Chindo Hicks, PhD
708-327-9070
chhicks@lumc.edu

PROFILE

Chindo Hicks is an international scientific expert in biostatistics, statistical genetics, and bioinformatics with more than ten years of research experience applied to biological and biomedical sciences. Dr. Hicks is a dynamic global professional with work experience at diverse organizations in Asia, Europe, and the USA.

MAJOR RESEARCH INTERESTS

- Multivariate analysis of high throughput gene expression and proteomics data. Modelling complex gene regulatory networks.
- Design of biological experiments, clinical and multicenter trials. Analysis of clinical and population studies data. Prediction of clinical outcomes. Correlating clinical information with gene expression profiles.
- Genetics and epigenetics of complex human diseases (cancer, diabetes, cardiovascular, developmental, neurodegenerative and aging).
- Genetic epidemiology, population and environmental studies with application to public health.
- Linkage and linkage disequilibrium mapping of genes associated with complex human diseases.
- Estimating genetic and polymorphic variation, gene effects and modeling gene x gene and genotype x environment interaction.

EDUCATION

Bachelor of Science *University of Agriculture, Brno, Czech Republic* Animal Genetics Two distinguished student awards, 1986 and 1987	1986
Master of Science *University of Agriculture, Brno, Czech Republic* Statistical Genetics	1989
Doctorate of Philosophy *Royal Veterinary and Agricultural University, Copenhagen, Denmark* Statistical Genetics	1995

HONORS AND AWARDS

NORDIC PhD Fellowship *Denmark, Scandinavian Council of Ministers*	1989-1992
Outstanding international research fellow *Ministry of Foreign Affairs, Jerusalem, Israel*	1997
Senior research fellowship *Science and Technology Agency (STA), Japan*	1997-1999
Outstanding young scientist award *Animal Science Technology Society, Japan*	August, 1998

RECENT PUBLICATIONS

1. **Hicks C**, Tang H, Havlioglu N, Cote J, Wu J. 2002. Systematic approaches to understanding alternative splicing of genes critical for neuronal survival and functions. Caspases and other genes. Neurobiolog. Aging. 23:S521-522.
2. Satoh M, **Hicks C**, Ishii K, Furukawa T. 2002. Choice of statistical model for estimating genetic parameters using restricted maximum likelihood in swine. J. Anim. Breed. Genet. 119:285-296.
3. Gu C, Rao DC, Stormo G, **Hicks C**, Province M. 2002. The role of gene expression microarray analysis in finding complex disease genes. Genet. Epidemiol. 23:37-56.
4. **Hicks C**, Tuinstra M, Pedersen J., Kofoid K, Dowell FE. 2002. Genetic analysis of feed quality and seed size in sorghum inbred lines and hybrids using analytical methods and NIRS. Euphytica. 127:31-40.
5. **Hicks C**, Werrenfeltz, S, Puett DJ, Singer A, Duval JM, Xu Y. 2005. Computational analysis and experimental validation of alternative splicing in matrix metalloproteinases (MMPs) and (TIMPs) in ovarian cancer. Proc. AARC. Oncogenomics. Dissecting Cancer through Genome Research. Feb. 2 – 6, San Diego.
6. Wang P, Yan B, Guo J, **Hicks C**, Xu Y. 2005. Structural genomics analysis of alternative splicing and its application in modeling structures of alternatively spliced variants. (In press).
7. **Hicks C**, Olman V, Dong S, Wang P, Xu, Y. 2005. Meta-analysis of the effects of co-expressed genes in multiple types of cancer. (In review, NAR).
8. **Hicks C**, Olman V, Wang P, Xu Y. 2005. Gene expression data analysis in subtypes of ovarian cancer using maximum covariance analysis. (In Review, Genome Biology).

RECENT EXPERIENCE

Research Associate *Biostatistics and Bioinformatics* *UCD Medical Center, Sacramento*	2002-2003
Senior Research Associate *Cancer Biostatistics and Bioinformatics* *University of Georgia*	2003-2005
Assistant Professor *Department of Epidemiology and Preventive Medicine* *Loyola University Stritch School of Medicine*	2005-