

**BIOGRAPHICAL SKETCH**

Provide the following information for the key personnel in the order listed for Form Page 2.  
Follow the sample format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME		POSITION TITLE	
Xiangning Chen		Assistant Professor	
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Guangxi Agricultural Institute, China	BA	1982	Agronomy
Institute of Genetics, Academia Sinica	MS	1988	Genetics/Biochemistry
Houston University Dept. of Biochem & Biophys.	PhD	1994	Genomics/Mol. Biology

**A. Positions and Honors****Positions**

- 1994-1997 Post doctoral fellow, Washington University School of Medicine, St. Louis, Missouri. High throughput genotyping technologies developing, automated DNA sequencing and analysis
- 1996-1998 National research service awards (NRSA) from National Institute of Health (1-F32-HG00156-01), SNP genotyping technology development
- 1997-1999 Research Instructor, Washington University School of Medicine, St. Louis, Missouri. SNP markers discovery and high throughput genotyping technologies development
- 1999-2000 Scientist, project leader, Cereon Genomics, LLC, Cambridge, Massachusetts. Development of single nucleotide polymorphism (SNP) markers for Arabidopsis and Maize, and implementation of large scale, high throughput genotyping technologies for genetic mapping and positional cloning of QTL gene
- 2001-2001 Senior Scientist, project leader, CuraGen Corporation, New Haven, Connecticut. Development of SNP genotyping technologies that use capillary DNA sequencers
- 2001-present Assistant professor, Virginia Institute for Psychiatric and Behavioral Genetics, Virginia Commonwealth University, Richmond, Virginia. SNP marker and genotyping technology development, high throughput genotyping for complex traits and candidate genes. Linkage and association studies of schizophrenia, nicotine dependence and major depression

**B. Selected Peer-Reviewed Publications**

*Dr. Chen has participated in the preparation and publication of over 20 papers, chapters and reviews, of which the following are a sample:*

- Chen X, Widger WR (1993) Physical genome map of the unicellular cyanobacterium *Synechococcus* sp. strain PCC 7002. *Journal of Bacteriology* **175**:5106-5116
- Widger WR, Chen X, Samartzidou H (1997) The physical Genome map of *Synechococcus* PCC 7002. In *Bacterial Genomes: Physical Structure and Analysis* Eds. deBruijn, F.J., Lupski, J.R., Weinstock, G. Chapman & Hall New York, New York. pp. 763-770
- Chen X, Kwok P-Y (1997) Template-directed dye-terminator incorporation (TDI) assay: a homogeneous DNA diagnostic method based on fluorescence resonance energy transfer. *Nucleic Acids Research* **25**:347-353
- Chen X, Zehnbauser B, Gnirke A, Kwok P-Y (1997) Fluorescence energy transfer detection as a homogeneous DNA diagnostic method. *Proc. Natl. Acad. Sci. USA*. **94**:10756-10761
- Chen X, Livak KJ, Kwok P-Y, 1998. A homogeneous, ligase-mediated DNA diagnostic test. *Genome Res.* **8**: 549-556
- Kwok P-Y, Chen X (1998) Detection of single nucleotide variations. In *Genetic Engineering: Principles and methods*. Ed. Setlow, J. K. Plenum Press New York. **20**:125-134

- Chen X, Kwok P-Y (1999) Homogeneous Genotyping Assays for Single Nucleotide Polymorphisms with Fluorescence Resonance Energy Transfer Detection. *Genetic Analysis (Biomolecular Engineering)* **14**:157-163
- Chen X, Levine L, Kwok P-Y (1999) Fluorescence polarization in homogeneous nucleic acid analysis. *Genome Research* **9**:492-498
- Kwok P-Y, Chen X (1999) Methods and kits for nucleic acid analysis using fluorescence resonance energy transfer. *US Patent* 5945283
- Kwok P-Y, Chen X, Levine L (200). Fluorescence polarization in nucleic acid analysis. *US patent* 6180408
- Hsu TM, Chen X, Duan S, Miller RD, Kwok P-Y (2001) Universal SNP genotyping assay with fluorescence polarization detection. *BioTechniques* **31**:560-570
- Chen X (2002) Multiple sequencible and ligatable structures for genomic analysis. *US patent application*, patent pending
- Chen X (2003) Allele specific PCR for genotyping. *US patent application*, patent pending
- van den Oord EJCG, Jiang Y, Riley BP, Kendler KS, Chen X (2003) FP-TDI SNP scoring by manual and statistical procedures: A study of error rates and types. *BioTechniques* **34**:610-623
- Chen X (2003) Fluorescence polarization for single nucleotide polymorphism genotyping. *Combinatorial Chem & High Throughput Screening* **6**:213-223
- Chen X, Sullivan PF, Single nucleotide polymorphism genotyping: Biochemistry, protocol, cost and throughput. *Pharmacogenomics Journal*, in press
- Kwok P-Y, Chen X, Detection of single nucleotide polymorphisms. *Current Issues in Molecular Biology*, in press

### C. Research Support

#### **Active**

R01 AA11408                      Prescott (PI)                      09/01/02 - 08/31/06                      Co-I

NIH/NIMH/NIAAA

An Irish Affected Sib Pair Study of Alcohol Dependence

The goal of this project is to detect the genomic location of susceptibility loci (SL) for alcoholism.

R01 MH41953                      Kendler (PI)                      04/01/99 - 02/28/04                      Co-I

NIH/NIMH

The Genetic Epidemiology of Schizophrenia in Ireland

This is a competitive renewal that seeks support to critically extend the Irish Study of High Density Schizophrenia Families by collecting 500 proband-parent triads for family-based association studies.

VTSF #8520012                      Kendler (PI)                      12/01/01 - 06/30/04                      Co-I

Virginia Tobacco Settlement Foundation

Candidate Genes for Nicotine Dependence in Humans

The goal is to identify and characterize the individual genes that determine vulnerability to nicotine dependence

#### **Pending**

R01 MH41953                      Kendler (PI)                      12/01/03 - 11/31/08                      Co-I

NIH/NIMH

The Genetic Epidemiology of Schizophrenia in Ireland

The aim is to screen two known high-risk haplotypes identified in two high-risk samples for causal variation and to catalog numerous human populations and primate lineages for the associated regions. Variants identified would be assessed for functionality.