

Stanford



Hua Tang

Professor of Genetics and, by courtesy, of Statistics

 NIH Biosketch available Online

 Curriculum Vitae available Online

Bio

BIO

Dr. Tang received her PhD in Statistics, with a minor in Genetics, from Stanford University in 2002. From 2002 to 2006, she was on faculty in the PHS division at the Fred Hutchinson Cancer Research Center. Dr. Tang joined the Stanford Genetics Department in 2007. The goals of her research are to better understand the evolutionary forces that have shaped the pattern of genetic variation in humans, as well as to elucidate the genetic architecture of complex traits and diseases in the context of human evolution.

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Professor (By courtesy), Statistics
- Member, Bio-X
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

PROFESSIONAL EDUCATION

- AB, Harvard and Radcliffe College , Biology (1997)
- PhD, Stanford University , Statistics (minor Genetics) (2002)

LINKS

- Tang Lab Website: <http://med.stanford.edu/tanglab/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Research in our laboratory develops and applies statistical methods for analyzing patterns of human genetic variation, which underlie the phenotypic diversity of our species. We are collaborating on various genome-wide studies focusing on stratified or recently admixed populations. These studies offer unique opportunities to elucidate the evolutionary forces that have shaped the patterns of genetic variation in humans, to uncover the genetic basis of complex traits, and to shed light on the mechanisms that lead to diverse phenotypes and disparate disease risks among populations.

Teaching

COURSES

2016-17

- Statistical Genetics of Complex Traits: BIOS 259 (Win)
- Statistical and Machine Learning Methods for Genomics: BIO 268, BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

2015-16

- Statistical and Machine Learning Methods for Genomics: BIO 268, BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Huaying Fang

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Genome-wide characterization of shared and distinct genetic components that influence blood lipid levels in ethnically diverse human populations.** *American journal of human genetics*
Coram, M. A., Duan, Q., Hoffmann, T. J., Thornton, T., Knowles, J. W., Johnson, N. A., Ochs-Balcom, H. M., Donlon, T. A., Martin, L. W., Eaton, C. B., Robinson, J. G., Risch, N. J., Zhu, et al
2013; 92 (6): 904-916
- **Genetic Architecture of Skin and Eye Color in an African-European Admixed Population** *PLOS GENETICS*
Beleza, S., Johnson, N. A., Candille, S. I., Absher, D. M., Coram, M. A., Lopes, J., Campos, J., Araujo, I. I., Anderson, T. M., Vilhjalmsson, B. J., Nordborg, M., Correia e Silva, A., Shriver, et al
2013; 9 (3)
- **Genome-Wide Association Studies of Quantitatively Measured Skin, Hair, and Eye Pigmentation in Four European Populations** *PLOS ONE*
Candille, S. I., Absher, D. M., Beleza, S., Bauchet, M., McEvoy, B., Garrison, N. A., Li, J. Z., Myers, R. M., Barsh, G. S., Tang, H., Shriver, M. D.
2012; 7 (10)
- **Ancestral Components of Admixed Genomes in a Mexican Cohort** *PLOS GENETICS*
Johnson, N. A., Coram, M. A., Shriver, M. D., Romieu, I., Barsh, G. S., London, S. J., Tang, H.
2011; 7 (12)
- **Worldwide human relationships inferred from genome-wide patterns of variation** *SCIENCE*
Li, J. Z., Absher, D. M., Tang, H., Southwick, A. M., Casto, A. M., Ramachandran, S., Cann, H. M., Barsh, G. S., Feldman, M., Cavalli-Sforza, L. L., Myers, R. M.
2008; 319 (5866): 1100-1104
- **Reconstructing genetic ancestry blocks in admixed individuals** *AMERICAN JOURNAL OF HUMAN GENETICS*
Tang, H., Coram, M., Wang, P., Zhu, X., Risch, N.
2006; 79 (1): 1-12
- **Variation and genetic control of protein abundance in humans** *NATURE*
Wu, L., Candille, S. I., Choi, Y., Xie, D., Jiang, L., Li-Pook-Than, J., Tang, H., Snyder, M.
2013; 499 (7456): 79-82
- **Association of DXA-derived Bone Mineral Density and Fat Mass With African Ancestry** *JOURNAL OF CLINICAL ENDOCRINOLOGY & METABOLISM*
Ochs-Balcom, H. M., Preus, L., Wactawski-Wende, J., Nie, J., Johnson, N. A., Zakharia, F., Tang, H., Carlson, C., Carty, C., Chen, Z., Hoffman, T., Hutter, C. M., Jackson, et al
2013; 98 (4): E713-E717
- **Variants in CXADR and F2RL1 are associated with blood pressure and obesity in African-Americans in regions identified through admixture mapping** *JOURNAL OF HYPERTENSION*
Shetty, P. B., Tang, H., Tayo, B. O., Morrison, A. C., Hanis, C. L., Rao, D. C., Young, J. H., Fox, E. R., Boerwinkle, E., Cooper, R. S., Risch, N. J., Zhu, X.

2012; 30 (10): 1970-1976

- **Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes** *CELL*
Chen, R., Mias, G. I., Li-Pook-Than, J., Jiang, L., Lam, H. Y., Chen, R., Miriami, E., Karczewski, K. J., Hariharan, M., Dewey, F. E., Cheng, Y., Clark, M. J., Im, et al
2012; 148 (6): 1293-1307
- **Human genetic variation altering anthrax toxin sensitivity** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Martchenko, M., Candille, S. I., Tang, H., Cohen, S. N.
2012; 109 (8): 2972-2977
- **Joint Testing of Genotype and Ancestry Association in Admixed Families** *GENETIC EPIDEMIOLOGY*
Tang, H., Siegmund, D. O., Johnson, N. A., Romieu, I., London, S. J.
2010; 34 (8): 783-791
- **Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies** *JOURNAL OF THE AMERICAN COLLEGE OF CARDIOLOGY*
Assimes, T. L., Holm, H., Kathiresan, S., Reilly, M. P., Thorleifsson, G., Voight, B. F., Erdmann, J., Willenborg, C., Vaidya, D., Xie, C., Patterson, C. C., Morgan, T. M., Burnett, et al
2010; 56 (19): 1552-1563
- **Molecular and Evolutionary History of Melanism in North American Gray Wolves** *SCIENCE*
Anderson, T. M., vonHoldt, B. M., Candille, S. I., Musiani, M., Greco, C., Stahler, D. R., Smith, D. W., Padhukasahasram, B., Randi, E., Leonard, J. A., Bustamante, C. D., Ostrander, E. A., Tang, et al
2009; 323 (5919): 1339-1343
- **Characterizing the admixed African ancestry of African Americans** *GENOME BIOLOGY*
Zakharia, F., Basu, A., Absher, D., Assimes, T. L., Go, A. S., Hlatky, M. A., Iribarren, C., Knowles, J. W., Li, J., Narasimhan, B., Sidney, S., Southwick, A., Myers, et al
2009; 10 (12)
- **Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE study** *HUMAN MOLECULAR GENETICS*
Assimes, T. L., Knowles, J. W., Basu, A., Iribarren, C., Southwick, A., Tang, H., Absher, D., Li, J., Fair, J. M., Rubin, G. D., Sidney, S., Fortmann, S. P., Go, et al
2008; 17 (15): 2320-2328
- **IMPROVING POPULATION-SPECIFIC ALLELE FREQUENCY ESTIMATES BY ADAPTING SUPPLEMENTAL DATA: AN EMPIRICAL BAYES APPROACH** *ANNALS OF APPLIED STATISTICS*
Coram, M., Tang, H.
2007; 1 (2): 459-479
- **Recent genetic selection in the ancestral admixture of Puerto Ricans** *AMERICAN JOURNAL OF HUMAN GENETICS*
Tang, H., Choudhry, S., Mei, R., Morgan, M., Rodriguez-Cintron, W., Burchard, E. G., Risch, N. J.
2007; 81 (3): 626-633
- **A statistical method for chromatographic alignment of LC-MS data** *BIOSTATISTICS*
Wang, P., Tang, H., Fitzgibbon, M. P., McIntosh, M., Coram, M., Zhang, H., Yi, E., Aebersold, R.
2007; 8 (2): 357-367
- **Reduced selection leads to accelerated gene loss in Shigella** *GENOME BIOLOGY*
Hershberg, R., Tang, H., Petrov, D. A.
2007; 8 (8)
- **Combining multiple family-based association studies.** *BMC proceedings*
Tang, H., Peng, J., Wang, P., Coram, M., Hsu, L.
2007; 1: S162-?
- **Genomewide evolutionary rates in laboratory and wild yeast** *GENETICS*
Ronald, J., Tang, H., Brem, R. B.
2006; 174 (1): 541-544

- **Locally weighted transmission/disequilibrium test for genetic association analysis** *14th Genetic Analysis Workshop*
Hsu, L., Yu, X. S., Houwing-Duistermaat, J. J., Uh, H. W., El Galta, R., Lebec, J. J., Tang, H.
BIOMED CENTRAL LTD.2005
- **A newly discovered founder population: the Roma/Gypsies** *BIOESSAYS*
Kaaydjieva, L., Morar, B., Chaix, R., Tang, H.
2005; 27 (10): 1084-1094
- **Estimation of individual admixture: Analytical and study design considerations** *GENETIC EPIDEMIOLOGY*
Tang, H., Peng, J., Wang, P., Risch, N. J.
2005; 28 (4): 289-301
- **Genetic structure, self-identified race/ethnicity, and confounding in case-control association studies** *AMERICAN JOURNAL OF HUMAN GENETICS*
Tang, H., Quertermous, T., Rodriguez, B., Kardia, S. L., Zhu, X. F., Brown, A., Pankow, J. S., Province, M. A., Hunt, S. C., Boerwinkle, E., Schork, N. J., Risch, N. J.
2005; 76 (2): 268-275
- **Ethnicity and human genetic linkage maps** *AMERICAN JOURNAL OF HUMAN GENETICS*
Jorgenson, E., Tang, H., Gadde, M., Province, M., Leppert, M., Kardia, S., Schork, N., Cooper, R., Rao, D. C., Boerwinkle, E., Risch, N.
2005; 76 (2): 276-290
- **Geographic distribution of disease mutations in the Ashkenazi Jewish population supports genetic drift over selection** *AMERICAN JOURNAL OF HUMAN GENETICS*
Risch, N., Tang, H., Katzenstein, H., Ekstein, J.
2003; 72 (4): 812-822
- **Categorization of humans in biomedical research: genes, race and disease.** *Genome biology*
Risch, N., Burchard, E., Ziv, E., Tang, H.
2002; 3 (7): comment2007-?
- **Frequentist estimation of coalescence times from nucleotide sequence data using a tree-based partition** *GENETICS*
Tang, H., Siegmund, D. O., Shen, P. D., Oefner, P. J., Feldman, M. W.
2002; 161 (1): 447-459
- **Locating regions of differential variability in DNA and protein sequences** *GENETICS*
Tang, H., Lewontin, R. C.
1999; 153 (1): 485-495