

YUHONG TANG, Ph.D
Genomics/Microarray Facility Manager
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SCIENTIFIC RESEARCH EXPERIENCE

Aug, 2006-Present: Genomics/Microarray Facility Manager

The Samuel Roberts Noble Foundation, Inc., Ardmore, OK

- Establish and improve service in DNA sequencing, marker analysis, and microarray analysis for Noble Foundation research community and its collaborators.
- Introduce and adapt current genomics techniques to the Noble Foundation community.

Jan, 2003-July, 2005: Senior research scientist

Microarray Core Facility, Oklahoma Medical Research Foundation, Oklahoma City, OK

- Performing microarray data analyses and providing bioinformatics services for collaborators from OMRF, OUHSC, OU and other clients;
- Organizing weekly discussion about technical and scientific issues related to microarray in the core facility;
- Acting as a bridging personal to coordinate the communication between the wet lab and analysis groups;
- Acting as OMRF Campus liaison for OKBIOS (Oklahoma Bioinformatics Society);

Jan, 2001-December, 2002: Research scientist

Advanced Center for Genome Technology (ACGT), University of Oklahoma, Norman, OK

- Conducted EST research project “Identification of circadian genes from day- and night-specific cDNA libraries”. Carried out research work, ranging from bench work (including cDNA library construction and EST DNA sequencing) to bioinformatics work (including sequence assembly and annotation);
- Involved in genomic DNA sequencing techniques, including Cosmid, BAC and PAC shot-gun sequencing and gap closures;
- Guided a undergraduate student Terrell E. John Swanson through his senior thesis “Sequencing and Analysis of the *MAT-1* locus in *Ustilago hordei*”;
- Managed EST data processing and annotation using Unix shell scripts;

May, 1998 - August, 2000: Postdoctoral Research Associate

US Plant, Soil, and Nutrition Laboratory, USDA-ARS, Cornell University, Ithaca, NY

- Mapped the conserved genomic region harboring the aluminum tolerance locus between wheat and barley;
- Confirmed aluminum tolerance mechanism involving organic acid exudation for Atlas 66 using bioassay;

- Initiated effort to isolate aluminum tolerance gene in wheat using Chinese Spring wheat deletion lines by differential display;

August, 1992 - May, 1998: Research Assistant

Molecular Cytogenetics Laboratory, Genetics Program, Clemson University, Clemson, SC

- Constructed and maintained an intra-specific cross of a F2 mapping population of Corolla Fasciation x "Clark" ;
- Constructed a soybean linkage map with molecular makers generated from various mapping techniques, including random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), restriction fragment length polymorphism (RFLP), random amplified microsatellite polymorphism (RAMP);
- Characterized a meristematic mutation-fasciation in soybean, *Glycine max* (L.) Merr.;
- Constructed tissue specific lambda ZapII cDNA libraries (apical meristem, leaf tissue and embryo) and use these clones for EST and mapping analysis;

September, 1989 - July, 1992: Master degree graduate student

Institute of Genetics, Chinese Academy of Sciences, Beijing, P. R. China

- Participated in "863" National Research Project "Genetic Engineering of Cotton with *Bt* (*Bacillus thuringiensis*) Endotoxin Gene through *Agrobacterium tumefaciens* Mediated Somatic Embryogenic Transformation".

EDUCATION

September, 2000 – December, 2004

University of Oklahoma, Norman, Oklahoma

Master degree: computer science, focusing on large scale data analysis

August, 1992 - May, 1998

Clemson University, Clemson, South Carolina

Ph.D.: Interdisciplinary Genetics Program with emphasis on Molecular Developmental

Biology & Genetics

Doctoral Dissertation Title: Developmental and Molecular Characterization of Meristematic Mutation in Soybean, *Glycine max* (L.) Merr.

Awards: Recipient of the Wade Stackhouse Graduate Research Fellowship, July, 1993 - June, 1996

September, 1989 - July, 1992

Institute of Genetics, Chinese Academy of Sciences, Beijing, P. R. China

Master degree: Genetics

Master Degree Thesis: Transformation of Cotton, *Gossypium hirsutum* [L.] with *Bacillus thuringiensis* Endotoxin Gene.

September, 1985 - July, 1989

Beijing Normal University, Beijing, P. R. China

Bachelor Degree: Biology

Teaching Experience: Intern-Instructor of the First High School of Beijing, Beijing, P.R. China

SPECIALTIES

Bioinformatics in Genomics and microarray: Microarray data analysis, both static pair-wise comparison and dynamics clustering; Trained in statistical knowledge used in data analysis; Familiar with annotation and analysis packages, including Spotfire and PathwayAssist. Skilled at genomic and EST sequence assembly and annotation using Staden package, phredPhrap, Consed and Cross_match; Familiar with various molecular databases, such as Genbank, ExPasy and Zfin etc.; Experienced with NCBI Analytical Package.

Computer Skills: Familiar with programming languages, including C, C++, Perl and Shell scripts and Matlab; Experienced with operating system, including Windows and Unix; Experienced in database design and implementation using database system Oracle 9i.

Genetics Analytic Tools: Linkage analysis-Mapmaker, Pedigree analysis-NTSYS.

Molecular lab techniques: cDNA library construction, library screening, Southern and Northern analyses, BAC, PAC and EST sequencing; marker techniques, including isozyme, RAPD, RFLP, EST, RAMP, AFLP.

Cytology: light microscopy sectioning, chromosome preparation, scanning electron microscopy, image processing.

Tissue Culture: somatic embryogenic regeneration, shoot regeneration, gene transformation.

Analytical Methods: high performance liquid chromatography (HPLC).

PEER REVIEWED PUBLICATIONS

- Vagner A, Benedito, Ivone Torres-Jerez, Jeremy D. Murray, Andry Andrianakaja, Stacy Allen, Klementina Kakar, Maren Wandrey, Jérôme Verdier, Hélène Zuber, Thomas Ott, Sandra Moreau, Andreas Niebel, Tancred Frickey, Georg Weiller, Ji He, Xinbin Dai, Patrick X. Zhao, Yuhong Tang, and Michael K. Udvardi. A gene expression atlas of the model legume *Medicago truncatula*. (Submitted to Plant Journal).
- Anand A, Uppalapati SR, Ryu CM, Allen SN, Kang L, Tang Y, Mysore KS. (2008) Salicylic Acid and Systemic Acquired Resistance Play a Role in Attenuating Crown Gall Disease Caused by *Agrobacterium tumefaciens*. *Plant Physiol.* 146(2):703-15. Epub 2007 Dec 21.
- Marina Naoumkina, Mohamed A. Farag, Lloyd W. Sumner, **Yuhong Tang**, Chang-Jun Liu, and Richard A. Dixon 2007 Different mechanisms for phytoalexin induction by pathogen and wound signals in *Medicago truncatula* PNAS published October 30, 2007, 10.1073/pnas.0708697104.
- Teaster ND, Motes CM, **Tang Y**, Wiant WC, Cotter MQ, Wang Y, Kilaru A, Venables BJ, Hasenstein KH, Gonzalez G, Blancaflor EB, and Chapman KD. 2007 N-Acylethanolamine Metabolism Interacts with Abscisic Acid Signaling in *Arabidopsis thaliana* Seedlings. *Plant Cell* 19: 2454–2469.
- Anand A, Krichevsky A, Schornack S, Lahaye T, Tzfira T, **Tang Y**, Citovsky V, Mysore KS. 2007 *Arabidopsis* VIRE2 INTERACTING PROTEIN2 Is Required for *Agrobacterium* T-DNA Integration in Plants. *Plant Cell* 19:1695-708.
- Zhu H, **Tang Y**, Ivanciu L, Centola M, Lupu C, Taylor FB Jr, Lupu F. (2007) Temporal dynamics of gene expression in the lung in a baboon model of *E. coli* sepsis. *BMC Genomics.* 26:8:58.
- Lawrence S, **Tang Y**, Frank MB, Dozmorov I, Jiang K, Chen Y, Cadwell C, Turner S, Centola M, Jarvis JN. (2007) A dynamic model of gene expression in monocytes reveals differences in immediate/early response genes between adult and neonatal cells. *J Inflamm (Lond).* 16:4:4.
- Deavours BE, Liu CJ, Naoumkina MA, **Tang Y**, Farag MA, Sumner LW, Noel JP, Dixon RA. (2006) Functional analysis of members of the isoflavone and isoflavanone O-methyltransferase enzyme families from the model legume *Medicago truncatula*. *Plant Mol Biol.* 62(4-5):715-33.

- Bakkeren G, Jiang G, Warren RL, Butterfield Y, Shin H, Chiu R, Linning R, Schein J, Lee N, Hu G, Kupfer DM, **Tang Y**, Roe BA, Jones S, Marra M, Kronstad JW. (2006) Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. *Fungal Genet Biol.*43:655-66.
- Jarvis JN, Petty HR, **Tang Y**, Frank MB, Tessier PA, Dozmorov I, Jiang K, Kindzelski A, Chen Y, Cadwell C, Turner M, Szodoray P, McGhee JL, Centola M. (2006) Evidence for chronic, peripheral activation of neutrophils in polyarticular juvenile rheumatoid arthritis. *Arthritis Res Ther.* 8:R154.
- Szodoray P, Alex P, Frank MB, Turner M, Turner S, Knowlton N, Cadwell C, Dozmorov I, **Tang Y**, Wilson PC, Jonsson R, Centola M. (2006) A genome-scale assessment of peripheral blood B-cell molecular homeostasis in patients with rheumatoid arthritis. *Rheumatology (Oxford).* 45:1466-76.
- Li C, **Tang Y**, Li F, Turner S, Li K, Zhou X, Centola M, Yan X, Cao W. (2006) 17beta-estradiol (betaE2) protects human retinal Muller cell against oxidative stress in vitro: evaluation of its effects on gene expression by cDNA microarray. *Glia.* 53:392-400.
- Yu X, **Tang Y**, Li F, Frank MB, Huang H, Dozmorov I, Zhu Y, Centola M, Cao W. (2005) Protection against hydrogen peroxide-induced cell death in cultured human retinal pigment epithelial cells by 17beta-estradiol: a differential gene expression profile. *Mech Ageing Dev.* 126:1135-45.
- Dozmorov IM, Centola M, Knowlton N, **Tang Y**. (2005) Mobile classification in microarray experiments. *Scand J Immunol.* 62 Suppl 1:84-91.
- Hitchon CA, Alex P, Erdile LB, Frank MB, Dozmorov I, **Tang Y**, Wong K, Centola M, El-Gabalawy HS. (2004) A distinct multicytokine profile is associated with anti-cyclical citrullinated peptide antibodies in patients with early untreated inflammatory arthritis. *J Rheumatol.* 31:2336-46.
- Dozmorov I, Knowlton N, Tang Y, Shields A, Pathipvanich P, Jarvis JN, Centola M. Hypervariable genes--experimental error or hidden dynamics. *Nucleic Acids Res.* 2004 32(19):e147.
- Zimmerman RA, Dozmorov I, Nunlist EH, **Tang Y**, Li X, Cowan R, Centola M, Frank MB, Culkin DJ, Lin HK. (2004) 5alpha-Androstane-3alpha,17beta-diol activates pathway that resembles the epidermal growth factor responsive pathways in stimulating human prostate cancer LNCaP cell proliferation. *Prostate Cancer Prostatic Dis.* 7:364-74.
- Nunlist EH, Dozmorov I, **Tang Y**, Cowan R, Centola M, Lin HK. (2004) Partitioning of 5alpha-dihydrotestosterone and 5alpha-androstane-3alpha, 17beta-diol activated pathways for stimulating human prostate cancer LNCaP cell proliferation. *J Steroid Biochem Mol Biol.* 91:157-70.
- Dozmorov I, Knowlton N, Tang Y, Centola M. (2004) Statistical monitoring of weak spots for improvement of normalization and ratio estimates in microarrays. *BMC Bioinformatics.* 5:5:53.
- **Tang Y.**, Garvin D.F., Kochian L.V., Sorrells M.E., and Carver B.F. (2002) Physiological genetics of aluminum tolerance in the wheat cultivar Atlas 66. *Crop Sci.* 42: 1541-1546.
- Karakaya HC, **Tang Y**, Cregan PB, Knap HT (2002) Molecular mapping of the fasciation mutation in soybean, *Glycine max* (Leguminosae) *American Journal of Botany* 89:559-565.
- **Tang, Y.**, M.E. Sorrells, L.V. Kochian, and D.F. Garvin. (2000) Identification of RFLP Markers Linked to the Barley Aluminum Tolerance Gene Alp. *Crop Science.* 40: 778-782.
- **Tang, Y.**, and H. T. Knap (1998) Fasciation mutation enhances meristematic activity and alters pattern formation in soybean. *International Journal of Plant Science* 159:249-260.
- **Tang, Y.**, and H. T. Skorupska. (1997) Expression of fasciation mutation in apical meristems of soybean, *Glycine max* (LEGUMINOSAE). *American Journal of Botany* 84:328-335.