**Date Prepared:** February 28, 2021

**NAME:** Liming Liang

**ACADEMIC TITLE:** Associate Professor of Statistical Genetics

**WORK ADDRESS:** 655 Huntington Ave, Building 2, Room 207, Boston, MA 02115

**EMAIL:** lliang@hsph.harvard.edu

**EDUCATION:**

1995 - 1999 Applied Mathematics B.S. South China University of Technology

Minor degree: Computer Science

1999 - 2002 Applied Mathematics M.S. South China University of Technology

2002 - 2004 Statistics and Probability M.S. Michigan State University

2004 - 2009 Biostatistics Ph.D. University of Michigan (Advisor:

Goncalo Abecasis)

**ACADEMIC APPOINTMENTS:**

2009-2015 Assistant Professor of Statistical Genetics Epidemiology Harvard Chan SPH

2009-2015 Assistant Professor of Statistical Genetics Biostatistics Harvard Chan SPH

2015 - present Associate Professor of Statistical Genetics Epidemiology Harvard Chan SPH

2015 - present Associate Professor of Statistical Genetics Biostatistics Harvard Chan SPH

**HOSPITAL/AFFILIATED INSTITUTIONAL APPOINTMENTS:**

2018 - present Consultant Massachusetts General Hospital

**OTHER PROFESSIONAL APPOINTMENTS:**

2013 Scientific Advisory Committee Member Chinese National Twin Registry

2013 – 2016 Advisory board, member Tute Genomics

**COMMITTEE SERVICE:**

DEPARTMENTAL/SCHOOL AND UNIVERSITY SERVICE:

**Harvard University level or inter-school**

2017 Symposium organizing committee member: How Disadvantage Gets “Under the Skin”: Using Epigenomic Methods to Better Understand & Address Health Disparities

2018 Harvard Initiative for Learning and Teaching (HILT) lunch meeting for curriculum and pedagogical practices, with the theme: *“Intentional” teaching and learning practices*

**Harvard T.H. Chan School level or inter-department**

2009 Genomics/Computational Biology Curriculum Committee (Epidemiology & Biostatistics), member

2010 - 2015 PQG seminar, chair

2011 - 2012 2012 Epigenetics Workshop, co-organizer and co-moderator http://www.hsph.harvard.edu/departments/nutrition/announcements/2012-epigenetics-workshop.html

2011 - 2012 Transdisciplinary Research Center on Energetics and Cancer (TREC) Genetics/Genomics/Epigenetics working group, co-chair

2011 - 2015 Transdisciplinary Research Center on Energetics and Cancer (TREC), Scientific Advisory Committee, member (Genetic Epidemiology and Statistics)

2011 - present PQG Student/Postdoc Travel Fund Award review committee, member

2012 Program in Quantitative Genomics (PQG) 2012 conference organizing committee, member

2013 - 2015 Transdisciplinary Research Center on Energetics and Cancer (TREC) Genetics/Genomics/Epigenetics working group, Chair

2013, 2016, 2021 Harvard SPH Post-doc association (PDA) travel award reviewer

2014 - present HSPH Chinese Students & Scholars Association, faculty advisor

2018 - present HSPH Chinese Student Health Club, faculty advisor

2020 - present HSPH Faculty council, department of epidemiology representative

2021 - present HSPH Faculty council, co-chair

**Department level**

2009 Department of Biostatistics, Program in Quantitative Genomics Research Computing Committee, member

2009 Department of Epidemiology, Review Committee of Epidemiology Methods Area of Interest, member

2009 - present Department of Epidemiology, Admissions Committee (genetic epidemiology and statistical genetics area), member

2011 - 2017 Department of Epidemiology, Written exam committee for genetic epidemiology

2012 - present Department of Biostatistics, Curriculum committee

2012 - present Department of Epidemiology, Methods committee of the written exam, member

2013 - present Department of Epidemiology, Seminar series for the Program in Genetic Epidemiology and Statistical Genetics (PGSG), chair

2019 Department of Biostatistics, “Pipeline into Biostatistics” Symposium, mentor for students (Quoc Nguyen, Ana Pilar Stevens, and Daisy Hernandez Grinnell)

**PROFESSIONAL SOCIETIES:**

2003 - present Member American Statistical Association

2005 - present Member American Society of Human Genetics

**GRANT REVIEW ACTIVITIES:**

2011 The India Alliance, partnership between The Wellcome Trust, UK and the Government of India

2011 AXA Research Fund, http://www.axa-research.org/home

2013 Netherlands Organisation for Scientific Research (NWO)

2014 Israel Science Foundation (ISF)

2014 NIH (R25)

2014 Communicable Diseases-Public Health Research Grant (CD-PHRG), Ministry of Health (MOH), Singapore.

2014 Italian Ministry of Health (MOH)

2016 - 2017 GTOE CL & Outcome CL Am. Heart Assoc.

2018 The Netherlands Organisation for Health Research and Development (ZonMw) and the E-Rare 3 group of national research funding agencies

2018 - 2019 Israel Science Foundation (ISF)

2020 Medical Research Council (MRC), UK

2021 The Wellcome Trust, UK

**EDITORIAL ROLES:**

Ad hoc reviewer

|  |  |
| --- | --- |
| 2010- | Nature |
| 2009- | Nature Methods |
| 2013- | Nature Communication |
| 2013- | Genome Research |
| 2014- | Genome Medicine |
| 2010- | Genome Biology |
| 2012- | American Journal of Human Genetics |
| 2012- | PLoS Genetics |
| 2009- | PLoS Computational Biology |
| 2012-  2016- | Nucleic Acids Research  International Journal of Epidemiology |
| 2014- | Human Molecular Genetics |
| 2013- | Genetic Epidemiology |
| 2013- | Epigenetics |
| 2012- | Epidemiology |
| 2011- | Human Heredity |
| 2010- | Statistics in Medicine |
| 2010- | Genetics |
| 2011- | Genetica |
| 2009- | Physiological Genomics |
| 2011- | Frontiers in Statistical Genetics and Methodology |
| 2011- | G3: GENES, GENOMES, GENETICS |
| 2012- | Pigment Cell & Melanoma Research |
| 2011- | European Journal of Human Genetics |
| 2011 | Invited reviewer for the Pacific Symposium on Biocomputing 2011 (conference reviewer), session *Genome-wide association mapping and rare alleles: from population genomics to personalized medicine* |
| 2018/2020 | Invited judge for American Statistical Association Statistics in Genomics and Genetics' Distinguished Student Paper |

***Other editorial roles***

2010 - present Review Editor, Frontiers in Statistical Genetics and Methodology

2011 - 2012 Host editor for a special topic “Mapping complex disease traits with global gene expression” for the journal of Frontiers in Genetics

2011 - present Editorial Board Member, Journal of Biometrics & Biostatistics

2019 - present **Statistical Review Board, American Society for Nutrition**, for all ASN journals including the *American Journal of Clinical Nutrition* (AJCN), the *Journal of Nutrition*, *Advances in Nutrition*, and *Current developments in Nutrition.*

2020 - present Guest Associate Editor, PLoS Genetics

**OTHER PUBLIC SERVICE:**

|  |  |
| --- | --- |
| **Date(s)** | **Invited National Academy of Medicine workshop** |
| August 2015 | Committee on Food Allergies: Global Burden, Causes, Treatment, Prevention, and Public Policy Workshop, August 31-Sept 1, 2015 |
| **Date(s)** | **Invited NIH workshop** |
| Expected 2022 | NIAID Workshop: Analytical Challenges in Omics Research on Asthma and Allergy, June 29-30, 2020 (postponed to 2022 due to COVID-19 pandemic) |

|  |  |
| --- | --- |
| **Date(s)** | **Doctorate dissertation exam committee** |
| 2015 | Jun Li, Tongji Medical College, [Huazhong University of Science and Technology](http://en.wikipedia.org/wiki/Huazhong_University_of_Science_and_Technology), Wuhan, China |
| 2019 | Chief Ben-Eghan, Department of Human Genetics, McGill University, Montreal, Canada |

**HONORS AND DISTINCTIONS:**

1996 - 1998 The University's Scholarship South China University of Technology

1998 Procter & Gamble Scholarship Procter & Gamble Guangzhou Ltd, China

2000 - 2001 Graduate Student Scholarship South China University of Technology

2002 Dr. Koo Fellowship Michigan State University, East Lansing, Michigan

2005 - 2008 Rackham Graduate School University of Michigan, Ann Arbor, MI

Travel Grant

2007 American Society of Human Genetics, Pre-doctoral Presentation Award Finalist, 57th Annual Meeting, San Diego, California

2008 - 2009 Rackham Pre-doctoral Fellowship, University of Michigan, Ann Arbor, Michigan

2008 American Society of Human Genetics, Pre-doctoral Presentation Award Finalist, 58th Annual Meeting, Philadelphia, Pennsylvania

2008 - 2009 Election to the Honor Society of Phi Kappa Phi, University of Michigan, Ann Arbor, Michigan

2015 **Invited presentation and discussion**, **National Academy of Medicine**, Committee on Food Allergies: Global Burden, Causes, Treatment, Prevention, and Public Policy Workshop, Washington, DC, title “Genetic and epigenetic effects on allergy related diseases and traits”

2017 2016 **Ten** **Most Influential Research Award** from the Chinese Diabetes Society at its 21th annual meeting on November 25, 2017

## FUNDED GRANTS AND UNFUNDED PROJECTS:

**ACTIVE:**

10/30/17–10/29/22 **Genetic and epigenetic variants responsible for kidney diseases and related traits**

Guangdong Provincial People’s Hospital 7811033-01 (Yu, X.; Liang L.)

Total Direct Cost: $78,466

Role: **Principal Investigator**

The goal of this project is to identify genetic and epigenetic variants responsible for kidney diseases and related traits based on samples and genome-wide genetic and genomic data collected by the First Affiliated Hospital of Sun Yat-Sen University.

06/01/18-05/31/23 **Boston Obesity Nutrition Research Center**

NIH/NIDDK P30DK46200-26 (Fried, S)

Total Direct Cost: $246,339

Role: Co-Investigator

The Boston Nutrition Obesity Research Center (BNORC) provides resources and supports studies in the area of obesity and nutrition through its 4 cores. The Epidemiology and Genetics core provides consultation on clinical and epidemiological study design and data analysis, access to longitudinal datasets at Harvard and serves as a liaison between BNORC members and the Harvard Partners Genotyping Facility for access to high-throughput genotyping. The center also funds pilot studies, travel scholarships, and organizes scientific meetings.

09/01/19-08/31/23 **Inter-generational Link of Cardio-Metabolic Risk: Integrate Multi-OMICs with Birth Cohort**

Johns Hopkins Univ (NIH) 1R01HD098232-01 (MPI Wang/Liang)

Total Direct Cost: $304,741

Role: **Principal Investigator**

We propose to leverage the exceptional resources of the Boston Birth Cohort (BBC), one of the largest, NIH-funded urban low-income minority birth cohorts in the U.S., coupled with the latest high-throughput genome-wide methylation profiling and metabolome profiles to (1) identify fetal cord blood DNA methylation signature for long-term adverse cardio-metabolic outcomes up to age 21 years, (2) identify fetal cord blood metabolome signature for long-term adverse cardio-metabolic outcomes up to age 21 years, and (3) examine the role of maternal folate status for child long-term cardio-metabolic outcomes up to age 21 years.

01/01/20-12/31/22 **Genes, environment, and Prodromal features of Parkinson disease**

DOD GRANT12889122 (Ascherio, Alberto B.)

Total Direct Cost: $990,082

Role: Co-Investigator

The purpose of the proposed project is to integrate information on environmental risk factors, phenotypic characteristics, and a PD-specific genetic score to develop novel, low cost and scalable strategies for the early identification of PD in the general population. The identification of these individuals would provide an invaluable opportunity to implement interventions aiming to delay or arrest the neurodegenerative process.

01/01/20-08/31/24 **Metabolomics a novel tool for investigating the pathogenesis of Age-related Macular Degeneration**

MEEI (NIH) R01EY030088-01 (Hussain)

Total Direct Cost: $57,550

Role: **Site-PI**

We propose to assess the association between systemic and localized eye metabolomic profiles, and to identify metabolic signals of AMD progression. Our central hypothesis is that patients with AMD have a distinct biofluid and tissue metabolome, and that patients with a high-risk of AMD progression (AMD-progressors) also have a distinct metabolomic profile. Dr. Liang will lead statistical analyses in Aim 1 to 3 to further characterize the metabolome of AMD; to characterize the metabolome of AMD progressors and identify potential biomarkers of progression; and to evaluate the relationship between metabolomics and genomics in AMD.

07/01/20-06/30/25 **Intergenerational impact of maternal trauma history on preschoolers’ behavior and health outcomes: Assessing links with caregiving sensitivity and DNA methylation**

NIH/NICHD R01HD098153 (Gelaye, B.)

Total Direct Cost: $933,950

Role: Co-Investigator.

This study seeks to better understand maternal trauma history as a driver of behavior and physical health problems in 3-year-old children. We will examine the impact of maternal trauma on their children’s behavior (internalizing and externalizing behaviors) and physical health (body mass index and wheezing). Dr. Liang will guide the statistical aspects of the data analysis for this study and will supervise the post-doc programmer during the years 3-5. He will supervise all statistical analyses and participate in manuscript preparation.

07/01/20-06/30/24 **Asprosin, Body Weight, and Risk of Type 2 Diabetes in Men and Women**

Brown University (NIH) R01DK125403-01 (Qi, Sun)

Total Direct Cost: $142,887

Role: Co-Investigator.

We will characterize the distribution of Asprosin, a newly identified hormone from white adipose tissue, in blood circulation, and evaluate its potential predictive and/or causal role for the development of obesity and type 2 diabetes (T2D) among women who participated in the national Women’s Health Initiative (WHI) and among men who participated in the Health Professionals Follow-Up Study (HPFS), each with 20 years of follow-up. We will investigate relevant genetic variations, plasma levels of biochemical markers, obesity and type 2 diabetes incidence using state-of-the-art methodology. Achieving the specific aims in our application will be a major step toward the timely and cost-efficient development of novel diagnostic and therapeutic strategies for the prevention and control of obesity and type 2 diabetes.

07/16/20-06/30/22 **Examining tissue-specific DNA methylation after prenatal exposure to arsenic among infants with spina bifida**

Children's Hospital Boston (NIH) 5R21ES030784-02 (Maitreyi, Mazumdar)

Total Direct Cost: $50,000

Role: Co-Investigator

We will supervise the design, data processing, analysis, and interpretation of the WGBS and RNAseq datasets. Libraries will be generated in a core facility. Briefly, for methylation analysis ~1µg of total DNA will undergo bisulfide treatment sequencing. For RNA analyses ~1ug of total RNA will undergo mRNA selection and high coverage sequencing (~40 M reads per sample). Sequencing will be performed using an Illumina

HiSeq 2000 with paired ends read of 150 base pairs.

08/12/20-07/31/24 **Infant blood epigenome and risks of IgE sensitization, obesity, and asthma: MARC-35/43 cohorts**

NIH/NIAID R01AI148338 (MPI Liang/Hasegawa)

Total Direct Cost: $1,083,251

Role: **Contact Principal Investigator**

In ongoing racially/ethnically-diverse cohorts (52% African-American or Hispanic) of U.S. children, the investigators will define the role of blood DNA methylation during infancy in the development of IgE sensitization, overweight/obesity, and incident asthma. This research has the potential to offer novel approaches for the primary prevention of childhood asthma.

03/15/21-01/31/25 **Lifestyle Interventions, Metabolites, Microbiome, and Diabetes Risk**

NIH R01DK127601-01 (Hu, F)

Total Direct Cost: $429,600

Role: Co-Investigator

This grant builds upon a large ongoing randomized clinical trial (PREDIMED-Plus) to examine the effects of an intensive lifestyle intervention consisting of an energy-reduced Mediterranean diet, increased physical activity and weight loss on changes in body composition, plasma and stool metabolites, and risk of type 2 diabetes. It will also evaluate whether the benefits of the lifestyle intervention on diabetes risk differ by individuals’ metabolic profile. The findings may enhance our understanding of the metabolic pathways through which lifestyle interventions reduce diabetes risk including changes in metabolites and gut microbiome and inform the development of more effective personalized nutrition and lifestyle interventions for the prevention of diabetes.

08/15/21-04/30/23 **Circulating plasma metabolites, lifestyle factors, and mortality risk**

NIH/NIA 1R21AG070375 (Guasch-Ferre, Marta)

Total Direct Cost: $150,000

Role: Co-Investigator.

Recent advances in high-throughput metabolomic studies have shown promise in elucidating potential pathways underpinning aging processes and longevity. However, data in human populations are still constrained by small sample sizes and a limited number of metabolites profiled. Existing studies have also not integrated data on diet and lifestyle to evaluate the associations of interest in a comprehensive manner. A better understanding of aging-related metabolic alterations and whether metabolite profiles are modulated by lifestyle factors is crucial to develop effective strategies to promote health and well-being. The main goal is to identify novel metabolite profiles associated with mortality and prolonged longevity and investigate whether the metabolomic signatures of lifestyle factors are associated with mortality and longevity. We propose to leverage unique resources from two large U.S. cohorts with long follow-up and extended lifespan data: the NHS and HPFS.

08/16/21-6/30/26 **Dietary Biomarkers Development Center at Harvard University**

NIH/NIDDK 1U2CDK129670-01 (Hu, Frank)

Total Direct Cost: $1,151,284

Role: **PI of Data Analysis Core**

This study proposes to create a state-of-the-art Dietary Biomarker Development Center at Harvard University to systematically catalog validated metabolomic signatures of important food sources of protein and carbohydrates in the US diets.

**PENDING:**

09/01/21-08/31/26 **Serological profiling of the human virome and Alzheimer disease risk in a military population**

NIH Pending (Bjornevik, K)

Total Direct Cost: $2,696,241

Role: Co-Investigator

The idea that certain microbial infections can trigger Alzheimer’s disease (AD) has recently gained traction. In some studies, specific neurotropic viruses and bacteria were found more commonly in AD patients compared to others, and recent discoveries also link infections to specific parts of the pathology underlying the disease. Our proposed study aims to evaluate whether viral and bacterial infections during early (ages 20-40 years) and middle (ages 40-65) adulthood are associated with AD risk. The project has the potential to contribute with groundbreaking results on the potential role of infections in AD.

09/01/21-08/31/26 **Preterm Birth and Child Long-term Cardiometabolic Risk: Integrate Proteomics with Birth Cohort**

NIH Pending (Hu, F)

Total Direct Cost: $509,058

Role: Co-Investigator

This subcontract is intended to provide support for the investigators to provide input in all stages of the project including study design, data analysis and interpretation and manuscript and report preparation. The team will also direct and conduct statistical analyses related to proteomics data.

09/01/21-08/31/26 **Mediterranean diet, Metabolites, and Cardiovascular Disease**

NIH/NHLBI Pending (Hu, F)

Total Direct Cost: $490,992

Role: Co-Investigator

To goal of this study is to examine the effects of the PREDIMED dietary interventions on CVD risk and metabolic syndrome -a signature of CVD risk- and to determine if an improvement in the metabolic profile resulting from the dietary intervention mediates the benefits of the Mediterranean diet on CVD risk.

**COMPLETED (NIH format):**

09/30/10-09/29/13 **Using GWAS Data for Enhanced Mendelian Randomization Studies**

NIH/NIMH RC4 MH092707 (Kubzansky)

Total Direct Cost: $305,804

Role: Co-Investigator

This proposal addresses the difficulty of using observational data to drawing causal inferences on treatment effects. We propose capitalizing on the GWAS data to allow four important innovations in MR studies.

09/01/08-05/31/13 **Genetics of Coronary Disease in Type 2 Diabetes**

NIH/NHLBI R01 HL073168 (Doria)

Total Direct Cost: $73,575

Role: Co-Investigator

The major goals of this project are to confirm the results of the 300k DNA-pooling screen by analyzing individual DNA samples in an expanded set of 850 early-onset T2D cases and 850 non-diabetic controls.

09/15/14-7/31/17 **Weight-Loss Diet Intervention on Cardiometabolic Factors of Gut Microbiota**

NIH R01 DK100383 (Qi)

Total Direct Cost: $310,132

Role: Co-Investigator

The study integrates the newly-developed, targeted metabolomic methods and global gene expression profiling to comprehensively evaluate the effects of weight-loss diets varying in macronutrient compositions on the long-term changes in serum levels of the novel cardiometabolic factors related to gut microbiota metabolism; and to investigate the mechanisms at molecular and gene expression levels.

04/01/09-02/28/15 **Genetic Markers of CHD in Type 2 Diabetes**

NIH/NHLBI R01 HL071981 (Qi)

Total Direct Cost: $304,865

Role: Co-Investigator

The primary goal of this application is to examine genetic determinants of atherosclerosis in diabetes on the inflammatory and endothelial dysfunction pathways that mediate the vessels’ response to atherogenic factors. We propose to investigate variability in 20 genes belonging to these pathways is related to CHD among diabetic men and women in the Nurses’ Health Study and Health Professionals’ Follow-up Study.

12/01/11-11/30/16 **Genetics and Gene Expression Profiling in Asthma**

NIH/NHLBI R01 HL086601-04 (Raby)

Total Direct Cost: $34,423

Role: **(subaward) Principal Investigator**

We propose to develop and apply novel statistical methods to expression quantitative trait locus (eQTL) mapping and subsequently combine the eQTL maps with asthma GWAS.

12/01/84 - 02/28/23 **Risk Factors of CVD in Women**

NIH/NHLBI 2R01HL034594-32A1 (Manson, Qi)

Total Direct Cost: $26,018

Role: Co-Investigator

The overarching goal of this competing renewal is to fill important gaps in knowledge regarding the metabolomics of CHD, using an exceptionally cost-efficient design that leverages existing resources from three large and well-established U.S. cohorts: the Nurses’ Health Study (NHS), the NHS2, and the Vitamin D and OmegA-3 TriaL (VITAL, men and Women, ~20% African Americans).

09/01/15-06/30/21 **Metabolomics and risk of Parkinson's Disease**

NIH/NINDS 3R01NS089619-05 (Ascherio A.)

Total Direct Cost: $667,057

Role: Co-Investigator

To identify Parkinson disease years before it becomes clinically manifest, we are proposing a novel approach that will take advantage of the peripheral blood and detailed lifestyle and medical information collected from over 80,000 individuals who were followed for up to 25 years. By comparing the blood levels of hundreds of compounds between the blood of individuals who developed Parkinson disease and the blood of individuals of the same age and sex who remained healthy, we expect to make novel discoveries on the etiology of Parkinson disease and to be able to develop a method for the early identification of Parkinson disease in other populations.

07/01/18-06/30/20 **Identification of exosome signature in serum from ALS patients**

NIH R21NS104609-01A1 (Butovsky, O.)

Total Direct Cost: $18,070

Role: **(subaward) Principal Investigator**

The aim of this project is to analyze Aim 1 and Aim 2, which identify serum exosome-based RNA and proteimic signature in ALS progression and investigate the difference in sALS and fALS (c9orf72 and SOD1).

03/26/19-02/28/23 **Metabolomics Signature Underlying Diet, Lifestyle and Gut Microbiota for Diabetes.**

NIH R01DK119268-01(Qi)

Total Direct Cost: $151,181

Role: Co-Investigator

The goal of the proposal is to perform high-throughput metabolomics profiling of plasma collected at baseline from 1,000 T2D incident cases and 1,000 matched controls in a Hispanic cohort to identify ‘T2D-metabotypes’ (novel metabolites associated with incident T2D). We will also perform cross-population replication and comparison in non-Hispanic populations by including 1,500 T2D incident cases and 1,500 matched controls from the Nurses’ Health Study (NHS) and the Health Professionals Follow-up Study (HPFS).

07/01/18-06/30/21 **Metabolomic Predictors of MS Outcomes**

DOD W81XWH1810341 (Ascherio A.)

Total Direct Cost: $199,467

Role: Co-Investigator

To explore relation between plasma metabolomic profile at the time of disease onset with clinical and imaging outcomes in multiple sclerosis.

09/01/18-06/30/23 **Long-term health consequences of birth by cesarean section.**

NIH R01HD093761-01A1 (Chavarro J.)

Total Direct Cost: $374,820

Role: Co-Investigator

We propose to address this issue by evaluating the association between births by cesarean section with known risk factors for chronic disease risk, including longitudinal trajectories in risk biomarkers, and to gain further insights into the biological underpinnings of these relations by evaluation how cesarean delivery impacts longitudinal trajectories in whole genome DNA methylation patterns and gut microbiota patterns.

01/01/18-12/31/22 **The effects of environmental exposures on semen quality and the sperm epigenome**

NIH/BWH R01ES028712-02 (Hart, J)

Total Direct Cost: $84,162

Role: Co-Investigator

The proposed subcontract will support the scientific contributions of Drs. Liang, Chavarro, Hauser and Adamkiewicz. Specifically, this subcontract will support Dr. Liang's scientific contribution with his expertise in epigenetic epidemiology and bioinformatics, Dr. Chavarro's scientific contribution with his expertise in reproductive epidemiology and male factor infertility, Dr. Hauser's scientific contribution with his expertise in the reproductive effects of endocrine disrupting chemicals and Dr. Adamkiewicz scientific contributions and expertise in indoor air pollution assessment.

01/01/16-12/31/20 **Does arsenic increase risk of neural tube defects in a highly-exposed population?**

NIH/CHB R01ES026317-04 (Mazumdar, M; Christiani, D.)

Total Direct Cost: $474,937

Role: Co-Investigator

This project will utilize a case-control study design to enroll infants with myelomeningocele, a common subtype of neural tube defect, to investigate how maternal arsenic exposure may contribute to increased risk.

04/15/19-03/31/24 **Food-Based Biomarkers, Diet Quality, and Cardiometabolic Health**

NIH/NIDDKD 1R01DK120870-01 (Sun)

Total Direct Cost: $390,405

Role: Co-Investigator

Novel biomarkers are needed to facilitate more accurate and objective measurements of food intake. The study will help to identify food markers that aid in better characterization of human diet, examination of associations with cardiometabolic diseases, and design of precision nutrition strategies for improving diet quality and health.

07/01/18-06/30/20 **Integrating Genetics of Gene Expression into Pathway Analysis for Skin SCC GWAS**

NIH R03CA219779-01A1 (Jiali, H.)

Total Direct Cost: $11,223

Role: Co-Investigator

The goal of this project is to apply pathway analysis to SCC GWAS to systematically assess the associations of biological pathways with SCC risk.

09/30/15-05/31/18 **Identifying epigenetic mechanisms underlying age-related disease risk in CHARGE**

NIH U34 AG051418 (Murabito, J.)

Total Direct Cost: $23,598

Role: Co-Investigator

Perform pilot studies to identify the most useful epigenetic measurements for study. This will include pilot studies of emerging technologies to assess different epigenetic measurements, and their potential as mechanisms underlying age-dependent disease risk, and to develop new methods to predict epigenomic marks in different cell and tissue types.

09/16/16-08/31/17 **Whole Blood MicroRNAs as Risk and Survival Biomarkers for ARDS**

NIH R56 HL134356 (Christiani, D.)

Total Direct Cost: $35,136

Role: Co-Investigator

This project’s objective is to develop and validate miRNA biomarkers in whole blood of potential utility in early diagnosis, prognosis, and treatment of ARDS.

07/01/16-06/30/17 **Investigating the Link between Cancer and Neurodegenerative Disease**

Dept. of Veteran’s Affairs Dept. of Veteran’s Affairs (Driver, J.)

Total Direct Cost: $33,642

Role: IPA/Contractor

To further investigate the inverse epidemiologic association between cancer and Alzeimer’s Disease, to investigate the association between metformin use and the risk of both diseases, and to characterize the genetic overlap between them using available GWAS data.

06/15/14-02/29/18 **Improving polygenic prediction using large next-generation data sets**

NIH/NIGMS R01 GM105857 (Sunyaev)

Total Direct Cost: $191,312

Role: Co-Investigator

The goal of this project is to develop statistical methods to improve polygenic prediction of quantitative and case-control traits from GWAS chip data and sequencing data, accounting for cross-ethnic diversity and the advantages of incorporating functional information.

07/01/14-04/30/18 **Environmental Obesogens and Weight Change in the POUNDS LOST Trial**

NIH/NIEHSR01 ES022981-04 (Sun)

Total Direct Cost: $17,274

Role: Co-Investigator

The proposed investigation will utilize the rich data and resources in the POUNDS LOST Trial to prospectively examine human PFC exposure in relation to a wide array of outcomes, including weight loss, weight regain, and change of body fat distribution, adipokines, thyroid hormones, and gene expression profiles in adipose tissue, to determine the possible contribution by PFCs to adipogenesis.

04/01/13-01/31/17 **Unified Methods for Sequence-based Association Studies**

NIGMS R01 GM104411-02 (Xiong)

Total Direct Cost: $168,329

Role: **Site Principal Investigator**

The goals of this study are to develop novel and powerful statistical methods for sequence-based association studies and QTL (eQTL) analysis which leverage high dimensional data reduction and functional data analysis techniques to integrate multiple variants across a given genomic region or a pathway, and unify family and population-based design to use various types of family and unrelated individual data sampled from any population structure.

07/01/16 – 06/30/17 **Biostatistics and Bioinformatics Branch**

NIH/NICHD/DIPHRNIH IPA (Albert, P.)

Total Direct Cost: $33,996

Role: IPA/Contractor

As a statistical/bioinformatics scientist, Professor Liang's primary duties are to collaborate with faculty members on the design and analysis of "omics" outcomes in large cohort studies, lead an independent research program developing new statistical methods for the analysis of "omics" data, and to teach and mentor graduate students in the department. Professor Liang is also expected to perform professional service in leading biostatistics, epidemiology, and bioinformatics societies.

09/22/08-07/31/14 **Gene Environment EBV Interactions in the Etiology of NPC**

NIH/NCIR01 CA115873 (Adami)

Total Direct Cost: $2,238,641

Role: Co-Investigator

This is a large, population-based case-control study of nasopharyngeal carcinoma (NPC) in Guangxi Region and Guangdong Province in southeastern China, where NPC is endemic. Our aims are to identify the main effects of Epstein-Barr virus strains, diet, smoking, and genetic variation in candidate susceptibility genes, as well as the interactions across these factors, in the etiology of NPC. This study is the first of its kind in the region with the world’s highest incidence of NPC.

02/17/12-01/31/15 **Methods to Identify Genetic Markers That Interact with Multiple Environmental Exposure**

NCIR21 CA165920-01 (Kraft, PI)

Total Direct Cost: $150,000

Role: Co-Investigator

We propose two analytic frameworks that flexibly model the interactions between a genetic marker and multiple measured exposures. We hypothesize that these approaches will be more powerful than tests that focus on a single exposure, or consider multiple exposures individually, in series.

05/01/12-04/30/16 **Obesity Genes, Energy Regulation in Response to Weight-Loss Diets**

NIH/NIDDKR01 DK091718 (Qi)

Total Direct Cost: $316,478

Role: Co-Investigator

The goal of this project is to examine genetic associations with long-term weight changes and gene-diet interactions. We will also assess the association of obesity gene variants with: 1) psychiatric measures for food craving, fullness, and hunger; 2) biochemical markers regulating energy intake and expenditure, including leptin, insulin, ghrelin, GLP-1, adiponectin and RBP4; and 3) adipose gene expression profile.

09/01/11-06/30/16 **DNA Methylation as a Biomarker of Exposure and Effect for Particles and Metals**

NIH/NIEHSR01ES15172 (Schwartz, J.)

Total Direct Cost: $298,874

Role: Co-Investigator

The goals of this proposal are to identify signature epigenetic changes that can be used as biomarkers of environmental exposure, especially to air pollution, where no such biomarkers exist, but also heavy metals, to identify pathways of cardiovascular disease whose methylation patterns are disturbed by particles and heavy metals, and to examine epigenetic changes as predictive of subsequent development of cardiovascular disease in a longitudinal study.

09/01/12-08/31/14 **Integrating Genetics of Gene Expression into Pathway Analysis for Melanoma GWAS**

NIH/NCIR03 CA167741-01 (Zhang, PI)

Total Direct Cost: $7,619

Role: Co-Investigator

To systematically assess the genetic associations of biological pathways with melanoma risk using pathway-based approaches for the genome-wide association study (GWAS) on melanoma. We plan to group the genetic association signals from melanoma GWAS into biological pathways and systematically assess the associations between the biological pathways and melanoma risk.

07/02/14-06/30/16 **Environmental Chemicals, Exosomal miRNAs in Ovarian Follicles, and IVF Success**

NIH/NIEH R21 ES 024236 (Hauser PI)

Total Direct Cost: $4,936

Role: Co-Investigator

The objective of the proposed study is to determine if follicular fluid (FF) levels of BPA and DEHP metabolites are associated with miRNA profile in FF isolated exosomes and with oocyte maturation and day 3 embryo quality. We will also use mediation analysis to estimate the indirect effects of BPA and DEHP metabolites on oocyte maturation and embryo quality mediated through FF isolated exosomes miRNA expression.

10/30/17-10/29/18 **Genetic and epigenetic variants responsible for kidney diseases and related traits**

SYSU-ID [2016]109 Sun Yat Sen University (Yu, X.; Liang L.)

Total Direct Cost: $36,323

Role: **Principal Investigator**

The goal of this project is to identify genetic and epigenetic variants responsible for kidney diseases and related traits based on samples and genome-wide genetic and genomic data collected by the First Affiliated Hospital of Sun Yat-Sen University.

07/01/14-06/30/19 **Dietary Interventions, Metabolites, and Risk of Type 2 Diabetes**

NIH/NIDDKR01DK102896-04 (Hu, F.)

Total Direct Cost: $416,133

Role: Co-Investigator

The goal of this project is to examine whether the changes in metabolic profiles induced by the dietary interventions mediate the benefits of the Mediterranean diet on diabetes, using a cost-effective case-cohort design.

05/19/08-04/30/23 **Harvard Clinical and Translational Science Center (UL1)**

NIH/NCRR1UL1TR002541-01 (Nadler, L.)

Total Direct Cost: $75,000

Role: Co-Investigator

The Harvard Catalyst Biostatistics Program supports Harvard clinical and translational investigators. Drawing on a team of highly skilled biostatisticians from the Harvard academic and hospital community, the program offers consultations on a range of topics to researchers as they design new studies.

01/07/15-12/31/19 **School Inner-City Asthma Intervention Study**

CHB (CBD/NIH/NIAID) U01 AI110397 (Phipatanakul W / Gold, D.)

Total Direct Cost: $167,228

Role: Co-Investigator/**Sub-contract Principal Investigator**

This study is to determine the role of a school-based environmental intervention on asthma health outcomes in urban children with asthma and discover novel mechanistic biomarkers through nasal epigenetic and transcriptomic marks.

09/01/18-08/31/21 **Circulating plasma metabolites, diet, and risk of type 2 diabetes**

NIH/NIDDKR01DK112940-01A1 (Hu, F.)

Total Direct Cost: $80,450

Role: Co-Investigator

The goal of this proposal is to evaluate the associations of individual metabolites and broader metabolomic profiles and their potential pathways with subsequent type 2 diabetes (T2D) risk among women in the Nurses’ Health Study (NHS) and men in the Health Professionals’ Follow-up Study (HPFS), ongoing prospective cohorts with detailed measurements of diet and lifestyle.

05/03/16-03/31/21 **Preterm Birth, Maternal and Cord Blood Metabolome, and Child Metabolic Risk**

NIH/NIDDK5R01HD041702-14 (MPI: Wang, Hu)

Total Direct Cost: $72,150

Role: Co-Investigator

Using a life-course framework, we proposed to conduct a comprehensive and systemic investigation of preterm birth and maternal and fetal metabolic characteristics in relation to development of adverse metabolic outcomes among children in the Boston Birth Cohort.

04/01/18-03/31/22 **Dietary Patterns and Risk of Cardiovascular Disease**

NIH/NHLBIR01HL060712-16A1 (Hu, F.)

Total Direct Cost: $460,758

Role: Co-Investigator

This study will be the first and largest of its kind to prospectively evaluate adherence to three recommended dietary patterns and cardiovascular disease risk in four large prospective US cohorts with diverse racial/ethnic groups. The study will also examine the interconnections between healthy eating patterns, plasma metabolite profiles, and gut microbes in Hispanic and non-Hispanic white populations. Our study will inform evidence-based dietary recommendations and help improve current guide.

08/20/17-06/30/21 **Mediterranean diet, Metabolites, and cardiovascular Disease**

NIH/NHLBIR01HL118264-05 (Hu, F)

Total Direct Cost: $443,582

Role: Co-Investigator

The goal of this study is to examine the effects of the PREDIMED dietary interventions on CVD risk and metabolic syndrome -a signature of CVD risk- and to determine if an improvement in the metabolic profile resulting from the dietary intervention mediates the benefits of the Mediterranean diet on CVD risk.

04/01/19-03/31/23  **Saliva and Plasma Metabolomic Signatures of Diabetes Progression in a Hispanic Cohort**

NIH/NIDDKR01DK120560-01 (Bhupathiraju)

Total Direct Cost: $366,920

Role: Co-Investigator

In the proposed project, we plan to examine both plasma and saliva metabolomic profiles of type 2 diabetes progression. While most studies have used plasma as a biofluid to measure metabolites, saliva is a non-invasive easily accessible alternative to plasma to measure metabolites related to diabetes risk. Saliva may also present with distinct metabolic pathways for disease progression.

**TEACHING AND TRAINING**:

TEACHING IN HARVARD CHAN SCHOOL COURSES

|  |  |  |  |
| --- | --- | --- | --- |
| Date | Title | Institution | Experience |
| 2009 | Epid 507 Genetic Epidemiology | Harvard SPH | Lecturer |
| 2010 | Bios 235 Regression and Analysis of Variance | Harvard SPH | Lecturer |
| 2010 | Epid 293 Analysis of Genetic Association Study using unrelated samples | Harvard SPH | Lecturer |
| 2011, 2013, 2015 | Epid 222 Genetic Epidemiology of Diabetes and its Complications | Harvard SPH | Lecturer |
| 2011 - present | Epid293 Analysis of Genetic Association Studies | Harvard SPH | Primary Instructor |
| 2012, 13, 17 | Epid507 Genetic Epidemiology | Harvard SPH | Co-instructor with 1-2 other instructors |
| 2014, 15, 19 | Epid507 Genetic Epidemiology | Harvard SPH | Primary instructor with 1-2 other instructors |
| 2015.12 | Harvard Catalyst Biostatistics course: Methods of Analysis of Genetic Studies | Harvard SPH | Organizer and lecturer |
| 2015, 2018 Spring 2 | BIO257/BST247 Advanced Statistical Genetics | Harvard SPH | Primary instructor with 3 other instructors |
| 2016.10 | Metabolomics nanocourse | Harvard SPH | Lecturer |
| Spring 2020, 2021 | BST281 Genomic Data Manipulation | Harvard SPH | Lecturer |

OTHER TEACHING EXPERIENCE

|  |  |  |  |
| --- | --- | --- | --- |
| 2002 -04 Fall | STT201 Statistical Methods | Michigan State University | Teaching Assistant |
| 2002 -04 Summer | STT201 Statistical Methods | Michigan State University | Instructor |
| 2007 | Biostat 815/615 Statistical Computing | University of Michigan | Teaching Assistant |

ADVISORY AND SUPERVISORY RESPONSIBILITIES

**Post-doc research fellow advisees**

1. 2011 – 2012 Hua Chen, Postdoc research fellow

Current position: Research Assistant Professor at the Center for Computational Genetics and Genomics, Temple University; Latest: Professor at Beijing Institute of Genomics, Chinese Academy of Science

2. 2011 – 2013 Xuefeng(Peter) Wang, Postdoc research fellow (co-mentor Xihong Lin)

Current position: Tenured faculty at H. Lee Moffitt Cancer Center & Research Institute, FL

3. 2012 – 2013 Baoshan Ma, Postdoc research fellow

2018 - 2019 Visiting scholar

Current position: Associate Professor at Dalian Maritime University, China

4. 2012 – 2014 Jinyan Huang, Postdoc research fellow

Current position: Associate Professor of Bioinformatics, Shanghai Institute of Hematology, State Key Laboratory Of Medical Genomics, Rui-jin Hospital, Shanghai Jiao Tong University School of Medicine

5. 2012 – 2014 Jun Chen, Postdoc research fellow (co-mentor Xihong Lin)

Current position: Senior Associate Consultant and Assistant Professor of Biostatistics, Division of Biomedical Statistics and Informatics, Mayo Clinic Rochester

6. 2012 – 2014 Chaolong Wang, Postdoc research fellow (co-mentor Xihong Lin)

Current position: Full professor at Tongji School of Public Health, Huazhong University of Science and Technology, China

7. 2014 – 2015 Ga Liao, Postdoc research fellow

Current position: Associate Professor, Director of Bioinformatics and Proteomics Platform, State Key Laboratory of Oral Diseases, West China School of Stomatology, Sichuan University, China

8. 2014 – 2019 Wonil Chung, Postdoc research fellow

Current position: Assistant Professor at Soongsil University, South Korea

**Awards**:

* Semifinalist for the 2018 Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research for the 68th Annual Meeting of the American Society of Human Genetics, San Diego, California, October 16-20, 2018.

9. 2016 – 2020 Jun Li, Postdoc research fellow

Current position: Research Scientist in Departments of Nutrition and Epidemiology at Harvard Chan SPH;

Assistant professor at Harvard Medical School/Brigham Women Hospital (Starting the end of 2021)

**Awards:**

* The Bernard Lown Scholarship in Cardiovascular Health Program (HSPH co-mentors Hu/Liang) 2014
* The New England Cardiovascular-Metabolic Fellowship Awards (American Diabetes Association co-mentors Hu/Liang) 2017-2019
* Pilot and Feasibility Award (BNORC co-mentors Hu/Liang) 2018-2020
* K99/R00 Award (NIDDK co-mentors Manson/Liang) 2019-2024
* 2020 Top 10% reviewers’ choice abstract, American Society of Human Genetics, Annual Meeting of the American Society of Human Genetics

10. 2016 – 2021 Yanjun Guo, Postdoc research fellow

Current position: Associate Professor at Tongji School of Public Health, Huazhong University of Science and Technology, China

**Awards:**

2019 Barry R. and Irene Tilenius Bloom Fellowship for outstanding postdoctoral fellows based on academic merit, leadership potential, and commitment to improving public health.

11. 2017 – 2020 Zhaozhong Zhu, Postdoc research fellow

Current position: Assistant Professor of Emergency Medicine at Harvard Medical School/Massachusetts General Hospital

**Awards:**

2017 Post-Doc Association Travel Fellowship, HSPH

2018 Program in Quantitative Genomic Travel Fellowship, HSPH

2018 Rose Traveling Fellowship, HSPH

2018 Top 10% reviewers’ select abstract, American Society of Human Genetics, Annual Meeting of the American Society of Human Genetics

K01 Award (NIAID co-mentors Camargo/Liang) 2021-2026

Junior Faculty Member Award from the journal *Metabolism* for his work for obesity and COVID-19 (Zhu et al 2020 *Metabolism*)

12. 2020 – 2021 Jiahui Si, Postdoc research fellow

Current position: Research fellow at Peking University, school of public health

13. 2020 – present Xikun Han, Postdoc research fellow

14. 2020 – present Jie (Jack) Hu, Postdoc research fellow

**Awards**:

2019 Semifinalist for the Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research for the 69th Annual Meeting of the American Society of Human Genetics, Houston, Texas, October 15-19, 2019.

2021 Connors-BRI Research Recognition Award, Discover Brigham 2021, Brigham Research Institute, November 3, 2021

15. 2021 – present Anat Yaskolka Meir, Postdoc research fellow

**Awards:**

Zuckerman-CHE Outstanding Israeli Female Postdoctoral Scholar at the Department of Epidemiology at Harvard University for the academic year, 2021-2022.

**Doctoral students (oral exam and dissertation advisor)**

1. 2010 – 2015 Zhonghua Liu, Department of Epidemiology (Co-advise with Xihong Lin).

Current position: Assistant Professor Department of Statistics and Actuarial Science, University of Hong Kong

2. 2012 – 2017 Yen-Chen (Anne) Feng, Department of Epidemiology.

Current position: Assistant Professor (tenure track) National Taiwan University

3. 2015 – 2018 Yichen Guo, Departments of Biostatistics and Environmental Health Science (Co-advise with David Christiani).

Current position: Joined Johnson & Johnson as data scientist

4. 2020 – present Jordan Rossen, Department of Epidemiology (co-advised with Alkes Price)

**Master students (research advisor)**

1. 2010 Xiaochen Lin, Department of Epidemiology

PhD at Brown University

Current Position: Optum

2. 2013 Wan Xu, Department of Biostatistics

Current Position: Bank of America

3. 2014 Yichen Guo, Department of Biostatistics,

Current Position: ScD program, Harvard Chan SPH

4. 2014 Yu Jiang, Department of Biostatistics

Current Position: PhD student at Penn State University

5. 2014 Jorge Eduardo Buendia-Buendia, Department of Biostatistics (CBQG)

Current Position: Computational biologist at the Broad Institute

6. 2014 Nicole Dah On Lee, Department of Biostatistics (CBQG)

7. 2015 Mark Chaffin, Department of Biostatistics (CBQG), June 2015

Current Position: Associate computational biologist, Broad Institute, Kathiresan lab

8. 2016 Weimiao Wu, Department of Biostatistics

Current Position: PhD program Yale University

9. 2016 Liu Cao, Department of Biostatistics (CBQG)

Current Position: Carnegie Mellon - University of Pittsburgh Ph.D. Program in Computational Biology

10. 2016 Qianyu Yuan, Department of Epidemiology

Current Position: PhD program in Environmental Health Science, Harvard Chan SPH

11. 2016 – 2018 Xinan Wang, Department of Biostatistics

Current Position: PhD program in Environmental Health Science, Harvard Chan SPH

12. 2017 Abhinav Reddy, Department of Biostatistics (CBQG)

13. 2017 Yi Ding, Department of Biostatistics

Current Position: Bioinformatics PhD program at UCLA

14. 2017 Tianyu Xia, Department of Biostatistics

15. 2017 – 2019 Yunqi Yang, Department of Biostatistics (CBQG)

Current Position: PhD in bioscience, University of Chicago

16. 2018 Tong Zhao, Department of Biostatistics (CBQG)

17. 2018 Zijie Zhao, Department of Biostatistics (CBQG)

18. 2018 Mengxi Yang, Department of Biostatistics (CBQG)

19. 2018 Mingrui Xu, Department of Biostatistics (CBQG)

20. 2019 Jiaxuan Zhao, Department of Biostatistics (CBQG)

21. 2019 Lu Zhu, Department of Epidemiology

22. 2019 Shujian Zhu, Department of Biostatistics (CBQG)

23. 2019 Qian Xiao, Department of Biostatistics (CBQG)

24. 2019 – 2021 Xin Xu, Department of Biostatistics (CBQG)

25. 2018 – 2021 Mingchen Ye, Department of Epidemiology

26. 2020 – present Tingyi Cao, Department of Biostatistics

Current Position: PhD program in Biostatistics, Harvard Chan SPH

27. 2020 – present Wenyi Wang, Department of Biostatistics

28. 2021 – present Zicheng Wang, Department of Biostatistics

29. 2021 – present Yingzhe Zhang, Department of Epidemiology

**Undergraduate students (research advisor)**

1. 2021 – present Lillian Petersen, Harvard College

2. 2021 – present Garyk Brixi, Harvard College

**Awards**: Harvard College Research Program (HCRP) summer research award (2021)

**Research Analyst**

1. 2020 – 2021 Yuxiang Chen

**Visiting Students**

1. 2014 – 2015 Jun Li Tongji Medical College, [Huazhong University of Science and Technology](http://en.wikipedia.org/wiki/Huazhong_University_of_Science_and_Technology), supported by the HSPH Bernard Lown scholarship

2. 2014 Yunhua Xiang School of Statistics, Renmin University

3. 2014 – 2015 Rui Gao, School of Public Health, Sun Yat-Sen University (Division of cancer prevention research, Sun Yat-sen University cancer center)

4. 2015 Biqi Wang, Peking University, school of public health

5. 2016 – 2017 Youyuan Yaom, Sun Yat-sen University

6. 2016 Shaun Aron, Wits Health Consortium, South Africa

7. 2016 Jacqueline Gao, Harker School, San Jose, California

8. 2016 – 2017 Yuan Lei, Tongji Medical College, [Huazhong University of Science and Technology](http://en.wikipedia.org/wiki/Huazhong_University_of_Science_and_Technology)

9. 2016 – 2017 Xiaohui Du, Tongji Medical College, [Huazhong University of Science and Technology](http://en.wikipedia.org/wiki/Huazhong_University_of_Science_and_Technology)

10. 2017 – 2017 Bingchen Shan, MIT financial engineering MS program

11. 2017 – 2019 Yifei Lin, Department of Urology/ Institute of Urology, West China School of Medicine/West China Hospital, Sichuan University

**Awards:** Tuition scholarship for three modules in the 24th Summer Institute in Statistical Genetics, July 8-26, 2019, at the University of Washington in Seattle, Washington

12. 2018 – 2020 Jiahui Si, doctoral student from Peking University, school of public health

13. 2019 Anat Yaskolka Meir, doctoral student from Department of Public Health, Ben-Gurion University of the Negev, Israel

14. 2020 – 2021 Yingxi Yang, undergraduate student from Sun Yat-sen University

15. 2021 Xi (Cindy) Kang, undergraduate student from Northwestern University

**Doctoral oral exam and dissertation committee**

2009-2010 Yu-Chun Yen (Advisor: Pete Kraft)

2010-2012 Mitchell Machiel (advisor David Hunter)

2013-2015 Shasha Meng (Advisor: Jiali Han)

2013-2015 Tristan Hayeck (Advisor: Alkes Price)

2013-2015 Nancy Diao (Advisor: David Christiani)

2013-2016 Xin Li (Advisor: Jiali Han)

2013-2017 Zhaozhong Zhu (Advisor: David Christiani)

2013-2017 Mohammad Rahman (Advisor: David Christiani)

2014-2017 Kevin Galinsky (Advisor: Alkes Price)

2015-2016 Jia Zhong (Advisor: Andrea Baccarelli)

2016-2018 Carla Marquez (Advisor: Alkes Price)

2016-2020 Chi Gao (Advisor: Pete Kraft)

2017-2018 Rosie Martinez (Advisor: Andrea Baccarelli)

2017-2021 Xihao Li (Advisor: Xihong Lin)

2018-2020 Qianyu Yuan (Advisor: David Christiani)

2018-2020 Helian Feng (Advisor: Pete Kraft)

2019-2021 Fenglei Wang (Advisor: Walter Willett)

2020-present Jiaxuan (Jessie) Liu (Advisor: Lori Chibnik)

2021-present Xinyi Li (Advisor: Edward Giovannucci)

2021-present Chih-Fu Wei (Advisor: Maitreyi Mazumdar)

**Doctoral oral exam committee only**

2011 Xinyi Lin (member, advisor Xihong Lin, Department of Biostatistics)

2013 Alexandra Binder (chair, advisor Karin Michels, Department of Epidemiology)

**Master oral exam and dissertation committee**

2017 Helian Feng  Department of Biostatistics (CBQG), (Advisor: Pete Kraft)

**Other advising:**

**Junior faculty:**

* Jean McGee, Assistant Professor of Dermatology, Harvard Medical School (HMS) and physician Beth Israel Deaconess Medical Center (BIDMC) (as co-mentor on NIH K23 application)
* Kohei Hasegawa, Associate Professor of Emergency Medicine at Harvard Medical School (as advisor for the HSPH Biostatistics CBQG MS degree program)

**Postdoc funding mentoring:**

\* indicates successful application (newly funded award will be updated when notified)

* Kelly J Brunst, research fellow, Icahn School of Medicine at Mount Sinai (advisory committee on K99 application 2013)
* Roby Joehanes, research fellow, NHLBI (collaborator on K99 application 2013)
* Mary Townsend, research fellow, HSPH (advisory committee on K01 application 2014)
* Deirdre Tobias, research fellow, HSPH (advisory committee on K01 application 2014)
* Audrey Gaskins, research fellow, HSPH (advisory committee on K99 application 2015)
* Elena Colicino, research fellow, HSPH (co-mentor on K99 application 2015)
* Sylvia Ley, research fellow, HSPH (advisory committee on K99 application 2015)
* Fred Tabung, research fellow, HSPH (co-mentor on K99 application 2015)\*
* Shilpa Bhupathiraju, research fellow, HSPH (co-mentor on K01 application 2015)\*
* Jiantao Ma, research fellow, NHLBI (advisory committee on K22 application 2015)
* Olga Demler, research fellow, NIH (co-mentor on K01 application 2015 and 2016)\*
* Mike Mendelson, research fellow, NHLBI (collaborator on K99 application 2016)
* Sammy Elmariah, assist. prof, HSPH (advisory committee on K23 application 2016)
* Edward Yu, doctoral student, HSPH (consultant on F31 application 2016)\*
* Dong Wang, research fellow, HSPH (co-mentor on AHA postdoc fellowship 2016-2018)\*
* Changzheng Yuan, research fellow, HSPH (advisory committee on K99 application 2017)
* Elkhansa Sidahmed, research fellow, HSPH (advisory committee on K07 application 2017)
* Carmen Messerlian, research fellow, HSPH (co-mentor on K99 award application 2017)
* Sylvia Ley, research fellow, HSPH (collaborator on ADA application 2017)
* Sylvia Ley, research fellow, HSPH (advisory committee on K01 application 2017)
* Ambika Satija, research fellow, HSPH (advisory committee on K01 application 2017)
* Dong Wang, research fellow, HSPH (collaborator on K99 application 2017)
* Yang Hu, research fellow, HSPH (collaborator on AHA fellowship application 2017)
* Xiaochen Lin, research fellow, Brown University (reference for AHA fellowship 2017)\*
* Jun Li, research fellow, HSPH (co-mentor on K99/R00 application 2018)\*
* Zhaozhong Zhu, research fellow, HSPH (co-mentor on K01 application 2021-2026)\*
* Marta Guasch-Ferre, research fellow, HSPH (mentor team on AHA career development award application 2019)
* Danielle Haslam, research fellow, HSPH (co-sponsor for F32 application 2020)
* Danielle Haslam, research fellow, HSPH (co-mentor for ADA New England Cardiovascular-Metabolic Fellowship Awards 2020)
* Jie Hu, research fellow, HSPH (co-mentor on NHLBI BioData Catalyst Fellows Program 2020-2021)
* Jie Hu, research fellow, HSPH (co-mentor on AHA Career Development Award 2021)
* Andres Korat, research fellow, HSPH (primary mentor Yerby Fellowship 2020)
* Natalie McCormick, research fellow, HSPH (co-mentor on K99 application 2021-2026)
* Jie Hu, research fellow, HSPH (co-mentor on K99 application 2021-2026)
* Alaina Bever, PhD student Harvard-MIT, (co-mentor for F30 fellowship application 2021-, mentor Song/Meir at HSPH)
* Clemens Wittenbecher, research fellow, HSPH (co-mentor on K99 application 2021-2026)

**Student funding mentoring:**

Jess Marden (former Jessica Daniel), mentored on her AHA grant application and advising one aim (the gene environment interaction paper to study SES and genetic risk of dementia predicting cognitive function and dementia) in her dissertation (2013).

**INVITED PRESENTATIONS:**

**Local**

2009 *The 1000 Genomes Project,* Program in Molecular and Genetics Epidemiology journal club, HSPH

2010 *Enhancing the Power of eQTL Mapping: A Catalog of 6,000 cis eQTLs in Lymphocytes,* FBAT seminar, HSPH

2010 *Enhancing the Power of eQTL Mapping: A Catalog of 6,000 cis eQTLs in Lymphocytes,* Program in Molecular and Genetics Epidemiology, HSPH

2010 *Enhancing the Power of eQTL Mapping: A Catalog of 6,000 cis eQTLs in Lymphocytes*, [Brigham and Women's Hospital](http://www.brighamandwomens.org/)

2011*Genome-wide mapping of methyl quantitative trait loci and complex traits*, Quantitative Issues in Cancer Research Working Seminar, HSPH

2012*Illumina 450K array normalization pipeline*, Epigenetics Working Group Meeting, HSPH

2012 *Statistical analysis of methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*,Epigenetics Workshop, HSPH

2012*Genome-wide association study on the variation of quantitative trait may help identify important genetic variants for complex diseases, an example of CHD risk in T2D patients*, Gene-Environment interaction working group, HSPH

2012 *Methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*, Boston University Probability and Statistics Seminar

2012 *Cross tissue methylation prediction and calibration*, Epigenetics Working Group Meeting, HSPH

2012 *Cross tissue methylation prediction and calibration*, EPA Clean Air Center research group meeting, HSPH

2012 *Methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*, Program in Quantitative Genomics short course, HSPH

2013 *Methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*, Center for Biomedical Informatics, Harvard Medical School

2013 *Challenges in big data analysis*, Dana-Farber cancer institute, Boston, MA

2014*Effective adjustment of differential cell populations in epigenome-wide association studies*, Psychiatric Genetics and Translational Research Seminar, Massachusetts General Hospital

2014 *Individual and pathway analyses for metabolomics profile related to body mass index*, Metabolomics working group, HSPH

2015*Statistical approaches to the analyses of multidimensional data including OMICS and epigenetic data,* Novartis, Cambridge, MA

2015*Detection of epigenomic biomarkers for asthma related traits and implication in patient stratification for cost-effective therapy selection,* Novartis, Cambridge, MA

2017 *Biostatistics and Genomics*, Tow of Sharon, MA

2017 *From Gene to Global*, Harvard China Think Big Team Campus visit, Cambridge, MA

2017*Metabolomic footprints of the 14-point PREDIMED Mediet score,* OMICS Advances, Applications and Translation in Nutrition and Epidemiology,

Boston, MA

2017 *Detection of cell specific effect in methylation study using mixture of cell types*, How Disadvantage Gets “Under the Skin”: Using Epigenomic Methods to Better Understand & Address Health Disparities Symposium, Boston, MA

2018 *Opening remark*, Public Health Symposium for Young Leaders in China, Boston, MA

2018 *Using DNA Methylation to Evaluate Aging*, Harvard Business School, Boston, MA

2018 *Molecular Profiling of Complex Clinical Traits*, lightning talk, Biostatistics Department, HSPH, Boston, MA

2019 *From Gene to Global*, Winsor School Global Forum, Boston, MA

2019 *Polygenic risk and causal inference based on Mendelian randomization: examples in cardiovascular diseases*, Brigham and Women's Hospital, Boston, MA

**National**

2010 International Chinese Statistical Association (ICSA), Applied Statistics Symposium. Indianapolis, IN

2012 Joint Statistical Meetings (JSM), eQTL and causal analysis section

2012*Two eQTL databases from lymphoblastoid cell lines*, 1000 Genomes Project, Functional Interpretation Group meeting.

2013*Methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*, NIH Heart, Lung and Blood Institute, Framingham, MA

2014 *Effective adjustment of differential cell populations in epigenome-wide association studies*, Short Course on Mathematical Sciences in Obesity, University of Alabama at Birmingham

2014 *Environmental, Familial, and Leukocyte-Associated Variance of Methylation Quantitative Trait Loci in the Human Genome*, Joint Statistical Meetings (JSM)

2015 **National Academy of Medicine**, Committee on Food Allergies: Global Burden, Causes, Treatment, Prevention, and Public Policy Workshop, Washington, DC, title “Genetic and epigenetic effects on allergy related diseases and traits”

2017 *Genotypes, Alleles, and Linkage Disequilibrium (LD)*, Brown University, RI

2021 *GWAS Introduction and Post-GWAS Applications*, Brown University, RI (via Zoom)

2021 *Investigating Complex Disease Epidemiology Through Multi-omics*, NICHD Biostatistics and Bioinformatics Branch (BBB) Seminar, Rockville, MD (via Zoom)

**International**

2010 Sun Yat-Sen University, Guangzhou, China

2010 The Eighth ICSA International Conference: Frontiers of Interdisciplinary and Methodological Statistical Research. Guangzhou, China

2011 The Second International Conference on Quantitative Biology and Bioinformatics in Modern Medicine, Dublin, Ireland

2011 South China University of Agriculture, Guangzhou, China

2011 The 4th Paris Workshop on Genomic Epidemiology. Paris, France

2013McGill University and Génome Québec Innovation Centre

2013 *In search of genes involved in complex human diseases*. Peking Union Medical College, China

2013 *Methylation quantitative trait loci and epigenetic networks underlying asthma-related traits*. Tongji Medical College, Wuhan, China

2013 *In search of genes involved in complex human diseases*. Sun Yat-Sen University, Cancer Research Center, China

2014 *Effective adjustment of differential cell populations in epigenome-wide association studies*, Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies, Banff, CA

2014*Analytical methods for high dimensional GWAS, methylation and metabolomics data*, Peking University, China

2014 *eQTL Data in Pathway Analysis*, GlaxoSmithKline, Shanghai, China

2014 *Analyses of metabolomics data*. McGill University and Génome Québec Innovation Centre

2015 The third Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, Kyoto, Japan

2015 *Statistical approaches to the analyses of multidimensional data including OMICS and epigenetic data,* SYMPOSIA ON PREDIMED, NUTRITION, OMICS & SYSTEM EPIDEMIOLOGY, University of Navarra, Pamplona, Spain

2015 *Statistical approaches to the analyses of multidimensional data including OMICS and epigenetic data*, Zhejiang University, Hangzhou, China

2015 *Statistical approaches to the analyses of multidimensional data including OMICS and epigenetic data*, Zhejiang University, Hangzhou, China

2015 *Statistical approaches to the analyses of multidimensional data including OMICS and epigenetic data*, Sichuan University, Chengdu, China

2016 The fourth Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, Kyoto, Japan

2017 *Detection of cell specific effect in methylation study using mixture of cell types*, Guangdong Medical College, Dongguan, China

2017 *Detection of cell specific effect in methylation study using mixture of cell types*, Second Military Medical College affiliated hospital, Shanghai, China

2017 *Power and method to detect cell-type-specific associations in EWAS using cell mixture samples*, CAS-MPG Partner Institute for Computational Biology, Shanghai, China

2017 *Detection of cell specific effect in methylation study using mixture of cell types*, West China School of Stomatology, Chengdu, China

2017*Detection of cell specific effect in methylation study using mixture of cell types*, Guangdong General Hospital, Guangzhou, China

2017 *Power and method to detect cell-type-specific associations in EWAS using cell mixture samples*, Fudan University, Shanghai, China

2018*Power and method to detect cell-type-specific associations in EWAS using cell mixture samples*, Peking University, Beijing, China

2018 *Molecular Profiling of Complex Clinical Traits*, McGill University, Montreal, Canada

2019 *Polygenic risk and causal inference based on Mendelian randomization: examples in cardiovascular diseases*, Fudan University Zhongshan Hospital, Shanghai, China

2020 *Multi-omics integrative approaches for cardiometabolic diseases and traits*. The 6th Annual Nutrition Omics Symposium. US/Spain (virtual)

2020 *Epigenome-wide association study and causal inference for cardiovascular diseases*, China Heart Congress (virtual)

2021 *Multi-fluid, multi-omics approaches to identify disease/trait related metabolomic markers*. The 7th Annual Nutrition Omics Symposium, US/Spain (virtual)

2021 *Epigenome-wide association study and causal inference for cardiovascular diseases*, Symposium on Frontiers in Cardiometabolic Health, China (virtual)

**INVENTIONS/PATENTS:**

US PATENT APPLICATION N° 12/665,602

Title: Method for testing a subject through to have asthma

UK PATENT APPLICATION N° 1401385.8 (International patent in progress)

Title: Method for identifying patients with eosinophil IgE mediated allergic inflammation

US PATENT APPLICATION (Harvard legal office submitting 002806-091450)

Title: Methods for measuring methylation age

**COMMUNITY SERVICE ACTIVITIES:**

2016 Youth Public Health Symposium, Shanghai, Harvard Center . Organizer

<https://www.hsph.harvard.edu/diversity/symposium-shanghai-china-2016/>

2018- Annual Public Health Symposium for Young Leaders, HSPH, Boston. Organizer and faculty advisor

<https://www.hsph.harvard.edu/public-health-symposium-for-young-leaders-in-china/>

2019 Winsor School, Global forum invited talk, Boston, MA <https://www.winsor.edu/uploaded/News/Global_Forum_2019_%E2%80%93_Workshops_and_Guest_Presenters.pdf>

**BIBLIOGRAPHY:**

**Complete list of peer-reviewed publications**

**(Total publications since 2006 = 254, numbers by years: 2022=6, 2021=32, 2020=23, 2019=29, 2018=17, 2017=30, 2016=18, 2015=21, 2014=16, 2013=23, 2012=12, 2011=7, 2010=10, 2009=4, 2008=1, 2007=4, 2006=1)**

**Google scholar citation (Feb 28, 2022)**

|  | **All** | **Since 2017** |
| --- | --- | --- |
| [Citations](javascript:void(0)) | 44852 | 23813 |
| [h-index](javascript:void(0)) | 79 | 67 |
| [i10-index](javascript:void(0)) | 186 | 179 |

**Annotation in the following citations:**

**# advisee (N=97 papers),**

**\* senior/co-senior/corresponding author (N=38 papers),**

**^ first/co-first author (N=12 papers)**

**2006**

1. Li M, Atmaca-Sonmez P, Othman M, Branham KE, Khanna R, Wade MS, Li Y, **Liang L**, Zareparsi S, Swaroop A, Abecasis GR. (2006) CFH haplotypes without the Y402H coding variant show strong association with susceptibility to age-related macular degeneration. ***Nat Genet.*** 38(9):1049-1054. PMC1941700.

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2. Libioulle C, Louis E, Hansoul S, Sandor C, Farnir F, Franchimont D, Vermeire S, Dewit O, de Vos M, Dixon A, Demarche B, Gut I, Heath S, Foglio M, **Liang L**, Laukens D, Mni M, Zelenika D, Van Gossum A, Rutgeerts P, Belaiche J, Lathrop M, Georges M. (2007) Novel Crohn disease locus identified by genome-wide association maps to a gene desert on 5p13.1 and modulates expression of PTGER4. ***PLoS Genet.*** 3(4):e58. PMC1853118 interests exist.

3. Moffatt MF, Kabesch M, **Liang L^**, Dixon AL, Strachan D, Heath S, Depner M, von Berg A, Bufe A, Rietschel E, Heinzmann A, Simma B, Frischer T, Willis-Owen SA, Wong KC, Illig T, Vogelberg C, Weiland SK, von Mutius E, Abecasis GR, Farrall M, Gut IG, Lathrop GM, Cookson WO. (2007) Genetic variants regulating ORMDL3 expression contribute to the risk of childhood asthma. ***Nature.*** 448(7152):470-473. PMID: 17611496.

4. **Liang L^**, Zollner S, Abecasis GR. (2007) GENOME: a rapid coalescent-based whole genome simulator. ***Bioinformatics.*** 23(12):1565-1567. PMID: 17459963.

5. Dixon AL, **Liang L^**, Moffatt MF, Chen W, Heath S, Wong KC, Taylor J, Burnett E, Gut I, Farrall M, Lathrop GM, Abecasis GR, Cookson WO. (2007) A genome-wide association study of global gene expression. ***Nat Genet.*** 39(10):1202-1207. PMID: 17873877.

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7. **Liang L^**, Chen WM, Sham PC, Abecasis GR. (2009) Variance components linkage analysis with repeated measurements. ***Hum Hered.*** 67(4):237-247. PMC2880721.

8. Chen W, **Liang L**, Abecasis GR. (2009) GWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. ***Bioinformatics.*** 25(2):284-285. PMC2732294.

9. Cookson W, **Liang L**, Abecasis G, Moffatt M, Lathrop M. (2009) Mapping complex disease traits with global gene expression. ***Nat Rev Genet.*** 10(3):184-194. PMC4550035.

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