

Priyam Singh

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Research and Professional Experience

Post-doctoral Fellow, Jan 2009-Present

The Jackson Laboratory, Bar Harbor, ME. Advisor: Joel Graber, PhD.

Working to determine whether significant abnormalities in the relative abundance of transcript isoforms differing at the 3'-end exist in microarray samples from human patients with Diffuse large B-cell lymphoma, mammary cancer, metastatic melanoma and colon cancer. Collaborating with biologists to generate and analyze microRNA and mRNA next generation "deep-sequencing" in a mouse leukemia model to determine contribution of microRNA activity in alternative isoform abundance.

Graduate Research Assistant, 2004-2009

The Jackson Laboratory, Bar Harbor, ME. Advisor: Joel Graber, PhD.

Collaborated to develop a novel microarray probe-level analysis algorithm and applied it to a mouse leukemia model to discriminate histologically similar subtypes of mouse lymphoma samples based on differences in the 3'-untranslated region; Demonstrated the critical importance of measuring changes in the distribution of alternative isoforms, as well as overall transcript levels and provided a possible link between genotoxic stress and alternative 3'-processing; Performed extensive DNA/RNA sequence analysis to determine that difference in isoforms differing at the 3'-end arise from both systematic selection of 3'-processing sites and differential degradation instigated by microRNA activity; Performed western blot analysis to determine protein levels of alternative 3'-processed genes. Collaborated extensively with molecular biologists at the Jackson Laboratory; Created and developed a database (PACdb) to store 3'-processing sites for 14 organisms; Trained 11 undergraduate students in the Jackson Laboratory summer student program to learn PERL and Bioinformatics skills.

Graduate Research Assistant, 2002-2004

Biomolecular Engineering Research Center (BMERC), Boston, MA

Advisor: Joel Graber and Temple Smith

Developed a software suite to locate 3'-processing sites using large-scale dataset of ESTs (Expressed Sequence Tags); Performed alignment of ESTs to genome and mapped alignment coordinates with gene information to determine 3'-processing sites in *Arabidopsis thaliana*. Developed extensive error checking and testing programs to assign confidence level to 3'-processing sites based on multiple criteria.

Undergraduate Research Assistant, 2001-2002

Batzer Lab, Louisiana State University, Baton Rouge, LA. Advisor: Mark Batzer, PhD.
Designed and maintained laboratory website; designed a database to systematically record ALU mobile elements.

Bioinformatics Programmer/Analyst, 2001

Syngenta Biotech Inc, Research Triangle Park, Raleigh, NC.

Supervisor: Michael Peterson, PhD.

Collaborated with plant biologists and database experts to identify genes required for viability at the seedling stage of development of *Arabidopsis thaliana*; Developed web-based forms using PERL/CGI to enable plant biologists to interact with complex merged tables in an Oracle database to retrieve genes matching multiple experimental criterion; Created web form to retrieve and access information regarding thousands of genes in record time (less than 5 seconds).

Education

May 2009	Ph.D. in Bioinformatics, Boston University. Dissertation: "Characterization of alternative mRNA 3'-processing in mouse progenitor B-cell lymphoma." (Defended Dec. 2008)
May 2004	M.S. in Bioinformatics, Boston University.
May 2002	B.S. in Computer Science, Louisiana State University (LSU).

Computer Skills

Languages:	C/C++, Perl, R, MATLAB, HTML, XHTML/CSS, PHP, ASP, XML, SQL
Microarray Analysis	"Affy"(Affymetrix) Statistical package, Bioconductor, RMA (Robust Multichip Average), R/MANNOVA, GenePattern
Applications and Tools:	MySQL, Gibbs Sampler, Improbizer, UCSC Genome Browser, BLAT, standalone BLAST, Ensembl, Biomart, Gene Ontology(GO), ClustalW, JMP, Primer3, GSEA (Gene Set Enrichment Analysis), Ingenuity Pathway Analysis, DAVID
Operating System	Macintosh OS X, Linux (Suse), Windows

Awards

- Best Poster Presentation, RNA Turnover Meeting, Asheville, NC, Oct 2008
- Dean Arthur Honor Award for Outstanding Academic Achievement. 2000-2001
- Non-Resident Tuition Waiver Award for International Students, 1999-2002
- Dean Honor's List Louisiana State University, 1998-2002
- LSU Honors Program Participant, 1998-2002

Memberships

- RNA Society
- International Society for Computational Biology (ISCB)
- BU Bioinformatics Student Group
- BU Student Association of Graduate Engineers (SAGE)
- LSU Ambassador

Publications

Liu D**, Brockman JM**, Dass B, Hutchins LN, **Singh P**, McCarrey J, MacDonald C, Graber JH. "Systematic variation in mRNA 3'-processing signals during mouse spermatogenesis". Nucleic Acid Research, 2007 Jan 12; 35(1): 234-246.

Evsikov AV, Graber JH, Brockman JM, **Singh P**, Holbrook AE, Hampl A, Oh B, Eppig JJ, Solter D, Knowles BB. "Cracking the egg: developmental dynamics and molecular transitions from the fully grown oocyte to embryo. Genes and Development", 2006 Oct 1; 20(19): 2713-2727.

Brockman JM**, **Singh P****, Liu D, Quinlan S, Salisbury J, Graber JH. "PACdb: PolyA Cleavage Site and 3'-UTR Database". Bioinformatics, 2005 Sep 15; 21(18): 3691-3

Hutchins LN, Murphy SM, **Singh P**, Graber JH. "Position-Dependant motif characterization using nonnegative matrix factorization". Bioinformatics, 2008 Dec 1;24(23):2684-90

Manuscripts in Preparation

Singh P, Mills KD, Graber JH. "Systematic and global changes in processing of mRNA 3'-untranslated regions characterize clinically distinct B-lymphoid subtypes". In review (Cancer Cell).

Brockman JM**, **Singh P****, Graber JH, De Vries W. "Multiple cis-elements affect transcript stability during the oocyte to embryo transition".

Brockman JM, **Singh P**, Graber JH. "PACdb 2: An update of the PolyA Cleavage Site and 3'-UTR Database."

**** contributed equally**

Presentations

"Systematic changes in mRNA 3'-processing discriminate between histologically similar tumors". Oral presentation at RNA Regulatory Mechanisms Implicated in Human Diseases Both Rare and Common, Asheville, NC, Oct 2008.

“Characterization of alternative mRNA processing in progenitor B-cell lymphoma”. Oral presentation at Maine Biomedical and Medical Sciences Symposium (MBMSS), Salisbury Cove, ME, April 2008.

“Discovery and characterization of 3'-UTR regulatory elements during the mouse oocyte to embryo transition”. Poster presentation at RNA Society Conference, University of Wisconsin-Madison, Madison, WI, May 2007.

“Characterization of Post-transcriptional Mis-regulation of mRNAs in Progenitor B-cell Lymphoma”. Oral presentation at Maine Biomedical and Medical Sciences Symposium (MBMSS), Salisbury Cove, ME, April 2007.

“Discovery and Characterization of 3'-UTR Regulatory Elements”. Poster presentation at Maine Biomedical and Medical Sciences Symposium (MBMSS), Salisbury Cove, ME, April 2006.

“PACdb PolyA Cleavage Site and 3'-UTR Database. Poster presentation at Intelligent Systems for Molecular Biology (ISMB), Renaissance Center, Detroit, MI, June 2005.

“PACdb: PolyA Cleavage Site and 3'-UTR Database. Poster presentation at Research in Computational Molecular Biology (ISMB), Massachusetts Institute of Technology, Cambridge, MA, May 2005.

“PACdb: PolyA Cleavage Site and 3'-UTR Database. Poster presentation at Maine Biomedical and Medical Sciences Symposium (MBMSS), Salisbury Cove, ME, April 2005.

References:

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