Renesh Bedre

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SUMMARY OF QUALIFICATIONS

- 7-years' experience in transcriptomics, genomics, statistical, and bioinformatics data analysis
- Extensive experience with large-scale NGS data analysis, including sequence filtering, genome mapping, assembly, gene expression analysis, co-expression networks, alternative splicing, genotyping, population genomics, phylogenetics, molecular marker discovery (SNP and SSR), plant physiology, PCR, enrichment, functional annotation, and visualization
- Designed experiments and collected data for genetic analysis
- Designed and implemented automated software pipelines for RNA-seq and RAD-seq data analysis
- Developed and implemented parallel computing algorithms for large-scale NGS data analysis
- Web server and databases development (Django) for transcriptomics data analysis
- Applied High Performance Computers (HPC) and parallel computing for NGS data
- Communicated scientific results to variety of audiences and published manuscripts in peer-reviewed journals
- Contributed to project proposal writings
- Conducted bioinformatics workshops, guest lectures, and training to students and co-workers
- Worked closely with collaborators to achieve project goals

EDUCATION

Louisiana State University, Baton Rouge, Louisiana , 2011-2016
Ph.D. in Agronomy, 2016, Concentration in Bioinformatics, genomics, transcriptomics, statistics, and plant biology
Dissertation title**:** Genome-wide transcriptome analysis of cotton (*Gossypium hirsutum* L.) to identify genes in response to *Aspergillus flavus* infection, and development of RNA-Seq data analysis pipeline

Indian Institute of Information Technology, 2009-2011, Allahabad, Uttar Pradesh, India
M.S in Bioinformatics, 2011
Dissertation title**:** A new information-based numerical presentation for detection of gene using digital signal processing (DSP) Approach

Dr. Babasaheb Ambedkar Marathwada University, 2005-2009, Aurangabad, Maharashtra, India
    B.S in Pharmacy

RESEARCH EXPERIENCE

Postdoctoral Research Associate, Texas A&M AgriLife Research, Weslaco, TX, Oct 2016-Present

- Identification of conserved gene regulatory network modulated by *Bactericera cockerelli* (tomato-potato psyllid) and bacterium *Candidatus* Liberibacter solanacearum (CLso) in potato and tomato
- Global characterization of alternative splicing in sugarcane modulated by smut pathogen, *Sporisorium scitamineum*
- Comparative gene expression profiling between resistant and susceptible tomato genotypes against tomato-potato psyllid (*Bactericera cockerelli*)
- Genotyping and SNP marker discovery using RAD-seq in spinach
- Comparative gene expression profiling and phenotypic analysis between two potato genotypes in response to drought stress
- Physiological data analysis in drought responsive potato plants
- Developed algorithms, software (web tool), and database for gene family enrichment analysis
- Utilized High performance computers (HPC), biostatistics, and parallel computing for large-scale NGS data analysis
- Contributed to project proposal writing for JGI Community Science Program (CSP), 2018 (got funded)
- Bioinformatics training to students and co-workers

Project keywords: Transcriptomics, genomics, gene expression, NGS, RNA-seq, RAD-seq, gene co-expression networks, genotyping, population genomics, phylogenetics, SNP markers, PCR, enrichment analysis, biostatistics, algorithms, software, and databases

Graduate Research Assistant, Louisiana State University Agricultural Center, Baton Rouge, LA, Aug 2011-Aug 2016

- Identification of genes regulatory changes in cotton pericarp and seed tissue associated with to toxigenic and atoxigenic strain of *A. flavus*
- Performed comparative transcriptomics analysis of two contrasting rice genotypes to study drought tolerance and development of SNP markers
- Identified spliced variants (alternative spliced transcripts) from rice RNA-seq data for drought stress regulated genes
- Designed and implemented automated pipeline for RNA-Seq data analysis using parallel computing for sequence quality filtering, assembly, mapping, variant calling (SNPs/INDEL), functional annotation and gene expression analysis (in Python and Bash)
- Performed genome-wide transcriptome analysis of leaf and root tissue of halophyte *Spartina alterniflora* to identify genes involved in salt tolerance and SSR marker development (Roche/454 GS FLX+ System)

- Co-expression gene network analysis to study gene interaction under biotic and abiotic stresses in plants
- miRNA discovery, structure and target prediction in Rice and *Spartina alterniflora*
- Utilized High performance computers (HPC), biostatistics, and parallel computing for large-scale NGS data analysis

Graduate Teaching Assistant, Indian Institute of Information Technology, Allahabad, UP, India, 2009-2011
- Performed Meta-analysis of clinical trials using R and RevMan
- Discovered new mapping method for detection of coding regions in genes using Digital Signal Processing (DSP) Approach
- Worked on protein docking, molecular modeling, and QSAR studies
- Studied and implemented machine learning algorithms

RELEVANT SKILLS

- **Operating Systems**:
  Linux/UNIX (Red Hat, Ubuntu, Mandriva, Fedora), Windows (7, 8, 10), Macintosh OS

- **Programming Experience**:
  Proficient - Python, Perl, R, Bioconductor, Biopython, Django, PostgreSQL, BioPerl, Bash, HPC, PBS, MySQL, HTML, CSS, git, svn
  Working Knowledge - C, C++, Java, SAS, MATLAB, PHP, MongoDB, Hadoop

- **Bioinformatics tools**:
  HISAT, StringTie, Ballgown, Bowtie, TopHat, Cufflinks, Cuffmerge, Cuffcompare, Cuffdiff, Stacks Pipeline, DESeq2, DEGseq, featureCounts, HTSeq, AStalavista, BWA, STAR, Trinity, ABySS, CAP3, Velvet, SOAPdenovo, WGCNA, BLAST, Blast2GO, GATK, SAMtools, MISA, Primer3, ClustalW, MEGA, PHYLIP, ClueGO, BiNGO, topGO, topKEGG, CLC workbench, Augustus, Fgenesh++, NCBI SRA toolkit, RiceNet, Infernal, InterPro, HMMER, RNAfold, Mfold, psRNATarget, AutoDock, Molegro, Hex

- **Biological databases:**
  NCBI, UniProt, Phytozome, TAIR, CDD, SMART, PlantGDB, NCBI SRA, ENA, Pfam, Rfam, Rice Genome Annotation Project, PlnTFDB, Gramene, miRBase, PMRD, PLACE, PlantCARE, Cotton Genome Project, Sugarcane genome

- **Visualization:**
  Matplotlib, IGV, Circos, Cytoscape, Genesis, R, MATLAB

- **Applications:**
  MS Office, LibreOffice, EndNote, GIMP, Mendeley Desktop, Rstudio, Review Manager (RevMan)

- **Personal Skills:**

Excellent written and verbal communication skills
Proficient in English, Hindi and Marathi languages
Eager and fast learner
Ability to perform work individually or in team, multiple work simultaneously

FELLOWSHIPS AND AWARDS

- **Publons Peer Review Awards 2018** for placing in the top 1% of reviewers
- **Gerald O. Mott Meritorious Student Award** from Crop Science Society of America, 2015
- **Travel Grant Award** from LSU Graduate School to attend XXII, Plant and Animal Genome Conference, 2014
- **GATE scholarship** from Ministry of Human Resources and Development, Govt. of India. 2009-2011
- All India Rank 28th in National Level Pharmacy Talent Search Examination, 2007

PROFESSIONAL MEMBERSHIPS AND SERVICES

- Member, **Crop Science Society of America**
- Member, **American Phytopathological Society (APS)**
- Member, U.S. Department of Energy **Joint Genome Institute** (DOE JGI)
- Member, **Bioinformatics Organization**
- Committee Member, **Graduate Student Association** (GSA) of department of School of Plant, Environmental and Soil Sciences at Louisiana State University, 2015-2016
- Committee Member, **Indian Student Association (ISA)** at Louisiana State University, 2014-2015
- Member, **Biostar** Bioinformatics community
- Member, **Bioclues** (BIOinformatics CLUb for Experimenting Scientists)
- Invited speaker at **Young Scientists - Rio Grande Valley** meeting, Apr 19, 2018
- Conducted **Advanced Bioinformatics Workshop**, Nov 20 to Nov 23, 2017 at ESPOL, Guayaquil, Ecuador
  Web: https://reneshbedre.github.io/blog/ecuador_workshop.html
  Media: https://www.youtube.com/watch?v=gGxJtNQcTBo&feature=youtu.be
- Delivered an online class on "Introduction to Bioinformatics" on Nov 2016 at **ESPOL, Ecuador**
- Conducted an online practical training on "Bioinformatics data analysis" on Dec 2016 at **ESPOL, Ecuador**
- **APS Foundation Student Travel Award** reviewer (3 reviews), 2018
- **Manuscript Reviewer (19 reviews)**, Scientific Reports-Nature, PLOS ONE, Molecular Genetics and Genomics, Neural Computing and Applications, Interdisciplinary Sciences: Computational Life Sciences, CBAB-Crop Breeding and Applied Biotechnology
  Publons https://publons.com/author/1282617/renesh-bedre#profile
- **Volunteer**, Third Science Conclave: An Interaction with Nobel Laureates held at IIIT Allahabad, India, 2010

PUBLICATIONS AND CONFERENCES

Google Scholar: https://scholar.google.com/citations?user=6pv2AiMAAAAJ&hl=en
Citations: 86 (Independent: 63)

Published:

- Sengupta S, Mangu V, Sanchez L, **Bedre R**, Joshi R, Rajasekaran K, Baisakh N. An Actin Depolymerizing Factor from the Halophyte Smooth Cordgrass, *Spartina alterniflora* (*SaADF2*) is Superior to its Rice homolog (*OsADF2*) in Conferring Drought and Salt Tolerance when Constitutively Overexpressed in Rice. Plant biotechnology journal. 2018 May 31. (**IF:6.305**)

- Mehanathan M, **Bedre R**, Mangu V, Rajasekaran K, Bhatnagar D, Baisakh N. Identification of candidate resistance genes of cotton against *Aspergillus flavus* infection using a comparative transcriptomics approach. Physiology and Molecular Biology of Plants. 2018 Mar 22:1-7. (**IF:1.151**)

- Solis J, Gutierrez A, Mangu V, Sanchez E, **Bedre R**, Linscombe S, Baisakh N. Genetic mapping of quantitative trait loci for grain yield under drought in rice under controlled greenhouse conditions. Frontiers in chemistry. 2018 Jan 8; 5:129. (**IF:3.994**)

- **Bedre R** and Mandadi K. GenFam: A new web application for gene family-based classification and functional enrichment analysis of plant genomes. bioRxiv doi: https://doi.org/10.1101/272187. (**preprint**)

- Gupta A, **Bedre R**, Thapa SS, Sabrin A, Wang G, Dassanayake M, Grove A. Global awakening of cryptic biosynthetic gene clusters in *Burkholderia thailandensis*. ACS chemical biology. 2017 Nov 8;12(12):3012-21. (**IF:4.995**)

- **Bedre R**, Mangu VR, Srivastava S, Sanchez LE, Baisakh N. Transcriptome analysis of smooth cordgrass (*Spartina alterniflora* Loisel), a monocot halophyte, reveals candidate genes involved in its adaptation to salinity. BMC genomics. 2016 Aug 19;17(1):657. (**IF:3.729**)

- **Bedre RH**, Raj U, Misra SP, Varadwaj PK. Antiviral therapy with nucleotide/nucleoside analogues in chronic hepatitis B: A meta-analysis of prospective randomized trials. Indian Journal of Gastroenterology. 2016 Mar 1;35(2):75-82.

- **Bedre R**, Raj U, Varadwaj P. Efficacy of Sucralfate in Reflux Disease in comparison to H2–Receptor Antagonist: A Meta-Analysis of Randomized Trials. Biology, Engineering, Medicine and Science Reports. 2016;2(1).

- **Bedre R**, Rajasekaran K, Mangu VR, Timm LES, Bhatnagar D, Baisakh N. Genome-Wide Transcriptome Analysis of Cotton (*Gossypium hirsutum* L.) Identifies Candidate Gene Signatures in Response to Aflatoxin Producing Fungus *Aspergillus flavus*. Plos One. 2015;10(9). (**IF:2.766**)

- Zandkarimi H, **Bedre R**, Solis J, Mangu V, Baisakh N. Sequencing and expression analysis of salt-responsive miRNAs and target genes in the halophyte smooth cordgrass (*Spartina alternifolia* Loisel). Molecular biology reports. 2015 Aug 1;42(8):1341-50. (**IF:1.889**)

- Khan NA, **Bedre R**, Parco A, Bernaola L, Hale A, Kimbeng C, Pontif M, Baisakh N. Identification of cold-responsive genes in energycane for their use in genetic diversity analysis and future functional marker development. Plant science. 2013 Oct 1;211:122-31. (**IF:3.712**) (Khan and Bedre has equal contribution)

- Lee S, Rajasekaran K, Ramanarao MV, **Bedre R**, Bhatnagar D, Baisakh N. Identifying

cotton (*Gossypium hirsutum* L.) genes induced in response to *Aspergillus flavus* infection. Physiological and molecular plant pathology. 2012 Oct 1;80:35-40. (**IF:1.395**)

Book Chapters:

- Irigoyen S, **Bedre RH**, Scholthof KB, Mandadi KK. Genomic Approaches to Analyze Alternative Splicing, A Key Regulator of Transcriptome and Proteome Diversity in *Brachypodium distachyon*. In Brachypodium Genomics 2018 (pp. 73-85). Humana Press, New York, NY.
- Joshi, Rohit, Venkata Ramanarao Mangu, **Renesh Bedre**, Luis Sanchez, Whitney Pilcher, Hana Zandkarimi, and Niranjan Baisakh. "Salt Adaptation Mechanisms of Halophytes: Improvement of Salt Tolerance in Crop Plants." InElucidation of Abiotic Stress Signaling in Plants, pp. 243-279. Springer New York, 2015.

Poster and oral presentations:

- Bernaola, L.,**Bedre, R.**, Stout, M. 2018. Mycorrhizal colonization affects rice gene expression of resistance traits in response to herbivore feeding. International Rice Research Conference (IRRC), Singapore. Oct 15- 17. (Oral)
- Awika, H.,**Bedre, R.**, Marconi, T., Badillo, I., Mandadi, K.K., Avila, C.A. 2018. Differential gene expression profile between resistant and susceptible tomato genotypes in response to tomato-potato psyllid (*Bactericera cockerelli*) infestation. American Society of Horticultural Sciences (ASHS), Washington, DC. July 30- August 3.
- Awika, H.,**Bedre, R.**, Marconi, T., Enciso, J., Jung, J., Mandadi, K.K., Avila, C.A. 2018. Development of molecular markers associated to spinach growth parameters. American Society of Horticultural Sciences (ASHS), Washington, DC. July 30- August 3. (Oral)
- Awika, H.,**Bedre, R.**, Marconi, T., Badillo, I., Mandadi, K.K., Avila, C.A. 2018. Resistance to the tomato-potato Psyllid (*Bactericera cockerelli*) in *Solanum habrochaites*. American Society of Plant Biology (ASPB), Montréal, Quebec. July 14-18.
- **Bedre, R.**, Scholthof, K.-B.G., Figueroa, M., Djamei, A., Zuccaro, A., Kazan, K., Powell, J., Vogel, J.P., and Mandadi, K.K. 2018. A gene atlas of diverse grass-microbe interactions in Brachypodium and Setaria. The 13th DOE Joint Genome Institute Annual Genomics of Energy & Environment User Meeting Annual Meeting, San Francisco, CA. 13-16 March.
- **Bedre, R.**, Irigoyen, S., Ramasamy, M., and Mandadi, K.K. Integration of Bioinformatics and Omics Technologies in Crop Improvement. The 76th Annual Meeting of the Subtropical Agriculture and Environments Society, February 9, 2018, Monte Alto, TX.
- Badillo-Vargas, I.E., **Bedre, R.**, Esparza-Díaz, G., Avila, C., and Mandadi, K.K. Tissue-specific transcriptional responses of the potato psyllid related to the horizontal and vertical transmission of the bacterial pathogen causing zebra chip disease of potato. The 76th Annual Meeting of the Subtropical Agriculture and Environments Society, February 9, 2018, Monte Alto, TX.
- **Bedre R**, Irigoyen S, Schaker P, Monteiro-Vitorello C, Mandadi KK. Genome-wide characterization of alternative splicing patterns in sugarcane modulated during infection with smut pathogen, *Sporisorium scitamineum*. The Annual Meeting of the American Phytopathological Society, August 5-9, 2017, San Antonio, TX.
- Badillo-Vargas, I.E., **Bedre, R.**, Esparza-Díaz, G., Avila, C., and Mandadi, K.K. Tissue-specific transcriptional responses related to the horizontal and vertical transmission of a bacterial pathogen by its insect vector. The Annual Meeting of the American

Phytopathological Society, August 5-9, 2017, San Antonio, TX.

- Venkata M., **Bedre R**., Zandkarimi, H. Baisakh, N. "Looking at the Bright Side of an Invasive Species: *Spartina alterniflora* from an Abiotic Stress Tolerance Perspective." Plant and Animal Genome XXIII Conference. In Plant and Animal Genome XXIII Conference, January 10-14, 2015, San Diego, CA.
- Zandkarimi, H., Venkata M., **Bedre R**., Baisakh, N. "Expression Profiling of miRNAs and Their Target Genes Under Salt Stress in the Halophyte Smooth Cordgrass (*Spartina alterniflora* Loisel)." In Plant and Animal Genome XXIII Conference, January 10-14, 2015, San Diego, CA.
- Venkata M., Timm, L.S., Joshi, R., **Bedre R**., Baisakh, N. "Translation of Halophyte Transcriptome Resources to Improve Salt and Drought Stress Tolerance in Rice." 2014 International meeting, At Long Beach, CA, USA.
- **Bedre R**., Venkata M., Srivastav S., Sanchez E., Solis J., Pereira A. & Baisakh N., (2014) Genome-wide transcriptome analysis of the halophyte grass *Spartina alterniflora* reveals molecular basis of its salt adaptation responses. In Plant and Animal Genome XXII Conference, January 11-15, 2014, San Diego, CA.
- Bernaola L., Parco A., Hale A., **Bedre R**., Kimbeng C., Gravois K., Baisakh, N. (2012) Mining genes for cold tolerance in sugarcane toward development of functional markers. In Plant and Animal Genome XX Conference, January 14-18, San Diego, CA.

Four first author manuscripts are under preparation

REFERENCES

- **Kranthi Mandadi, Ph.D.** (Supervisor)
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  Texas A&M University System
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  School of Plant, Environmental and Soil Sciences
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Renesh Bedre, Ph.D.