

NAME: Degui Zhi, Ph.D.

PRESENT TITLE:

Associate Professor
Center for Precision Health
School of Biomedical Informatics & School of Public Health
University of Texas Health Science Center at Houston

WORK ADDRESS:

7000 Fannin St Suite 820
Houston, TX 77030
Office Phone: (713) 500-3629
Email: Degui.Zhi@uth.tmc.edu

CITIZENSHIP: China

UNDERGRADUATE EDUCATION:

1993-1997 B.S. in computer science, Peking University (Beijing University)

GRADUATE EDUCATION:

1997-1999 M.Sc. in computer science, National University of Singapore

POSTGRADUATE TRAINING:

2001-2006 Ph.D. in Bioinformatics, University of California, San Diego.

MILITARY SERVICE (IF APPLICABLE): None

ACADEMIC & ADMINISTRATIVE APPOINTMENTS:

| | |
|-----------|---|
| 2009-2015 | Assistant Professor, Section on Statistical Genetics, Department of Biostatistics, School of Public Health, University of Alabama at Birmingham |
| 2014-2016 | Member, Biostatistics Core, Nutrition Obesity Research Center (NORC), University of Alabama at Birmingham |
| 2010-2016 | Associate Scientist, Nutrition Obesity Research Center (NORC), University of Alabama at Birmingham |
| 2015-2016 | Associate Professor with Tenure, Department of Biostatistics, School of Public Health, University of Alabama at Birmingham |
| 2016- | Associate Professor, Department of Biostatistics, School of Public Health, University of Texas Health Science Center at Houston |
| 2016- | Associate Professor, School of Biomedical Informatics, University of Texas Health Science Center at Houston |

PREVIOUS RESEARCH EXPERIENCE

- 1997-1999 Graduate student researcher, Department of Computer Science, School of Computing, National University of Singapore
- 1999-2000 Full-time research assistant, Department of Computational Science, National University of Singapore
- 2000-2001 Research assistant, Department of Computer Science and Engineering, University of California, Santa Cruz
- 2001 Summer intern, Arena Pharmaceutical Inc., San Diego
- 2001-2006 Research assistant, Department of Computer Science, University of California, San Diego
- 2004 Summer visiting student researcher, Max Planck Institute for Molecular Genetics, Berlin, Germany
- 2004-2006 Visiting research assistant, Burnham Institute, La Jolla, California
- 2006-2009 Postdoctoral fellow, Department of Plant and Microbial Biology, University of California, Berkeley.

PROFESSIONAL MEMBERSHIPS

- International Society of Computational Biology (ISCB), 2006-present
- Sigma Xi, 2007-present
- Reuter Insight Expert, 2008-present
- American Society of Human Genetics, 2008-present
- American Association for the Advancement of Science, 2007-present

HONORS AND AWARDS:

- First class award (top 10), National Mathematics Olympic, Liaoning Province, China, 1992.
- Max-Planck-Society fellowship, 2004.
- Travel award, Workshop on Genomic Impact of Eukaryotic Transposable Elements, 2006.
- Outstanding Poster award (4 out of 171), RECOMB, 2007.
- NIH Pathway to independence K99/R00, 2007-2012.
- Best Paper award, the Science Unbound Foundation, for Best paper by a UAB based investigator in the area of statistical genetics, 2013.

EDITORIAL POSITIONS:

EDITORIAL BOARD

| | |
|--|-------|
| Review editor, Frontiers in Statistical Genetics and Methodology | 2010- |
| Review editor, Frontiers in Bioinformatics and Computational Biology | 2011- |
| Review editor, Frontiers in Evolutionary and Population Genetics | 2011- |
| Review editor, Frontiers in Epigenetics | 2011- |
| Editorial board member, Journal of Medical Statistics and Informatics | 2012- |
| Academic editor, PLOS ONE | 2013- |
| Academic editor, PeerJ | 2015- |

GUEST EDITORIAL ACTIVITY

| | |
|---|------|
| Guest editor, Biomedical Data Integration, Modeling, and Simulation in the Era of Big Data and Translational Medicine. BioMed Research International | 2014 |
| Guest editor, Research Topic: Identification of rare genetic variants contributing to human diseases. Frontiers in Genetics , | 2015 |

SERVICE ON NATIONAL GRANT REVIEW PANELS, STUDY SECTIONS, COMMITTEES:

| | | |
|-----------------------------|---|-----------------|
| Ad hoc reviewer | NIH IAR Reviewer Challenge Grants Panel ZRG1 PSE-C/J (58) R | 2009 |
| Reviewer | Italian Ministry of Health Researchers Call | 2010,2011, 2013 |
| Ad hoc Statistical reviewer | NIH MGB Section | 2010 |
| Reviewer | Tuskegee/UAB partnership pilot grant | 2010 |
| Reviewer | Portuguese Foundation for Science and Technology, Diagnostic, Therapies and Public Health Evaluation Panel | 2012 |
| Reviewer | Kansas City Area Life Sciences Institute (KCALS) Patton Trust Grant Program | 2012 |
| Reviewer | NIH RFA-RM-14-001: Computational Analyses Exploiting Reference Epigenomic Maps [ZRG1 IMST-R (51) R] study section panel | 2014 |
| Reviewer | NIH K99/R00 Grants Panel ZGM1 TWD-Y (KR) | 2014, 2014 |
| Ad hoc Reviewer | NIH IRAP Study Section | 2015 |
| Ad hoc Reviewer | NIA review panel on the Social and Behavioral Science of Aging | 2015 |

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| Ad hoc Reviewer | NIH BMRD panel | 2016 |
| Reviewer | Pennsylvania Department of Health Final Performance Review | 2016 |
| Reviewer | NIH BD2K Mentored Career Development Award study section panel | 2016 |
| Reviewer | NIH NIGMS R35 panel | 2017 |
| Reviewer | NIH review panel for Mechanisms of Disparities in Chronic Liver Diseases and Cancer | 2017 |
| Reviewer | NIH review panel for Social Epigenomics Research Focused on Minority Health and Health Disparities | 2018 |
| Ad hoc Reviewer | NIH BDMA panel | 2018 |

SERVICE ON THE UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER AT HOUSTON COMMITTEES:

SERVICE ON SBMI COMMITTEES:

Member, Faculty Search Committee, Center for Precision Health, School of Biomedical Informatics, UTHealth, 2016-2017

Member, Faculty Search Committee, Center for Systems Medicine, School of Biomedical Informatics, UTHealth, 2017

Member, Curriculum Committee, School of Biomedical Informatics, UTHealth, 2016-

Member, Data Governance Committee, School of Biomedical Informatics, UTHealth, 2016-

Speaker, SBMI PASS Day 2018

SERVICE ON UTHEALTH COMMITTEES:

None

SERVICE TO THE COMMUNITY:

JOURNAL AND CONFERENCE REFEREES

Advances in Bioinformatics 2009

American Journal of Clinical Nutrition 2014

Bioinformatics 2006, 2007, 2008, 2009, 2009, 2010, 2011, 2013, 2013, 2013, 2015, 2015, 2016, 2017, 2018, 2018

BMC Bioinformatics 2012, 2013, 2016

BMC Genetics 2012

Computational and Mathematical Methods in Medicine 2013

Computational Statistics and Data Analysis 2009, 2010

European Conferences on Computational Biology (ECCB) 2006
European Journal of Clinical Investigation 2011
Frontiers in Genetics 2011, 2013, 2014, 2015
Genes 2010
Genetic Epidemiology 2012, 2013, 2015
Genetics Research 2012
Genome Medicine 2016 2018
Genome Research 2011
Human Genetics 2012
Human Heredity 2010, 2014
International Journal of Obesity 2014
Int'l Conf. on Research in Computational Molecular Biology (RECOMB) 2005, 2016, 2018
ICIBM 2016 2018
ISMB 2018
Journal of Biomedicine and Biotechnology 2010
Journal of Computational and Graphical Statistics 2012
Journal of Medical Genetics 2012
Journal of Obesity 2012
Molecular Biology and Evolution 2009
Molecular Ecology Resources 2015
Molecular Systems Biology 2008
Nature Biotechnology 2011(co-review)
Nature Communications 2013
Nature Methods 2011
Nucleic Acids Research 2007, 2011
Obesity 2014
PeerJ 2015
PLOS Genetics 2015, 2017
PLOS ONE, 2012, 2013, 2015
Respiratory Research, 2013
Science Translational Medicine 2018

CONFERENCE ORGANIZATION

Member, UAB Research Computing Day Program Committee, 2011

Co-investigator, Workshop on next-generation sequencing data analysis, 2011, (NIH R13 grant funded, PI: Cui)

Co-Investigator, Short Course on next-generation sequencing data analysis, 2011-2014, (NIH R25 grant funded, PI: Tiwari)

Session Chair, Next-generation sequencing data analysis, ENAR, 2011.

Co-organizer, UAB Microbiome Resource Workshop, 2015

Chair, Publicity Committee, ICIBM, 2016

Member, Program Committee, ICCABS 2017

Co-Chair, Program Committee, ICIBM 2018

Member, Programmer Committee, ISMB 2018

Member, Programmer Committee, RECOMB-seq 2018

SERVICE TO THE OTHER UNIVERSITY COMMITTEES:

Leader, SSG Journal Club, Biostatistics Department, SOPH, UAB, 2009 - 2015

Member, Admission Committee, Biostatistics Department, SOPH, UAB, 2009-2010, 2012-2016

Member, SSG curriculum committee, Biostatistics Department, SOPH, UAB, 2010

Member, SSG overseas connection task force, Biostatistics Department, SOPH, UAB, 2010

Member, SSG Professional Development Workshop Organization Committee, Biostatistics Department, SOPH, UAB, 2010

Member, UAB Research Computing Day Program Committee, 2011

Alternate Senate, UAB faculty senate, 2011 – 2013

Member, UAB faculty senate finance committee, 2011 – 2013

Grader, UAB Department of Biostatistics qualifying exams, 2014, 2015

Member, SOPH UWIRC review committee, UAB 2014

CONFERENCE AND INVITED TALKS

Resolving difference between nearly identical repeats in fragment assembly, RECOMB satellite meeting on DNA sequencing and characterizations, Stanford, CA, May, 2002.

Comparative genomics analysis of Alu gene conversions, 1st International Conference and Workshop on Genomic Impact of Eukaryotic Transposable Elements, Asilomar, CA, April, 2006.

Alignment-free local structural comparison by Writhe decomposition, Workshop on Algorithms in Bioinformatics (WABI), Philadelphia, PA, September, 2007.

An optimization framework for the inference of nontrivial protein domain architecture and ancient homology, University of Tennessee, Knoxville, TN, April, 2008.

Beyond Sequence Alignment: An optimization framework for the inference of nontrivial protein domain architecture and ancient homology, Section on Statistical Genetics, School of Public Health, University of Alabama, Birmingham, AL, July, 2008.

A sequence alignment-based optimization framework for the inference of nontrivial protein domain architecture and ancient homology, Computational Systems Biology Seminar, University of Georgia, Athens, GA, July, 2008.

Repeat, Repeat, Repeat (Analysis of genomic repeats), Beijing Genome Institute, Shenzhen, Guangdong, China, December, 2008.

A sequence alignment-based optimization framework for the inference of nontrivial protein domain architecture and ancient homology, Tongji University, Shanghai, China, December, 2008.

Protein structural comparison, classification, and function prediction in the structural genomics era, University of Tennessee, Knoxville, TN, February, 2009.

Bayesian Hierarchical Models for Quantifying Methylation Levels by Next-generation Sequencing, *Annual Meeting of ENAR*, New Orleans, LA, March, 2010.

Bayesian Analysis of Rare Variants with Disparate Effects in Association Studies, *Annual Meeting of ENAR*, Miami, FL, March, 2011.

Genotype calling and haplotype inference from next-generation sequencing data. Emory University, Atlanta, GA, March, 2012.

Genotype calling and haplotype inference from next-generation sequencing data. HitSEQ SIG of ISMB, Long Beach, CA, July, 2012.

From genetics to epigenetics. Sino-US summer school for translational biomedical informatics (3S-TBI2013) Suzhou, Jiangsu Province, China, June, 2013.

Genotype calling from NGS data: incorporating haplotype information in reads. NGS workshop, International Conference on Intelligent Biology and Medicine (ICIBM), Nashville, TN, August, 2013

Next-generation bioinformatics for next-generation sequencing: genotype calling and haplotype phasing. Department of Computer and Information Sciences, University of Alabama at Birmingham, Birmingham, AL, Oct, 2014.

Inferring genotypes and haplotypes from Next-generation sequencing data. Molecular and Human Genetics Department, Baylor College of Medicine, Houston, TX, Nov, 2014.

Inferring genotypes and haplotypes from Next-generation sequencing data. University of Alabama, Tuscaloosa, AL, Mar, 2016.

Identical-by-Descent in TOPMed samples. TOPMed Steering Committee and External Advisory Panel meeting, Tysons, VA, Nov, 2017.

SPONSORSHIP OF CANDIDATES FOR POSTGRADUATE DEGREE: (include names and years)

PhD COMMITTEE CHAIR

Guodong Wu UAB BST 2009-2014

Current position: Biostatistician, Lovelace Respiratory Research Institute

Masters STUDENT CHAIR

Guodong Wu UAB BST MS 2011

Dongning He UAB BST MS 2015

Dongmei Sun UAB BST MSPH 2013-2015

PHD DISSERTATION COMMITTEE

Celeste Yang UAB BST 2013

Aditi Shendre UAB EPI 2016

Lindsay Jones UAB BST 2015

Anh N Do UAB EPI 2017

Rachel Brewer UAB Nutrition 2015

Gene Sher UCF CS 2017

Ardalan Naseri UCF CS 2016-

Cheng Li (external reviewer) UTHealth Epi 2018

MS DISSERTATION COMMITTEE

Peng Li UAB BST 2011

Ngan Thanh Tran UAB EPI 2014

Mingyao Lu UTHealth Epi 2017-

STUDENT ADVISOR

Dongning He UAB BST MS 2013-2015

Dongmei Sun UAB BST MSPH 2013-2015

Fuchenchu Wang UAB BST MS 2015-2016

Megan Yanik UAB BST MSPH 2015-2016

Ruth Amaku UTHealth Epi MPH 2018-

Srisha Neshangi UTHealth Epi MPH 2018-

Robert Men UTHealth Epi MS 2018-

Ruth Amaku UTHealth Epi MPH 2018-

Jane Ibekwe UTHealth SBMI MS 2018-

Stella Ibekwe UTHealth SBMI MS 2018-

OTHER STUDENT MENTOR

| | | |
|--------------------------|--|-----------|
| Alexey Aleshin | UCB Undergrad student research | 2007 |
| Shravan Gopal | UAB Graduate student research | 2009 |
| Hua Zhong | UAB Graduate student research | 2009 |
| Nirmal Choradia | UAB MD student intern | 2011 |
| Yue Pan | UAB's NIGMS-funded Bursary Award for short course | 2012 |
| Xin Geng | UAB's NIGMS-funded Bursary Award for short course | 2013 |
| Aditi Shendre | UAB's NIGMS-funded Bursary Award for short course | 2013 |
| Matthew Ainsworth | UAB Predoctoral Training in Obesity-Related Research Program | 2015-2016 |
| Swati Goyal | UTHealth SBMI MS student | 2016-2017 |
| Laila Bekhet | UTHealth SBMI MS student | 2017 |
| Jie Zhu | UTHealth Biostat PhD student | 2018- |

SPONSORSHIP OF POSTDOCTORAL FELLOWS: (include names and years)

| | |
|--|-----------|
| Kirk Williams (co-mentor with David Allison) | 2009-2011 |
| Samad Jahandideh | 2010-2012 |
| Curtis Holliman (co-mentor with Hemant Tiwari) | 2011-2014 |
| Xueyan Zhao | 2015-2016 |
| Bijie Bie | 2016-2016 |
| Xin Geng | 2016- |
| Soyeon Kim | 2016-2017 |

TEACHING RESPONSIBILITIES:

As Course Master

2011, UAB BST695 Special Topics in Statistical Genomics
 2012, UAB BST612 Intermediate Statistical Analysis
 2013, UAB BST775 Statistical Methods for Genetic Analysis I
 2015, UAB BST775 Statistical Methods for Genetic Analysis I
 2015, UAB BST675 Introduction to Statistical Genetics
 2016, UAB BST676 Genomic Data Analysis

2018, UHealth BMI6334 Deep Learning for Biomedical Informatics

Guest Lectures

2010, UAB BST676 Genomic Data Analysis

Role: gave 2 Guest lectures on Next-generation sequencing data analyses.

2011, UAB BST795 Faculty Research Area Seminar

Role: gave 1 guest lecture.

2011, NIGMS SHORT COURSE ON STATISTICAL GENETICS AND GENOMICS, UAB, Birmingham, AL.

Role: Course instructor on Software demonstration of exome sequence data analysis.

2012, NHGRI SHORT COURSE ON NEXT-GENERATION SEQUENCING: TECHNOLOGY AND STATISTICAL METHODS, UAB, Birmingham, AL.

Role: Course instructor on Assembling NGS data.

2012, NIGMS SHORT COURSE ON STATISTICAL GENETICS AND GENOMICS, UAB, Birmingham, AL.

Role: Course instructor on Software demonstration of exome sequence data analysis.

2012, UAB GBS722 Bioinformatics Course

Role: gave 1 guest lecture.

2013, NHGRI SHORT COURSE ON NEXT-GENERATION SEQUENCING: TECHNOLOGY AND STATISTICAL METHODS, UAB, Birmingham, AL.

Role: Course instructor on Variant calling and assembly from NGS data.

2013, NIGMS SHORT COURSE ON STATISTICAL GENETICS AND GENOMICS, UAB, Birmingham, AL.

Role: Course instructor on Software demonstration of genotype imputation.

Role: Course instructor on Software demonstration of exome sequence data analysis.

Role: Course instructor on Genotype calling from NGS data.

2014, NHGRI SHORT COURSE ON NEXT-GENERATION SEQUENCING: TECHNOLOGY AND STATISTICAL METHODS, UAB, Birmingham, AL.

Role: Course instructor on Variant calling and assembly from NGS data.

Role: Course instructor on Software demonstration of RNA-seq data analysis.

2014, UAB BST776 Statistical Methods for Genetic Analysis II

Role: Guest lecturer on pathway-based association analysis.

Role: Guest lecturer on epigenetics.

2015, NHGRI SHORT COURSE ON NEXT-GENERATION SEQUENCING: TECHNOLOGY AND STATISTICAL METHODS, UAB, Birmingham, AL.

Role: Course instructor on Variant calling and assembly from NGS data.

Role: Course instructor on Software demonstration of Genome sequencing data analysis.

2017, UTHealth SBMI Foundation 1

Role: gave 1 guest lecture on Introduction to Bioinformatics

2018, UTHealth BMI 7302

Role: gave 1 guest lecture on Introduction to Bioinformatics

2018, UTHealth SBMI Foundation 1

Role: gave 1 guest lecture on Introduction to Bioinformatics

MENTORING ACTIVITIES:

CURRENT CLINICAL SERVICE RESPONSIBILITIES:

CURRENT GRANT SUPPORT:

NIH/NHGRI R01HG010086 (Zhang&Zhi) 06/01/2018-03/31/2022

Title: Scalable methods for identity by descent
\$600,000 (current year total cost)

The aim of the project is to develop and evaluate accurate and efficient methods and tools for detecting Identity-by-Descent (IBD) and local ancestry information in large genotyped cohorts, resources of increasing importance in the era of precision medicine. If successful, this project will advance genetic research by offering efficient informatics tools to researchers that can reveal detailed genetic relationships in very large genotyped cohorts.

Role: PI.

Cancer Prevention and Research Institute of Texas RP170668 (Zheng) 9/1/2017-8/31/2022

Title: Data Science and Informatics Core for Cancer Research
\$1,549,315 (Year 1 total cost)

The goal of this project is to establish a Data Science and Informatics Core to support cancer prevention and research in Texas by data science and informatics infrastructure and methodologies for data analysis and mining.

Role: Co-Investigator.

NIH/NHGRI U01HG009454 (Tao) 09/28/2016-07/31/2019

METADATA APPLICATIONS ON INFORMED CONTENT TO FACILITATE BIOREPOSITORY
DATA REGULATION AND SHARING
\$456,710 (current year total cost)

Role: Co-Investigator.

R01LM011829 (Tao) 09/01/2014 - 08/31/2019

NLM/ NIH \$256,410

Title: Patient Medical History Representation, Extraction, and Inference from EHR Data

Project Goal: Develop an ontology and semantic-based temporal relation modeling and reasoning tool.

Role: Co-Investigator.

AHA 17IG33660386 (Xu)

04/01/2017-03/31/2019

Title: Developing a data discovery index to facilitate precision medicine research in cardiovascular diseases

Project Goal: This project focuses on facilitating findability and accessibility of cardiovascular dataset across different repositories. If the proposed framework succeeds, we will be able to establish a sustainable discovery system prototype with a user interface that allows for simple and rapid navigation and information distribution for the cardiovascular community, thus enabling improved discoverability of biomedical datasets.

Role: Co-Investigator

NIH/NIAMS R01AR064280 (Brown)

08/26/2014-06/30/2019

Association of Genetic and Autoantibody Signatures with SLE Clinical Course

Role: Co-Investigator.

PAST GRANT SUPPORT:

NIH R01 HG008115 (Yu, Zhang, & Zhi)

09/10/2014-06/30/2018

Title: Next-Generation Bioinformatics for Next-Generation Sequencing

\$361,108 (Year 1 direct costs)

The goals of this project are to develop an improved computational system for calling of rare genetic variants and haplotypes and for integrating genetic data sets of different compositions and generated by different platforms.

Role: PI.

USDA/NIFA #2015-67015-22975 (Liu)

01/15/2015-01/14/2018

Title: Whole Genome Mapping of Disease Resistance/Susceptibility-Associated SNPs in Catfish

Role: Subcontract-PI.

NIH R01 HL091357 (Arnett)

04/01/2015-02/28/2019

First year direct: \$699,303

Title: Genomewide Association Study of Lipid Response to Fenofibrate and Dietary Fat

Role: Co-investigator.

People differ in the ways their bodies process dietary fats and in the ways they respond to drugs meant to lower elevated blood lipids, often risk factors of cardiovascular disease. By studying the building blocks of lipids and the chemicals that lipids are broken down into via metabolomics profiling of 350 metabolites, this project seeks to determine which genetic factors influence people's blood lipid concentrations after eating a high-fat meal or after taking a lipid-lowering drug. Ultimately, this research may help doctors more accurately assess people's risk of cardiovascular disease and more effectively prescribe drugs to prevent disease.

NIH R01 HL055673 (Arnett)

06/01/13 – 04/30/17,

First year direct: \$626,073.

Title: HyperGEN: Genetics of Left Ventricular Hypertrophy.

Left ventricular (LV) remodeling and hypertrophy occurs frequently in the general population and is a strong predictor of myocardial infarction, heart failure, and stroke. Using whole exome

sequencing, this project will identify novel genes contributing to LV hypertrophy, and evaluate their relevance in a cell-based system to identify new pathways for future treatment.

Role: co-Investigator.

AHA CVGPS (Arnett)

02/01/2015-01/31/2017

First year direct: \$500,000.

Title: Epigenetic Determinants of Left Ventricular Structure and Function in Hypertensive African Americans

Role: co-Investigator.

This project will investigate the genome-wide epigenomic association to left ventricular structure and function in the African Americans of the HyperGEN cohort.

NIH/NIDDK P30 DK056336 Allison (PI)

06/15/12 – 5/31/17

UAB Nutrition Obesity Research Center

One's nutritional intake can have profound positive or negative consequences on health. So too does obesity, or excess body fat, have profound effects, usually negative, on health, quality of life, and lifespan. Beyond these broad generalities, however, much remains unknown in these domains, and misinformation and superstition abound. Our center advances knowledge on these critical contributors to health and disease through scientific inquiry that is both rigorous and creative.

Role: Co-Investigator.

NIH/NHGRI R25 HG006110 (Tiwari)

Title: Short Course on Next-Generation Sequencing Technology and Statistical Methods

04/27/11 – 1/31/17

\$48,584 (first year direct)

To offer an annual short course focused on technological and statistical approaches pertaining to next-generation sequencing applied to complex human disorders and quantitative traits.

Role: Co-investigator

NIH/NCI R01 CA186646 (MPI: Brown/Vachon)

Title: Molecular characterization of myeloma and related asymptomatic precursor conditions

07/01/2014-05/31/2019

\$551,870 (Year 1 direct costs)

The purpose of this study is to identify microRNAs associated with the presence of MM and its asymptomatic precursor states and to characterize the role miRNAs in regulating gene transcription.

Role: Co-Investigator.

NIH/NCI R01 AR064820 (Brown)

Title: association of genetic and autoantibody signatures with SLE clinical course

08/26/2014-06/30/2019

\$482,631 (Year 1 direct costs)

The purpose of this study is to characterize complex interactions between variation in DNA sequence and autoantibody profiles with the rate of progression and severity of lupus-associated nephritis and severe organ damage, which are more common among ethnic minorities.

Role: Co-Investigator.

USDA/NIFA Proposal #2014-07991 (Liu)

Enhancing Low-Oxygen Tolerance of Catfish Using Genomics and Genetics

09/30/2014-09/29/2016

Role: Subcontract-PI.

In this project, we will identify DNA markers that are closely linked to low-oxygen tolerance, validate such markers for their utilities in predicting tolerance levels for low oxygen, and use such markers to select female channel catfish and male blue catfish.

NIH R21 AA023273 (PI: Darley-Usmar & Singal)

Translational Bioenergetics in Patients with Alcoholic Liver Disease

05/01/15-04/30/17

\$143,750

Roles: Co-Investigator.

In this application we will test the hypothesis that alcoholic liver disease patients with severe cellular bioenergetic defects and low oxidative burst activity detectable in monocytes and neutrophils will progress more rapidly to liver failure and be unresponsive to corticosteroid treatment.

NIH R56HL125061 (PI: Shrestha)

Genetic Variants In Calcium Channel And Binding Proteins Underlying cIMT In HIV

09/01/15-08/31/16

\$528,085 (Year 1 direct costs)

Roles: Co-Investigator.

Atherosclerosis is an important cardiovascular complication that is accelerated and accentuated among HIV- positive individuals. The proposed project will examine defective genes that alter biological mechanisms of calcium channel pathways, exacerbated by HIV, which lead to plaque development. Findings from the study will assist in understanding a mechanism and pathway of atherosclerosis, necessary for development of innovative interventions and treatments.

NIH R01 HL126737 (Liu)

Title: Metabolic Reprogramming in Myofibroblasts as a Mechanism of Pulmonary Fibrosis

01/01/2016-12/31/2019

Role: Co-investigator.

We aim to determine the role of aerobic glycolysis in the establishment and sustainment of the myofibroblastic phenotypes and lung fibrosis. The studies should improve understanding of the roles of aerobic glycolysis in the pathogenesis of lung fibrosis, and suggest glycolytic inhibitor being a novel therapeutic approach aimed at decreasing the severity of lung fibrosis.

UA System Collaborative Research Initiation Program (Tang&Zhi)

01/01/2015-12/31/2015

\$5,000 (Year 1 direct costs)

Communicating risk through social media big data: The case of the 2014 Ebola outbreak

Role: PI.

NIH R01 CA154643 Skibola (PI)

03/01/13 – 04/30/2016

Resequencing and Functional Studies to Identify Casual Gene Variants of Lymphoma

Non-Hodgkin lymphoma (NHL) is the fifth most common cancer in the U.S and will account for over 66,000 newly diagnosed cases and 20,000 deaths in the U.S. and 300,000 cases and 175,000 deaths worldwide in 2010. We will perform genetic studies that will aid in the identification of common genetic variants that cause lymphoma. These studies will increase our understanding of how lymphoma develops in the body and provide new ways to screen, prevent and treat lymphoma.

Role: Co-Investigator.

NIH/NIA R01 AG033682 Allison (PI)

03/15/10 – 2/29/16

Body Composition, Energetics and Longevity

Over 50 million Americans are obese and are therefore predicted to live less long than they would otherwise live. Whether reductions in overall obesity or selected aspects of fatness among obese persons will prolong life remains the subject of active debate and controversy.

The proposed research will help provide information to inform that dialogue.

Role: Co-Investigator.

NIH R01 HL104135 (Arnett)

08/15/2010 – 05/31/2015,

Yearly Cost: \$924,356.

Title: Epigenetic Determinants of Lipid Response to Dietary Fat and Fenofibrate.

In this project, we will identify novel epigenetic variations that predict individuals who respond poorly to dietary fat or favorably to fenofibrate which will lead to the development of targeted interventions to more effectively prevent and treat hypertriglyceridemia.

Role: co-Investigator.

NIH/NHLBI P01 HL114470 Thannickal (PI)

Therapeutic Targeting of the Myofibroblast in Fibrotic Lung Disease

10/1/13 – 7/31/18

The major goal of this translational program project grant is to develop novel anti-fibrotic therapies targeting myofibroblasts in fibrotic lung disease.

Roles: co-Investigator

SAIC-FREDERICK, INC, NCI Chemical Biology Consortium Task Order S08-221ST TO4aSAIC (Gillespie)

Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression.

04/01/2013 – 11/30/2014

Role: co-Investigator.

NIH R00 RR024163 (Pathway to independence, Independent Phase)

Title: Algorithms for protein structural classification and function prediction.

07/15/2009 – 05/31/2014,

Yearly Total Cost: \$244,046.

Role: PI.

NIH K99 RR024163 (Pathway to independence, Mentored Phase)

Title: Algorithms for protein structural classification and function prediction.

09/15/2007 – 06/30/2009,

Yearly Cost: \$73,440.

Role: PI.

Degui Zhi

UAB NORC Special ARRA Pilot/Feasibility Grant (Zhi)

Title: Differential gene expression of ribosomal proteins and its implication to obesity.

06/01/2010 – 05/31/2011,

Yearly Cost: \$25,000.

Role: PI.

SAIC-FREDERICK, INC, NCI Chemical Biology Consortium Task order S08-221ST TO4 (Gillespie)

Title: Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression.

07/02/2010 – 06/30/2012

Yearly Cost:

Role: co-Investigator.

UAB NORC Pilot/Feasibility Grant (Zhi)

Title: Expression of ribosomal protein genes and pseudogenes in adipose and its implications to obesity

06/01/2011 – 05/31/2013,

Yearly Cost: \$25,000.

Role: PI.

PUBLICATIONS: (List ONLY those published or accepted for publication.
DO NOT INCLUDE PAPERS SUBMITTED FOR PUBLICATION
OR IN PREPARATION. Use the citation style noted below.
Separate the publications into the following categories.)
Date order should be oldest (first) to current (last)

A. Abstracts

1. A. Aleshin, and **D. Zhi***. “Recombination-associated sequence homogenization of neighboring Alu elements—The signature of nonallelic gene conversion”, *CSHL Biology of Genomes*, 2008.
2. **D. Zhi**, and N. Liu. “Bayesian network model for SNP calling in shallow sequencing with haplotype based prior”, *Annual Meeting of The American Society of Human Genetics*, 2009.
3. Guodong Wu, Nengjun Yi, Devin Absher, and **Degui Zhi**. “Bayesian Hierarchical Models for Quantifying Methylation Levels by Next-generation Sequencing”, *Annual Meeting of ENAR*, 2010.
4. G. Wu, N. Yi, D. Absher, **D. Zhi**. “Quantification of Methylation Levels by Next-generation Sequencing”, *Annual Meeting of The American Society of Human Genetics*, 2010.
5. N. Yi, **D. Zhi**. “Hierarchical Generalized Linear Models For Detecting Rare Variants With Disparate Effects In Association Studies”, *Annual Meeting of The American Society of Human Genetics*, 2010.

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C. Invited Articles (Reviews, Editorials, etc.) in Journals

1. Wu H, Wu MC, **Zhi D**, Santorico SA, Cui X: **Statistics for Next Generation Sequencing - Meeting Report.** *Front Genet* 2012, **3**:128. PMID: PMC3395795.
2. Bairong Shen, Andrew E. Teschendorff, **Degui Zhi**, and Junfeng Xia: Biomedical Data Integration, Modeling, and Simulation in the Era of Big Data and Translational Medicine - Editorial. *BioMed Research International* 2014, Volume 2014, Article ID 731546. PMID: PMC4131419.

D. Chapters

1. **Degui Zhi**, Kui Zhang, Genotype Calling and Haplotype Phasing from Next Generation Sequencing Data. In Somnath Datta, and Dan Nettleton (Editors): *Statistical Analysis of Next Generation Sequence Data*. Springer. 2014.
2. Xin Geng, **Degui Zhi** and Zhanjiang Liu, Genome-wide Association Studies of Performance Traits. In Liu (Editor) *Bioinformatics in Aquaculture*. John Wiley & Sons, 2017

E. Books

F. Other Professional Communications

G. Visiting Professorships