

Arun S. Seetharam

Research Scientist IV
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Summary

- Highly organized and efficient in multitasking environments.
- Able to prioritize projects effectively to accomplish objectives creatively and on time.
- Over 10 years of experience in bioinformatics data analyses, with an excellent publication record.
- Worked on over 35 eukaryotic genome assembly and annotation projects.
- Developed open source programs, pipelines and scripts for streamlining data analyses.

Education

May, 2012	Ph.D. in Biology <i>Indiana State University, Terre Haute, Indiana, United States</i> Dissertation: "Phylogenomics: Molecular Evolution in the Genomics Era" Supervisor: Gary W. Stuart, Ph.D. OGP: 3.97/4.00
Mar, 2006	M.Sc. Agriculture (Plant Biotechnology) <i>University of Agricultural Sciences, Dharwar, Karnataka, India</i> Thesis: "In silico EST data-mining for elucidation of repeat biology and functional annotation in sorghum, <i>Sorghum bicolor</i> (L.) moench" Supervisor: B. Fakrudin, Ph.D. OGP: 9.26/10.00
Jun, 2003	B.Sc. Agriculture <i>University of Agricultural Sciences, Bangalore, Karnataka, India</i> Major: Agronomy OGP: 9.09/10.00

Positions

Feb 2016 - present	Research Scientist IV (<i>previously Associate Scientist</i>) <i>Dept. of Ecology, Evolution, and Organismal Biology/ Genome Informatics Facility, Iowa State University, Ames, Iowa</i>
Jan 2014 - Jan 2016	Post-Doctoral Research Associate <i>Genome Informatics Facility, Iowa State University, Ames, Iowa</i>
Jul 2012 - Dec 2013	Post-Doctoral Research Associate <i>Bioinformatics Core, Purdue University, West Lafayette, Indiana</i>
Aug 2007 - May 2012	Teaching Assistant <i>Dept. of Biology, Indiana State University, Terre Haute, Indiana</i>
Jan 2007 - Jun 2007	Research Associate <i>University of Agricultural Sciences, Dharwar, Karnataka, India</i>
Aug 2006 - Jan 2007	Technical Assistant <i>University of Agricultural Sciences, Dharwar, Karnataka, India</i>

Work Experience

Research Scientist IV, Iowa State University

- Research, investigate, develop, evaluate and implement methods for analyzing various types of data, extracting meaningful information relevant for understanding and solving biological problems at a molecular level.
- Developing and building novel cyber-infrastructure at GIF by developing pipelines, scripts, and tutorials, thereby consolidating knowledge of bioinformatics to advance science. The resources developed are open source and accessible to everyone, helping the community and expanding available resources to accelerate the use of bigdata.
- Manage day to day activities of the Bioinformatics core facility operation, including managing of personnel, billing and resource monitoring.
- Engage and support collaborative research with faculty to develop research proposals for extramural grant funding.

Post-Doctoral Researcher, Iowa State University

- Genome assembly and annotation of *Seriola dorsalis*
- The teosinte (*Zea mays* ssp. *parviglumis*) *de novo* genome assembly and annotation
- Genome assembly and annotation for the basal grass species, *Streptochaeta angustifolia*
- Detecting genome selection pressure for oil and yield traits during Soybean improvement
- Using GMOD tools to setup genome portal for the newly sequenced genomes
- Pathway analyses for a non-model species using protein expression data
- High throughput CRISPR experiments to test efficacy of various PAM and seed constructs
- Nematode gland cell (single cell RNAseq) transcriptome profiling
- GWAS studies to identify pathogenic loci in *Fusarium* spp
- Comparing DGE between wild type and bzip60 mutant *Arabidopsis* lines
- NCBI-BLAST optimizations on XSEDE resources (TACC: Stampede)
- Generating genetic map for Teosinte using GBS data from the mapping population
- Teosinte *de novo* transcriptome assembly and Presence-Absence Variants (PAV) analyses
- Clustering metabolomics data for different tissues from various location
- Testing microbiota under various diet conditions for Primates
- Developing genomic resources for Pacific White Shrimp (*Litopenaeus vannamei*)
- RNA-Seq: DGE analyses of ALS disease in mouse
- Single cell transcriptome analyses of retinal cells in mouse
- Effect of various Fe supplements on gut biota of rats
- DGE analyses of *Phytophthora sojae* during soybean infection
- *Seriola de novo* RNA seq analyses (transcriptome assembly and differential gene expression).
- RNA-Seq: DGE analyses of Soybean against fungal inoculations
- Rice Genome Sequencing: PacBio Error Correction
- RNA-seq: DGE analyses of *Pichia* spp. for various sources of carbon
- GC3 plots for chromosomes of various fungal species

Post-Doctoral Researcher, Purdue University

- Analyses of 5-HmC and 5-mC changes during differentiation of human leukemia cells
- Defining epigenetic programming during flight expeditions in differentiating embryonic stem cells
- Organized workshop on basic UNIX for biologists (multiple times)
- Organized workshop on phylogenomics
- BarSeq: Developing barcoded yeast libraries for screening efficacy of drugs
- SynColi: generating synthetic *E. coli* genome, with minimal required genes for survival
- RNASeq: Differential gene expression of 4 different apple genotypes during fruiting stages
- RADSeq: Gene flow and dispersal evolution in *Lasthenia* species
- Assembling the lichen moth tree of life (using transcriptome data)
- Resolving Classes of Pucciniomycotina and Ustilaginomycotina through phylogenomic analyses

Graduate Student, Indiana State University, Terre Haute

- Developing whole genome, non-alignment based methods for phylogenomics (for dissertation)

- Co-taught graduate level course in Bioinformatics (BIO487/587) program. Shared responsibility for lectures, exams, homework assignments, and grades.
- Taught undergraduate level labs in the Genetics (BIO382L) program. Full responsibility for lectures, exams, homework assignments, and grades.
- Teaching assistant (teaching and grading duties): Exploration of Biological Phenomena (BIO 112L), Genetics Lab (BIO 382L) and Recombinant DNA technology (BIO 582L)
- Mentoring: Hannah Smith (Biology major) summer semester, 2009. Construction of improved green/red switch gene as a marker for inducible recombination and transposition in Zebrafish (project guided by Dr. Gary Stuart).
- Mentoring: Vincent Keller (Biology major) spring semester, Fall 2009. Conservation of C2H2 Zinc finger genes in genomes (Project guided by Dr. Gary Stuart)

Research Associate, University of Agricultural Sciences, Dharwar, India

- Worked on the Pigeon Pea Genomics Initiative under Indo-US Agriculture Knowledge Initiative at Institute of Agri-biotechnology, funded by Directorate of Biotechnology, Government of India. I Was involved in identifying differentially expressed genes during drought conditions using cDNA subtraction method.

Technical Assistant, University of Agricultural Sciences, Dharwar, India

- Worked on developing genetic linkage map and QTL analysis for charcoal rot resistance in Sorghum, funded by Directorate of Biotechnology, Government of India.

Synergistic Activities

- **Bioinformatics Workbook** (available at bioinformaticsworkbook.org): Co-author of an online book on Bioinformatics, that is continuously updated and freely available to everyone. This “living” book provides guides for ever changing tools and methods commonly used in data analyses. This book has over thousand visitors every month.
- **Contributing and developing open source programs and scripts** for data analyses:
 - 🔗 [SequelTools](#): A suite of tools for working with PacBio Sequel raw sequence data
 - 🔗 [phylostratr](#): a R framework for phylostratigraphy
 - 🔗 [fagin](#): Classify genes based on syntenic relationship
 - 🔗 [GenomeQC](#): web-server for computing assembly and annotation metrics
 - 🔗 [pyrpipe](#): pyrpipe: python RNA-Seq pipeliner
- **Publicly available, pipeline and scripts development** for running routine bioinformatics tasks:
 - 🔗 [ISUgenomics/common_analyses](#): optimized scripts for commonly used programs
 - 🔗 [ISUgenomics/common_scripts](#): simple utility scripts to enhance efficiency
 - 🔗 [ISUgenomics/StampedeBLAST](#): NCBI-BLAST optimization pipeline for XSEDE-Stampede
 - 🔗 [ISUgenomics/basic_UNIX_2015](#): workshop materials for learning basic UNIX scripting
- **Installation/management of programs on clusters**: responsible for installation and management of bioinformatics programs ISU-HPC clusters Lightning3 (now decommissioned), Condo and HPC-Class. Programs were installed via environmental modules for dynamically load/unload any programs as needed.
- **Genome portal development**: For *Seriola* spp. ([SeriolaDB.org](#)) and for Soybean Cyst Nematode ([SCNbase.org](#)), currently hosting genome and related resources in a centralized database. This website uses ISU’s custom *Drupal/Tripal* back-end and *Chado* database schema. Many plugins like *JBrowse*, *Appollo*, *BioMart*, *InterMine* are being actively developed for these portals.
- **Posters and participation**: Actively participated in many international conferences to present posters (26) and talks (10). Also attended multiple workshops (3) in the field of NGS/programming.
- **Journal Editor**: Editorial Board member for the journals *BMC Genomics*, *Plants* and *Frontiers*.

- **Peer reviewing:** Active reviewer for many biology journals, including *Scientific Reports*, *BMC Bioinformatics*, *BMC Genomics*, *PeerJ*, and many MDPI open access journals. Complete review activity is available at publons.com/researcher/1276739/arun-seetharam.

Grants

2019	Co-PI	<i>The prediction of plant and animal orphan genes with comparative genomics and data mining</i> Agency: Extreme Science and Engineering Discovery Environment (XSEDE) Status: Awarded (\$6,461)
2018	Co-PI	<i>The molecular hallmark of epigenetic control in high performing yeasts</i> Agency: Presidential Interdisciplinary Research Initiative (PIRI), ISU Status: Awarded (\$50,000)
2015	Co-PI	<i>Genome assembly and annotation of Red Abalone, Yellowtail, Soybean Cyst Nematode, and Spiny Softshell Turtle</i> Agency: Extreme Science and Engineering Discovery Environment (XSEDE) Status: Awarded (\$50,680)
2017	Co-PI	<i>The prediction of plant & animal orphan genes with comparative genomics & data mining</i> Agency: Extreme Science and Engineering Discovery Environment (XSEDE) Status: Awarded (\$3,376)
2015	SRP	<i>Orphan genes: An untapped genetic reservoir of novel traits driving evolutionary adaptation and crop improvement</i> Agency: National Science Foundation (PGRP) (NSF 16-505) Status: Awarded (\$2,275,000)
2014	Co-I	<i>Genomic resource development of Yellow Tail, Teosinte, Soybean and Streptochaeta</i> Agency: Extreme Science and Engineering Discovery Environment (XSEDE) Status: Awarded (\$111,158)
2014	PI	<i>Testing approaches for assembling the Teosinte genome</i> Agency: Extreme Science and Engineering Discovery Environment (XSEDE) Status: Awarded

Honors and Awards

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|---|--------------------|
| - Post-doctoral fellowship , Iowa State Univ., Ames, IA | 2014 - 2016 |
| - Post-doctoral fellowship , Discovery Park, Purdue Univ., W. Lafayette, IN | 2012 - 2013 |
| - Student Travel Grant , ISBRA 2010, Univ. of Connecticut, Storrs, CT | 2010 |
| - Graduate Student Travel Grant , Indiana State Univ., Terre Haute, IN | 2008 |
| - Graduate Student Assistantship , Indiana State Univ., Terre Haute, IN | 2007 - 2012 |
| - JN Tata Scholar , The JN Tata Endowment for the Higher Education scholarship. | 2007 |
| - University Merit Scholarship , University of Agricultural Sciences, Bangalore | 1999 - 2003 |
| - Five Gold medals at 38th Convocation , Univ. of Agricultural Sciences, Bangalore | 2003 |
| <ul style="list-style-type: none"> • Best (Boy) Student of the Year, LAg's Foundation, Karnataka Gold medal. • Best Undergraduate Student of the Year, B.K. Garudachar Centenary Gold medal. • Best Student of the Year, Sri R. Gundu Rao Gold medal. • Highest OGPA for the University, Sri Ragi Lakshmanaiah Gold medal. • Overall Performance, University of Agricultural Sciences, Bangalore, Gold medal | |

Skills

- **Programming languages:** proficient in Bash/UNIX command-line and scripting. Intermediate in scripting languages R, Python and Perl. Basic knowledge of C/C++, Ruby, Haskell.
- **Developing and building novel bioinformatics cyber-infrastructure**, including data analyses pipelines, scripts, and tutorials
- **Genome assembly** using various data-sets (short reads, long reads, optical maps, Hi-C and genetic maps), and programs (Canu, Falcon, Flye, MaSuRCA, SOAP *de novo* etc.)
- **Genome annotation** using various methods: *ab initio*, homology based methods, including software workflows like MAKER, BRAKER, GeneSAS etc.
- **Metagenomics analyses**, both shotgun (metagenome assembly, binning and annotation) and *16s rRNA* amplicon-based (Qiime, Mothur) workflows
- **Proteomics and metabolomics analyses:** statistical test, abundance estimation, differential expression, enrichment, and pathway analyses
- **NGS based analyses and workflows:** expert in data analyses and interpretation including RNAseq, MeDIP-Seq, ChIP-Seq, Iso-Seq etc.
- **Variant calling** (GATK, FreeBayes) and **GWAS** analyses (Tassel)
- **Comparative genomics analyses** including ortholog identification, phylogenetics, phylogenomics, functional annotation, adaptive evolution tests etc.
- **Population genomics analyses** including detecting selection patterns, genomic variation, genetic map construction, QTL analyses, understanding the evolutionary processes affecting genomes.
- **Server management** skills, including installation of programs and packages (via containers, environmental modules, conda package manager etc.), running web-server and general maintenance
- **Molecular biology** skills including cloning, recombination, expression, protein purification including common protocols (DNA/RNA/protein isolation, PCR, vector/plasmid design, transformation).
- **Microbiology**, general aseptic techniques and common bacterial/yeast culture techniques.
- **Immunological assays, cell culturing and plant tissue culturing** and many other routine wet-lab experiments.

Publications*

Pre-prints/in-press

1. S. Tittes, A. Lorant, S. McGinty, J. F. Doebley, J. B. Holland, J. d. J. Sánchez-González, **A. S. Seetharam**, M. Tenaillon, and J. Ross-Ibarra. Not so local: the population genetics of convergent adaptation in maize and teosinte. *bioRxiv*, 2021

Peer-reviewed Articles

37. J. Li, U. Singh, P. Bhandary, J. Campbell, Z. Arendsee, **A. S. Seetharam**, and E. Wurtele. Foster thy young: enhanced prediction of orphan genes in assembled genomes. *Nucleic Acids Research*, 12 2021. gkab1238
36. **A. S. Seetharam**[†], Y. Yu[†], S. Belanger, L. G. Clark, B. C. Meyers, E. A. Kellogg, and M. B. Hufford. The *Streptochoaeta* genome and the evolution of the grasses. *Frontiers in Plant Science*, 12:2165, 2021
35. M. B. Hufford, **A. S. Seetharam**, M. R. Woodhouse, K. M. Chougule, S. Ou, J. Liu, W. A. Ricci, T. Guo, A. Olson, Y. Qiu, R. Della Coletta, S. Tittes, A. I. Hudson, A. P. Marand, S. Wei, Z. Lu, B. Wang, M. K. Tello-Ruiz, R. D. Piri, N. Wang, D. w. Kim, Y. Zeng, C. H. O'Connor, X. Li, A. M. Gilbert, E. Baggs, K. V. Krasileva, J. L. Portwood, E. K. S. Cannon, C. M. Andorf, N. Manchanda, S. J. Snodgrass, D. E. Hufnagel, Q. Jiang, S. Pedersen, M. L. Syring, D. A. Kudrna, V. Llaca, K. Fengler, R. J. Schmitz, J. Ross-Ibarra, J. Yu, J. I. Gent, C. N. Hirsch, D. Ware, and R. K. Dawe. *De novo* assembly, annotation, and comparative analysis of 26 diverse maize genomes. *Science*, 373(6555):655–662, 2021
34. T. Khan[†], **A. S. Seetharam**[†], J. Zhou, N. J. Bivens, D. J. Schust, T. Ezashi, G. Tuteja, and R. M. Roberts. Single Nucleus RNA Sequence (snRNAseq) Analysis of the Spectrum of Trophoblast Lineages

- Generated From Human Pluripotent Stem Cells in vitro. *Frontiers in Cell and Developmental Biology*, 9:1881, 2021
33. U. Singh, J. Li, **A. S. Seetharam**, and E. S. Wurtele. pyrpipe: a Python package for RNA-Seq workflows. *NAR Genomics and Bioinformatics*, 3(2), 06 2021. lqab049
 32. N. Bornowski, K. J. Michel, J. P. Hamilton, S. Ou, **A. S. Seetharam.**, J. Jenkins, J. Grimwood, C. Plott, S. Shu, J. Talag, M. Kennedy, H. Hundley, V. R. Singan, K. Barry, C. Daum, Y. Yoshinaga, J. Schmutz, C. N. Hirsch, M. B. Hufford, N. de Leon, S. M. Kaeppler, and C. R. Buell. Genomic variation within the maize stiff-stalk heterotic germplasm pool. *The Plant Genome*, n/a(n/a):e20114
 31. W. A. Shell, M. A. Steffen, H. K. Pare, **A. S. Seetharam.**, A. J. Severin, A. L. Toth, and S. M. Rehan. Sociality sculpts similar patterns of molecular evolution in two independently evolved lineages of eusocial bees. *Communications Biology*, 4(253), 2021
 30. K. Murugan, S. K. Suresh, **A. S. Seetharam.**, A. J. Severin, and D. G. Sashital. Systematic in vitro specificity profiling reveals nicking defects in natural and engineered CRISPR-Cas9 variants. *Nucleic Acids Research*, 49(7):4037–4053, 03 2021
 29. D. E. Hufnagel, M. B. Hufford, and **A. S. Seetharam.** SequelTools: A suite of tools for working with PacBio Sequel raw sequence data. *BMC Bioinformatics*, 21(429), 2020
 28. J. Liu, **A. S. Seetharam.**, K. Chougule, S. Ou, K. W. Swentowsky, J. I. Gent, V. Llaca, M. Woodhouse, N. Manchanda, G. G. Presting, D. Kudrna, M. Alabady, C. Hirsch, K. Fengler, D. Ware, T. Michael, M. Hufford, and K. Dawe. Gapless assembly of maize chromosomes using long read technologies. *Genome Biology*, 21(121), 2020
 27. S. Ou, J. Liu, K. M. Chougule, A. Fungtammasan, **A. S. Seetharam.**, J. C. Stein, V. Llaca, N. Manchanda, A. M. Gilbert, S. Wei, et al. Effect of sequence depth and length in long-read assembly of the Maize inbred NC358. *Nature Communications*, 11(1):1–10, 2020
 26. K. Murugan, **A. S. Seetharam.**, A. J. Severin, and D. G. Sashital. CRISPR-Cas12a has widespread off-target and dsDNA-nicking effects. *Journal of Biological Chemistry*, pages jbc-RA120, 2020
 25. N. Manchanda, J. L. Portwood, M. R. Woodhouse, **A. S. Seetharam.**, C. J. Lawrence-Dill, C. M. Andorf, and M. Hufford. GenomeQC: A quality assessment tool for genome assemblies and gene structure annotations. *BMC genomics*, 21(193), 2020
 24. A. M. Elashry, S. S. Habash, P. Vijayapalani, N. Brocke-Ahmadinejad, R. Blümel, **A. S. Seetharam.**, H. Schoof, and F. M. Grundler. Transcriptome and parasitome analysis of beet cyst nematode *Heterodera schachtii*. *Scientific Reports*, 10(1):1–12, 2020
 23. R. E. Masonbrink, C. Purcell, S. Boles, A. Whitehead, J. Hyde, **A. S. Seetharam.**, and A. J. Severin. An annotated genome for *Haliotis rufescens* (Red Abalone) and resequenced green, pink, pinto, black and white abalone species. *Genome biology and evolution*, 2019
 22. R. Masonbrink, T. R. Maier, U. Muppirala, **A. S. Seetharam.**, E. Lord, P. S. Juvale, J. Schmutz, N. T. Johnson, D. Korkin, M. G. Mitchum, et al. The genome of the soybean cyst nematode (*Heterodera glycines*) reveals complex patterns of duplications involved in the evolution of parasitism genes. *BMC Genomics*, 20(1):119, 2019
 21. S. N. Barnes, R. E. Masonbrink, T. R. Maier, **A. S. Seetharam.**, A. S. Sindhu, A. J. Severin, and T. J. Baum. *Heterodera glycines* utilizes promiscuous spliced leaders and demonstrates a unique preference for a species-specific spliced leader over *C. elegans* sl1. *Scientific reports*, 9, 2019
 20. Z. Arendsee, J. Li, U. Singh, P. Bhandary, **A. S. Seetharam.**, and E. S. Wurtele. fagin: synteny-based phylostratigraphy and finer classification of young genes. *BMC Bioinformatics*, 20(1):1–14, 2019
 19. Z. Arendsee, J. Li, U. Singh, **A. S. Seetharam.**, K. Dorman, and E. S. Wurtele. phylostratr: A framework for phylostratigraphy. *Bioinformatics*, btz171, 2019

18. R. Masonbrink, T. R. Maier, **A. S. Seetharam.**, P. S. Juvale, L. Baber, T. J. Baum, and A. J. Severin. SCNBase: a genomics portal for the soybean cyst nematode (*Heterodera glycines*). *Database*, 2019(1), 11 2019. baz111
17. P. Bhandary, **A. S. Seetharam.**, Z. W. Arendsee, M. Hur, and E. S. Wurtele. Raising orphans from a metadata morass: A researcher's guide to re-use of public'omics data. *Plant Science*, 267:32–47, 2018
16. J. T. Trujillo, **A. S. Seetharam.**, M. B. Hufford, M. A. Beilstein, and R. A. Mosher. Evidence for a unique DNA-dependent RNA polymerase in cereal crops. *Molecular biology and evolution*, 35(10):2454–2462, 2018
15. C. M. Purcell, **A. S. Seetharam.**, O. Snodgrass, S. Ortega-García, J. R. Hyde, and A. J. Severin. Insights into teleost sex determination from the *Seriola dorsalis* genome assembly. *BMC Genomics*, 19(31), 2018
14. M. Cao, M. Gao, C. L. Lopez-Garcia, Y. Wu, **A. S. Seetharam.**, A. J. Severin, and Z. Shao. Centromeric DNA facilitates nonconventional yeast genetic engineering. *ACS synthetic biology*, 6(8):1545–1553, 2017
13. J. N. Cullen, A. Lithio, **A. S. Seetharam.**, Y. Zheng, G. Li, D. Nettleton, and A. O'Connor. Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. *Veterinary Microbiology*, 207(2017):267–279, 2017
12. M. Cao, **A. S. Seetharam.**, A. J. Severin, and Z. Shao. Rapid isolation of centromeres from *Scheffersomyces stipitis*. *ACS synthetic biology*, 6(11):2028–2034, 2017
11. R. E. Masonbrink, A. J. Severin, and **A. S. Seetharam.** Comparative genomics of Soybean and other legumes. In *The Soybean Genome*, pages 83–93. Springer, 2017
10. B. Chowdhury[†], **A. S. Seetharam[†]**, Z. Wang, Y. Liu, A. C. Lossie, J. Thimmapuram, and J. Irudayaraj. A study of alterations in DNA epigenetic modifications (5mC and 5hmC) and gene expression influenced by simulated microgravity in human lymphoblastoid cells. *PLOS ONE*, 11(1):e0147514, 2016
9. **A. S. Seetharam.**, A. Gomez, C. M. Purcell, J. R. Hyde, P. D. Blood, and A. J. Severin. NCBI-BLAST programs optimization on XSEDE resources for sustainable aquaculture. In *Proceedings of the 2015 XSEDE Conference: Scientific Advancements Enabled by Enhanced Cyberinfrastructure*, page 4. ACM, 2015
8. C. Xue, **A. S. Seetharam.**, O. Musharova, K. Severinov, S. J. J. Brouns, A. J. Severin, and D. G. Sashital. CRISPR interference and priming varies with individual spacer sequences. *Nucleic acids research*, 43(22):10831–10847, 2015
7. **A. S. Seetharam.**, E. Kawaler, Z.-Q. Du, M. F. Rothschild, and A. J. Severin. Microbiome analyses of pacific white shrimp (*Litopenaeus vannamei*) collected from disparate geographical locations. *Genomics data*, 6:67, 2015
6. **A. S. Seetharam.** and G. W. Stuart. Whole genome phylogeny for 21 drosophila species using predicted 2b-RAD fragments. *PeerJ*, 1:e226, 2013
5. **A. S. Seetharam.** and G. W. Stuart. A study on the distribution of 37 well conserved families of C2H2 zinc finger genes in Eukaryotes. *BMC genomics*, 14(1):420, 2013
4. Rajkumar, F. Bashasab, S. P. Kavil, Y. Girma, **A. S. Seetharam.**, D. Dadakhalandar, B. H. Gurusiddesh, A. M. Patil, M. Thudi, S. B. Bhairappanavar, Y. D. Narayana, P. U. Krishnaraj, B. M. Khadi, and M. Y. Kamatar. Molecular mapping of genomic regions harbouring QTLs for root and yield traits in sorghum (*Sorghum bicolor* l. Moench). *Physiology and Molecular Biology of Plants*, 19(3):409–419, 2013
3. **A. S. Seetharam.** and G. W. Stuart. Whole genome phylogenies for multiple Drosophila species. *BMC research notes*, 5(1):670, 2012
2. **A. S. Seetharam.**, Y. Bai, and G. W. Stuart. A survey of well conserved families of C2H2 zinc-finger genes in *Daphnia*. *BMC genomics*, 11(1):276, 2010

1. S. R. Pallam-Reddy, F. Bashasab, Rajkumar, S. M. Punnuri, **A. S. Seetharam.**, M. S. Kuruvinashetti, I. K. Das, and N. Seetharama. Molecular mapping of genomic regions harboring QTLs for stalk rot resistance in sorghum. *Euphytica*, 159(1-2):191-198, 2007

* see my ORCID [0000-0002-6789-9298](https://orcid.org/0000-0002-6789-9298) profile for the up-to-date publications list.

† equal contribution - shared first-author

Thesis and Dissertations

1. **A. S. Seetharam.** *Phylogenomics: Molecular Evolution in the Genomics Era*. PhD thesis, Indiana State University, Terre Haute, IN, United States of America, 2012
2. **A. S. Seetharam.** *in silico* EST datamining for elucidation of repeats biology and functional annotation in Sorghum [*Sorghum bicolor* (L.) Moench.]. Master's thesis, University of Agricultural Sciences, Dharwad, Karnataka, India, 2006

Academic Memberships

Society for the Study of Evolution (SSE)	2020-current
Research Data Alliance (RDA)	2020-current
International Society for Computational Biology	2019-current
American Society of Plant Biology: Plantae Community	current
MaizeGDB: Maize Cooperator	2020-current
Indiana Academy of Sciences	current
The Bioinformatics Organization, Inc	current
IEEE Computational Intelligence Society	2019
Society for Molecular Biology and Evolution	2013
Student Government Association at Indiana State University	2008

Attended Workshops

Tassel Hackathon (Tassel Program), at Buckler Lab, Cornell University, Ithaca, NY	Nov, 2015
GMOD Training , by Generic Model Organism Database (GMOD) online	May, 2014
iPlant Tools and Services Workshop , at Purdue University, West Lafayette, IN	May, 2012
Workshop on Molecular Evolution , at Marine Biological Laboratory, Woods Hole, MA	May, 2010

Talks and Lectures

1. **Genome evolution in the Andropogoneae tribe of grasses**, talk presented at *Zaevolution Webinar series* conducted by Prof. Rubén Rellán-Álvarez, NC State University, Raleigh, NC. September 29, 2021.
2. **Coming of age: complete genomes and accurate gene annotations**, lead talk, presented at *Advances and Future Outlook in Biotechnology and Crop improvement for Sustainable Productivity conference*, University of Horticultural Sciences, Bagalkot, Karnataka, India. November 24-27, 2020.
3. **Complete genomes and accurate annotations: Are we there yet?**, talk presented at University of California, Riverside, CA. April 29, 2020.
4. **Consolidated approach for characterizing genomic structural variants across the maize NAM founders**, talk presented at *Zaevolution Webinar series* conducted by Prof. Jeffrey Ross-Ibarra, University of California, Davis, CA. April 22, 2020.
5. Guest lecturer for the course *EEOB 561: Evolutionary and Ecological Genomics* offered by Dr. Matthew Hufford, Iowa State University, Ames, IA. Spring 2020.

6. **Optimizing Orphan Gene Prediction: Case Study using *Arabidopsis thaliana* Genome** talk presented at Biomedical Sciences Seminar Series at Veterinary Medicine, Iowa State University, Ames, IA. February 21, 2019.
7. Guest lecturer for the course *Agron 523: Molecular Plant Breeding* offered by Dr. Thomas Lubberstedt, Iowa State University, Ames, IA. Spring 2019.
8. Guest lecturer for the course *BCB 590: Introduction to Next-Generation Sequencing* offered by Dr. Usha Muppirala, Iowa State University, Ames, IA. Fall 2015.
9. **Developing genomic resources for agricultural research**, talk presented at *Celebrating 50 Years Graduate Education in Biology*, Indiana State University, Terre Haute, IN. October 3, 2015.
10. Guest lecturer for the course *Gen 349X: The genome perspective in biology* offered by Dr. Jeffery K. Beetham, Iowa State University, Ames, IA. Spring 2015.
11. **Developing genomic resources for Teosinte, Seriola and Streptochoeta**, Talk presented at *Plant and Animal Genomes XXIII conference*, San Diego, California. January 9-14, 2015.
12. Guest lecturer for the course *EEOB 561X: Evolutionary and Ecological Genomics* offered by Dr. Matthew B. Hufford, Iowa State University, Ames, IA. Spring 2014.
13. Guest lecturer for the course *ENTM 595: Systematics and Phylogenetic Methods* offered by Dr. Jennifer Zaspel, Purdue University, West Lafayette, IN. Fall 2013.
14. **Next Gen Phylogenomics: overview of non-traditional methods**, talk presented at *Bioinformatics Seminar series from Department of Statistics*, Purdue University, West Lafayette, IN. March 26th 2013.
15. **Multi-locus *Drosophila* Phylogenomics using TypeIIB enzyme target sites**, talk presented at *Indiana Academy of Sciences annual meeting*, Purdue University, West Lafayette, Indiana. March 10, 2012.
16. **Whole Genome Phylogeny of *Drosophila* spp. based on Singular Value Decomposition analysis**, talk presented at *Indiana Academy of Sciences Fall meeting*, Indiana University, Kokomo, Indiana. October 22-23, 2009.

Conference Posters

51. A. Phillips, T. AuBuchon-Elder, **A. S. Seetharam.**, M. Hufford, E. Kellogg, and J. Ross-Ibarra. Implications of whole genome duplication on local adaptation in *Andropogon gerardi*. *Poster presented at Botany 2021 virtual conference* July 19-23, 2021
50. D. S. Senchina, **A. S. Seetharam.**, and M. A. Perera. Tissue-Specific Metabolite Profiling of Bloodroot (*Sanguinaria canadensis* L., Papaveraceae) Extracts using Liquid Chromatography-Tandem Mass Spectrometry (LC/MS). *Poster presented at Botany 2021 virtual conference* July 19-23, 2021
49. S. J. Snodgrass, J. Engelhorn, **A. S. Seetharam.**, M. Khaipho-Burch, J. Ross-Ibarra, T. Hartwig, and M. B. Hufford. Variance Component Analysis of MOA-seq identified transcription factor binding sites for 143 maize traits. *Poster presented at Evolution 2021 virtual conference* June 21-25, 2021
48. S. J. Snodgrass, J. Engelhorn, **A. S. Seetharam.**, M. Khaipho-Burch, J. Ross-Ibarra, T. Hartwig, and M. B. Hufford. Find-cis: High-resolution mapping of functional cis-elements in the maize drought response. *Poster presented at 63rd Annual Maize Genetics Conference, held virtually* March 8-12, 2021
47. J. Li, U. Singh, **A. S. Seetharam.**, and E. Wurtele. Annotating and characterizing the orphan genes of *zea mays* b73 and nam lines. *Poster presented at 63rd Annual Maize Genetics Conference, held virtually* March 8-12, 2021
46. Y. Qiu, K. M. Chougule, **A. S. Seetharam.**, M. B. Hufford, D. Ware, R. K. Dawe, and C. N. Hirsch. Maize pan-genome construction using 26 nam genome assemblies. *Poster presented at 63rd Annual Maize Genetics Conference, held virtually* March 8-12, 2021

45. N. Manchanda, K. Chougule, A. Olson, K. Fengler, **A. S. Seetharam.**, V. Llaca, G. Zastrow-hayes, S. Wei, I. Braun, M. Lopez, W. Ployaram, S. Zarecor, Z. Lu, J. Walley, M. Nelson, K. Wang, D. Adams, D. Ware, B. Schmitz, M. Woodhouse, N. Lauter, C. Andorf, C. Lawrence-Dill, and M. Hufford. Sequence, assembly and annotation of maize inbred b104. *Poster presented at 63rd Annual Maize Genetics Conference, held virtually March 8-12, 2021*
44. **A. S. Seetharam.**, M. R. Woodhouse, S. J. Snodgrass, N. Manchanda, S. Ou, R. D. Coletta, M. Syring, J. L. Portwood, R. K. Dawe, C. N. Hirsch, and M. B. Hufford. Consolidated approach for characterizing genomic structural variants across the maize nam founders. *Poster presented at 62nd Annual Maize Genetics Conference, held virtually March 12-15, 2020*
43. N. Manchanda, **A. S. Seetharam.**, K. A. Fengler, V. Llaca, G. Zastrow-Hayes, I. Braun, M. D. Lopez, W. Ployaram, S. Zarecor, Z. Lu, K. Chougule, J. W. Walley, M. D. Yandeu-Nelson, K. Wang, R. J. Schmitz, M. R. Woodhouse, N. Lauter, C. M. Andorf, C. J. Lawrence-Dill, and M. B. Hufford. Sequence, assembly and annotation of maize inbred b104: A maize transformation resource. *Poster presented at 62nd Annual Maize Genetics Conference, held virtually March 12-15, 2020*
42. C. Hirsch, C. O'Connor, T. Guo, R. DellaColetta, X. Li, **A. S. Seetharam.**, K. Chougule, B. Wang, Z. Lu, S. Ou, Z. Li, P. Monnahan, J. Liu, X. Wei, M. Woodhouse, K. Fengler, A. Gilbert, C. Andorf, J. Gent, J. Yu, S. McGaugh, D. Ware, M. B. Hufford, and R. K. Dawe. Characterizing the maize pan-genome and effects on phenotypic variation. *Poster presented at 62nd Annual Maize Genetics Conference, held virtually March 12-15, 2020*
41. A. Phillips, T. AuBuchon, **A. S. Seetharam.**, M. B. Hufford, and E. Kellogg. Persistence and evolution of polyploid complexes within a species. *Poster presented at 62nd Annual Maize Genetics Conference, held virtually March 12-15, 2020*
40. S. Chudalayandi, M. Sayadi, **A. S. Seetharam.**, R. E. Masonbrink, and A. J. Severin. Bioinformatics workbook: Case study. *Poster presented at Plant and Animal Genomes XXVIII conference, San Diego, California. January 11-15, 2020*
39. E. S. Wurtele, U. Singh, P. Bhandary, J. Li, and **A. S. Seetharam.** Targets of Opportunity: The Birth of Orphan Genes, Exemplified in Yeast, Arabidopsis, Maize and Humans. *Poster presented at Plant and Animal Genomes XXVIII conference, San Diego, California. January 11-15, 2020*
38. R. Masonbrink, T. R. Maier, **A. S. Seetharam.**, T. J. Baum, and A. J. Severin. The genome of the soybean cyst nematode (*Heterodera glycines*). *Poster presented at Plant and Animal Genomes XXVIII conference, San Diego, California. January 11-15, 2020*
37. **A. S. Seetharam.**, N. Manchanda, S. Banerjee, M. R. Woodhouse, J. D. Campbell, C. Andorf, E. K. Cannon, E. S. Wurtele, and M. B. Hufford. A novel, evidence-weighted pipeline for improving maize gene structure annotations. *Poster presented at 61st Annual Maize Genetics Conference, St. Louis, Missouri. March 14-17, 2019*
36. S. Chudalayandi, **A. S. Seetharam.**, R. E. Masonbrink, M. Sayadi, and A. J. Severin. A living bioinformatics workbook. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California. January 12-16, 2019*
35. D. E. Hufnagel, M. B. Hufford, and **A. S. Seetharam.** SequelQC: Analyzing PacBio Sequel raw sequence quality. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California. January 12-16, 2019*
34. R. E. Masonbrink, T. Maier, **A. S. Seetharam.**, P. S. Juvale, L. Baber, M. G. Mitchum, A. J. Severin, and T. J. Baum. SCNBase: A genomics portal for the soybean cyst nematode (*Heterodera glycines*). *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California. January 12-16, 2019*
33. **A. S. Seetharam.**, Z. W. Arendsee, and E. S. Wurtele. Optimizing orphan gene prediction: Case study using *Arabidopsis thaliana* genome. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California. January 12-16, 2019*

32. R. E. Masonbrink, C. Purcell, S. Boles, A. Whitehead, **A. S. Seetharam.**, J. Hyde, and A. J. Severin. Genomic resources for California Abalone species. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California.* January 12-16, 2019
31. R. E. Masonbrink, T. Maier, U. Muppirala, **A. S. Seetharam.**, E. Lord, P. S. Juvale, J. Schmutz, N. Johnson, M. G. Mitchum, D. Korkein, S. E. Akker, B. Mimee, M. E. Hudson, A. J. Severin, and T. J. Baum. The genome of the Soybean Cyst Nematode (*Heterodera glycines*). *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California.* January 12-16, 2019
30. M. Woodhouse, E. R. Cannon, R. K. Dawe, M. B. Hufford, D. Ware, **A. S. Seetharam.**, D. E. Hufnagel, J. Stein, and N. Manchanda. Gene copy number variation in the maize pan-genome. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California.* January 12-16, 2019
29. **A. S. Seetharam.**, M. Woodhouse, J. Liu, D. E. Hufnagel, S. Pedersen, K. Chougule, J. Stein, D. Ware, R. K. Dawe, and M. B. Hufford. Comparative analyses of NAM founder lines using whole genome assemblies. *Poster presented at Plant and Animal Genomes XXVII conference, San Diego, California.* January 12-16, 2019
28. **A. S. Seetharam.** and E. S. Wurtele. Maximizing gene prediction using traditional gene finding pipelines. *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
27. **A. S. Seetharam.**, C. Purcell, R. E. Masonbrink, O. Snodgrass, S. Teo, J. Hyde, and A. J. Severin. Sequencing albacore (*Thunnus alalunga*) genome to identify sex specific markers. *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
26. **A. S. Seetharam.**, C. Purcell, R. E. Masonbrink, S. Chudalayandi, M. Drawbridge, J. Hyde, and A. J. Severin. Genome assembly and annotation for almaco jack (*Seriola rivoliana*). *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
25. R. E. Masonbrink, **A. S. Seetharam.**, S. Chudalayandi, J. Hyde, C. Purcell, and A. J. Severin. The red abalone genome and the consequences of inbreeding in white abalone aquaculture. *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
24. R. E. Masonbrink, T. Maier, **A. S. Seetharam.**, E. Lord, P. S. Juvale, B. Mimee, S. E. Akker, A. J. Severin, and T. J. Baum. A trio of evolutionary mechanisms give rise to a diversity of parasitic effector genes in the Soybean Cyst Nematode. *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
23. P. Blood, N. Ghaffari, **A. S. Seetharam.**, L. Pipes, R. Singh, J. Abante, A. J. Severin, C. D. Johnson, and C. E. Mason. Fast, flexible, and free: Enabling large-scale genome assembly and analysis with the bridges supercomputer. *Poster presented at Plant and Animal Genomes XXVI conference, San Diego, California.* January 13-17, 2018
22. R. E. Masonbrink, T. Maier, U. Muppirala, **A. S. Seetharam.**, P. Juvale, A. J. Severin, and T. J. Baum. Scnbase: A community resource for soybean cyst nematode (*heterodera glycines*) genomics. *Poster presented at Plant and Animal Genomes XXV conference, San Diego, California.* January 14-18
21. A. J. Severin, C. Purcell, M. Carter, R. E. Masonbrink, **A. S. Seetharam.**, J. Hyde, and L. Baber. *Seriola Genomics* and the knowledge repository *serioladb.org*. *Poster presented at Plant and Animal Genomes XXV conference, San Diego, California.* January 14-18, 2017
20. **A. S. Seetharam.**, C. Purcell, R. E. Masonbrink, A. J. Severin, and J. Hyde. Development of a genomic toolkit for *Haliotis* species. *Poster presented at Plant and Animal Genomes XXV conference, San Diego, California.* January 14-18, 2017
19. **A. S. Seetharam.**, A. J. Severin, M. B. Hufford, L. Clark, and E. Kellogg. *Streptochaeta angustifolia*: a keystone genome for understanding evolution of cereals and grains. *Poster presented at Plant and Animal Genomes XXIV conference, San Diego, California.* January 9-13, 2016

18. A. J. Severin, **A. S. Seetharam.**, C. Purcell, and J. Hyde. Sex determination and diversity of *Seriola dorsalis* in three distinct geographical location. *Poster presented at Plant and Animal Genomes XXIV conference, San Diego, California.* January 9-13, 2016
17. **A. S. Seetharam.**, Z. Lang, Z. Lemmon, A. J. Severin, J. Doebley, J. Lai, and M. B. Hufford. The teosinte (*Zea mays* ssp. *parviglumis*) *de novo* genome assembly and annotation. *Poster presented at 57th Annual Maize Genetics Conference, St. Charles, Illinois.* March 12-15, 2015
16. **A. S. Seetharam.**, Z. Lang, Z. Lemmon, A. J. Severin, J. Doebley, J. Lai, and M. B. Hufford. The teosinte (*Zea mays* ssp. *parviglumis*) *de novo* genome assembly. *Poster presented at Plant and Animal Genomes XXIII conference, San Diego, California.* January 9-14, 2015
15. A. J. Severin, **A. S. Seetharam.**, C. Purcell, and J. Hyde. Genome assembly for *Seriola lalandi*. *Poster presented at Plant and Animal Genomes XIII conference, San Diego, California.* January 9-14, 2015
14. A. Jamison, **A. S. Seetharam.**, and E. M. Tuttle. Molecular ecology and the use of molecular methods of identification of three different parasitic genera. *Poster presented at Symposium: A Celebration of Student Research and Creativity, Indiana State University, Terre Haute, Indiana.* April 4-5, 2012
13. V. M. Keller, **A. S. Seetharam.**, and G. W. Stuart. A RAD-tag sampling method for deep level whole genome phylogenies. *Poster presented at 19th annual meeting of the Society for Molecular Biology and Evolution, Kyoto, Japan.* June 26-30, 2011
12. **A. S. Seetharam.**, V. M. Keller, and G. W. Stuart. Study on conservation and distribution of C2H2 zinc-finger genes in eukaryotes. *Poster presented at 6th International Symposium on Bioinformatics Research and Applications (ISBRA) University of Connecticut, Storrs, Connecticut.* May 23-26, 2010
11. A. Jamison, **A. S. Seetharam.**, and E. M. Tuttle. Identification of avian malarial parasites, using RFLPs to distinguish three parasitic genera. *Poster presented at Symposium: A Celebration of Student Research and Creativity, Indiana State University, Terre Haute, Indiana.* April 21, 2010
10. **A. S. Seetharam.** and G. W. Stuart. Single calculation whole genome phylogenies for multiple *Drosophila* species. *Poster presented at 17th annual meeting of the Society for Molecular Biology and Evolution, Iowa City, Iowa.* June 3-7, 2009
9. V. M. Keller, **A. S. Seetharam.**, and G. W. Stuart. Conservation of C2H2 zinc finger genes in genomes. *Poster presented at Undergraduate Research Conference, Butler University, Indianapolis, Indiana.* April 18, 2009
8. V. M. Keller, **A. S. Seetharam.**, and G. W. Stuart. Evolutionary origin analysis of zinc finger genes. *Poster presented at Symposium: A Celebration of Student Research and Creativity, Indiana State University, Terre Haute, Indiana.* April 8, 2009
7. **A. S. Seetharam.** and G. W. Stuart. Novel chordate phylogeny based on improved Singular Value Decomposition (SVD) analysis. *Poster presented Symposium: A Celebration of Student Research and Creativity, Indiana State University, Terre Haute, Indiana.* April 8, 2009
6. **A. S. Seetharam.** and G. W. Stuart. Novel chordate phylogeny based on improved SVD analysis. *Poster presented at Indiana Academy of Sciences Fall meeting, University of Evansville, Evansville, Indiana.* October 23-25, 2008
5. **A. S. Seetharam.** and G. W. Stuart. Phylogenomics of metazoans based on SVD analysis. *Poster presented at 4th International Symposium on Bioinformatics Research and Applications Georgia State University, Atlanta, Georgia.* May 6-8, 2008
4. **A. S. Seetharam.** and G. W. Stuart. Phylogenomics of metazoans based on SVD analysis. *Abstract presented at 11th annual ISU research Showcase, Indiana State University, Terre Haute, Indiana.* April 2, 2008
3. P. R, F. Bashasab, **A. S. Seetharam.**, P. Pallam-Reddy, Srinivasa Reddy, and M. S. Kuruvinashetti. Drought tolerance studies in sorghum. *Poster presented at the Northeast Agricultural and Biological Engineering Conference, Montreal, Quebec, Canada.* July 30 - August 2, 2006

2. **A. S. Seetharam.**, F. Bashasab, and M. S. Kuruvinashetti. Genic ssrs in sorghum EST database: patterns, abundance and distribution. *Poster presented at the International conference on biotechnology approaches for alleviating malnutrition and health, Bangalore, Karnataka, India.* January 9-11, 2006
1. **A. S. Seetharam.**, F. Bashasab, P. R, S. R. Pallam-Reddy, and M. S. Kuruvinashetti. *in silico* functional annotation and mapping of microsatellite contained ESTs of sorghum. *Poster presented at the International conference on biotechnology approaches for alleviating malnutrition and health, Bangalore, Karnataka, India.* January 9-11, 2006

References

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