Priya Ranjan

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EDUCATION

Ph.D. in Forest Molecular Genetics and Biotechnology (Bioinformatics) Michigan Technological University, Houghton, MI, 2005

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. Systems biology knowledgebase (KBASE) funded by Department of Energy (**DOE**) (2011-)
2. Genome / transcriptome sequencing using new sequencing technologies
3. Identification of conserved cis-elements in co-expressed genes and its use in creating designer promoter
4. 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 (2007-). **BESC** is one of three nationwide, part of a $375 million federal investment in basic research on biofuels.
5. 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 -).

PROFESSIONAL EXPERIENCE

July 2010 – Present: **Research scientist**, University of Tennessee, Knoxville

June 2008 – July 2010: **Post Doctoral Research associate**, Oak Ridge National Lab, TN (Administered by **Oak Ridge Associated Universities** for **ORNL**)

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. Tuskan GA, Chen JG, DiFazio S, Patricia Faivre-Rampant, Gaudet M, Harfouche A, Jorge V, Labbe JL, **Ranjan P**, Sabatti M, Street N, Tschaplinski TJ, Yin TM. The obscure events contributing to the evolution of an incipient sex chromosome in Populus – A retrospective working hypothesis (***Submitted***).

2. Slavov GT, DiFazio SP, Martin J, Schackwitz W, Muchero W, Rodgers-Melnick E, Lipphardt M, Pennacchio C, Hellsten U, Pennacchio L, Gunter LE, **Ranjan P**, Strauss SH, Rokhsar D, Tuskan GA. Strong Geographic Structure and Linkage Disequilibrium in Black Cottonwood. (***Submitted***)

3. Abraham P, Adams R, Giannone JR, Kalluri UC, **Ranjan P**, Erickson B, Shah M, Tuskan GA, Hettich RL. 2011. Defining the boundaries and characterizing the landscape of functional genome Expression in vascular tissues of *Populus* using Shotgun Proteomics. **DOI: 10.1021/pr200851y.**

4. Yin TM, Davis M, Gunter L, Zhang X, **Ranjan P**, Sykes R, and Tuskan GA. 2010. Differential expression of genetic loci underlying above- and below-ground lignin contents in Populus. **PLoS ONE** 5(11): e14021. doi:10.1371/journal.pone.0014021.

5. **Ranjan P**, Yin T, Zhang X, Kalluri U C, Yang X, Jawdy S, Tuskan GA 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*

6. 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.

7. 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**

8. Kalluri UC, Hurst G, Lankford P, **Ranjan P**, Pelletier D. Shotgun proteome profile of Populus developing xylem. **Proteomics**. 2009 (21): 4871-80.

9. Rao MR, Halfhill MD, Abercrombie LG, **Ranjan P**, Abercrombie JM, Gouffon JS, Saxton AM, and Stewart CN. 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.

10. Yang X, Kalluri UC, Jawdy S, Gunter LE, Yin TM, Tschaplinski TJ, Weston DJ, **Ranjan P**, and Tuskan GA. 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

11. Abercrombie JM, Halfhill MD, **Ranjan P**, Rao MR, Saxton AM, Yuan JS and Stewart NC. Transcriptional responses of Arabidopsis thaliana plants to As (V) stress. **BMC Plant Biology** 2008, 8:87

12. **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.

13. Joshi CP, Bhandari S, **Ranjan P**, Kalluri UC, Liang X, Fujino T, and Samuga A: Genomics of cellulose biosynthesis in poplars. **New Phytologist** 164: 53-61, 2004.

CONFERENCE PUBLICATIONS

14. DiFazio S, Slavov G, Rodgers-Melnick E, Martin J, Schackwitz W, Ranjan P and Gerald Tuskan: Inferring the evolutionary history of Populus trichocarpa from whole genome resequencing data. BMC Proceedings 2011, 5(Suppl 7):O1

15. Tuskan GA, Slavov G, DiFazio S, Muchero W, **Ranjan P**, Schackwitz W, Martin J, Rokhsar D, Sykes R, Davis M, Studer M and Wyman C: Populus resequencing: towards genome-wide association studies. BMC Proceedings 2011 5(Suppl 7):I21.

BOOK CHAPTERS

16. Tsai C-J, **Ranjan P**, DiFazio SP, Tuskan GA and Johnson V (2011) Poplar Genome Microarrays. In: Joshi CP and DiFazio SP (eds), Genetics, Genomics and Breeding of Crop Plants: Poplar Genome Microarrays, Taylor and Francis.

17. Stewart, C. N., Jr., Y. Peng, L. G. Abercrombie, M. D. Halfhill, M. R. Rao, **P. Ranjan**, J. Hu, R. D. Sammons, G. R. Heck, P. J. Tranel, J. S. Yuan 2010. Genomics of glyphosate resistance. Pp in V. Nandula (ed). Glyphosate Resistance in Weeds. **Wiley-Blackwell.**

RESEARCH SUMMARY / COMPLETED PROJECTS

1. Setting up a pipeline for the automated analysis of next generation sequencing data.
2. Identification of conserved cis-elements in co-expressed genes and its use in creating designer promoter.
3. Design of Illumina SNP array for Populus association study to identify genetic variations associated with cell wall traits. (In collaboration with JGI)
4. Design of Illumina SNP array for improving assembly in Physcomitrella Patens.
5. Narrowing down of candidate genes in QTL intervals related to liginin content.
6. EST analysis: Eucalyptus sequence: Help in gene annotation of Eucalyptus genome.
7. SNP analysis using **454 dataset** in *Populus* at Bioenergy Science center.
8. Developed an algorithm for automated identification and intensity determination of metabolites in GC/MS dataset from *Populus* and switchgrass samples.
9. Integration of poplar genetic maps, QTL information with Poplar genome browser using CMAP/GMOD at University of Tennessee (**NSF** funded project).

10. Development of tools and database for accessing and analysing QTL data (**NSF** funded project).

11. Development of a database with web interface for cross-referencing multiple microarray platforms in *Populus.*(**NSF** funded project)

12. 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**)

13. Binding site analysis of enzymes in cephalosporin biosynthetic pathway. (Funded by department of Biotechnology, Govt. of India)

14. 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

5. Next generation sequencing: Data and analysis. Guest Lecture, University of Tennessee, 2009

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

1) **Panelist for the 2011 NSF** graduate research fellowship program, with service on the panel Genetics and Evolutionary Biology

2) **Associate editor**, BMC research notes

3) **Associate editor**, The Journal of Plant Genomics.

4) **Ad hoc reviewer** for following journals: a) **International Journal of Plant genomics**, b) **Bioinformatics**, c) **plant journal**, d) **Tree genetics and genomes, e) plant genome**

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.