Renesh Bedre

1225 N FM 491 RD APT 2101, Mercedes, TX 78570
C: 225-636-4761 | E: renesh.bedre@agnet.tamu.edu | W: https://reneshbedre.github.io/
ORCID ID: 0000-0001-8874-5100 | ResearcherID: Q-9617-2018

SUMMARY OF QUALIFICATIONS

- 8-years of experience in bioinformatics and statistical data analysis related to omics datasets (transcriptome and whole genome sequencing)
- Extensive experience in large-scale gene expression profiling, sequence assemblies, molecular biomarker discovery, functional annotation, GWAS, development of algorithms and software pipelines, and data visualization
- Gene ontology, gene co-expression network, pathway, and gene family analysis
- Developed and implemented automated software pipelines for analysis of omics datasets (RNA-seq, RAD-seq, GBS) generated from NGS platforms
- Meta-analysis of randomized clinical trials to estimate and compare the efficacy and adverse effects of drugs
- Developed and implemented algorithms, standalone software programs, web servers, and databases for high-throughput data analysis and visualization
- Data integration of multiple heterogeneous omics databases
- Proficient in Python, R/Bioconductor, Perl, PostgreSQL, Bash, Django, open-source bioinformatics tools, HPC, parallel computing, CyVerse, and GitHub
- Worked closely with multi-disciplinary collaborators to achieve project goals
- Communicated scientific results and reports to variety of audiences and published manuscripts in peer-reviewed journals
- Conducted bioinformatics workshops, guest lectures, and training to research scientists and students

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 AND PROFESSIONAL EXPERIENCE

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

- Identification of conserved gene regulatory network and long non-coding RNAs (lncRNAs) from potato and tomato transcriptome (RNA-seq) modulated by insect *Bactericera cockerelli* and bacterium *Candidatus* Liberibacter solanacearum
- Global characterization of alternative splicing in sugarcane modulated by smut pathogen, *Sporisorium scitamineum*
- Development of gene atlas for grass-microbe interactions in Brachypodium and Setaria
- Large-scale genotyping, SNP marker discovery, genotype imputation and GWAS in spinach (RAD-seq GBS) and tomato (AgSeq GBS) using whole genome sequencing
- Comparative gene expression profiling between resistant and susceptible tomato genotypes against insect *Bactericera cockerelli*
- Comparative gene expression profiling and physiological phenotypic analysis between two potato genotypes in response to drought stress
- Phylogenetic characterization of *Phytophthora nicotianae* isolates from citrus orchards using ITS sequencing
- Tissue-specific transcriptome analysis of *Bactericera cockerelli* organs involved in horizontal and vertical transmission of bacterium *Candidatus* Liberibacter solanacearum
- Developed software pipelines for analysis of omics datasets (RNA-seq, RAD-seq, GBS) generated from NGS platforms
- Developed standalone software programs, dockerized tools, web servers, and databases for high-throughput data analysis and visualization
- Algorithm development and implementation, parallel computing, statistical analysis, large-scale data analysis, database handling, and high-performance computers (HPC)
- Integrated multiple heterogenous omics databases
- Project proposal writing for JGI Community Science Program (CSP), 2018 (got funded)
- Conducted bioinformatics workshops, guest lectures, and training to research scientists and students

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

- Identification of gene regulatory changes using RNA-seq in cotton infected with different strains of *A. flavus*
- Comparative transcriptomics (RNA-seq) analysis of for drought and salt tolerance in rice and development of SNP markers
- Genome-wide transcriptome analysis (RNA-seq) in *Spartina alterniflora* for gene and biomarker discovery in response to salt stress
- Identification and characterization miRNA and their targets in rice and *Spartina alterniflora* using high-throughput sequencing

- Analysis of bacterial (*Burkholderia thailandensis*) transcriptome (RNA-seq) to identify biosynthetic gene clusters
- Identification of gene expression changes in rice associated with beneficial arbuscular mycorrhizal fungi (AMF) using RNA-seq
- Co-expression gene network analysis to study gene interaction under biotic and abiotic stresses in plants
- 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
- 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

Technical:

- Linux, Mac, Windows, Python, R/Bioconductor, Perl, PostgreSQL, Bash, Django, open-source bioinformatics tools, HPC, CyVerse, Docker, GitHub, PBS, MATLAB, visualization, biological databases, EndNote

Personal Skills:

- Excellent written and verbal communication skills
- Proficient in English
- Ability to perform work independently or in a collaborative team
- Rapidly test and use new technologies

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, American Phytopathological Society (APS), Joint Genome Institute (DOE JGI)**, **Bioinformatics Organization, Biostar Bioinformatics community, Bioclues (BIOinformatics CLUb for Experimenting Scientists)**
- Committee Member, **Graduate Student Association (GSA)** at Louisiana State University, 2015-2016
- Committee Member, **Indian Student Association (ISA)** at Louisiana State University, 2014-2015
- 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
- **APS Foundation Student Travel Award** reviewer (3 reviews), 2018
- Manuscript Reviewer (23 reviews)
  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: 113 (Independent: 78)

Three first author and two co-author manuscripts are under review

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.
- 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.
- 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.
- **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.
- 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.

- **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.
- **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).
- 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.
- 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. (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.

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:

- **Bedre, R.**, Irigoyen, S., Schaker, P.D.C., Monteiro-Vitorello, C.B., Da Silva, J.A., Mandadi, K.K. 2019. Characterization of Alternative Splicing Patterns Modulated by Biotrophic Smut Pathogen in Sugarcane. Plant and Animal Genome XXVII Conference, San Diego, CA. Jan 11- 16.
- 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.

REFERENCES

- **Kranthi Mandadi, Ph.D.** (Supervisor)
  Texas A&M AgriLife Research & Extension Center
  Texas A&M University System
  Phone: (956) 969-5683
  Email: kkmandadi@tamu.edu

- **Niranjan Baisakh, Ph.D.** (Ph.D. Supervisor)
  School of Plant, Environmental and Soil Sciences
  Louisiana State University AgCenter
  Phone: (225) 578-1300
  Email: NBaisakh@agcenter.lsu.edu

- **Kanniah Rajasekaran**, **Ph.D.** (Project collaborator)
  Food and Feed Safety Research
  USDA-ARS-SEA-Southern Regional Research Center
  Phone: (504) 286-4482
  Email: Rajah.Rajasekaran@ars.usda.gov