

Priya Ranjan

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EDUCATION

Ph.D. in Forest Molecular Genetics and Biotechnology (Bioinformatics) Michigan Technological University, Houghton, MI, 2006

M.S. in Biotechnology Indian Institute of Technology (IIT Bombay), Mumbai, India, 2001

B.S. in Chemistry with Honors TM Bhagalpur University, Bhagalpur, India, 1999

CURRENT RESEARCH PROJECTS

1. Application of functional genomics tools for improving productivity of Lignocellulosic biomass for biofuels production as part of Bioenergy science center (**BESC**) funded by Department of Energy (**DOE**) (2007-). **BESC** is one of three nationwide, part of a \$375 million federal investment in basic research on biofuels.
2. Identification of genes and gene networks involved in natural resistance of plant cell walls to microbial and enzymatic deconstruction for biofuels production as part of Bioenergy science center (**BESC**) funded by Department of Energy (**DOE**) (2007 -).
3. Genome / transcriptome sequencing using new sequencing technologies as part of Bioenergy science center (**BESC**) funded by Department of Energy (**DOE**) (2007 -2012).

PROFESSIONAL EXPERIENCE

June 2008 – present: **Post Doctoral Research associate**, Oak Ridge National Lab, TN

Oct2006 - June 2008: **Post Doctoral Research associate**, University of Tennessee, Knoxville

Jan2006 - Oct 2006: **Post doctoral research scientist**, Michigan Technological University

2002 – 2005: **Research Assistant**, Michigan Technological University

Spring 2004: **Teaching Assistant**, Michigan Technological University (Tools in bioinformatics)

1999 – 2001: **Research Assistant**, IIT Bombay, Mumbai, India

Summer 2000: **Research Assistant**, National Institute of Immunolgy, New Delhi, India

PUBLICATIONS

1. Yin, T.-M., M. Davis, L. Gunter, X. Zhang, **P. Ranjan**, R. Sykes, and G.A. Tuskan. 2010. Differential expression of genetic loci underlying above- and below-ground lignin contents in *Populus*. **PLOS Genetics** In review.
2. **Ranjan P**, Yin T, Zhang X, Kalluri U C, Yang X, Jawdy S, Tuskan G A Bioinformatics-based identification of candidate genes from QTLs associated with cell wall traits in *Populus*, **BioEnergy Research** 2009 DOI [10.1007/s12155-009-9060-z](https://doi.org/10.1007/s12155-009-9060-z)
3. Yuan Y, Chung J-D, Fu X, Johnson VE, **Ranjan P**, Booth SL, Harding SA, Tsai C-J: Alternative splicing and gene duplication differentially shaped the regulation of isochorismate synthase in *Populus* and *Arabidopsis*. **Proceedings of the National Academy of Sciences USA** 2009, 106:22020-22025.
4. Yuan J, Halfhill M, Abercrombie L, Rao M, Zhou X, .. **Ranjan P** et al. (2009) Functional genomics analysis of *Conyza canadensis* (horseweed) with special reference to the evolution of non-target site glyphosate resistance. *Weed Science: In Press*
5. Udaya Kalluri, Gregory Hurst, Patricia Lankford, **Priya Ranjan**, Dale Pelletier. **Shotgun proteome profile** of *Populus* developing xylem. **Proteomics**. 2009 (21):4871-80.
6. Rao, M.R.,M.D. Halfhill, L.G Abercrombie, **P. Ranjan**, J.M. Abercrombie, J.S. Gouffon, A.M. Saxton, and C.N. Stewart,Jr. 2009. Phytoremediation and phytosensing of chemical contaminants, RDX and TNT:identification of the required target genes. **Functional and Integrative Genomics** DOI [10.1007/s10142-009-0125-z](https://doi.org/10.1007/s10142-009-0125-z).
7. Xiaohan Yang , Udaya C. Kalluri , Sara Jawdy , Lee E. Gunter , Tongming Yin , Timothy J. Tschaplinski , David J. Weston , **Priya Ranjan** , and Gerald A. Tuskan. F-box Gene Family is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. **Plant Physiol**. First published on September 5, 2008; [10.1104/pp.108.121921](https://doi.org/10.1104/pp.108.121921)
8. Jason M Abercrombie, Matthew D Halfhill, **Priya Ranjan**, Murali R Rao, Arnold M Saxton, Joshua S Yuan and C Neal Stewart Jr: Transcriptional responses of *Arabidopsis thaliana* plants to As (V) stress. **BMC Plant Biology** 2008, 8:87
9. **Ranjan P**, Kao Y, Jiang H, C.P. Joshi, S.A. Harding and C.J. Tsai: Suppression Subtractive hybridization-mediated **transcriptome analysis** from multiple tissues of aspen (*Populus tremuloides*) trees altered in phenylpropanoid metabolism. **Planta**, 219: 694-704, 2004.
10. C.P. Joshi, S. Bhandari, **P. Ranjan**, U. C. Kalluri, X. Liang, T. Fujino, and A. Samuga: Genomics of cellulose biosynthesis in poplars. **New Phytologist** 164: 53-61, 2004.

BOOK CHAPTER

11. Tsai C-J, **Ranjan P**, DiFazio SP, Tuskan GA and Johnson V (2009) Poplar Genome Microarrays. In: Joshi CP and DiFazio SP (eds), Genetics, Genomics and Breeding of Crop Plants: Poplar. Science Publishers, Enfield, New Hampshire (*in press*).

RESEARCH SUMMARY / COMPLETED PROJECTS

1. Design of Illumina SNP array for Populus association study to identify genetic variations associated with cell wall traits. (In collaboration with JGI)
2. SNP analysis using **454 dataset** in *Populus* at Bioenergy Science center.
3. Developed an algorithm for automated identification and intensity determination of metabolites in GC/MS dataset from *Populus* and switchgrass samples.
4. Integration of poplar genetic maps, QTL information with Poplar genome browser using CMAP/GMOD at University of Tennessee (**NSF** funded project).
5. Development of tools and database for accessing and analysing QTL data (**NSF** funded project).
6. Development of a database with web interface for cross-referencing multiple microarray platforms in *Populus*. (**NSF** funded project)
7. Analysis of **expressed sequence tags** in aspen tissues and characterization of copia elements in Arabidopsis genome: A bioinformatics approach at Michigan Technological University. Funded by Michigan Life sciences corridor (**MLSC**)
8. Binding site analysis of enzymes in cephalosporin biosynthetic pathway. (Funded by department of Biotechnology, Govt. of India)
9. Production, characterization and purification of α -1,2 Mannosyl transferase from recombinant *E.coli*. (Funded by department of Biotechnology, Govt. of India)

SEMINARS / TEACHING

1. Plant based Edible vaccines, Michigan Technological University, 2003
2. Bioinformatics and Drug design, Michigan Technological University, 2004
3. Conducted one week training for high school students in bioinformatics in Michigan Technological University as part of summer youth program, 2006.

4. Identification of candidate genes underlying Lignin QTLs in poplar genome. 2nd
Bioenergy Science center (BESC) retreat, Chattanooga, TN, Dec 2008

POSTERS / CONFERENCES

1. Comparison of metabolic changes in control and transgenic aspen by functional evaluation of expressed sequence tag(EST), Great Lakes Bioinformatics retreat, Hartland, Michigan , 2002
2. Diversity, distribution and features of LTR retrotransposons in selected plant genomes, Annual ESC/BRC graduate research forum, 2005
3. A Database For Cross-Reference Of Multiple Microarray Platforms In Populus, PAG XV, San Diego, 2007
4. 1st Bioenergy Science center (BESC) retreat, Townsend, Maryville, TN, Feb 2008

OTHER PROFESSIONAL ACTIVITIES

Ad hoc reviewer for following journals

1. **International Journal of Plant genomics,**
2. **Bioinformatics,**
3. **plant journal,**
4. **Tree genetics and genomes**

SKILLS

❖ Bioinformatics

1. Metabolic profiling Analysis

AMDIS, XCMS package of R

2. Sequence analysis

Blast package from NCBI (blastall, formatdb, fastacmd, blastclust, blastpgp), mpiblast for parallel processors, WU-blast2 package, RECON for identification of sequence repeats in a genome, EMBOSS, GCG Wisconsin package, cap3, staden package, phred, phrap, TIGR assembler.

3. Next generation sequencing technology, 454 illumina data analysis

Pyrobayes, MOSAIK, Gigabayes, MIRA2, Velvet etc.

4. Phylogenetic analysis

Mega4, clustalw, PHYLIP, PAUP, TreeView,

5. Microarray data analysis

Genespring, Base-BioAarray Software environment, Bioconductor package of R

6. Other miscellaneous packages

Bioperl, NCBI C++ toolkit, Rasmol, web lab viewer, various databases

❖ STATISTICS

1. SAS programming for univariate and multivariate statistics
2. R-package

❖ IT

1. Programming languages

C, C++, java, Visual Basic

2. Scripting and Mark-up languages

Perl, PHP, XML, HTML, Javascript

3. Database Technology

mysql, MS Access, Base-BioAarray Software environment

Operating systems

Linux, MS-DOS, Win NT/9x/2000/XP/Vista, Macintosh, Sun workstation,

Experience as system administrator

4. Multimedia packages

Adobe Photoshop 7, Macromedia Flash, Gif animator, GD Perl module for graphics,
R graphics.