Renesh Bedre

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SUMMARY OF QUALIFICATIONS

- Application of bioinformatics, statistical, and machine learning methods to analyze high-throughput genomics and transcriptomics datasets
- High performance data analysis and biological interpretation of high-throughput sequencing datasets
- Development of novel methods, software, automated analysis pipelines, statistical models, databases, and visualization tools to effectively analyze large-scale datasets
- Data integration of multiple heterogeneous omics databases
- Fully proficient in Python, R/Bioconductor, PostgreSQL, Linux/Unix, HPC, Nextflow and GitHub
- Worked closely with multi-disciplinary collaborators to achieve project goals
- Communicated scientific results and reports via peer-reviewed journals, conferences, workshops and invited talks
- Strong analytical, problem solving and learning skills to resolve complex issues

EDUCATION

Ph.D. in Computational biology and Bioinformatics
Louisiana State University (LSU), Baton Rouge, Louisiana, 2011-2016
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

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

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

RESEARCH AND PROFESSIONAL EXPERIENCE

Postdoctoral Research Associate, Texas A&M AgriLife Research, Weslaco, TX, Oct 2016-Present
Graduate Research Assistant, Louisiana State University, Baton Rouge, LA, Aug 2011-Aug 2016

Graduate Teaching Assistant, Indian Institute of Information Technology, Allahabad, UP, India, 2009-2011

- Transcriptomics (Total RNA-seq, mRNA-seq and small RNA-seq) analysis for uncovering transcriptional/post-transcriptional gene regulation, gene discovery, gene co-expression networks, long non-coding RNAs (lncRNAs), and miRNAs in plants, bacteria and insects (See J2, J5, J6, J8, J9, J12, J13, J14, J15, P4, P5, P8, P11)
- Genomics (RAD-seq GBS, AgSeq GBS and ITS-seq) analysis to discover population structure, genetic diversity, genome-wide association (GWA), taxonomy and phylogeny, and SNP markers (See J1, J4, P2)
- Development of gene atlas for grass-microbe interactions (See P9)
- Functional annotation and enrichment analysis (GO, GSEA, KEGG, GenFam, Gene networks) (See J2, J5, J7, J8, J9, J12, J14, J15, S1, N1)
- Development of software (standalone and web-based), automated analysis pipelines (Nextflow) and databases to analyze high-throughput sequencing (HTS) datasets (See S1, S2, S3, N1)
- Statistical analysis and machine learning to analyze HTS generated omics datasets (See J2, J5, J7, J8, J9, J12, J14, J15, S1, N1)
- Meta-analysis of clinical trials (See J10, J11)

RELEVANT SKILLS

Technical:

- Linux/Unix, Mac, Windows, Python, R/Bioconductor, Perl, PostgreSQL, MySQL, Bash, Django, open-source bioinformatics tools, High-performance computing (HPC), Nextflow, 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, HONORS AND AWARDS

Publons Peer Review Awards 2018 for placing in the top 1% of reviewers
Gerald O. Mott Meritorious Student Award, Crop Science Society of America (CSSA), 2015
Travel Grant Award, LSU Graduate School, 2014
GATE scholarship, Government of India. 2009-2011
All India Rank 28th in National Level Pharmacy Talent Search Examination, 2007

Invited speakers and workshops:

Young Scientists - Rio Grande Valley meeting, Apr 19, 2018
    "Integration of Bioinformatics and Omics Technologies in Crop Improvement"
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

Research Grants:
Department of Energy-Joint Genome Institute, Community Science Program, 2018 (RNA-sequencing and analysis credits for ~312 samples)
"Gene atlas of diverse grass-microbe interactions in Brachypodium and Setaria"
Media: https://jgi.doe.gov/csp-2018-mandadi-gene-atlases-grass-microbe-interactions/

PROFESSIONAL MEMBERSHIPS AND SERVICES

Society and Association Member:
Crop Science Society of America (CSSA)
American Phytopathological Society (APS)
Joint Genome Institute (DOE JGI)
Bioinformatics Organization
Biostar Bioinformatics community**,**
Bioclues (BIOinformatics CLUb for Experimenting Scientists)
Graduate Student Association (GSA), LSU, 2015-2016
Indian Student Association (ISA), LSU, 2014-2015

Editorial Board:
Computational biology and bioinformatics

Journal Scientific Reviewer:
Plant Physiology (2)
Frontiers in Plant Science (2)
Neural Computing and Applications (6)
Agronomy (2)
Physiology and Molecular Biology of Plants (2)
Interdisciplinary Sciences: Computational Life Sciences (1)
Scientific Reports (9)
Plos One (8)
Genes (2)
Journal of Fungi (2)
Molecular Genetics and Genomics (1)
Crop Breeding and Applied Biotechnology (1)

Others:
APS Foundation Student Travel Award reviewer (3 reviews), 2018
Volunteer, Third Science Conclave: An Interaction with Nobel Laureates held at IIIT Allahabad, India, 2010

BIBLIOGRAPHY

Google Scholar: https://scholar.google.com/citations?user=6pv2AiMAAAAJ&hl=en
Citations: 128 (Independent: 83)

PEER REVIEWED

Journal papers:

J1. Kandel DR, **Bedre RH**, Mandadi KK, Crosby K, Avila CA. Genetic Diversity and Population Structure of Tomato (*Solanum lycopersicum*) Germplasm Developed by Texas A&M Breeding Programs. American Journal of Plant Sciences. 2019 Jul 11;10(7):1154-80.
J2. **Bedre R**, Irigoyen S, Schaker PD, Monteiro-Vitorello CB, Da Silva JA, Mandadi KK. Genome-wide alternative splicing landscapes modulated by biotrophic sugarcane smut pathogen. Scientific Reports. 2019 Jun 20;9(1):8876.
J3. **Bedre R**, Irigoyen S, Petrillo E, Mandadi K. New Era in Plant Alternative Splicing Analysis Enabled by Advances in High-Throughput Sequencing (HTS) Technologies. Frontiers in plant science. 2019;10:740.
J4. Awika H, **Bedre R**, Yeom J, Marconi T Enciso J, Mandadi K, Jung J, Avila C. Developing Growth-Associated Molecular Markers Via High-Throughput Phenotyping in Spinach. The Plant Genome. 2019 Aug 1
J5. 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. 2019 Jan;17(1):188-205.
J6. 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.
J7. 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.
J8. 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.
J9. **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.
J10. **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.
J11. **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).
J12. **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).
J13. 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.
J14. 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)

J15. 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.

Software and databases:

S1. GenFam: Gene Family based classification and enrichment analysis (http://mandadilab.webfactional.com/home/)

S2. RseqFilt: automated sequence filtering analysis tool for high-throughput RNA-seq data (https://github.com/reneshbedre/RseqFilt)

S3. bioinfokit: Bioinformatics data analysis and visualization toolkit (https://github.com/reneshbedre/bioinfokit)

Book chapters:

B1. 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.

B2. 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:

P1. Kandel DR, **Bedre RH**, Mandadi KK, Crosby K, Avila CA. Genetic Diversity and Population Structure of Texas A&M Tomato (*Solanum lycopersicum*) Breeding Germplasm. American Society of Horticultural Sciences (ASHS), Las Vegas. July 21- July 25, 2019.

P2. Awika H, Marconi T, **Bedre R,** Mandadi KK, Avila CA. Assessing Minor Alleles as Risk Factors in Spinach White Rust Disease Severity. American Society of Horticultural Sciences (ASHS), Las Vegas. July 21- July 25, 2019.

P3. **Bedre R**, Irigoyen S, Schaker PDC, Monteiro-Vitorello CB, Da Silva JA, Mandadi KK. Characterization of Alternative Splicing Patterns Modulated by Biotrophic Smut Pathogen in Sugarcane. Plant and Animal Genome XXVII Conference, San Diego, CA. Jan 11- 16, 2019.

P4. Devisetty U, Castillo-Siri A, Palos KR, Bedre R, Mandadi K, Lyons E, Beilstein MA, Nelson A. Comparative Genomic and Transcriptomic Analyses of Functionally Characterized Arabidopsis lncRNAs Reveals Conservation in Unexpected Places. Plant and Animal Genome XXVII Conference, San Diego, CA. Jan 11- 16, 2019 (Oral).

P5. Bernaola L, **Bedre R**, Stout M. Mycorrhizal colonization affects rice gene expression of resistance traits in response to herbivore feeding. International Rice Research Conference (IRRC), Singapore. Oct 15- 17, 2018. (Oral)

P6. Awika H, **Bedre R**, Marconi T, Badillo I, Mandadi KK, Avila CA. 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, 2018.

P7. Awika H, **Bedre R**, Marconi T, Enciso J, Jung J, Mandadi KK, Avila CA. Development of molecular markers associated to spinach growth parameters. American Society of Horticultural Sciences (ASHS), Washington, DC. July 30- August 3, 2018. (Oral)

P8. Awika H, **Bedre R**, Marconi T, Badillo I, Mandadi KK, Avila CA. Resistance to the tomato-potato Psyllid (*Bactericera cockerelli*) in *Solanum habrochaites*. American Society of Plant Biology (ASPB), Montréal, Quebec. July 14-18, 2018**.**

P9. **Bedre R**, Scholthof KBG, Figueroa M, Djamei A, Zuccaro A, Kazan K, Powell J, Vogel JP, and Mandadi, KK. 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, 2018.

P10. **Bedre R**, Irigoyen S, Ramasamy M, and Mandadi KK. Integration of Bioinformatics and Omics Technologies in Crop Improvement. The 76th Annual Meeting of the Subtropical Agriculture and Environments Society, Monte Alto, TX. February 9, 2018.

P11. Badillo-Vargas IE, **Bedre R**, Esparza-Díaz G, Avila C, and Mandadi KK. 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, Monte Alto, TX. February 9, 2018

P12. **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, San Antonio, TX. August 5-9, 2017.

P13. Badillo-Vargas IE, **Bedre R**, Esparza-Díaz G, Avila C, and Mandadi KK. 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, San Antonio, TX. August 5-9, 2017.

P14. 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, San Diego, CA. January 10-14, 2015.

P15. 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, San Diego, CA. January 10-14, 2015.

P16. Venkata M, Timm, LS, 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.

P17. **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, San Diego, CA. January 11-15, 2014.

P18. 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, San Diego, CA. January 14-18.

NON-PEER REVIEWED

N1. **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.