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I. EDUCATION

Ph.D. (Biochemistry) Louisiana State University, Baton Rouge. 2005
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II. PROFESSIONAL EXPERIENCE

07/18 – present Associate Professor, Department of Genetics, Rutgers, the State University of New Jersey
11/12 – present Full Member, Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey
01/12 – present Full Member, Human Genetic Institute of New Jersey, Rutgers, the State University of New Jersey
01/12 – 06/18 Assistant Professor, Department of Genetics, Rutgers, the State University of New Jersey
08/06 – 12/11 Postdoctoral Fellow, Department of Human Genetics, University of Utah School of Medicine, Salt Lake City.
05/05 – 08/06 Postdoctoral Fellow, Department of Biological Sciences, Louisiana State University, Baton Rouge.
01/03 – 05/05 Graduate Research Assistant, Louisiana State University, Baton Rouge. Advisor: Dr. Mark Batzer.
07/01 – 12/02 Graduate Teaching Assistant, Louisiana State University, Baton Rouge.

III. PUBLICATIONS (*: equal contribution; †: equal contribution; #: corresponding author; underlined: trainees)

1. Peng, C., L. Niu, J. Deng, J. Yu, X. Zhang, C. Zhou, **J. Xing**[#], and J. Li[#] (2018) Can-SINE dynamics in the giant panda and three other Caniformia genomes. *Mobile DNA* 9:32 (14 pages)

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3. Wang S., J. D. Mandell, Y. Kumar, N. Sun, M. T. Morris, J. Arbelaez, C. Nasello, S. Dong, C. Duhn, X. Zhao, Z. Yang, S. S. Padmanabhuni, D. Yu, R. A. King, A. Dietrich, N. Khalifa, N. Dahl, A. Y. Huang, B. M. Neale, G. Coppola, C. A. Mathews, J. M. Scharf, Tourette International Collaborative Genetics Study (TIC Genetics) (including H. Poisner and Y. Zhang), Tourette Syndrome Genetics Southern and Eastern Europe Initiative (TSGENESEE), Tourette Association of America International Consortium for Genetics (TAAICG), T. V. Fernandez, J. D. Buxbaum, S. De Rubeis, D. E. Grice, **J. Xing**, G. A. Heiman, J. A. Tischfield, P. Paschou, A. J. Willsey, M. W. State (2018) *de novo* sequence and copy number variants are strongly associated with Tourette Disorder and implicate cell polarity in pathogenesis. *Cell Reports* 24:3441–3454
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5. Fan Z., A. Zhou, N. Osada, J. Yu, J. Jiang, P. Li, L. Du, L. Niu, J. Deng, H. Xu, **J. Xing**, B. Yue, and J. Li (2018) Ancient hybridization and admixture in macaques (genus *Macaca*) inferred from whole genome sequences. *Molecular Phylogenetics and Evolution* 127:376-386
6. Zhou, A., Y. Zhang, Y. Sun[#], and **J. Xing**[#] (2018) PipelineDog: a simple and flexible pipeline construction and maintenance tool. *Bioinformatics* 34:1603–1605
7. Sun, N., C. Nasello, L. Deng, N. Wang, Y. Zhang, Z. Xu, Z. Song, R. A. King, Z. Pang, **J. Xing**, G. A. Heiman, K. Kwan, and J. A. Tischfield (2018) The *PNKD* gene is associated with Tourette Disorder and Tic disorder in a multiplex family. *Molecular Psychiatry* 23:1487-1495
8. Tong K.*, O. Pellón-Cárdenas*, V. R. Sirihorachai, B. N. Warder, O. A. Kothari, A. O. Perekatt, E. E. Fokas, R. L. Fullem, A. Zhou, J. K. Thackray, H. Tran, L. Zhang, **J. Xing**, and M. P. Verzi (2017) Degree of tissue differentiation dictates susceptibility to BRAF-driven colorectal cancer. *Cell Reports* 21:3833–3845
9. Wang, N.*, Y. Zhang*, E. Gedvilaite, J. Loh, T. Lin, X. Liu, C. Liu, D. Kumar, R. Donnelly, K. Raymond, E. H. Schuchman, D. Sleat[#], P. Lobel[#], and **J. Xing**[#] (2017) Using whole-exome sequencing to investigate the genetic bases for lysosomal storage diseases of unknown etiology. *Human Mutation* 38:1491-1499
10. Nguyen A. L.*, D. Marin*, A. Zhou, A. S. Gentilello, E. M. Smoak, Z. Cao, A. Fedick, Y. Wang, D. Taylor, R. T. Scott Jr., **J. Xing**, N. Treff, and K. Schindler (2017)

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11. Rustagi, N., A. Zhou, W. S. Watkins, E. Gedvilaite, S. Wang, N. Ramesh, D. Muzny, R. A. Gibbs, L. B. Jorde[#], F. Yu[#], and **J. Xing**[#] (2017) Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. *BMC Genomics* 18:396
 12. Willsey, A. J.^{*}, T. V. Fernandez^{*}, D. Yu[†], R. A. King[†], A. Dietrich[†], **J. Xing**[†], S. J. Sanders, J. D. Mandell, A. Y. Huang, P. Richer, L. Smith, S. Dong, K. E. Samocha, Tourette International Collaborative Genetics (TIC Genetics) (including E. Gedvilaite, S. Wang, Y. Zhang, A. Zhou), Tourette Syndrome Association International Consortium for Genetics (TSAICG), B. M. Neale, G. Coppola, C. A. Mathews, J. A. Tischfield, J. M. Scharf, M. W. State, and G. A. Heiman (2017) *De novo* coding variants are strongly associated with Tourette Disorder. *Neuron* 94: 486-499
 13. Ha H., N. Wang, and **J. Xing**[#] (2017) Library construction for high-throughput mobile element identification and genotyping. *Methods in Molecular Biology* 1589:1-15
 14. Viljetic B^{*}, L. Diao^{*}, J. Liu^{*}, Z. Krsnik^{*}, S. H. R. Wijeratne, R. Kristopovich, M. L. Kraushar, J. Song, **J. Xing**[#], K. C. Chen[#], M. R. Rasin[#] (2017) Multiple roles of PIWIL1 in mouse neocortico-genesis. *bioRxiv* doi: <https://doi.org/10.1101/106070>
 15. Jadot, M., M. Boonen, J. Thirion, N. Wang, **J. Xing**, C. Zhao, M. Qian, H. Zheng, J. Everett, D. Moore, D. Sleat, and P. Lobel (2017) Accounting for protein subcellular localization. *Molecular and Cellular Proteomics* 16: 194-212
 16. Kumar, N., M. Srivillibhuthur, K. D. Walton, A. Zhou, W. J. Faller, A. O. Perekatt, O. J. Sansom, D. L. Gumucio, **J. Xing**, E. M. Bonder, N. Gao, M. P. Verzi (2016) A YY1-dependent increase in aerobic metabolism is indispensable for intestinal organogenesis. *Development* 143: 3711-3722
 17. Sleat, D.[#], E. Gedvilaite, Y. Zhang, P. Lobel, and **J. Xing**[#] (2016) Analysis of large-scale whole exome sequencing data to determine the prevalence of genetically-distinct forms of neuronal ceroid lipofuscinosis. *Gene* 593:284-291
 18. Alexander, J., H. Potamianou, **J. Xing**, L. Deng, I. Karagiannidis, F. Tsetsos, P. Drineas, Z. Tarnok, R. Rizzo, T. Wolanczyk, L. Farkas, P. Nagy, U. Szymanska, C. Androutsos, V. Tsironi, A. Koumoula, C. Barta, TSGeneSEE, P. Sandor, C. L. Barr, J. Tischfield, P. Paschou, G. A. Heiman, and M. Georgitsi (2016) Targeted re-sequencing approach of candidate genes implicates rare potentially functional variants in Tourette Syndrome etiology. *Frontiers in Neuroscience* 10:428 (7 pages)
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- patterns of genomic variation and admixture in gray wolves. *Genome Research* 26: 163-173 (PMCID: 4728369)
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 24. Parrish N. F., K. Fujino, Y. Shiromoto, Y. W. Iwasaki, H. Ha, **J. Xing**, A. Makino, S. Kuramochi-Miyagawa, T. Nakano, H. Siomi, T. Honda, and K. Tomonaga (2015) piRNA derived from ancient viral processed pseudogenes suggests transgenerational sequence-specific immunity in mammals. *RNA* 21:1691-1703 (PMCID: 4574747)
 25. Platt II R. N., Y. Zhang, D. J. Witherspoon, **J. Xing**, A. Suh, M. S. Keith, L. B. Jorde, R. D. Stevens, and D. A. Ray (2015) Targeted capture of phylogenetically-informative Ves SINE insertions in genus *Myotis*. *Genome Biology and Evolution* 7:1664-1675 (PMCID: 4494050)
 26. Kwak Y., Y. Kim, **J. Xing**, and K. Han (2015) Evolutionary fate of SVA2 elements in primate genomes. *Genes & Genomics* 37:153-159
 27. Song J., J. Liu, S. L. Schnakenberg, H. Ha, **J. Xing**, and K. C. Chen (2014) Variation in piRNA and transposable element content in strains of *Drosophila melanogaster*. *Genome Biology and Evolution* 6(10):2786-2798 (PMCID: PMC4224344)
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35. Wang S., J. Lachance, S. Tishkoff, J. Hey, and **J. Xing**[#] (2013) Apparent variation in Neanderthal admixture among African populations is consistent with gene flow from non-African populations. *Genome Biology and Evolution* 5(11): 2075-2081 (PMCID: 3845641)
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37. Wu W., E. A. Clark, G. J. Stoddard, W. S. Watkins, M. S. Esplin, T. A. Manuck, **J. Xing**, M. W. Varner, and L. B. Jorde (2013) Effect of interleukin-6 polymorphism on risk of preterm birth within population strata: a meta-analysis. *BMC Genetics* 14:30 (9 pages, PMCID: 3639799)
38. Witherspoon D. J., Y. Zhang, **J. Xing**, W. S. Watkins, H. Ha, M. A. Batzer, and L. B. Jorde (2013) Mobile Element Scanning (ME-Scan) identifies thousands of novel Alu insertions in diverse human populations. *Genome Research* 23(7):1170-1181 (PMCID: 3698510)
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51. Roos C., D. Zinner, L. S. Kubatko, C. Schwarz, M. Yang, D. Meyer, S. D. Nash, **J. Xing**, M. A. Batzer, M. Brameier, F. H. Leendertz, T. Ziegler, D. Perwitasari-Farajallah, T. Nadler, L. Walter and M. Osterholz (2011) Nuclear versus mitochondrial DNA: Evidence for hybridization in colobine monkeys. *BMC Evolutionary Biology* 11:77 (13 pages, PMID: 3068967)

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IV. RESEARCH SUPPORT

ACTIVE

R01MH092293

06/2018 - 03/2023

NIH/NIMH

1/7 Collaborative Genomic Studies of Tourette Disorder

Role: Co- Investigator (MPI: Gary Heiman, Jay Tischfield)

R01HD082242 MPI 12/2017 - 11/2022

NIH/NICHD

Association of the Maternal Exome with Risk of an Aneuploid Conception

Principal Investigator (MPI: Karen Schindler, Jinchuan Xing)

U24HG008956 01/2016 - 11/2019

NIH/NHGRI

NHGRI Genome Sequencing Program Coordinating Center

Co-Investigator (MPI: Tara Matisse, Steve Buyske)

U01HG007419 09/2013 - 05/2019

NIH/NHGRI

Population Architecture Using Genomics and Epidemiology (PAGE), Phase II -
Coordinating Center

Co-Investigator (MPI: Tara Matisse, Steve Buyske)

COMPLETED

CAUT12APS006 06/2012 - 06/2018

New Jersey Governor's Council for Medical Research and Treatment of Autism

Elucidating Genetic Components of Autism and Related Disorders

Co-Investigator (PI: Linda Brzustowicz)

R00HG005846 04/2012 - 02/2016

NIH Pathway to Independence Award (K99/R00)

NIH/NHGRI

High-throughput Mobile Element Genotyping Using Next-generation Sequencing

Principal Investigator

Busch Biomedical Grant 07/2012 - 05/2014

Busch Biomedical Grant Program

Correlating piRNA and mobile element expression in human individuals

Principal Investigator (Co-PI Kevin Chen)

K99HG005846 09/2010 - 03/2012

NIH Pathway to Independence Award (K99/R00)

NIH/NHGRI

High-throughput Mobile Element Genotyping Using Next-generation Sequencing

Principal Investigator

V. PRESENTATIONS

Invited Talks and Platform Presentations

From primate to human: What we can learn from genomic data Department of Biology, Temple University, Philadelphia, PA, Nov 2018. *Invited talk*

From primate to human: What we can learn from genomic data Featured CHES Research Evening, Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, New Brunswick, NJ, Oct 2018. *Invited talk*

Population genetics and disease gene identification in the genomics era College of Life Sciences, Sichuan University, Chengdu, Sichuan, China, May 2018. *Invited talk*

Investigate lysosomal disease etiology by exome sequencing International Symposium on Molecular Evolution and Medicine, Philadelphia, PA, Sep 2017. *Platform Presentation*

Lighthouses for safe harbors: using mobile element insertions to identify genomic regions for gene therapy FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Big Sky, MT, Jun 2017. *Platform Presentation*

Understanding human genomic variation via high-throughput sequencing Genomic Instability & Cancer Genetics Research Program Meeting, Rutgers Cancer Institute of New Jersey, New Brunswick, NJ, Dec 2016. *Invited talk*

Disease gene identification in the genomics era ChemBio specialization program (CK2), Dankook University, Cheonan, Korea, Oct 2016. *Invited talk*

Understanding mobile element biology using high-throughput sequencing International Conference of the Korean Society for Molecular and Cellular Biology, Seoul, Korea, Oct 2016. *Invited talk*

Understanding human genomic variation via high throughput sequencing The Human Genetics Association of New Jersey Conference, New Brunswick, NJ, Sep 2016. *Invited talk*

Novel Candidate Genes that Modify Chronic Obstructive Pulmonary Disease Susceptibility Human Genetics in New York City Second Symposium, New York, NY, Jun 2016. *Invited talk*

Disease gene identification in the genomics era Institute of Development and Regenerative Biology, Hangzhou Normal University, Hangzhou, Zhejiang, China, May 2016. *Invited talk*

Understanding genomic variation via high throughput sequencing Center for primate translational medicine research, Kunming University of Science and Technology, Kunming, Yunnan, China, Apr 2015. *Invited talk*

Understanding genomic variation via high throughput sequencing College of Life Sciences, Sichuan University, Chengdu, China, Apr 2015. *Invited talk*

Pedigree-based disease-gene identification using high-throughput sequencing Columbia University Seminars in Genetic Epidemiology, Columbia University, New York, NY, Dec 2014. *Invited talk*

VAAST projects at Rutgers VAAST developer annual meeting, University of Utah, Salt Lake City, UT, Jun 2014. *Invited talk*

- Understanding human genomic variation via high throughput sequencing School of Molecular Biosciences, Washington State University, Pullman, WA, Feb 2014. *Invited talk*
- Disease gene identification using high throughput sequencing data Department of Nuclear Medicine, Tianjin Medical University General Hospital, Tianjin, China, Jan 2014. *Invited talk*
- Understanding human genomic variation via high throughput sequencing Department of Biological Sciences, Texas Tech University, Lubbock, TX, Dec 2013. *Invited talk*
- Disease gene identification in the genomics era – a case study of Tourette syndrome The Interactive Group in Human Genetics, Rutgers, the State University of New Jersey, Piscataway, NJ, Jul 2013. *Invited talk*
- Characterization of piRNA genomic distribution and expression variation in human individuals FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Big Sky, MT, Jun 2013. *Platform Presentation*
- Understanding human evolutionary history in the genomics era Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, New Brunswick, NJ, Nov 2012. *Invited talk*
- Population dynamics of human mobile elements 63rd Fujihara Seminar, a new horizon of retroposon research, Kyoto, Japan, Aug 2012. *Invited talk*
- Mobile elements demonstrate that *Australopithecus* effective population size was twice that of *Homo* FASEB Summer Research Conferences on Mobile DNA in Mammalian Genomes, Snowmass, CO, Aug 2011. *Platform Presentation*
- Toward a more uniform sampling of human genetic diversity The American Society of Human Genetics 59th annual meeting, Honolulu, HI, Oct 2009. *Platform Presentation*
- Genetic variation associated with mobile elements in an individual human genome The genome instability satellite meeting of the American Society of Human Genetics 58th annual meeting, Philadelphia, PA, Nov 2008. *Platform Presentation*
- Under the genomic radar: the stealth model of *Alu* amplification FASEB Summer Research Conferences on Mobile Elements in Mammalian Genomes 2005, Tucson, AZ, Jun 2005. *Platform Presentation*
- Under the genomic radar: the stealth model of *Alu* amplification CBMM Seminar Series, Louisiana State University, Baton Rouge, LA, May 2005. *Platform Presentation*

VI. TEACHING

- Fall 2018 Genomes (01:447:451), Rutgers, the State University of New Jersey
- Fall 2013-2015, 2017 Effective Communication Skills in Genetics (01:447:430), Rutgers, the State University of New Jersey
- Spring 2013 Honors Seminar (01:447:404), Rutgers, the State University of New Jersey

VII. PROFESSIONAL SERVICE

Editorial Activities

Associate Editor: Gene (2013-2016)

Editorial Board: Analytical Biochemistry (2012-), Gene (2011-), Mobile DNA (2014-)

Guest Editor: Comparative and Functional Genomics, for the special issue "Genomic Impact of Transposable Elements in Mammals" (2012)

Ad-hoc Review Activities

Study sections:

Member, NIH Genetic Variation and Evolution (2017)

Member, Busch Biomedical Research Award (2013, 2014, 2016)

Member, NIH NIEHS Special Emphasis Panel (2013)

Grant proposals:

National Science Foundation (NSF)

Louisiana Board of Regents' Research Competitiveness Subprogram

Netherlands Organisation for Health Research and Development (ZonMw)

Arabian Gulf University Research Committee

Book Chapter:

Human Evolutionary Genetics

Scientific Writing and Communication

Writing in the Biological Sciences

Journal articles (26 journals, >100 articles): American Journal of Human Genetics, Analytical Biochemistry, Annals of Human Genetics, Bioinformatics, Biotechniques, BMC Bioinformatics, BMC Genetics, Gene, Genetica, Genome Biology and Evolution, Genome Research, Genomics, European Journal of Human Genetics, Human Immunology, Human Molecular Genetics, Human Mutation, International Journal of Molecular Sciences, Mobile DNA, Molecular Biology and Evolution, Nucleic Acids Research, PLoS Computational Biology, PLoS Genetics, PLoS One, Recent Patents on Food, Nutrition & Agriculture, Systematic Biology, Zoological Science.

Professional Societies

Member, American Heart Association 2014 - 2015

Member, American Association for the Advancement of Science 2010 - 2012

Member, American Society of Human Genetics 2007 - present

Full Member, Sigma Xi 2007

Member, American Society for Microbiology 2006

VIII. HONORS & AWARDS

2011 Nominee for the Searle Scholars Program

- 2010 Science Program for Excellence in Science - The American Association for the Advancement of Science
- 2009 ASHG Trainee Research Award finalist - The American Society of Human Genetics
- 2005 The Robert Scott and Louise Pierce Allen Award for the outstanding graduate student in biochemistry - Louisiana State University, Baton Rouge, LA