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EDUCATION AND TRAINING:

- **Ph.D.** in Forest Molecular Genetics and Biotechnology (Bioinformatics) Michigan Technological University, Houghton, MI, 2005
- **MS** in Biotechnology Indian Institute of Technology (IIT Bombay), Mumbai, India, 2001
- **BS** in Chemistry with Honors TM Bhagalpur University, Bhagalpur, India, 1999

RESEARCH AND PROFESSIONAL EXPERIENCE:

- Senior Staff Scientist, Biosciences, Oak Ridge National Laboratory 2021-present
- Research Assistant Professor, University of Tennessee, Knoxville 2015-2021
- Research Scientist, University of Tennessee, Knoxville 2010-2015
- Postdoctoral Fellow, Oak Ridge National Laboratory 2008-2010
- Postdoctoral researcher, University of Tennessee, Knoxville 2006-2008
- Graduate Teaching/Research Assistant, Michigan Tech University 2002-2006

AWARDS

- Recognition as outstanding University of Tennessee inventor (December 2018); Innovation awards ceremony, University of Tennessee, Knoxville (for patent related to key genes regulating cell wall recalcitrance).
- Best paper award silver prize in original article category for "The *Physcomitrella patens* chromosome-scale assembly reveals moss genome structure and evolution" Published in THE PLANT JOURNAL Volume 93, Issue 3, Pages 515–533, February 2018.
- ACM SIGSOFT Distinguished Paper Award for "The Impact of Configurability in Bioinformatics Software" Published in Proceedings of the 33rd ACM/IEEE International Conference on Automated Software Engineering (ASE). Pages 757-767, September 2018.

SOFTWARE DEVELOPMENT:

Contributions to open-source software development as part of DOE KBase infrastructure

- **https://github.com/pranjan77**
- **https://github.com/kbasecollaborations**
- **https://github.com/kbaseapps**
- **https://kbase.us**

PUBLICATIONS:

- Labbé J., Muchero W., Czarnecki O., Wang J., Wang X., Bryan A.. Ranjan P.. et al. Mediation of plant–mycorrhizal interaction by a lectin receptor-like kinase. *Nature Plants*. 2019;5(7):676-680.
- Arkin, A. P., Cottingham, R. W., Henry, C. S., Harris, N. L., Stevens, R. L., Maslov, S., …Ranjan, P., et al. (2018). KBase: the United States department of energy systems biology knowledgebase. *Nature Biotechnology*, *36*(7).
- Bryan, A. C., Zhang, J., Guo, J., Ranjan, P., Singan, V., Barry, K., … others. (2018). A variable polyglutamine repeat affects subcellular localization and regulatory activity of a Populus ANGUSTIFOLIA protein. *G3: Genes, Genomes, Genetics*, *8*(8), 2631–2641.

- Zhang, J., Yang, Y., Zheng, K., Xie, M., Feng, K., Jawdy, S. S., …Ranjan, P., .. others. (2018). Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of HCT 2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in Populus. *New Phytologist*, *220*(2), 502–516.
- Yin, H., Guo, H.-B., Weston, D. J., Borland, A. M., Ranjan, P., Abraham, P. E., … others. (2018). Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. *BMC Genomics*, *19*(1), 588.
- Cashman, M., Cohen, M. B., Ranjan, P., & Cottingham, R. W. (2018). Navigating the maze: the impact of configurability in bioinformatics software. In *Proceedings of the 33rd ACM/IEEE International Conference on Automated Software Engineering* (pp. 757–767).
- Muchero, W., Sondreli, K. L., Chen, J.-G., Urbanowicz, B. R., Zhang, J., Singan, V., Ranjan, P… others. (2018). Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant--pathogen interactions in a tree. *Proceedings of the National Academy of Sciences*, *115*(45), 11573–11578.
- Weighill, D., Jones, P., Shah, M., Ranjan, P., Muchero, W., Schmutz, J., … Jacobson, D. (2018). Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. *Frontiers in Energy Research*, *6*, 267997. https://doi.org/10.3389/fenrg.2018.00030
- Lang, D., Ullrich, K. K., Murat, F., Fuchs, .. Ranjan, P., ..Schmutz, J. and Rensing, S. A. (2018), The *Physcomitrella patens* chromosome-scale assembly reveals moss genome structure and evolution. Plant J, 93: 515–533. doi:10.1111/tpj.13801
- Weston, D. J., Turetsky, M. R., Johnson, .. Ranjan, P., Jacobson, D., Lilleskov, E. A., Clymo, R. S. and Shaw, A. J. (2018), The Sphagnome Project: enabling ecological and evolutionary insights through a genus-level sequencing project. New Phytol, 217: 16–25. doi:10.1111/nph.14860
- Plett, J.M., Yin, H., Mewalal, R., Hu, R., Li, T., Ranjan, P., Jawdy, S., De Paoli, H.C., Butler, G., Burch-Smith, T.M. and Guo, H.B., 2017. *Populus trichocarpa* encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. *Scientific reports*, *7*(1), p.382.
- Abraham, P. E., Wang, X., Ranjan, P., Nookaew, I., Zhang, B., Tuskan, G. A. & Hettich, R. L. Integrating mRNA and Protein Sequencing Enables the Detection and Quantitative Profiling of Natural Protein Sequence Variants of *Populus trichocarpa*. *J. Proteome Research* 14, 5318–5326 (2015).
- Rambani, A., Rice, J. H., Liu, J., Lane, T., Ranjan, P., Mazarei, M., Pantalone, V., Stewart, C. N., Staton, M. & Hewezi, T. The methylome of soybean roots during the compatible interaction with the soybean cyst nematode. *Plant Physiology* 168, 1364–1377 (2015).
- Yang, X., Cushman, J. C., Borland, A. M., Edwards, E. J., Wullschleger, S. D., Tuskan, G. A., Owen, N. A., Griffiths, H., Smith, J. A. C., De Paoli, H. C. & others. A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. *New Phytologist* 207, 491–504 (2015).
- Muchero, W., Guo, J., DiFazio, S. P., Chen, J.-G., Ranjan, P., Slavov, G. T., Gunter, L. E., Jawdy, S., Bryan, A. C., Sykes, R., Ziebell, A., Klapste, J., Porth, I., Skyba, O., Unda, F., El-Kassaby, Y. A., Douglas, C. J., Mansfield, S. D., Martin, J., Schackwitz, W., Evans, L. M., Czarnecki, O. & Tuskan, G. A. High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. *BMC Genomics* 16, 24 (2015).
- Evans, L. M., Slavov, G. T., Rodgers-Melnick, E., Martin, J., Ranjan, P., Muchero, W., Brunner, A. M., Schackwitz, W., Gunter, L., Chen, J.-G. & others. Population genomics of *Populus trichocarpa* identifies signatures of selection and adaptive trait associations. *Nature Genetics* 46, 1089–1096 (2014).
- Myburg, A. A., Grattapaglia, D., Tuskan, G. A., Hellsten, U., Hayes, R. D., Grimwood, J., Jenkins, J., Lindquist, E., Tice, H., Bauer, D. & others. The genome of *Eucalyptus grandis*. *Nature* 510, 356–362 (2014).
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- Geraldes, A., Difazio, S. P., Slavov, G. T., Ranjan, P., Muchero, W., Hannemann, J., Gunter, L. E.,

Wymore, A. M., Grassa, C. J., Farzaneh, N. & others. A 34K SNP genotyping array for Populus trichocarpa: design, application to the study of natural populations and transferability to other *Populus* species. *Molecular Ecology Resources* 13, 306–323 (2013).

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- Abraham, P., Adams, R., Giannone, R. J., Kalluri, U., Ranjan, P., Erickson, B., Shah, M., Tuskan, G. A. & Hettich, R. L. Defining the boundaries and characterizing the landscape of functional genome expression in vascular tissues of Populus using shotgun proteomics. *Journal of Proteome Research* 11, 449–460 (2012).
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- Joshi, C. P., Bhandari, S., Ranjan, P., Kalluri, U. C., Liang, X., Fujino, T. & Samuga, A. Genomics of cellulose biosynthesis in poplars. *New Phytologist* 164, 53–61 (2004).
- Ranjan, P., Kao, Y.-Y., Jiang, H., Joshi, C. P., Harding, S. A. & Tsai, C.-J. Suppression subtractive hybridization-mediated transcriptome analysis from multiple tissues of aspen (*Populus tremuloides*) altered in phenylpropanoid metabolism. *Planta* 219, 694–704 (2004).

SYNERGISTIC ACTIVITIES:

- Outreach activities at various conferences as senior Bioinformatics Scientist in KBase (2014-2020)

- Panelist, National Science Foundation (NSF), Graduate Research Fellowship Program (GRFP), Genetics and Evolutionary Biology Panel, 2011 and 2014
- Reviewer of several peer-reviewed journals including 1) *Bioinformatics*, 2) *Plant Journal*, 3) *Tree Genetics and Genomes*, 4) *Plant Genome*, 5) *International Journal of Plant Genomics*