

Arun S. Seetharam

Associate Scientist
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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 10 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: “ <i>In silico</i> 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	Associate Scientist <i>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

Associate Scientist, 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 Big Data.
- 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 bz1p60 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
- Differential gene expression of 4 different apple genotypes during fruiting stages
- Gene flow and dispersal evolution in *Lasthenia* species: RAD-seq project
- 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. Was involved in identifying differentially expressed genes during drought conditions using cDNA subtraction methods.

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 as 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**: currently in charge of installation and management of bioinformatics programs ISU-HPC clusters Condo, Nova and HPC-Class. These programs are installed using environmental modules and allow users to dynamically load/unload any programs as needed.
- **Genome portal development**: For *Seriola* spp. (SeriolaDB.org) and for Soybean Cyst Nematode (SCN-base.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.
- **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)
2019	Co-I	<i>Investigating gestational glyphosate exposure-induced adverse outcome pathways</i> Agency: National Institutes of Health-RO1 Status: Pending
2019	Co-PI	<i>The Molecular Hallmark of Epigenetic Control in High Performing Yeasts</i> Agency: National Science Foundation (EFRI) Status: pre-proposal accepted, invited for a full proposal.
2019	Co-PI	<i>Epigenetics 1: Exploring 4D Epigenomics to Elucidate Novel Design Rules in High-performing Yeasts</i> Agency: National Science Foundation (URoL) Status: Pending
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

- 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
• 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. Ou, J. Liu, K. M. Chougule, A. Functammasan, **Seetharam, Arun**, J. Stein, V. Llaca, N. Manchanda, A. M. Gilbert, X. Wei, C.-S. Chin, D. E. Hufnagel, S. Pedersen, S. Snodgrass, K. Fengler, M. Woodhouse, B. P. Walenz, S. Koren, A. M. Phillippy, B. T. Hannigan, R. K. Dawe, C. Hirsch, M. Hufford, and D. Ware. Effect of sequence depth and length in long-read assembly of the Maize inbred NC358. *bioRxiv*, 2019
2. D. E. Hufnagel, M. B. Hufford, and **Seetharam, Arun S.** SequelTools: A suite of tools for working with PacBio Sequel raw sequence data. *bioRxiv*, 2019
3. K. Murugan, **Seetharam, Arun S.**, A. J. Severin, and D. G. Sashital. Pervasive off-target and double-stranded DNA nicking by CRISPR-Cas12a. *bioRxiv*, 2019
4. N. Manchanda, J. L. Portwood, M. R. Woodhouse, **Seetharam, Arun**, C. J. Lawrence-Dill, C. M. Andorf, and M. Hufford. GenomeQC: A quality assessment tool for genome assemblies and gene structure annotations. *bioRxiv*, 2019
5. **Seetharam, Arun**, U. Singh, J. Li, P. Bhandary, Z. Arendsee, and E. S. Wurtele. Maximizing prediction of orphan genes in assembled genomes. *bioRxiv*, 2019
6. J. Liu, **Seetharam, Arun S.**, 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. *bioRxiv*, 2020

REVIEW

1. P. Bhandary, **Seetharam, Arun S**, 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

BOOK CHAPTER

1. R. E. Masonbrink, A. J. Severin, and **Seetharam, Arun S**. Comparative genomics of Soybean and other legumes. In *The Soybean Genome*, pages 83–93. Springer, 2017

RESEARCH ARTICLES

22. A. M. Elashry, S. S. Habash, P. Vijayapalani, N. Brocke-Ahmadinejad, R. Blümel, **Seetharam, Arun**, H. Schoof, and F. M. Grundler. Transcriptome and parasitome analysis of beet cyst nematode *Heterodera schachtii*. *Scientific Reports*, 10(1):1–12, 2020
21. R. Masonbrink, T. R. Maier, **Seetharam, Arun S**, P. S. Juvalé, 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
20. Z. Arendsee, J. Li, U. Singh, P. Bhandary, **Seetharam, Arun**, 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, **Seetharam, Arun**, K. Dorman, and E. S. Wurtele. phylostratr: A framework for phylostratigraphy. *Bioinformatics*, btz171, 2019
18. R. E. Masonbrink, C. Purcell, S. Boles, A. Whitehead, J. Hyde, **Seetharam, Arun S**, 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
17. S. N. Barnes, R. E. Masonbrink, T. R. Maier, **Seetharam, Arun**, 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
16. R. Masonbrink, T. R. Maier, U. Muppirala, **Seetharam, Arun S**, E. Lord, P. S. Juvalé, 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
15. J. T. Trujillo, **Seetharam, Arun S**, 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
14. C. M. Purcell, **Seetharam, Arun S**, 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
13. M. Cao, M. Gao, C. L. Lopez-Garcia, Y. Wu, **Seetharam, Arun S**, A. J. Severin, and Z. Shao. Centromeric DNA facilitates nonconventional yeast genetic engineering. *ACS synthetic biology*, 6(8):1545–1553, 2017
12. J. N. Cullen, A. Lithio, **Seetharam, A S**, 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
11. M. Cao, **Seetharam, Arun S**, A. J. Severin, and Z. Shao. Rapid isolation of centromeres from *Scheffersomyces stipitis*. *ACS synthetic biology*, 6(11):2028–2034, 2017
10. B. Chowdhury, **Seetharam, Arun S**, 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. **Seetharam, Arun S**, 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, **Seetharam, Arun S**, 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. **Seetharam, Arun S**, 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. **Seetharam, Arun S** and G. W. Stuart. Whole genome phylogeny for 21 drosophila species using predicted 2b-RAD fragments. *PeerJ*, 1:e226, 2013
5. **Seetharam, Arun S** 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, B. Fakrudin, S. P. Kavil, Y. Girma, **Seetharam, Arun S**, D. Dadakhalandar, B. H. Gurusiddesh, A. M. Patil, M. Thudi, S. B. Bhairappanavar, et al. 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. **Seetharam, Arun S** and G. W. Stuart. Whole genome phylogenies for multiple Drosophila species. *BMC research notes*, 5(1):670, 2012
2. **Seetharam, Arun S**, 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. P. S. Reddy, B. Fakrudin, Rajkumar, S. M. Punnuri, **Seetharam, Arun S**, 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.

THESIS AND DISSERTATIONS

1. **Seetharam, Arun S**. *Phylogenomics: Molecular Evolution in the Genomics Era*. PhD thesis, Indiana State University, Terre Haute, IN, United States of America, 2012
2. **Seetharam, Arun S**. *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

PROFESSIONAL ACTIVITIES

ACADEMIC MEMBERSHIPS

International Society for Computational Biology	current
IEEE Computational Intelligence Society	current
Indiana Academy of Sciences	current
The Bioinformatics Organization, Inc	current
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. Guest lecturer for the course *EEOB 561: Evolutionary and Ecological Genomics* offered by Dr. Matthew Hufford, Spring 2020, Iowa State University.
2. Invited talk for Biomedical Sciences Seminar Series at Veterinary Medicine, Iowa State University, Ames, IA. February 21, 2019.
3. Guest lecturer for the course *Agron 523: Molecular Plant Breeding* offered by Dr. Thomas Lubberstedt, Spring 2019, Iowa State University.
4. Guest lecturer for the course *BCB 590: Introduction to Next-Generation Sequencing* offered by Dr. Usha Muppirala, Fall 2015, Iowa State University.
5. Invited talk for Celebrating 50 Years Graduate Education in Biology at Indiana State University, Terre Haute, IN. October 3, 2015.
6. Guest lecturer for the course *Gen 349X: The genome perspective in biology* offered by Dr. Jeffery K. Beetham, Spring 2015, Iowa State University.
7. Developing genomic resources for *Teosinte*, *Seriola* and *Streptochaeta*. *Talk presented at Plant and Animal Genomes XXIII conference, San Diego, California. January 9-14, 2015*
8. Guest lecturer for the course *EEOB 561X: Evolutionary and Ecological Genomics* offered by Dr. Matthew B. Hufford, Spring 2014, Iowa State University.
9. Guest lecturer for the course *ENTM 595: Systematics and Phylogenetic Methods* offered by Dr. Jennifer Zaspel, Fall 2013, Purdue University.
10. *Next Gen Phylogenomics: overview of non-traditional methods* March, 2013. Talk presented on March 26th 2013, for Bioinformatics Seminar series from Department of Statistics, Purdue University.
11. 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*
12. 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

40. S. Chudalayandi, M. Sayadi, **Seetharam, Arun S**, 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 **Seetharam, Arun S**. 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, **Seetharam, Arun S**, 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. **Seetharam, Arun S**, 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, **Seetharam, Arun S**, 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 **Seetharam, Arun S.** 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, **Seetharam, Arun S.**, P. S. Juvalé, 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. **Seetharam, Arun S.**, 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, **Seetharam, Arun S.**, 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, **Seetharam, Arun S.**, E. Lord, P. S. Juvalé, J. Schmutz, N. Johnson, M. G. Mitchum, D. Korkin, 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, **Seetharam, Arun S.**, 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
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