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, on time.
- Over 10 years of experience in bioinformatics data analyses, with an excellent publication record.
- Worked on 7 different eukaryotic genome assembly and annotation projects.
- Developed programs, pipelines and scripts for streamlining data analyses (open source).

EDUCATION

Indiana State University, Terre Haute, Indiana USA   **Aug 2007 - May 2012**
   Ph.D. in Biology.

   - OGP: 3.97/4.00
   - Dissertation Topic: "Phylogenomics: Molecular Evolution in Genomics era"
   - Advisor: Gary W. Stuart, Ph.D.

University of Agricultural Sciences, Dharwar, Karnataka.   **Dec 2003 - March 2006**
   M.Sc. Agriculture (Plant Biotechnology)

   - OGP: 9.26/10.00
   - Thesis Topic: "*In silico* EST data-mining for elucidation of repeats biology and functional annotation in sorghum, *Sorghum bicolor* (L.) moench"
   - Advisor: B. Fakrudin, Ph.D.

University of Agricultural Sciences, Bangalore, Karnataka.   **Aug 1999 - June 2003**
   B.Sc. Agriculture.

   - OGP: 9.09/10.00
   - Major: Agronomy

POSITIONS

Associate Scientist   **Feb 2016 - present**
   Genome Informatics Facility, Iowa State University, Ames, IA
Post-Doctoral Research Associate   **Jan 2014 - Feb 2016**
   Genome Informatics Facility, Iowa State University, Ames, IA
Post-Doctoral Research Associate   **Jul 2012 - Dec 2013**
   Bioinformatics Core, Purdue University, West Lafayette, IN
Adjunct Faculty   **Aug 2011 - May 2012**
   Dept. of Biology, Indiana State University, Terre Haute, IN
Teaching Assistant   **Aug 2007 - May 2012**
   Dept. of Biology, Indiana State University, Terre Haute, IN
Research Assistant   **May 2006 - Jun 2007**
   University of Agricultural Sciences, Dharwar, Karnataka, India

SYNERGISTIC ACTIVITIES

Publicly available, pipeline and scripts development. Repositories with useful scripts and pipelines for running routine bioinformatics tasks:
- *common_analyses*: scripts for most commonly used programs, optimized to run on clusters.
- *common_scripts*: simple utility scripts to efficiently run or manipulate the NGS data.
- *StampedeBLAST*: Optimized NCBI-BLAST program pipeline for the XSEDE (Stampede) cluster.
- *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 allows users to dynamically load/unload any programs as and when it is needed.

Publicly available tutorials for NGS analyses and workbook Actively contributing for developing a comprehensive wiki pages for various NGS data analyses. The pages include many custom pipelines as well as utility scripts that can be readily used for specific problems.

Genome portal development, SeriolaDB and SCNbase, currently hosting genome databases, using *Drupal/Tripal* backend and *Chado* database schema. Many plugins like *JBrowse, Appollo, BioMart* are being actively developed for these portals.

Posters and participations: Actively participated in many international conferences to present posters (25) and talks (3). Also attended multiple workshops (3) in the filed of NGS/programing.

GRANTS

1. **Co-I**, National Institutes of Health-RO1, Investigating gestational glyphosate exposure-induced adverse outcome pathways *(pending)* **2018**

2. **Co-I**, NSF grant proposal (EFRI), The Molecular Hallmark of Epigenetic Control in High performing Yeasts *(pending)* **2018**

3. **Co-I**, Extreme Science and Engineering Discovery Environment (XSEDE), The prediction of plant and animal orphan genes with comparative genomics and data mining. *(pending)* **2018**

4. **Co-PI**, Extreme Science and Engineering Discovery Environment (XSEDE), Genome Assembly and Annotation of Red Abalone, Yellowtail, Soybean Cyst Nematode and Spiny Softshell Turtle *(current)* **2016**

5. **Post-Doc**, NSF grant proposal (NSF 16-505), Orphan genes: An untapped genetic reservoir of novel traits driving evolutionary adaptation and crop improvement *(current)* **2015**

6. **Co-PI**, XSEDE research grant *(completed)* **2015**

7. **PI**, XSEDE start-up grant *(completed)* **2014**

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**
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

PUBLICATIONS

PRE-PRINTS

1. Zebulun Arendsee, Jing Li, Urminder Singh, **Arun S Seetharam**, Karin Dorman, and Eve Syrkin Wurtele. phylostratr: A framework for phylostratigraphy. *BioRxiv*, page 360164, 2018

RESEARCH ARTICLES

1. Rick E Masonbrink, Catherine Purcell, Sara Boles, Andrew Whitehead, John Hyde, **Arun S Seetharam**, and Andrew 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

2. Stacey N Barnes, Rick E Masonbrink, Thomas R Maier, **Arun S Seetharam**, Anoop S Sindhu, Andrew J Severin, and Thomas 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

3. Rick Masonbrink, Tom R Maier, Usha Muppirala, **Arun S Seetharam**, Etienne Lord, Parijat S Juvale, Jeremy Schmutz, Nathan T Johnson, Dmitry Korkin, Melissa 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

4. Joshua T Trujillo, **Arun S Seetharam**, Matthew B Hufford, Mark A Beilstein, and Rebecca A Mosher. Evidence for a unique dna-dependent rna polymerase in cereal crops. *Molecular biology and evolution*, 35(10):2454–2462, 2018

5. Catherine M. Purcell, **Arun S Seetharam**, Owyn Snodgrass, Sofia Ortega-García, John R. Hyde, and Andrew J. Severin. Insights into teleost sex determination from the *Seriola dorsalis* genome assembly. *BMC Genomics*, 19(31), 2018

6. Mingfeng Cao, Meirong Gao, Carmen Lorena Lopez-Garcia, Yutong Wu, **Arun S Seetharam**, Andrew Josef Severin, and Zengyi Shao. Centromeric dna facilitates nonconventional yeast genetic engineering. *ACS synthetic biology*, 6(8):1545–1553, 2017

7. J. N. Cullen, A. Lithio, **Seetharam, A. S.**, Y. Zheng, G. Li, D. Nettleton, and A.M. O'Connor. Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. *Veterinary Microbiology*, 207(2017):267–279, 2017

8. Mingfeng Cao, **Arun S Seetharam**, Andrew Josef Severin, and Zengyi Shao. Rapid isolation of centromeres from *Scheffersomyces stipitis*. *ACS synthetic biology*, 6(11):2028–2034, 2017

9. Basudev Chowdhury, **Arun S Seetharam**, Zhiping Wang, Yunlong Liu, Amy C. Lossie, Jyothi Thimmapuram, and Joseph 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

10. **Arun S Seetharam**, Antonio Gomez, Catherine M Purcell, John R Hyde, Philip D Blood, and Andrew 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

11. Chaoyou Xue, **Arun S Seetharam**, Olga Musharova, Konstantin Severinov, Stan J J. Brouns, Andrew J Severin, and Dipali G Sashital. Crispr interference and priming varies with individual spacer sequences. *Nucleic acids research*, 43(22):10831–10847, 2015

12. **Arun S Seetharam**, Emily Kawaler, Zhi-Qiang Du, Max F Rothschild, and Andrew J Severin. Microbiome analyses of pacific white shrimp (*Litopenaeus vannamei*) collected from disparate geographical locations. *Genomics data*, 6:67, 2015

13. **Arun S Seetharam** and Gary W Stuart. Whole genome phylogeny for 21 drosophila species using predicted 2b-rad fragments. *PeerJ*, 1:e226, 2013

14. **Arun S Seetharam** and Gary 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

15. Rajkumar, B. Fakrudin, S. P. Kavil, Y. Girma, **Arun, S. 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

16. **Arun S Seetharam** and Gary W Stuart. Whole genome phylogenies for multiple drosophila species. *BMC research notes*, 5(1):670, 2012

17. **Arun S Seetharam**, Yang Bai, and Gary W Stuart. A survey of well conserved families of c2h2 zinc-finger genes in *Daphnia*. *BMC genomics*, 11(1):276, 2010

18. P. Srinivasa Reddy, B. Fakrudin, Rajkumar, S. M. Punnuri, **Arun, S. 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

Review

1. Priyanka Bhandary, **Arun S Seetharam**, Zebulun W Arendsee, Manhoi Hur, and Eve Syrkin 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. Rick E Masonbrink, Andrew J Severin, and **Arun S Seetharam**. Comparative genomics of soybean and other legumes. In *The Soybean Genome*, pages 83–93. Springer, 2017

Thesis and Dissertations

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

2. **Arun 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

Professional avtivities

Acadamic Memberships

Society for Molecular Biology and Evolution	**2014**
Indiana Academy of Sciences	**2008 - 2012**
Student Government Association at Indiana State University	**2008**

Attended Workshops

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

Talks and Lectures

1. Guest lecture for the course *Agron 523: Molecular Plant Breeding* offered by Dr. Thomas Lubberstedt, Spring 2019, Iowa State University.

2. Guest lecture for the course *BCB 590: Introduction to Next-Generation Sequencing* offered by Dr. Usha Muppirala, Fall 2015, Iowa State University.

3. Invited talk for Celebrating 50 Years Graduate Education in Biology at Indiana State University, Terre Haute, IN. October 3, 2015.

4. Guest lecture for the course *Gen 349X: The genome perspective in biology* offered by Dr. Jeffery K. Beetham, Spring 2015, Iowa State University.

5. Developing genomic resources for Teosinte, Seriola and Streptochaeta. *Talk presented at Plant and Animal Genomes XXIII conference, San Diego, California. January 9-14, 2015*

6. Guest lecture for the course *EEOB 561X: Evolutionary and Ecological Genomics* offered by Dr. Matthew B. Hufford, Spring 2014, Iowa State University.

7. Guest lecture for the course *ENTM 595: Systematics and Phylogenetic Methods* offered by Dr. Jennifer Zaspel, Fall 2013, Purdue University.

8. *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.

9. 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*

10. 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*

References

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