BIOGRAPHICAL SKETCH

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NAME: Hua Tang

eRA COMMONS USER NAME (credential, e.g., agency login): TANGHUA

POSITION TITLE: Associate Professor, Stanford University School of Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Harvard University, Cambridge, Massachusetts	BA	6/1997	Biology
Stanford University, Stanford, California	PhD	8/2002	Statistics, minor Genetic

A. Personal Statement

My research aims to develop statistical methods for genomic and biomedical studies; my graduate training in Statistics and Genetics has enabled me to develop computationally efficient approaches for modeling complex biological problems. Recent work in my group has developed methods and applications of genome-wide association studies of complex traits in minority populations, such as the African American and Hispanic and Hispanic American populations. We have developed methods for quantifying the overlap in genetic architecture between populations, as well as methods for leveraging such overlap to enhance trait mapping and risk prediction. Applications of these methods include several large-scale GWAS in the multi-ethnic Kaiser Permanente Research Program on Genes, Environment, and Health (KP-RPGEH) cohort (103,006 individuals) and the Women's Health Initiative SNP Health Association Resource (WHI-SHARe, 12,000 African Americans and Hispanic Americans), and the Million Veterans Project (MVP). In parallel, we are developing statistical framework to elucidate causal variants and biological mechanisms underlying genotype-phenotype associations discovered by GWAS, by integrating molecular phenotypes, such as proteins or metabolites. Current I serve as a MPI on a proteomics project as part of the Enhancing Gene-Tissue-Expression (eGTEx) consortium, which aims to systematically characterize protein variation among tissues and between individuals.

B. Positions and Honors

2001 Summer intern, Genome Therapeutics Corporation, Waltham, MA

2002-2007 Assistant Member, Biostatistics and Biomathematics Program, Fred Hutchinson Cancer Research Center

2007-2009 Associate Member, Biostatistics and Biomathematics Program, Fred Hutchinson Cancer Research Center.

2002-2008 Affiliate Assistant Professor, Department of Biostatistics, University of Washington

2007-2009 Assistant Professor, Dept. of Genetics, Stanford University School of Medicine

2009-2016 Associate Professor, Dept. of Genetics, Stanford University School of Medicine

2010-2016 Associate Professor (by courtesy), Dept. of Statistics, Stanford University

2017- Professor, Dept. of Genetics, Stanford University School of Medicine

2017- Professor (by courtesy), Dept. of Statistics, Stanford University

Other Experience, Service and Professional Memberships

2000-	Member, American Society of Human Genetics
2002-	Member, Western North American Region of the International Biometric Society
2010-reviewer	NIH review panel for Fogarty International Research Collaboration Award (FIRCA), ad hoc
2014	NIH reviewer, ad hoc, BDMA (February, June).
2015-2021	Regular member, NIH BDMA study section
2015-2017	Scientific Program Committee, American Society of Human Genetics
2015-	Section Editor (Natural variation), PLoS Genetics

Honors and Awards

1994-1997	John Harvard Scholarship and Elizabeth Cary Agassiz Scholarship, Harvard University
1996-1997	Research Assistant, Dept of Health Care Policy, Harvard Medical School
1997	Gertrude Cox Scholarship, American Statistical Association
1998	National Science Foundation Predoctoral Fellowship Awardee
1998-2002	Howard Hughes Medical Institute Predoctoral Fellow
2008-2010	Alfred P. Sloan Research Fellow.
2015	Stanford Center at Peking University Faculty Fellowship.

C. Contribution to Science

Genome-wide association studies in minority populations. Collaborating on minority GWAS studies, we deeply appreciate the challenges in performing GWAS in minority populations. We are using our expertise to develop better analytic approaches, which improves the statistical power of these GWAS studies. For example, using an empirical Bayes approach that harness multi-ethnic evidence, Coram [2015] brought the number of significant lipid loci from 14 to 65 in African Americans. Research in this area has the potential to shed light on the shared and distinct genetic risk factors among ethnicities. We also envision that integrating information across ethnicities will enable a more complete understanding of the genetic basis of diseases, so that individuals of all ethnicities can benefit from the fruit of genomic medicine.

Coram MA, Fang H, Candille SI, Assimes TL, **Tang H.** (2017) Leveraging Multi-Ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. *Am J Hum Genet.* 97:30278-1. PMC5630193

Zaitlen N*, Pasaniuc B, Sankararaman S, Bhatia G, Zhang J, Gusev A, Young T, Tandon A, Pollack S, Vilhjálmsson BJ, Assimes TL, Berndt SI, Blot WJ, Chanock S, Franceschini N, Goodman PG, He J, Hennis AJ, Hsing A, Ingles SA, Isaacs W, Kittles RA, Klein EA, Lange LA, Nemesure B, Patterson N, Reich D, Rybicki BA, Stanford JL, Stevens VL, Strom SS, Whitsel EA, Witte JS, Xu J, Haiman C, Wilson JG, Kooperberg C, Stram D, Reiner AP, **Tang H***, Price AL*. (2014) Leveraging population admixture to characterize the heritability of complex traits. *Nat. Genet.* 46(12):1356-62. PMC4244251

Coram MA, Candille SI, Duan Q, Chan KHK, Li Y, Kooperberg C, Reiner AP, **Tang H.** (2015) Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. *Am J Hum Genet.* 96:740-52. PMCID: PMC4570551

Coram MA, Duan Q, Hoffmann TJ, Thornton T, Knowles JW, Johnson NA, Ochs-Balcom HM, Donlon TA, Martin LW, Eaton CB, Robinson JG; Risch NJ, Zhu X, Kooperberg C, Li Y, Reiner AP, **Tang H.** (2013) Genome-wide Characterization of Shared and Distinct Genetic Components that Influence Blood Lipid Levels in Human Populations. *Am J Hum Genet.* 92(6):904-16. PMCID: PMC3675231

Variation of protein abundance in humans. We have a long-standing interest in developing methods for high-throughput mass-spectrometry-based proteomic studies, and collaborated on the first large-scale

characterization of human proteome variation. We are currently investigating the protein abundance variation across multiple tissues through the NIH-GTEx consortium.

Wu L, Candille SI, Choi Y, Xie D, Jiang L, Li-Pook-Than J, **Tang H***, Snyder M*. (2013) Variation and genetic control of protein abundance in humans. *Nature,* 499(7456):79-82. PMCID: PMC3789121 *Joint corresponding authors.

Piening BD, Wang P, Bangur CS, Whiteaker J, Zhang H, Feng L, Keane JF, Eng JK, **Tang H**, Prakash A, McIntosh MW, Paulovich A. (2006) Quality Control Metrics for LC-MS Feature Detection Tools Demonstrated on Saccharomyces cerevisiae Proteomic Profiles. J. Proteomics Res. **5**:1527-34.

Wang P*, **Tang H,** Fitzgibbon MP, Coram M*, Zhang H, Yi E, Aebersold R, Mcintosh M. (2007) A statistical method for chromatographic alignment of LC-MS data. *Biostatistics* **8**:357-67.

Methods and analysis of human population genetic structure. Characterizing population structure using genetic information is a powerful approach in understanding human evolutionary history, as well as an essential step for eliminating confounding bias in genetic association studies. We developed a computational program for characterizing population structure based on SNP genotype data, *frappe*. Because of its computational efficiency, *frappe* was widely used in both population genetics analysis and genome-wide association studies (GWAS). Applying this program, we have analyzed US and world-wide populations, and provided important insights in the shared and distinct pattern of genetic variation in humans.

Tang H, Peng J., Wang P., and Risch N. (2005) Estimation of Individual Admixture: Analytical and Study Design Considerations. *Genet Epidemiol.* **28**:289-301.

Tang H, Quertermous T, Rodriguez B, Kardia SL, Zhu X, Brown A, Pankow JS, Province MA, Hunt SC, Boerwinkle E, Schork NJ, Risch NJ (2005) Genetic Structure, Self-Identified Race/Ethnicity and Confounding in Case-Control Association Studies. *Am J Hum Genet.* **76**:268-75. PMID: 15712363

Li JZ, Absher DM, **Tang H**, Southwick AM, Casto AM, Ramachandran S, Cann HM, Barsh GS, Feldman M, Cavalli-Sforza LL, Myers RM. (2008) Worldwide human relationships inferred from genome-wide patterns of variation. *Science*, 319: 1100-1104. PMID: 18292342.

Method for characterizing admixed ancestry and genetic association methods for admixed populations. Individuals with mixed ancestry pose special challenge and opportunities in genotype-trait association studies. We developed one of the first computational algorithms that accurately delineate ancestry origin, at each genomic location, using high-density SNP genotype data. Our 2006 paper motivated many follow-up studies in this field. We also developed the first algorithm of sub-continental principal component analysis in admixed populations; in a Hispanic cohort, we demonstrated that this approach is able to distinguishing between Northern versus Southern European ancestry origins, as well as identifying different indigenous AmerIndian ancestral groups. Using these tools, we performed association and admixture analysis of skin and eye color traits in the admixed Cape Verde population. This study not only help to explain how genes work together to control the full range of pigmentary phenotypic diversity, but also provide new insight into the evolution of these traits. Additionally, we have quantified fine-scale local ancestry for several large cohorts, including the African American participants in the Women's Health Initiative, which has enabled many other researchers to use the admixture mapping approach to study traits of their interest.

Tang H, Coram M, Wang P, Zhu X, Risch NJ. (2006) Reconstructing Genetic Ancestry Blocks in Admixed Individuals. *Am J Hum Genet.* **79**:1-12. PMID: 16773560. PMCID: PMC1474129.

Johnson NA, Coram MA, Shriver MD, Romieu I, Barsh G, London S, **Tang H**. (2011) Ancestral Components of Admixed Genomes in a Mexican Cohort. *PLoS Genet.* **7**:e1002410. PMID 22194699. PMCID: PMC3240599.

Beleza S, Johnson NA, Candille SI, Absher DM, Coram MA, Lopes J, Campos J, Araújo II, Anderson TM, Vilhjálmsson BJ, Nordborg M, Silva AC, Shriver MD, Rocha J, Barsh GS, **Tang H**. (2013) Genetic

architecture of skin and eye color in an African-European admixed population. *PLoS Genetics*, 9(3):e1003372. PMID: 23555287; PMCID: PMC3605137.

SciENcv bibliography:
http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/40626456/?sort=date&direction=descending

D. Research Support

Active

NIH RO1 GM073059/ NIGMS (PI: Tang) 03/01/05 – 04/30/18
Genetic Architecture of Complex Traits in Admixed Populations.
This project aims to develop new methods to improve the robustness and efficiency of case-control association studies, with applications to African Americans and Mexican Americans. A supplement was awarded (01/01/2010 – 12/31/2011) to support software development for estimating local ancestry. The focus of the current funding cycle is to develop analytic approaches for genome-wide association studies (including those using next-gen sequencing technologies) in genetically admixed populations.
Role: PI

NIH U01HG007611 (MPIs: Snyder/Tang) 04/24/14-03/31/18
Genotype-Tissue-Protein: proteomic variation and quantitative trait loci (pQTL)
This project will characterize the proteomic variation in multiple human tissues in ~150 GTEx donors using high-throughput mass-spectrometry.
Role: MPI

1I01BX002641-01A (Tsao/Chang) 10/01/15 – 09/30/18
VA-ORD
Title: Genetics of Cardiometabolic Diseases in the VA Population
The goal of this study is to investigate the genetic underpinnings of various cardiometabolic traits using genetic and phenotype data from the Million Veterans Program.
Role: Co-Investigator

Institutional support (PI: Tang) Stanford University 01/01/2007 –
The purpose of this institutional support is for PI to set up her lab and to explore novel, high-risk, projects.

Completed

Research Fellow Award (Tang) Alfred P. Sloan Foundation 9/16/08 – 9/15/12
Computational Methods for Molecular Evolution
The goal of this project is to develop statistical and computational methods for understanding the evolutionary processes that shapes the pattern of human genetic variation.
Role: PI

Transformative Innovation in Basic Bioscience Project (Tang) Stanford University 09/01/13 – 08/30/14
Computational approaches for post-transcriptional regulation.
The goal of this research is to develop and apply computational approaches to probe post-transcriptional regulatory mechanisms that influence protein abundance.