37. **Lu J**, Clark AG* (2010). Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in *Drosophila*. *Genome Research* 20: 212–227.
38. **Lu J**, Shen Y, Wu QF, Kumar S, He B, Carthew RW, Wang SM*, Wu CI* (2008). The birth and death of microRNA genes in *Drosophila*. *Nature Genetics* 40: 351–355; author reply in 42: 9–10.
39. **Lu J**, Fu Y, Kumar S, Shen Y, Zeng K, Xu A, Carthew RW, Wu CI* (2008). Adaptive evolution of newly emerged micro-RNA genes in *Drosophila*. *Molecular Biology and Evolution* 25: 929–938.
40. Wang HY, Fu Y, McPeek MS, Lu X, Nuzhdin S, Xu A, **Lu J**, Wu ML, Wu CI* (2008). Complex genetic interactions underlying expression differences between *Drosophila* races: analysis of chromosome substitutions. *Proceedings of the National Academy of Sciences of the United States of America* 105: 6362–6367.
41. Wu QF, Kim YC, **Lu J**, Xuan ZY, Chen J, Zheng YL, Zhou T, Zhang MQ, Wu CI, Wang SM* (2008). Poly A- transcripts expressed in HeLa cells. *PLOS ONE* 3(7): e2803.
42. Clark AG, Eisen MB, Smith DR, Bergman CM, Oliver B, Markow TA *et al* (2007). Evolution of genes and genomes on the *Drosophila* phylogeny. *Nature* 450: 203–218 (**Lu J** is a coauthor of this paper).
43. Shapiro JA, Huang W, Zhang C, Hubisz MJ, **Lu J**, Turissini DA, Fang S, Wang HY, Hudson RR, Nielsen R, Chen Z, Wu CI* (2007). Adaptive genic evolution in the *Drosophila* genomes. *Proceedings of the National Academy of Sciences of the United States of America* 104: 2271–2276.

44. **Lu J[#]**, Tang T[#], Tang H, Huang JZ, Shi SH*, Wu CI* (2006). The accumulation of deleterious mutations in rice genomes: a hypothesis on the cost of domestication. *Trends in Genetics* 22: 126–131.
45. Tang T[#], **Lu J[#]**, Huang J, He J, McCouch SR, Purugganan MD, Shi SH*, Wu CI* (2006). Genomic variation in rice - Genesis of highly polymorphic linkage blocks during domestication. *PLOS Genetics* 2(11): e199.
46. **Lu J**, Wu CI* (2005). Weak selection revealed by the whole-genome comparison of the X chromosome and autosomes of human and chimpanzee. *Proceedings of the National Academy of Sciences of the United States of America* 102: 4063–4067.
47. Tang H, Wyckoff GJ, **Lu J**, Wu CI* (2004). A universal evolutionary index for amino acid changes. *Molecular Biology and Evolution* 21: 1548–1556.
48. **Lu J**, Li WH, Wu CI* (2003). Comment on "Chromosomal speciation and molecular divergence-accelerated evolution in rearranged chromosomes". *Science* 302: 988.
49. **Lu J**, Lü J, Chen HX, Zhang WX, Dai ZH* (2002). Molecular phylogeny of *Drosophila auraria* species complex (in Chinese). *Acta Genetica Sinica* 29: 39–49.
50. Zhao Z, **Lu J**, Dai ZH* (2001). Genetic differentiation within *Drosophila auraria* species complex revealed by Random Amplified Polymorphic DNA (RAPD) (in Chinese). *Acta Zoologica Sinica* 47: 625–631.

4) BOOK CHAPTERS SINCE THE APPOINTMENT

1. Chen JH & **Lu J**, *Drosophila* and evolution (book chapter, in Chinese). In *Drosophila: the wonderful dew lover* edited by Jilong Liu & Wumin Deng (in press). Shanghai Scientific and Technical Publishers.