

Insuk Lee

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RESEARCH INTERESTS

- **Biological Data Mining:** biological feature selection and extraction, heterogeneous genomics data integration, evaluation of genome-scale data, pattern recognition or model selection from large-scale biological data, prediction of gene function, prediction of protein-protein interaction or gene functional association
- **Systems Biology:** network modeling of cellular system, topological analysis of biological network, prediction of system behavior

EDUCATION

- **University of Texas at Austin, TX** 09/1996 – 12/2002
Ph.D. in Molecular genetics & Microbiology
Advisor: Prof. Rasika M. Harshey
Dissertation: Importance of the Conserved TG/CA Dinucleotide Termini in Phage Mu Transposition: Similarities to Transposable Elements in the Human Genome
- **Texas State University at San Marcos, TX** 06/2000 – 12/2002
Finished 37 credit hours (31 of undergraduate, 6 graduate) in Computer Science
- **Western Illinois University, Macomb, IL** 09/1993 – 05/1996
M.S. in Biology
Advisor: Prof. Thomas Alton
Thesis: Genetic analysis of *Agrobacterium vir* region by generating gene fusion using bacterial transposon
- **Hanyang University, Seoul, Korea** 03/1986 – 02/1993 (military service: 02/1988 – 05/1990)
B.S. in Biology

AFFILIATIONS AND HONORS

- International Society for Computational Biology (ISCB)
- ISMB 2005 Travel Fellowship Award
- The L. Joe Berry Memorial Scholarship, University of Texas at Austin, 2001
- David Bruton, Jr. Fellowship, University of Texas at Austin, 2000
- Korean Honor Scholarship from Korean Consulate, 1999
- The Hal H. Ramsey, III Memorial Scholarship, University of Texas at Austin, 1999

- Academic Achievement Scholarship, Hanyang University, 1986, 1991, 1992

PROFESSIONAL SERVICE AND EXPERIENCE

- Journal Reviewing: *Ad hoc* reviewer for the **Genome Research**
- Long-term participant, IPAM Special Semester on “Proteomics: Sequence, Structure, Function”, UCLA, Spring 2004

RESEARCH EXPERIENCE AND ACCOMPLISHMENTS

Center for Systems and Synthetic Biology, University of Texas at Austin 01/2003 – Present
Post-doctoral fellow

- Developed new algorithm for integration of heterogeneous functional genomics data.
- Developed new algorithm to discover gene linkages from network context.
- Developed new algorithm to discover gene linkages from cDNA microarray data.
- Reconstructed probabilistic functional gene network for yeast (currently the most extensive and accurate gene network covering more than 80% of yeast proteome with high confidence), *M. tuberculosis*, and *C. elegans*.
- Improved algorithms discovering gene linkages from phylogenetic profile, high-throughput protein-protein interaction assays (yeast 2 hybrid and mass spectrometry analysis of cellular complex).
- Proposed topological models for large scale functional gene networks.

Department of Microbiology, University of Texas at Austin 09/1996 – 12/2002
Graduate research assistant

- Developed sensitive, plasmid-based assay system to monitor Mu transposition in vivo.
- Discovered general hierarchy of reactivity in highly conserved terminal dinucleotides of Mu.
- Discovered that the role of conserved terminal dinucleotide of Mu in assembly of a stable transpososome.
- Discovered the same pattern of terminal dinucleotides in human transposable elements using computational sequence analysis, and proposed a universal role of conserved terminal sequences of transposable elements in transpososome assembly.
- Discovered a new rule for suppression of terminal defects by MuB protein, as well as a role for metal ions in DNA opening at the termini.

Department of Biology, Western Illinois University, Macomb, IL 09/1993 – 05/1996
Graduate student

- Transposon mutagenesis and Expression analysis in the virulent gene *virD* region of *Agrobacterium Tumefaciens*.

Department of Chemistry, Western Illinois University, Macomb, IL 01/1994 – 08/1995
Research assistant

- Analysis of the inhibitory specificity and function of *Cucurbita maxima* trypsin inhibitor (CMTI)-V by site-directed mutagenesis.
- Cloning/expression/purification of CMTI-III and blood coagulation factor XIIa.

TEACHING EXPERIENCE

Department of Microbiology, University of Texas at Austin
Graduate teaching assistant

1997, 2000

- Instructor in undergraduate Microbiology Laboratory Course (MIC129K: Spring 1997, Spring 2000) and Public Health Bacteriology Laboratory (MIC361K: Fall 1997).

INVITED BOOK CHAPTER

1. **Insuk Lee**, Rammohan Narayanaswamy, Edward Marcotte. **2006** Bioinformatic prediction of yeast gene function. In **Yeast Gene Analysis** (ed M. Tuite and A. Brown), Elsevier. **In press**.
2. **Insuk Lee** and Edward Marcotte. **2006** Integrating Functional Genomics Data. In **Bioinformatics** (ed Jonathan Keith). Totowa, THE HUMANA. **In preparation**

JOURNAL PUBLICATIONS

1. **Insuk Lee**, Shailesh V. Date, Alex T. Adai, Edward Marcotte. **2004** A Probabilistic functional network of yeast genes. **Science** 306:1555-1558
2. Bork, P., Jensen, L.J., Von Mering, C., Ramani, A.K., **Lee I**, Marcotte, E.M. **2004** Protein interaction networks from yeast to human. **Curr. Opin. Struct. Biol.** 14:292-9
3. **Insuk Lee** and Rasika Harshey. **2003** Patterns of Sequence conservation at termini of LTR retrotransposons and DNA transposons in the human genome: Lessons from phage Mu. **Nucleic Acids Res.** 31:4531-4540
4. **Insuk Lee** and Rasika Harshey. **2003** The conserved CA/TG motif at Mu termini: T specifies stable transpososome assembly. **J. Mol. Biol.** 330:261-275
5. **Insuk Lee** and Rasika Harshey. **2001** Importance of the conserved CA dinucleotide at Mu termini. **J. Mol. Biol.** 314:433-444
6. Xue, Y., Bai, X., **Lee, I.**, Kallstrom, G., Ho, J., Brown, J., Stevens, A., and Johnson, A. W. **2000**. *Saccharomyces cerevisiae* RAI1 (YGL246c) is homologous to human DOM3Z and encodes a protein that binds the nuclear exoribonuclease Rat1p. **Mol. Cell. Biol.** 20:4006-4015.
7. Liu, J., Gong, Y., Prakash, O., Wen, L., **Lee, I.**, Huang J.,-K., and Krishnamoorthi, R. **1998**. NMR studies of internal dynamics of serine proteinase protein inhibitors: Binding region mobilities of intact and reactive-site hydrolyzed CMTI-III of the squash family and comparison with those of counterparts of CMTI-V of the potato I family. **Protein Science.** 7:132-141.
8. Wen, L., **Lee, I.**, Chen, G., Huang, J.,-K., Gong, Y., and Krishnamoorthi, R. **1995**. Changing the inhibitory specificity and function of CMTI-V by site-directed mutagenesis. **Biochem. Biophys. Res. Commun.** 207:897-902.

INVITED TALKS

1. Aug 2005 Monsanto company
2. June 2005 ISMB2005, Session on “Pathways, Networks, and Proteomics”
3. May 2005 Rosetta Inpharmatics Inc.

POSTER PRESENTATIONS

1. **Insuk Lee** and Edward Marcotte. A probabilistic Functional Gene Network of Yeast – Version2. **2005 ISMB**, Detroit, MI
2. **Insuk Lee** and Edward Marcotte. Linkage by context: Discovering functional linkages between proteins from their known interactions. **2004 RECOMB**, San Diego, CA
3. **Insuk Lee** and Rasika Harshey. The conserved CA/TG motif at Mu termini: T specifies stable transpososome assembly. **2002 Oxford workshop on site-specific recombination, genetic transposition and DNA dynamics**, Oxford, UK
4. **Insuk Lee** and Rasika M. Harshey. Isolation of Mu transposase mutants that suppress terminal base-pair defects in Mu DNA. **2000 Keystone symposia**, Santa Fe, New Mexico
5. **Insuk Lee** and Rasika M. Harshey. Identification of target DNA-binding subunits in the Mu transposase tetramer. **1999 FASEB summer research conferences**, Snowmass, Colorado.