

## Xiangqin Cui

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### EDUCATION AND TRAINING

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2001–2004, Postdoctoral training. Statistical Genetics, The Jackson Laboratory, Bar Harbor, ME (with Dr. Gary Churchill).  
1994–2001, Ph.D. Genetics, Iowa State University, Ames, IA (with Dr. Patrick Schnable).  
1991–1994, M.S. Molecular and Cytogenetics, Nankai University, Tianjin, P. R. China.  
1987–1991, B.A. Biology, Nankai University, Tianjin, P. R. China.

### RESEARCH EXPERIENCE

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2017– Present Associate Professor (Research track) and Director of Atlanta VA Medical Center Data Analytics Core, Department of Biostatistics and Bioinformatics, Emory University, Atlanta, GA  
2012– 2017 Associate Professor, Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL.  
2004–2012 Assistant Professor, Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL.  
2004–2009 Assistant Professor, Department of Medicine, Division of Genetic and Translational Medicine (later merged into Department of Genetics), University of Alabama at Birmingham, Birmingham, AL.  
2001–2004 Postdoctoral associate, The Jackson Laboratory, Bar Harbor, ME.  
1994–2001 Graduate Research Assistant, Iowa State University, Ames, IA.  
1991–1994 Graduate Research Assistant, Nankai University, Tianjin, China.

### COLLABRATION AND LEADERSHIP EXPERIENCE

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#### ***Funding Director of the Data Analytics Core at Atlanta VA Medical Center (2017-present)***

The Data Analytics Core provides analytics support for research and quality assurance at the Atlanta VA Medical center. The core consists of programmers working with VA databases to extract and cleaning data and statisticians working on study design, grant writing, and data analyses.

#### ***Director of the methodology core in Rheumatology NIH P60 program grant (2014-2017).***

The methodology core supported 6-7 faculty members with various expertise at 5% -10% effort level and two master statisticians. The function of the core was to support the analytic

needs of the projects (2 or 3 depending on cycles) and the research community. The main tasks were data analyses, grant writing support, study designs, new methods development, new investigator development, and community education. This grant was funded for more than 10 years and it was the third funding cycle under my direction. I had been a member of the core for 6 years before taking on the director role.

#### ***UAB CCTS BERD Member (2010-2017)***

I was a member of the Biostatistics, Epidemiology & Research Design (BERD) unit of UAB CCTS for 7 years. The UAB BERD had 4-6 biostatistics and epidemiology faculty members funded at variously level and one master level statistician. Collectively, the BERD members ran the weekly clinic, assisted analytical requests, and participated in all grant review panels for the whole UAB campus.

#### ***Biostatistics and Bioinformatics Resource in UAB O'Brien Center (2008-2017)***

The UAB O'Brien Center is a NIH P30 grant in the Nephrology Division of Department of Medicine. It only has cores families without projects. I was one of the two people forming the bioinformatics and biostatistics resource hosted in the administration core. Our job was to provide analytical help to the community need in grant writing and data analysis.

### **PUBLICATIONS (first and corresponding/senior authorship marked with \*\*)**

#### ***Book Chapters:***

1. Wu H, MK Kerr, **X Cui**, and GA Churchill (2003). MAANOVA: A software package for the analysis of spotted cDNA microarray experiments. Chapter 14 in *The analysis of gene expression data*. Edited by G. Parmigiani et al. Springer, New York, pp. 313–341.
2. **Cui X\*\*** and GA Churchill (2003). How many mice and how many arrays? Replication in mouse cDNA microarray experiments. In *Methods of microarray data analysis III*. Edited by Kimberly F. Johnson and Simon M. Lin. Kluwer Academic Publishers, Norwell, MA. Pp. 139-154.
3. Page G and **X Cui** (2008). Microarray. In *Wiley encyclopedia of clinical trials*. Edited by Ralph D'Agostino Lisa Sullivan, and Joseph Massaro. Wiley, Hoboken, NJ. ISBN: 978-0-471-35203-7.
4. **Cui X.\*\*** (2010). Experimental designs of high throughput biological experiments. Chapter 9 in “Statistical Bioinformatics” edited by Lee, Jae K. John Wiley & Sons, Inc., Hoboken, NJ, pp. 201–217.
5. Kennedy RE, and **X. Cui.\*\*** (2011). Experimental designs and ANOVA for microarray data. Book Chapter 8 in *Hand book of statistical bioinformatics* Edited by Henry Horng-Shing Lu, Bernhard Scholkopf, and Hongyu Zhao. Springer Heidelberg Dordrecht, London, pp. 151-169.

#### ***Journal Articles***

1. Song WQ, **XQ Cui**, WS Xu, XL Li, YK Peng, and RY Chen (1996). Micro-dissection and amplification of the terminal region from the long arm of the big M chromosome. *Vicia faba*. *Chinese Science Bulletin* 41: 361–364.

2. **Cui X\*\***, RP Wise, and PS Schnable (1996). The *rf2* nuclear restorer gene of male sterile T-cytoplasm maize. *Science* 272: 1334–1336.
3. Liu F.\* **X Cui**.\* HT Horner, H Weiner, and PS Schnable (2001). Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize. *Plant Cell* 13: 1063–1078.\* These authors contributed equally to this work. PMID: PMC135560
4. Skibbe DS, F Liu, TJ Wen, MD Yandeu, **X Cui**, J Jun Cao, CR Simmons, and PS Schnable (2002). Characterization of the aldehyde dehydrogenase gene families of *Zea mays* and *Arabidopsis*. *Plant Molecular Biology* 48: 751–764.
5. **Cui X,\*\*** AP Hsia, DA Ashlock, RP Wise, and PS Schnable (2003). Alternative transcription initiation sites and polyadenylation sites are recruited during *Mu* suppression at the *rf2* locus of maize. *Genetics* 163: 685–698. PMID: PMC1462470.
6. **Cui X,\*\*** MK Kerr, and GA Churchill (2003) Transformations for cDNA microarray data. *Statistical Applications in Genetics and Molecular Biology*. vol 2, issue 1, article 4.
7. **Cui X**, and GA Churchill (2003) Statistical tests for differential expression in cDNA microarray experiments. *Genome Biology*, 4:201. PMID: PMC154570
8. Lobenhofer E.K., **X Cui**, L. Bennett, P.L. Cable, G.A. Churchill, and C.A. Afshari (2004) Exploration of Low Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). *Toxicol Pathol.* 32(4):482-92.
9. Mrug M, TR Schoeb, R Li, **X Cui**, GA Churchill , and LM Guay-Woodford (2004). Kinesin 12 is predicted to modulate multiple phenotypes in the *cpk* mouse model of ARPKD. *J Am Soc Nephrol* 15:216A.
10. **Cui X,\*\*** JTG Hwang, J Qiu, NJ Blades, and G Churchill (2005). Improved statistical tests for differential gene expression by shrinking variance component estimates. *Biostatistics*. 6(1): 59–75.
11. Yao H, L , Y Fu, LA Borsuk, TJ Wen, DS Skibbe, **X Cui**, BE Scheffler, J Cao, SJ Emrich, DA Ashlock, and PS Schnable (2005). Evaluation of five ab initio gene prediction programs for the discovery of maize genes. *Plant Mol Biol.* 57(3): 445-60.
12. Mrug M, R Li, **X Cui**, TR Schoeb, GA Churchill, and LM Guay-Woodford (2005). Kinesin-related protein 12 is a candidate polycystic kidney disease modifier in the *cpk* mouse. *J Am Soc Nephrol.* 16(4): 905–16.
13. Allison DB, **X Cui**, GP Page, and M Sabripour (2006). Microarray data analysis: From disarray to consolidation and consensus. *Nat Rev Genet.* 7: 55–65.
14. **Cui, X,\*\*** and AE Loraine (2006). Global correlation analysis between redundant probe sets using a large collection of arabidopsis ath1 expression profiling data. *Comput Syst Bioinformatics Conf.* 2006: 223–226
15. **Cui, X,\*\*** J Affourtit, KR Shockley, Y Woo, and GA Churchill (2006). Inheritance patterns of transcript levels in f1 hybrid mice. *Genetics* 174: 627–637
16. Laudencia-Chinguanco, DL., BS Stamova, GR Laxo, XQ **Cui**, and OD Anderson (2006). Analysis of the wheat endosperm transcriptome. *J. Appl. Genet* 47: 287–302.

17. Allison DB, **X Cui**, GP Page, and M Sabripour (2006). Erratum: Microarray data analysis: From disarray to consolidation and consensus (Nature Reviews Genetics (2006) 7 (55-65) DOI: 10.1038/nrg1749). *Nature Review Genetics* 7(5):406.
18. Brand JPL, L Chen, **X Cui**, AA Bartolucci, AA Page, K Kim, K., S Barnes, S., V Srinivasasainagendra, TM Beasley, and DB Allison (2007). An adaptive alpha-spending algorithm improves the power of statistical inference in microarray data analysis. *Bioinformatics*, 1(10): 384–389. PMID: PMC1896052
19. Ye J, Cui X, Loraine A, Bynum K, Kim NC, White G, De Luca M, Garfinkel MD, Lu X, Ruden DM (2007). Methods for nutrigenomics and longevity studies in Drosophila: Effects of diets high in sucrose, palmitic acid, soy, or beef. *Methods Mol Biol.* 371:111–41.
20. Wu, X, J Wang, **X Cui**, L Maianu, B Rhees, J Rosinski, WV So, SM Willi, MV Osier HS Hill, GP Page, DB Allison, M Martin, and WT Garvey (2007). The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. *Endocrine*; 32(3):356.
21. Gao YZ, SY Guo, QZ Yin, **X Cui**, T. Hisamitsu, and XH Jiang (2007). Possible involvement of integrin signaling pathway in the process of recovery from restraint stress in rats. *Neurosci Bull.* 23(4):22935.
22. Mrug, M., J Zhou, **X Cui**, LM Guay-Woodford, N Hill-Kapturczak (2007). Thrombospondin 1, a latent TGF $\beta$  activator, is expressed abnormally in autosomal recessive polycystic kidney disease. *J Am Soc Nephrol* 18:360 A.
23. Mrug, M, J Zhou, Y Woo, **X Cui**, AJ Szalai1, J Novak, GA Churchill, and LM Guay-Woodford (2008). Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. *Kidney International* 73(1):63–76.
24. Mrug, M, J Zhou, Y Woo, **X Cui**, AJ Szalai1, J Novak, GA Churchill, and LM Guay-Woodford (2008). Overexpression of complement-component genes in Han: SPRD rats a model of polycystic kidney disease – Response. *Kidney International* 73(11):1325–1325
25. **Cui, X,\*\*** and AE Loraine (2009) Consistency analysis of redundant probe sets on affymetrix three-prime expression arrays and applications to differential mRNA processing. *PLoS ONE* 4(1):e4229. PMID: PMC2621337
26. PA Ioannidis, DB Allison, C Ball, C Furlanello, J Mangion, GP Page, V van Noort, I Coulibaly, **X Cui**, A Culhane, M Falci, L Game, G Jurman, T Mehta, E Petretto, JWang, M Axton (2009). Reproducibility of published microarrays gene expression analyses. *Nature Genetics* 41:178–186.
27. Zhu, H, G-J Li, L Ding, **X Cui**, H Berg, SM Assmann, and Y Xia (2009) Arabidopsis Extra Large G Protein 2 (XLG2) interacts with the G $\beta$  subunit of heterotrimeric G protein and functions in disease resistance. *Molecular Plant* 2(3):513–525. PMID: PMC2902900
28. Chen, L, GP Page, T Mehta, R Feng, and **X Cui.\*\*** (2009). Single nucleotide polymorphisms affect both cis- and trans-eQTLs. *Genomics* 93(6):501–8. PMID: PMC4041081
29. **Cui, X,\*\*** J Qiu, J Zhou, and M Mrug (2009). Validation of endogenous internal real-time PCR controls in renal tissues. *Am J Nephrol* 30:413–417. PMID: PMC2818397

30. Ulett, GC, RI Webb, KB Ulett, **X Cui**, WH Benjamin, M Crowley, and MA Schembri. (2010). Group B Streptococcus (GBS) urinary tract infection involves binding of GBS to bladder uroepithelium and potent but GBS-specific induction of Interleukin-1 $\alpha$ . *The Journal of Infectious Diseases* 201(6):866–70.
31. Thalacker-Mercer, A, LJ Dell’Italia, **X Cui**, JM Cross, and MM Bamman (2010). Differential Genomic Responses in Old vs. Young Humans Despite Similar Levels of Modest Muscle Damage After Resistance Loading. *Physiological Genomics* 40(3):141–9. PMC2825766
32. Qiu, J, and **X Cui**.\*\* (2010). Evaluation of a statistical equivalence test applied to microarray data. *Journal of Biopharmaceutical Statistics*, 20(2):240-66.
33. Zhou, J, X Ouyang, **X Cui**, TR Schoeb, LE Smythies, MR Johnson, LM Guay-Woodford, AB Chapman, and M Mrug (2010) Renal CD14 expression correlates with rates of cystic kidney disease progression. *Kidney International* 78(6):550–60. PMC2818397
34. Garvey WT, Wu X, A Patki, C Lara-Castro, **X Cui**, K Zhang, RG Walton, MV Osier, GL Gadbury, DB Allison, and M Martin M (2011). Genes and biochemical pathways in human skeletal muscle affecting resting energy expenditure and fuel partitioning. *Journal of Applied Physiology* Mar;110(3):746–55. PMC3070475
35. Gao L, Z Fang, K Zhang, D Zhi, and **X Cui**.\*\* (2011). Length bias correction for RNA-seq data in gene set enrichment analyses. *Bioinformatics* 7(5):662–669. doi: 10.1093/bioinformatics/btr005. PMC3042188.
36. Fang Z, and **X Cui**.\*\* (2011). Design and validation issues in next generation sequencing experiments. *Briefings in Bioinformatics* 12(3):280–287.
37. Chen Y, B Pat, JD Gladden, J Zheng, P Powell, C-C Wei, **X Cui**, A Husain, and LJ Dell’Italia (2011). Dynamic molecular and histopathological changes in extracellular matrix and inflammation in the transition to heart failure in isolated volume overload. *Circulation. AJP-Heart and Circulatory Physiology* 300(6):H2251–60. PMC3119090
38. Duell BL, AJ Carey, CK Tan, **X Cui**, RI Webb, M Totsika, MA Schembri, P Derrington, H Irving-Rodgers, AW Cripps, M Crowley, and GC Ulett (2012) Innate transcriptional networks activated in bladder in response to uropathogenic Escherichia coli drive diverse biological pathways and rapid synthesis of IL-10 for defense against bacterial urinary tract infection. *Journal of Immunology* 188(2):781–92.
39. Duarte CW, CD Willey, D Zhi D, **X Cui**, JJ Harris, LK Vaughan, T Mehta, RO McCubrey, NN Khodarev, RR Weichselbaum, and GY Gillespie (2012). Expression signature of ifn/stat1 signaling genes predicts poor survival outcome in Glioblastoma Multiforme in a subtype-specific manner. *PLoS One* 2012; 7(1):e29653. PMC3252343.
40. Reynolds RJ, **X Cui**, LK Vaughan, DT Redden, Z Causey, E Perkins, T Shah, LB Hughes; CLEAR Investigators, A Damle, M Kern, PK Gregersen, MR Johnson, and SL3Bridges Jr (2012). Gene expression patterns in peripheral blood cells associated with radiographic severity in African Americans with early rheumatoid arthritis. *Rheumatology International*. 33(1):129-37. doi: 10.1007/s00296-011-2355-3. PMC3769702
41. Moskowitz-Kassai E, L Mackelaite, J Chen, K Patel, DM Dadhania, SS Gross, P Chander, V Delaney, L Deng, L Chen, **X Cui**, M Suthanthiran, and MS Goligorsky MS (2012) Excretion

- of anti-angiogenic proteins in patients with chronic allograft dysfunction. *Nephrology Dialysis Transplantation*. 2012 Feb;27(2):494-7. Epub 2012 Jan 17. PMC3275786
42. Fang Z., R Du, and **X Cui**.\*\* (2012) Uniform approximation is more appropriate for Wilcoxon Rank-Sum Test in Gene Set Analysis. *PLoS One*. 7(2):e31505 Epub 2012 Feb 7. PMC3274536
  43. Zhou J, Ouyang X, Schoeb TR, Bolisetty S, **Cui X**, Mrug S, Yoder BK, Johnson MR, Szalai AJ, Mrug M (2012) Kidney Injury Accelerates Cystogenesis via Pathways Modulated by Heme Oxygenase and Complement. *J Am Soc Nephrol*. Jul;23(7):1161-71. PMC3380643
  44. Tan CK, AJ Carey, **X Cui**, RI Webb, WH Benjamin Jr., AW Cripps, M Crowley, KB Ulett, and GC Ulett. (2012) Genome-wide mapping of cystitis due to *Streptococcus agalactiae* and *Escherichia coli* in mice identifies a unique bladder transcriptome signifying pathogen-specific antimicrobial defense against urinary tract infection. *Infection and Immunity*. 80(9):3145-60. PMC3418756
  45. Wu H, M. Wu, D Zhi, S A Santorico, **X Cui**\*\* (2012) Statistics for Next Generation Sequencing--- Meeting Report. *Frontiers in Statistical Genetics and Methodology* doi:10.3389/fgene.2012.00128. PMC3395795
  46. Krejčí E, Pesevski Z, Dealmeida AC, Mrug M, Fresco VM, Argraves WS, Barth JL, **Cui X**, Sedmera D (2012) Microarray analysis of normal and abnormal chick ventricular myocardial development. *Physiol Res*. 2012 Jul 24;61 Suppl 1:S137-44.
  47. Fox ER, Musani SK, Barbalic M, Lin H, Yu B, Ogunyankin KO, Smith NL, Kutlar A, Glazer NL, Post WS, Paltoo DN, Dries DL, Farlow DN, Duarte CW, Kardina SL, Meyers KJ, Sun YV, Arnett DK, Patki AA, Sha J, **Cui X**, Samdarshi TE, Penman AD, Bibbins-Domingo K, Bůžková P, Benjamin EJ, Bluemke DA, Morrison AC, Heiss G, Carr JJ, Tracy RP, Mosley TH, Taylor HA, Psaty BM, Heckbert SR, Cappola TP, Vasani RS (2013) Genome-wide association study of cardiac structure and systolic function in African Americans: The Candidate Gene Association Resource (CARE) Study. *Circ Cardiovasc Genet*. 2013 Feb;6(1):37-46. PMID:PMC3591479
  48. Thalacker-Mercer A, Stec M, **Cui X**, Cross J, Windham S, Bamman M. (2013) Cluster analysis reveals differential transcript profiles associated with resistance training-induced human skeletal muscle hypertrophy. *Physiological Genomics* 17;45(12):499-507. PMID:PMC3680779.
  49. Johnson SL, SO. Hughes, **X Cui**, X Li, DB Allison, Y Liu, S Goodell, T Nicklas, T Power, KL Vollrath (2014) Portion sizes for children are associated with parental characteristics and the amounts parents serve themselves. *The American Journal of Clinical Nutrition*. 99(4):763-70. doi: 10.3945/ajcn.113.078311 PMID: PMC3953879
  50. Yang S, **Cui X**, Fang Z. (2014) "BCRgt: a Bayesian cluster regression-based genotyping algorithm for the samples with copy number alterations." *BMC Bioinformatics* 15: 74. doi:10.1186/1471-2105-15-74. PMID: PMC4003822
  51. Yan Q, Tiwari HK, Yi N, Lin WY, Gao G, Lou XY, **Cui X**, Liu N. (2014) Kernel-machine testing coupled with a rank-truncation method for genetic pathway analysis. *Genetic Epidemiology*, 38(5):447-56. doi: 10.1002/gepi.21813 PMID: PMC4073214

52. Qiu J; Qi Y; **Cui X** (2014) "Applying shrinkage variance estimators to the TOST test in high dimensional settings" *Statistics in Genetics and Molecular Biology*, 13(3):323-41. doi: 10.1515/sagmb-2013-0045.
53. Peng Y, Song L, Zhao M, Harmelink C, DeBenedittis P, **Cui X**, Wang Q, Jiao K. (2014) "Critical roles of miRNA-mediated regulation of TGF $\beta$  signalling during mouse cardiogenesis." *Cardiovasc Res.* 103(2):258-67. doi: 10.1093/cvr/cvu126. PMID: PMC4110444.
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55. Barnes J, Pat B, Chen YW, Powell PC, Bradley WE, Zheng J, Karki A, **Cui X**, Guichard J, Wei CC, Collawn J, Dell'Italia LJ. (2014) "Whole-genome profiling highlights the molecular complexity underlying eccentric cardiac hypertrophy." *Ther Adv Cardiovasc Dis.* 8(3):97-118
56. Cuna A, B Halloran, O Faye-Petersen, D Kelly, D Crossman, X Cui, K Pandit, N Kaminski, S Bhattacharya, A Ahmad, T J. Mariani and N Ambalavanan (2014). Alterations in Gene Expression and DNA Methylation During Murine and Human Lung Alveolar Septation. *Am J Respir Cell Mol Biol* 2014 Nov 11. [Epub ahead of print] PMID-in process
57. Stoll ML, R Kumar, C D Morrow, E J Lefkowitz, **X Cui**, A Genin, R Q Cron, C O Elson. Dysbiosis triggering abnormal humoral immune responses to commensal organisms in juvenile spondyloarthritis. (*Arthritis Research & Therapy*) 2014 Nov 30;16(6):486 PMID: PMC4272554
58. Ying Si, **X Cui**, S Kim, R Wians, R Sorge, S J. Oh, M Al-Sharabati, L Lu, G Claussen, T Anderson, S Yu, Dn Morgan, M Kazamel, P H. King (2014) "Smads as Muscle Biomarkers in Amyotrophic Lateral Sclerosis" *Annals of Clinical and Translational Neurology.* 1:778-787
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62. Yan Q, Tiwari HK, Yi N, Gao G, Zhang K, Lin WY, Lou XY, **Cui X**, Liu N. (2015) A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a

Generalized Linear Mixed Model. *Hum Hered.* 2015;79(2):60-8. doi: 10.1159/000375409. Epub 2015 Mar 10.

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65. Plyler ZE, Hill AE, McAtee CW, **Cui X**, Moseley LA, Sorscher EJ. (2015) SNP Formation Bias in the Murine Genome Provides Evidence for Parallel Evolution. *Genome Biol Evol.* 2015 Aug 6;7(9):2506-19. doi:10.1093/gbe/evv150. PMID: PMC4607513.
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69. Stephen Barnes, H.P. Benton, K. Casazza, S. cooper, X. **Cui**, X. Du, J. Engler, J.H. Kabarowski, S. Li, W. Pathmasiri, J.K. Prasain, M.B. Renfrow, H.K. Tiwari (2016) Training in metabolomics research. I. Designing the experiment, collecting an extracting samples and generating metabolomics data. *Jornal of Mass spectrometry* 2016 Jul;51(7):461-75. doi: 10.1002/jms.3782
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77. Atkinson TP, Centor RM, Xiao L, Wang F, **Cui X**, Van Der Pol W, Morrow CD, Ratliff AE, Crabb DM, Totten AH, Estrada CA, Faircloth MB, Waites KB. (2018) Analysis of the Tonsillar Microbiome in Young Adults with Sore Throat Reveals a High Relative Abundance of Fusobacterium necrophorum with Lower Diversity. PLoS One. 2018 Jan 19;13(1):e0189423. doi: 10.1371/journal.pone.0189423. eCollection 2018.
78. Garcia PL, Miller AL, Gamblin TL, Council LN, Christein JD, Arnoletti JP, Heslin MJ, Reddy S, Richardson JH, **Cui X**, van Waardenburg RCAM, Bradner JE, Yang ES, Yoon KJ. (2018) JQ1 Induces DNA Damage and Apoptosis, and Inhibits Tumor Growth in a Patient-Derived Xenograft Model of Cholangiocarcinoma. Mol Cancer Ther. 2018 Jan;17(1):107-118. doi: 10.1158/1535-7163.MCT-16-0922.
79. Hartman H, Wang Y, Schroeder H Jr, and **X Cui\*\*** (2018). Absorbance Summation as a novel approach to analyzing high-throughput ELISA data in the absence of a standard. PLOS ONE PLoS One. Jun 8;13(6):e0198528. doi: 10.1371/journal.pone.0198528.
80. Si Y, **X Cui**, D Crossman, J Hao, M Kazamel, Y Kwon, P H. King.(2018) Muscle MicroRNA Signatures as Biomarkers in Amyotrophic Lateral Sclerosis. Neurobiology of Disease (In Press)
81. Carson TL, Wang F, **Cui X**, Jackson BE, Van Der Pol WJ, Lefkowitz EJ, Marrow C, Baskin M. (2018) Associations between Race, Perceived Psychological Stress, and the Gut Microbiota in a Sample of Generally Healthy Black and White Women: A Pilot Study on the Role of Race and Perceived Psychological Stress. Psychosomatic Medicine (In Press)
82. Wu J, A Pendegraft, Q Yang, C Wang, B Christmann, T Lucious, T Seay, **X Cui**, C O. Elson, J Han, P Mannon. (2018) Expanded TCRβ CDR3 Clonotypes Distinguish Crohn's Disease and Ulcerative Colitis Patients. Mucosal Immunology (In Press)

***Articles submitted/under revision:***

Rachel A. Brewer, **Xiangqin Cui**, Nathan D. Miyasaki, Travis Ptacek, Ranjit Kumar, Yu-Hua Hsieh, Nianjun Liu, David B. Allison, Casey D. Morrow, Daniel L. Smith, Jr. Hyperphagia, Altered Nutrient Processing and Decreased Adiposity with Acarbose in Mice (Being revised for Journal of Nutrition)

Behring M, Shrestha S, Manne U, **Cui X**, Vazquez AI. Integrated analysis of copy number variation and RNA expression associated to nodal metastasis in invasive ductal breast carcinoma.

Huan Zhong, Degui Zhi, **Xiangqin Cui\*\***. Predicting Gene Expression Using DNA methylation in Two Human Populations. (Submitted to BMC Bioinformatics)

### *Articles in Preparation:*

## **PRESENTATIONS**

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### *Talks*

“Fertility restoration in cytoplasmic male sterile maize,” at the Interdepartmental Genetics Program Retreat, August 23, 1997.

“Characterization of *rf2*, a maize mitochondrial male sterility restorer gene,” at the All Iowa Genetics Symposium, June 19, 1998.

“Analyze cDNA microarray data using MAANOVA,” invited talk at Amgen, Inc. Thousand Oaks, CA, June 7, 2002.

“How many mice and how many arrays? Replication of cDNA microarray experiment,” invited talk at the CAMDA02 contest, Nov. 14–15, 2002, Durham, NC.

“The inheritance pattern of gene expression in mouse,” at the Microarray Research Coordination Network Retreat, Mohonk, NY, September 27–30, 2004.

“Statistical equivalence testing applied to microarray data,” at the Microarray Research Coordination Network Retreat, Mohonk, NY, September 19–23, 2005.

“Consistency assessment among multiple probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip,” CIS seminar series, October 24, 2007.

“Consistency assessment among redundant probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip,” Fifth Annual Rocky Mountain Bioinformatics, Snow Mass, CO, November 30–December 2, 2007.

“Statistical equivalence testing applied to microarray data,” SSG retreat, January 4, 2008.

“Statistical equivalence testing applied to microarray data,” ENAR, March 16–19, Washington, D.C., 2008.

“Microarray data analysis – established routines and new directions,” December 5, 2008, Florida State University, Tallahassee, FL.

“Interrogation of alternative splicing using microarray,” May 20, 2009, First International Biomedical Conference at Nankai, Tianjing, China.

“Identifying equivalently expressed genes using DNA microarrays,” May 21, 2009, Department of Statistics, Nankai University, Tianjin, China.

“Experimental design for microarray experiments,” May 23, 2009, Institute of Crop Sciences, the Chinese Academy of Agricultural Sciences, Beijing, China.

“Gene class enrichment analysis for RNA-seq data,” March 23, 2010, ENAR, New Orleans, LA.

“Length bias correction for RNA-seq data in gene set analyses,” March 22, 2011, ENAR, Miami, FL. (Invited)

“Equivalence testing of high dimensional expression data,” November 2011, Emory University, Atlanta, GA. (Invited)

“Equivalence evaluation of GBM primary tumors and xenografts”, August 4<sup>th</sup>, 2012, JSM San Diego (invited)

- “From arrays to NGS - methodology research in Omic equivalence and number crunching in collaboration research”, Feb 5<sup>th</sup>, 2013, Children’s National Medical Center. Washington DC. (Invited)
- “RNA-seq Data for Differential Expression Analysis”, May 13<sup>th</sup> 2014, Next Generation Sequencing Workshop, UNC Charlotte, NC.
- “New Findings for an Old Problem – qRT-PCR Data Normalization” June 25<sup>th</sup>, 2014. Department of Bioinformatics, Tongjin University. Shanghai, China (invited)
- “Uniform Approximation for Wilcoxon Rank-Sum Test in Gene Set Analysis” June 27<sup>th</sup>, 2014, The Third International Symposium on Biostatistics, Chengdu, China (invited)
- “Exploring Immune-Repertoire Sequencing Data” June 13<sup>th</sup>, 2016. ICSA Applied Statistics Symposium. Atlanta, GA.

### **Posters**

- Cui X**, WJ Chen, RP Wise, and PS Schnable. (1995). The *rf2* nuclear restore of *cmsT* encodes an aldehyde dehydrogenase, 37 Maize Genetics Conference, March 16–19, Asilomar, CA.
- Cui X**, F Liu, WJ Chen, RP Wise, and PS Schnable. (1996). The *rf2* nuclear restore of *cmsT* encodes an aldehyde dehydrogenase, 38<sup>th</sup> Maize Genetics Conference, March 14–17, St. Charles, IL.
- Liu F, **X Cui**, WJ Chen, AP Hsia, RP Wise, and PS Schnable. (1997). The biochemistry characterization of *rf2* protein which is required for *cmsT*, 39<sup>th</sup> Maize Genetics Conference, March 13–16, Clearwater Beach, FL.
- Cui X**, AP Hsia, RP Wise, and PS Schnable. (1998). Suppression of *rf2-m* alleles, 40<sup>th</sup> Maize Genetics Conference, March 19–20, Lake Geneva, WI.
- Cui X**, and PS Schnable. (1999). The physiological role of *rf2* independent of its *cms-T* restorer, 41<sup>st</sup> Maize Genetics Conference, March 11–14, Lake Geneva, WI.
- Cui X**, B Scheffler, C Simmons, RB Meely, and PS Schnable. (2000). Mutations in the maize *pd3* gene cause reduced levels of tolerance to anaerobic stress, annual meeting of the American Society of Plant Physiologists, July 15–19, San Diego, CA.
- Cui X**, and GA Churchill. (2002). The application of ratio by intensity plot in microarray normalization, MGED IV (Microarray and Chips: Algorithms and Applications), February 13–16.
- Cui X**, JTG Hwang, J Qiu, NJ Blade, S-W Tsaih, and GA Churchill. (2004). Improved statistical tests for differential gene expression by shrinking variance components estimates, International Conference on Analysis of Genomic Data, May 10–11, Boston, MA.
- Cui X**, J Affourtit, Y Woo, and GA Churchill. (2005). Inheritance Patterns of transcript levels in F1 hybrid mice. Plant and Animal Genomic XIII, January 15–19, San Diego, CA.
- Cui X**, and J Qiu. (2007). Identifying equivalently expressed genes using microarray. Gordon Conference: Toxicogenomics. June 24–29, New London, NJ.
- Cui X**, and A Loraine. (2007). Consistency assessment among redundant probe sets interrogating the same gene on the Affymetrix MOE430 GeneChip. Fifth Annual Rocky Mountain Bioinformatics, November 30–December 2, Snow Mass, CO.
- Mirel B, B J Keller, M Peleg, **X Cui**, and R Altman. (2009). Design of integrated translational bioinformatics systems. 2009. AMIA summit on translational bioinformatics (STB 2009), March 15–17, 2009.
- Kennedy R, and **X Cui**. (2009). Searching for efficient experimental design for differential DNA methylation studies, at ENAR 2009, March 15–18. San Antonio, TX.

- Cui X**, M Cook, Z Li, R Williams, K Hamre, and L Lu. (2010). Genetic and stress influence on DNA methylation in mouse hippocampus, at the 9<sup>th</sup> Complex Trait Community Conference (CTC 2010), May 7–10, Chicago, IL.
- Yang, C, and **X Cui**. (2011). Multi-group tests of equivalence for microarray data, ENAR, March 20–23, Miami, FL.
- Cuna, A., B. Halloran, O. Faye-Petersen, D. Kelly, D. Crossman, X. Cui, K. Pandit, N. Kaminski, S. Bhattacharya, A. Ahmad, T.J. Mariani and N. Ambalavanan. Alterations in Gene Expression and DNA Methylation during Murine and Human Lung Alveolar Septation. Octobr 23 2015, AAP Experience Nation Conference & Exhibition, Washington, DC.
- Wilson L, G. Trivedi; A. Sreedasyam;H. Kim; X. Cui; L. J Cseke; S. Barnes. Quantitative SWATH Proteomics Analysis of Tree Fungal Interactions under Nutrient Limiting Conditions. 63rd American Society for Mass Spectrometry (ASMS) Conference. May 31<sup>st</sup> - June 4th, 2015, St. Louis, MO.
- Rachel A. Brewer, Xiangqin Cui, Nianjun Liu, Nathan D. Miyasaki, Travis Ptacek, Ranjit Kumar, Casey D. Morrow, Daniel L. Smith, Jr. Acarbose treatment and the gut microbiota. Gerontological Society of America Annual Scientific Meeting. Nov 18-22 Orlando, FL.
- Elizabeth Ma, Minsung Kang, Xiangqin Cui, Wei Zhang, Yuchang Fu, W. Timothy Garvey, Circulating MicroRNA Species and Role in Human Insulin Resistance. American Diabetes Association conference. June 5-9, 2015; Boston, MS.
- McLean M, Bates GW, Cui X, Barnes S, Harper L. Peri-conception metabolomics in serum and follicular fluid of obese versus non-obese women undergoing IVF, at 63<sup>rd</sup> Annual Scientific Meeting of Society for Reproductive Investigation, Mar 16, 2011-18, 2016

## **TEACHING AND ADVISING**

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### ***Courses Taught at UAB:***

- BST 675 “Instroduction to Statistical Genetics,” Department of Biostatistics (Spring 2009, spring 2011, Spring 2013).
- BST 676 “Genomic Data Analysis,” Department of Biostatistics (Spring 2010, Spring 2012), revised course.
- BST 611 “Intermediate Statistical Analysis I” (online Spring 2015) (in class Fall 2015)
- BST 690 “Biostatic Consult and App Pro,” Department of Biostatistics (Summer 2009, Summer 2010, Summer 2011).
- BST 698 “Non-disertation Research” (Spring 2015, summer 2015)
- BST 626 “Statistical Languages: R and SAS” (Fall 2016)

### ***Guest Lectures at UAB:***

- “Introduction to Microarray Technology (Biology and Experimental Design),” CS640 (course title: Bioinformatics; primary instructor: Chengcui Zhang). Fall 2004.
- “Image processing,analysis,QC and normalization—Two Color,” in NSF Plant Microarray Short Course, June 14, 2005, Madison, WI; June 13, 2006.
- “Inferential Statistical Procedures - Linear Models,” in NSF Plant Microarray Short Course, June 14, 2005, Madison, WI.
- NIDDK short course at UAB: “Demonstration and Supervised Practice (Microarray).” May 4, 2005. Birmingham, AL.

- “Genomics, Bioinformatics, and Medicine,” in UAB K30 genetics lectures (organizer: Bruce Korf), Spring 2005, 2006, 2007, 2008.
- “Inferential Statistical Procedures—Linear Models” in the 2<sup>nd</sup> NSF Plant Microarray Short Course, August 2, 2006. Boston, MA.
- “Statistical Analysis of Microarray Data: Design, Normalization, and Statistical Inference” in Genet702 (course title: Animal Model Systems for Genetic and Genomic Analyses). Spring 2005, Spring 2007.
- “Design of Microarray Experiments,” in International Microarray Workshop, January 11, 2007; January 10, 2008, Tucson, AZ.
- “Statistical Aspects for the Polycystic Kidney Study,” in HMG703 (Title: Hughes Med-Grad “Quantitative Methods”). March 28, 2007; April 1, 2009.
- “Basic Statistics,” in Genetics Core Lecture Series (organizer: Scott Austin). August 17, 2007; Fall 2008.
- “Introduction to QTL Mapping,” in NSF Statistical Genetics Short Course, July 12, 2008, Birmingham, AL.
- “Software Demonstration of MAANOVA Package,” in the NSF Statistical Genetics Short Course, July 12, 2008, Birmingham, AL.
- “Permutation Methods,” in BST 765 (course name: Advanced Computational Methods; primary instructor: Rui Feng). Oct 1, 2008.
- “Arrays and Bioinformatics,” in Combined Fellow’s Physiology Conference (organizer: James Hagood), February 19, 2009.
- “Microarray Analysis and Related Topics,” in EPI 788 (course name: Molecular Epidemiology; primary instructor: Elizabeth Brown). Summer 2009, Summer 2011.
- “Introduction to Epigenetics/Epigenomics,” in Introduction to Statistical Genetics Workshop. New Orleans, LA., Feb 12, 2009.
- “Bioinformatics, Genomics, and Medicine,” in Vocabulary of Clinical & Translational Science (organizer: Jacqueline Ann Moss). Sep 18, 2009.
- “Analysis Issues of Microarray and Next-Generation Sequencing Data,” in the Genomics Block of GBS 722 (course name: GGS Bioinformatics: course master: Michael Crowley). Jan 26, 2011.
- “Microarray Data Analysis Software—R Based,” in the Bioinformatics Block of GBS 722 (course name: GGS Bioinformatics: course master: Chiquito Crasto). Feb 28, 2011.
- “Statistical Analyses of RNA-seq Data,” in BST 695 (course name: Special Topics; primary instructor: Degui Zhi). April 6, 2011.
- “Software Packages Affy, MAANOVA, and PowerAtlas,” in the NIGMS short course, Birmingham, AL, July 20, 2011.
- “Analysis of Whole Genome Transcriptome Sequencing Data,” in the NHGRI short course on Next Generation Sequencing, Birmingham, AL. December 19, 2011.
- “Introduction to R & Bio-conductor”. For NIGMS short course at UAB 7/9/2012
- “Affy, RMANOVA package demo”. For NIGMS short course at UAB 7/11/2012
- “Analysis of Whole Genome Transcriptome Sequencing Data,” in the NHGRI short course on Next Generation Sequencing, Birmingham, AL. December 12, 2012.
- “Introduction to R and Bioconductor”, in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/8/2013
- “RNAseq: Experimental Design and Data Analysis”, in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/11/2013

“Bowtie/TopHat, SAMTools, IGV, R packages for RNA-seq and CHIP-seq”, together with Hao Wu in the NIGMS short course on Statistical Genetics and Genomics, Birmingham, AL, 7/11/2013

“Transcriptome Analysis” in 3rd Short Course on Next-Generation Sequencing: Technology and Statistical Methods, Birmingham, AL, 12/18/2013

“Software Demonstration (RNA-Seq & Galaxy)” in 3rd Short Course on Next-Generation Sequencing: Technology and Statistical Methods, Birmingham, AL, 12/18/2013

“About RNA-seq” in WINGS Workshop in Next Generation Science, UNC Charlotte, May 13-14, 2014

“Introduction to R & Bio-conductor” in Short Course on Statistical Genetics and Genomics. Birmingham, AL, 4th 7/7/2014, 5<sup>th</sup> 7/27/2015, 6<sup>th</sup> 7/13/2016

“Transcriptome Analyses: Microarray and RNAseq” in Short Course on Statistical Genetics and Genomics. Birmingham, AL, 4th 7/10/2014, 5<sup>th</sup> 7/29/2015, 6<sup>th</sup> 7/11/2016

“Introduction to R & Bio-conductor” in Short Course on Next-Generation Sequencing: Technology and Statistical Methods. Birmingham, AL, 4<sup>th</sup> 12/15/2014, 5<sup>th</sup> 12/14/2015

“Transcriptome Analysis Using NGS” in Short Course on Next-Generation Sequencing: Technology and Statistical Methods. Birmingham, AL, 4<sup>th</sup> 12/17/2014, 5<sup>th</sup> 12/19/2015

“Experimental Design of Omics Experiments” in GBS 748: Advanced Graduate Course in Metabolomics, January 17th 2015; January 6<sup>th</sup>, 2016

“Interpretation of Metabolomics Analysis Results” in GBS 748: Advanced Graduate Course in Metabolomics, Feb. 9th 2015;

“Introduction to R and Bioconductor” in GBS 722: Bioinformatics, Feb. 11th-12th 2015; March 8-9, 2-016.

“Training in Experimental Design” 6/15/2015 in 3<sup>rd</sup> and 7/18/2016 4<sup>th</sup> Annual Workshop on Metabolomics.

“Statistical analysis using metaboanalyst” 7/20/2016 in 4<sup>th</sup> Annual Workshop on Metabolomics.

“Designing a Metabolomics Experiment” 12/2/2015 in One-Day Metabolomics Workshop

“Experimental Design & Statistics” 9/11/2015 in MIC 741: Topics in Professional Development

***Guest lectures at the Jackson Laboratory:***

“Data Quality Control and Normalization,” in the Workshop on Techniques in Gene Microarray

“Development and Analysis: Approaches to Heart, Lung, Blood, and Sleep Disorders.” Jackson Lab, Bar Harbor, ME April 24-28, 2002

“Data Transformation of cDNA Microarray,” in the Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes. Bar Harbor, ME, September 23, 2002

***At Iowa State University:***

Genetics Lab (Bio 301L)

***Student and Post-doctoral Fellow advised:***

Master students

Kathakali Ghosh (2005–2006) research advisor  
Liyan Gao (2009–2010 ) academic and research advisor  
Luqin Deng (2009–2012) academic and research advisor  
Ligong Chen (2010–2012) research advisor  
Xuelin Li (2013) research advisor  
Shaohua Yu (2013-2014) academic and research advisor  
Justin Leach (2014-2016) academic advisor  
Holly Hartman (2015) research advisor  
Lauren Wood (2015-2017) academic advisor  
Jiaying Hao (2016-2017) academic and research advisor  
Fuchenchu Wang (2016-2017) academic and research advisor

Ph.D students:

Lang Chen (2006-2008) dissertation Co-chair  
Celeste Yang (2010-2013) dissertation Chair  
Henry Roberson (2005–2008) academic advisor  
Jun Li (2005–2011) academic advisor  
Guoqiao Wang (2010–2013) academic advisor  
Amanda H. Pendegraft (2014- 2017) academic and research advisor

Postdocs

Richard Kennedy (2008–2011) Co-mentor  
Armrit Karki (2012-2012) mentor  
Jason Guichard (2012-2015) Co-mentor

Graduate disertation committees:

Hong Gao (Ph.D.) Department of Vision Science (2007-2009)  
Jacquelyn Zimmerman (Ph.D.) Department of Medicine, Division of Hematology & Oncology (2009–2012)  
Elizabeth Perkins (Ph.D.) Clinical Immunology and Rheumatology (2011–2012)  
Kathryn Royse (Ph.D.) Department of Epidemiology (2011–2014)  
Amanda Chou Sue (MS) Department of Epidemiology (2014)  
Lindsay Jones (Ph.D) Biostatistics (2013-2015)  
Michael Behring (Ph.D) Biostatistics (2015- 2018)  
Stephen Gragg (MD/Ph.D) NIH Medical Scientist Training (2016-2017)  
Yogasudha Veturi (Ph.D) Department of Biostatistics (2016-2017)

Summer interns

Tarik Trend, Emery Univresity, (2007) Intern advisor

***Junior faculty (NIH K awardee) mentored:***

Tomi Akinyemiju, Assistant Professor, Department of Epidemiology (2016-)  
Yuanyuan Li, Assistant Professor, Department of Biology (2016-)

**PROFESSIONAL SOCIETIES**

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American Association for the Advancement of Science (AAAS)	1997–2011
International Society for Computational Biology (ISCB)	2007–2012
The American Society of Human Genetics (ASHG)	2011–2015
American Statistical Association (ASA)	2002–present

International Chinese Statistical Association (ICSA) 2013–present  
Caucus for Women in Statistics (CWS) 2016-present

## **PROFESSIONAL SERVICES**

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**Editorial board:** Associate editor for *Frontiers in Epigenomics* (2011 - present)

Associate editor for *PeerJ* (Oct 2014 – present)

**Appointed microarray referee:** *Plant Cell* (2008–2011)

**Add hoc Referee for:**

Bioinformatics, Nature Genetics, Biostatistics, BioTechniques, Physiological Genomics, Theoretical and Applied Genetics, Computational Statistics & Data Analysis, JASA, BMC-Bioinformatics, BMC Evolutionary Biology Genetics, Euphytica, International Journal of Plant Genomics, Biometrical Journal of Biological Chemistry, The Annals of Statistics, Plant Physiology.

**National services:**

National conferences:

Organizer of the NHGRI-funded “Statistical Analysis for Next Generation Sequencing,” Birmingham, AL, Sept. 26–27, 2011.

Co-organizer of the 2<sup>nd</sup> NSF Plant Microarray Short Course (2006).

Scientific Committee member for annual Critical Assessment of Massive Data Analysis (CAMDA) conferences (2009–2014).

ENAR session chair for “Experimental Design, Power/Sample Size, and Survey Research” (March 2010), New Orleans, LA.

Organizer for invited session “Next Generation Sequencing,” at ENAR 2011, Miami, FL.

Program committee member for “Workshop on Computational Advances in Molecular Epidemiology (CAME),” Atlanta, GA. 2011.

Grant Reviews:

NSF Ad-hoc grant reviewer (2008)

NIH/NHLBI study section for RFA HL-11-002, "Common Pathogenetic Mechanisms of Lung Cancer and COPD" (2010)

NSFC grant review (May 2011)

NIH ZRG1\_HDM study section (May 2014) “Gene and environment interaction”

Others:

DNA Day Essay Contest judge (third annual essay contest for U.S./Canadian students in grades 7–12), April 2008.

Birmingham UseR group organizer (2014-present)

**University Services:**

UAB:

UAB Faculty Senate (2013-2015)

UAB Grievance and Termination Hearing Panel (2016-2017)

HSF-GEF Grant Review Committee (2010–2017)

School of Public Health:



Admission and Graduation Committee (2011–2015, chair 2013-2015)  
Award Nomination Committee (2012-2016)  
Norwood Award Selection Committee (2005–2013)  
Public Health Practice Committee (2016-2017)

Department:

Co-organizer for SSG Seminar (2005–2008)  
Department of Medicine Ph.D. Faculty Advisory Group (2007–2008)  
IGGP Graduate Program Admission Committee (2007–2009)  
Chair of the SSG StatGen Software Training Committee (2008)  
Organizer of the SSG Monthly Research Update Seminar (2009)  
Postdoctoral Trainee Research Day judge (2010).  
Organizer of the Bimonthly Biostatistics social event (SMA) (2007–2011)  
SSG Faculty Recruiting Committee (2007–2012)  
SSG Curriculum Committee (2008–2014)  
SSG programmer recruiting committee chair (2015)  
Biostatistics social chair (2012-2015)  
Graduate Student Admission Committee chair (2016-2017)

## HONORS

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Nankai University Scholarship, China	1988
Guanghua Scholarship, China	1992
Wang Kechang Scholarship, China	1993
Phi Kappa Phi, Iowa State University Chapter	1996
Fung Fellowship	1998
Stadler Research Fellowship	1999
1 <sup>st</sup> Runner up for CAMDA (Critical Assessment of Microarray Data Analysis) competition	2002
Best Paper Award, Science Unbound Foundation	2012

## GRANTS:

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### *Terminated due to Moving to Emory*

2P60AR048095-06A1 NIH (Cui) 9/1/08–6/30/18

*NIAMS Multidisciplinary Clinical Research Center—Methodology Core*

The objectives of the Methodology Core are: (1) to conduct cutting-edge research in arthritis and MSD by providing statistical, epidemiological, outcomes, and health-service expertise and leadership; (2) to support data collection, management, and analytic efforts of the MCRC projects; (3) to develop original research in methodology applicable to clinical research in arthritis and MSD; and (4) to nurture and support new investigators in arthritis and MSD.

Role: PI of Methodology Core

P30 DK07022 (Agarwal) 07/01/08–06/30/18

NIH/NIDDK

*UAB-UCSD O'Brien Core Center for Acute Kidney Injury Research*

Core Center will establish an interdisciplinary center of excellence in AKI-related research.

Role: Primary co-investigator in the Biostatistics/Bioinformatics Resource

8UL1TR000165-05 (Kimberly)

09/01/2015 – 8/31/2020

UAB Center for Clinical and Translational Science

To 1) establish a centralized communication structure to enhance collaboration between our research centers and programs across all fields of clinical and translational research, including pediatric and community groups; 2) train and develop clinical and translational investigators to become principal investigators and productive members of research teams; 3) facilitate utilization of existing resources and provide new resources; 4) emphasize novel interdisciplinary research that is important given our geographic location and history (i.e., health disparities research) and that utilizes our unique strengths (i.e., outcomes research and drug discovery); and 5) assess the progress of the CCTS toward its goals.

Role: Co-Investigator (major player in BERD)

NIH R01DK097107 (Mannon)

08/01/13 – 06/30/17

NIH/NIDDK

Ulcerative Colitis – Regulation of the IL-13 Receptor System

Role: Co-Investigator for data analysis

R01CA186646 (MPI, Brown/Vachon)

07/01/2014 – 03/31/2019

NIH/NCI

Molecular characterization of myeloma and related asymptomatic precursor states

The goal of this investigation is to identify and characterize the contribution of microRNAs (miRNA) in serum exosomes on the risk of multiple myeloma, and within the spectrum of its progression, the risk of asymptomatic precursor states, including monoclonal gammopathy of undetermined significance and smoldering myeloma.

Role: Co-Investigator for data analysis

NIH R25 GM093044 (Tiwari)

08/01/10 – 05/31/17

NIH/NIGMS

Short Course on Statistical Genetics and Genomics

To offer an annual statistical genetics short course to be focused on applying advanced quantitative approaches to the search for genes that predispose complex human disorders and quantitative traits.0.55

Role: co-director mainly in charge of hands-on component.

R01CA178441 (Tollefsbol)

04/01/2014 – 02/28/2019

NIH/NCI

Combinatorial Epigenetic-Based Prevention of Breast Cancer

Breast cancer is a significant health problem worldwide and is a leading cause of cancer morbidity and mortality. The overall goal of this application is to develop a combinatorial dietary approach consisting of green tea polyphenols and sulforaphane-rich broccoli sprouts for efficacious and safe use in preventing the epigenetic aberrations of breast cancer.

Role: Co-Investigator for data analysis

R01DK097423 (Mrug)

08/05/2013 – 06/30/2018

NIH/NIDDK

## Mechanisms of C3 Effects in ARPKD Pathogenesis

Our initial studies point to local intra-renal production of complement component 3 (C3), an axial component of complement pathway, as regulator of cystogenic pathway that dictates the pace of ARPKD progression. Therefore, we propose to establish key relationships of C3 effects in the pathogenesis of ARPKD and provide foundation for pre-clinical ARPKD studies targeting C3-regulated pathways

Role: Co-Investigator for data analysis

R21CA205501 (Yoon)

04/01/2016 – 03/31/2018

NIH/NCI

Developing Therapy for the Treatment of Cholangiocarcinoma Nutritional deficiencies and environmental Cholangiocarcinoma (CCA) is a fatal disease with a 5-year survival of less than 30%. We plan to use our recently established CCA patient-derived xenograft (PDX) models, the first such models reported and a unique resource, to develop effective therapy for patients with CCA. We will determine whether the combination of gemcitabine and the novel agent JQ1 (a targeted BET inhibitor) indirectly inhibits two proteins that contribute to CCA tumor progression and drug-resistance (c-Myc and Chk1), and produces synergistic cytotoxicity in CCA PDX models.

### ***Completed:***

#### GRANTS AS PI:

NIH 1R13HG005792

1/1/11–11/30/12

*Statistical Analyses for Next Generation Sequencing*

Organizing a two-day conference for biologists, bioinformaticians, and statisticians to discuss challenges and strategies in the next-generation sequencing data analysis.

UAB CAEG Partnership Pilot Program

8/15/10–8/14/11

*Unmasking Novel Cystogenic Pathways: Biological Knowledge-Based Statistical Pathway Analyses of Genome-Wide Gene Expression and DNA Methylation Data*

UAB Faculty Development Grant

8/1/08–7/31/09

*Toward the Integration of Genomics and Epigenomics—a Pilot Genome-wide Methylation Study to Characterize the Relationship Between DNA Methylation and Marker Genotype, Gene Expression, and Phenotype in Mouse RI Lines.*

UAB Center of Nutrition Research

8/1/05–7/31/06

*Characterizing the Diet/Nutrition Effect on Gene Alternative Transcripts Using Affymetrix Microarray Data.*

#### GRANTS AS CO-I:

R01GM085105 (Miller)

05/01/2014 – 02/28/2016

NIH/NIGMS

Prostaglandins in *C. Elegans* Fertilization

Nutritional deficiencies and environmental exposures can have a lasting, negative impact on gamete function and fertility. Prostaglandins are locally acting lipid hormones that are derived from dietary fats. This proposal aims to use the simple animal *Caenorhabditis elegans* to investigate fundamental mechanisms that couple nutritional status to gamete function via ovarian prostaglandins.

Role: Co-Investigator for data analysis

AICR 316184 (Tollefsbol)

01/01/2015 – 12/31/2016

American Institute for Cancer Research

Epigenetics of Early Life Exposure to Cancer Preventive Cruciferous Vegetables

Role: Co-Investigator for data analysis

R21CA182861 (MPI, Brown/Sanderson)

07/01/2014 – 06/30/2016

NIH/NCI

The Role of Exosome Heparanase and miRNAs as Biomarkers for Myeloma

The goal of the proposed Exploratory/Developmental investigation is to characterize the role of heparanase, a potent tumor regulator, and exosome miRNAs as biomarkers for early detection, classification and progression of individuals at highest risk for developing multiple myeloma from asymptomatic precursor states

Role: Co-Investigator for data analysis

1R01HL109785-01A1 (Dell'Isola)

04/01/12-03/31/16

*Mitochondrial Haplotype Influences LV Dysfunction in Heart Failure.*

Mitochondrial DNA Background Drives Disease Susceptibility and Gene Expression

Role: minor co-Investigate for supervising postdoc on the data analysis

NIH R21NS085497 (King)

09/01/13 – 08/31/15

NIH/NINDS

*Molecular Signatures of Amyotrophic Lateral Sclerosis in Skeletal Muscle*

Role: Co-Investigator for data analysis

NIH R25 GM093044 (Tiwari)

08/01/10 – 07/31/15

NIH/NIGMS

Short Course on Statistical Genetics and Genomics

To offer an annual statistical genetics short course to be focused on applying advanced quantitative approaches to the search for genes that predispose complex human disorders and quantitative traits.

Role: Deputy Director and teaching

1R01DK085027-01A1 (Allon)

7/1/2010–6/30/2014

NIH/NIDDK

*Vascular Abnormalities in Patients Receiving a Dialysis Access.*

This grant is to quantify preoperative arterial medial fibrosis in CKD patients receiving a fistula, and correlate it with fistula non-maturation.

Role: Co-Investigator for statistical genetics data analysis

S10-005 6/30/2010–12/30/2013  
DHHS SRI (Gillespie)  
*Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression*  
This project is to profile global gene expression, SNP genotype, and kinase activities in the GBM xenograph lines and compare them with the primary tumors.  
Role: Co-Investigator for statistical and bioinformatical analysis

UF11080 (Allison) 3/01/11 –3/31/14  
NSF/USF  
Integrating physiological and genetic mechanisms to understand the evolution of cold tolerance  
Identify, test, and integrate hypotheses about biochemical and physiological mechanisms underlying the evolution of cold tolerance in *Drosophila*.  
Role: Co-Investigator for data analysis

5R01DK083562 (Garvey) 8/1/2009–7/31/2013  
NIH/NIDDK  
*NR4A Orphan Receptors and Insulin Resistance*

VA RR&D Merit Review F7226R (Bamman) 3/1/10-6/30/13  
*Understanding Muscle Regeneration Impairment in Aging Veterans*  
The overarching goal of this project is to advance knowledge of the molecular mechanisms causing muscle regeneration impairment with increasing age.

2P30HD038985-06A2 (Percy) 9/1/08–6/30/13  
UAB Mental Retardation Research Center  
This project provides the environment and support for clinical and genetic study of mental diseases.

10A020 (Tollefsbol) 1/01/11-12/31/12  
AIFCR  
*Green Tea Polyphenols in the Prevention of Breast Cancer Initiation*

P50 HL77100 (Dell'Italia) 2/9/2005–12/31/2010  
NIH/NHLBI  
*SCCOR in Cardiac Dysfunction and Disease—Biostatistics Core*  
To unravel mechanisms of LV remodeling in three disparate forms of heart disease—volume overload of mitral regurgitation (MR), primary aldosteronism, and diabetic cardiomyopathy—that are resistant to standard medical therapy.

NIH U54CA100949 (Barnes) 9/9/03–8/31/2010  
Center for Gene-Nutrient Interaction (CNGI)  
This Center will focus on the identification of genetic pathways that may distinguish cancer cells from normal cells, and the extent to which dietary polyphenols with documented chemo preventive activity modulate these pathways.

1 P30 DK074038-02 (Guay-Woodford)  
NIH/NIDDK

9/30/05–8/31/10

*UAB Recessive PKD Research and Translational Core Center*

This center integrates existing intellectual and technological resources of the University and provides a set of services/resources to enable innovative investigations in the four thematic areas related to recessive PKD pathogenesis: (1) cilia-related biology, (2) regulation of epithelial transport pathways, (3) signaling pathways in epithelial differentiation, and (4) matrix biology and fibrosis.

R01DK68261 (Nagy)  
NIH/NIDDK

7/1/04 to 6/30/09

*Antipsychotic Drug-Induced Weight Gain*

The specific aim of this project is to determine, using a mouse model system, the mechanism(s) by which the new atypical antipsychotic drugs induce weight gain.

Susan G. Komen Breast Cancer Foundation (Frost)

12/1/07–11/30/09

*Targeting the Hedgehog Pathway in the Treatment of Breast Cancer*

1 R21 DK078522 (Guay-Woodford)  
NIH/NIDDK

6/1/06–5/30/11

*Genetics and Pharmacogenetics in FSGS (PPG Project 4)*

5 R01 HL075211 (Oparil)

NIH/NHLBI

7/1/04–6/30/08

*Estrogen Modulates Injury-Induced Inflammation*

Utilize a well-characterized rodent model to elucidate the fundamental cellular/molecular mechanisms by which ovarian hormones, particularly estrogen, modulate the inflammatory response to acute endoluminal vascular injury.

NIH R01AG020681 (Prolla)  
NIH/NIA

3/15/03 - 1/31/08

*Gene Expression Profiling, Caloric Restriction and Aging.*

To use microarrays for gene expression studies to understand the role of caloric restriction in promoting longevity in mice.

NSF 0217651 (Allison)  
NSF

10/01/02–08/31/06

*Design and Analysis of Microarray Gene Expression Studies in Plants: Toward Sound Statistical Procedures*

To develop statistical methods from a strong epistemological foundation for analysis of microarray data from plants.

NIH R01ES12933-01A1 (Ruden)  
NIH/NIEHS

04/01/05–03/31/10

*QTL and Microarray Mapping Lead Sensitivity Genes*

The hypothesis for this proposal is that one can identify some of the "protective genes" that make an organism resistant to the behavioral and developmental effects of lead toxicity using

quantitative trait loci (QTL) mapping techniques combined with microarray and sophisticated genetic analyses.

Burroughs Wellcome Fund (Guay-Woodford)

07/01/01–06/30/06

*Genetic Modifiers of Recessive Polycystic Kidney Disease: Implications for Pathogenesis and Therapeutics*

The specific aims of this project are: (1) to map QTL that modulate *cpk* renal cystic disease and those QTL that unmask and modulate the biliary phenotype in the mouse *cpk* model, (2) to determine whether these same QTL modulate *bpk*-associated renal and biliary traits, and 3) to test patients enrolled in our ARPKD Clinical Database to determine whether the human homologues of these renal and biliary QTL modulate disease expression in human ARPKD.

NIH 1 R21 HL72871 (Matalon)

10/01/01–09/30/06

*Modulation of Innate Immunity in Lung Transplantation*

The major goal of this project is to identify differences in the ability of *Ams* to kill gram-positive and gram-negative bacterial pathogens in lung-transplant patients.