

Asela Wijeratne

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PROFILE

Research Scientist with 10+ years of experience in designing, leading, and managing complex biology research projects; recent history includes leadership in bioinformatics core facility. Well-published team player with excellent quantitative, analytical, and problem-solving skills. Ability to work collaboratively with a diverse group of faculty and students, and to build a rigorous learning environment for students to achieve their goals.

EDUCATION

PENNSYLVANIA STATE UNIVERSITY, State College, PA

PhD in Biology | 2007

UNIVERSITY OF PERADENIYA, Sri Lanka

Bachelor of Science | 2000

CONTINUING EDUCATION / PROFESSIONAL DEVELOPMENT

JOHNS HOPKINS UNIVERSITY, Baltimore, MD (via Coursera)

Data Science Specialization Certificate (Nine Courses) | Certificate earned May 2015

GEORGIA INSTITUTE OF TECHNOLOGY (GEORGIA TECH), Atlanta, GA

Machine Learning (Professional Course) | 2015

STANFORD UNIVERSITY, Stanford, CA

Statistical Learning | 2014

SOFTWARE CARPENTRY FOUNDATION

Certified Instructor for Software Carpentry | 2014

RICE UNIVERSITY, Houston, TX (via Coursera)

Programming in Python | 2012

COLD SPRING HARBOR LABORATORY, Cold Spring Harbor, NY

Computational & Comparative Genomics | 2010

EXPERIENCE

ARKANSAS STATE UNIVERSITY, Jonesboro, AR

Instructor in Bioinformatics | Jan 2017 - present

UNIVERSITY OF MEMPHIS, Memphis, TN

Postdoctoral Researcher | Jan 2016 – Jan 2017

Used machine learning based approaches to find genomic regions for phylogenetics in beetles. Managed a project in longhorned beetle phylogenomics and evolution.

OHIO STATE UNIVERSITY, Wooster, OH

Research Scientist | Mar 2010 – Jan 2016

Taught and mentored students and postdocs to do molecular genetics and genomics research, and high-throughput data analysis projects. Conducted and coordinated experiments to support molecular genetic

EXPERIENCE – CONTINUED

research and high-throughput data analysis projects within and outside of The Ohio State University. Successfully completed 13 projects (10 published papers).

- Established sample preparation protocol for next generation sequencing: SNP genotyping, Genomic DNA, RNAseq, small RNA, RADtag, amplicon sequencing and genotype-by-sequencing (GBS).
- Automated sample preparation for next generation sequencing using a liquid handling robot.
- Optimized and automated data analyses protocol for SNP genotyping, RNAseq, small RNA, RADtag and amplicon sequencing.

OHIO STATE UNIVERSITY, Columbus, OH

ERICH GROTEWOLD LAB, DEPARTMENT OF PLANT MOLECULAR AND CELLULAR BIOLOGY

Postdoctoral Researcher | Jun 2007 – Feb 2010

Conducted research on transcription machineries and epigenetic modifications using genomics, molecular biological, biochemical, genetic, and computational biology approaches.

- Developed a high-throughput system to find mutations in the promoter regions allowing rapidly screening of mutations that affect the gene expression.
- Characterized a gene family important for chromatin remodeling.
- Instructed undergraduate and graduate students in the areas of genetics, molecular biology, and bioinformatics.

PENNSYLVANIA STATE UNIVERSITY, University Park, PA

Graduate Research Assistant | Aug 2002 – May 2007

Conducted research to understand the molecular genetic processes involved in male meiosis and early anther development using genomics, transcriptomic, molecular biological, cytological, genetic, and computational biological approaches.

- Identified a key gene important for meiosis and described a set of genes important for meiosis and anther development using microarray for the first time.
- Published five peer-reviewed papers.

TEACHING EXPERIENCE

- **Instructor:** Graduate level course on Methods in Horticulture and Crop Science: Analyzing RNA-seq data from a RIL population (HCS 7806) at the Ohio State University (Fall, 2015) (Other instructors: Leah McHale, PhD).
- **Instructor:** Graduate level course on Methods in High-throughput Sequence Data Analyses (PLNTPH 8300) at the Ohio State University (Spring, 2014) (Developed from scratch) (Other instructors: Tea Meulia, PhD, Saranga Wijeratne, MS).
- **Instructor:** Graduate level course on Molecular Techniques and Data Analysis (ENTMLGY 6703) at the Ohio State University. Other instructors: Omprakash Mittapalli, PhD and Larry Phelan, PhD (Spring, 2014).
- **Guest Lecturer:** Graduate level course: Agricultural Genomics (PLNTPH 7003): DNA sequence analysis and data handling at the Ohio State University. Instructors: Guo-Liang Wang, PhD and Eric Stockinger, PhD (Spring, 2013).

TEACHING EXPERIENCE– *CONTINUED*

- **Journal Club:** Organized a journal club on data analysis from July 1 to August 30, 2014.
- **Workshops:**
 - Software Carpentry workshops:
 - Monsanto company on May 28-29 (Shell and R).
 - Indiana University on September 17 -18, 2015 (Shell, Python and Git) (http://bit.ly/SCW_bloomington).
 - Next-Gen Sequence Analysis Workshop at Michigan State University (http://bit.ly/NGS_2015_week3).
 - Introduction to high-throughput data analysis at Ohio State University on August 18, 2013 (Number of participant 30).
 - Summer workshops on high-throughput data analysis on June 13 to July 31 (2013) (every Friday) at Ohio Agriculture Research and Development Center/Ohio State University (Number of participant 12).
 - Introduction to RNA-Seq approach to study gene expression and hands-on session using Galaxy, North East OHIO Bioinformatics workshop, College of Wooster, Wooster, OH, May 29, 2013 (Number of participant 40).
 - RNA-Seq Approach to Study Gene Expression Profiles in Non-Model Organisms, a tutorial session at Great Lakes Bioinformatics Conference, University of Michigan, Ann Arbor, MI, May 15-17, 2012 (Number of participant ~200).
 - Two-day summer workshops on high-throughput data analysis on July 16, 18 and July 30,31 (2012) at Ohio Agriculture Research and Development Center/Ohio State University (Number of participant 40).
 - Hands-on session on introduction to Galaxy on February 15, 2013 at Ohio Agriculture Research and Development Center/Ohio State University (Number of participant 10).
- **Teaching Assistant at Cold Spring Harbor Laboratory:** Frontiers and Techniques in Plant Science; Summer, 2005.
- **Teaching Assistant-Undergraduate Laboratories Courses in Department of Biology at The Pennsylvania State University:** (Biology 110, Biology: Basic Concepts and Biodiversity; fall, 2003 and 2004; Biology 240W - Biology: Function and Development of Organisms; spring, 2006 and 2007).
- **Mentoring undergraduate students, graduate students and visiting scholars:** Mentored and assisted in the planning and carrying out research projects, data analysis and development of new tools:
 - Graduate Students: Katja Macheimer (2008), Jessica Winburn (2007), Shaun Broderick (2013-2014), Matthew Kost (2013-2014), Anand Kumar (2014-2015).
 - Undergraduate students: Ben Chaney (2008), Stephen Kanzlemer (2008), Andrea Gonzalez (2008-2009), Gabrielle Coors and Michael Janning (Summer, 2012), Rakin Rouf, Douglas Code, Dagmawi Zegeye, Liang Cheng (Summer, 2013).
 - High school students: Martina Fraga (Summer 2011); Stefan Fraga (Summer 2013).
 - Visiting scholars: Gabriel Jose Villamil and David Gonzales (staff members from Philippine Genome Center).

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GRANTS

Recent submissions:

- Co-PI: Evolutionary Consequences of Multiple Horizontal Gene Transfer Events in an Invasive Insect (NSF proposal, 2014).
- Co-PI: Dissecting the role of microRNAs in the resistance phenotype of bed bugs (NSF pre-proposal, 2014).

Funded:

- OARDC instrument grant (2013 and 2014).
 - Co-PI: Targeted Identification of the SNP markers for Gene Cloning using the Solexa Genome Analyzer"; OARDC SEED Interdisciplinary Award #2008-044 (\$200,000; completed 2012).
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VOLUNTEER WORK

Reviewer for Scientific Journals

- Journal of Integrative Plant Biology
- The Plant Methods
- Frontiers in Plant Science
- Microbiological Research
- Journal of the American Society for Horticultural Science

Out-reach activities

- Participated as a speaker for Building with Biology Forum – Engineering the Mosquito at the Pink Palace Museum, Memphis TN (2016).
 - Mentored middle school students for Planting Science project (<http://www.plantingscience.org>) (2014 to present).
 - Conducted the “Breaking the Code” sessions for ~400 school children for Science of Agriculture (2011 to 2015).
 - Served as Judge at 22nd Annual Graduate Exhibition, The Pennsylvania State University.
 - Served as Judge at 71st and 72nd Pennsylvania Junior Academy of Science, Pennsylvania state meet.
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PUBLICATIONS

1. Pavinato VAC, Margarido GRA, **Wijeratne AJ**, Wijeratne S, Meulia T, Souza AP, Michel AP, Zucchi, MI. Restriction site associated DNA (RAD) for *de novo* sequencing and marker discovery in sugarcane borer, *Diatraea saccharalis* Fab.(Lepidoptera: Crambidae). *Molecular Ecology Resources*. doi: 10.1111/1755-0998.12583
2. Arismendi NL, Reyes M, Miller SA; **Wijeratne AJ**; Carrillo R. 2015. Infection of *Candidatus Phytoplasma ulmi* reduces the protein content and alters the activity of detoxifying enzymes in *Amplipcephalus curtulus*. *Entomologia Experimentalis et Applicata*. 157(3): 334-345
3. Sun L, Rodriguez GR, Clevenger JP, Illa-Berenguer E, Lin J, Blakeslee JJ, Liu W, Fei Z, **Wijeratne, A**, Meulia T, van der Knaap E. 2015. Candidate gene selection and detailed morphological evaluations of fs8.1, a quantitative trait locus controlling tomato fruit shape. *J. Exp. Bot.* 66(20): 6471–6482. Epub ahead of print 2015 Jul 14. doi:10.1093/jxb/erv361.

PUBLICATIONS – CONTINUED

4. Bautista M, Anita M, Bhandary B, **Wijeratne AJ**, Michel AP, Hoy CW, Mittapalli O. 2015. Evidence for tradeoffs in detoxification and chemosensation gene signatures in *Plutella xylostella*. *Pest Manag Sci*. 71(3):423–432. Epub ahead of print 2014 Jun 13. doi: 10.1002/ps.3822.
5. Broderick SR, Wijeratne S, **Wijeratne AJ**, Chapin LJ, Meulia T, Jones ML. 2014. RNA-sequencing reveals early, dynamic transcriptome changes in the corollas of pollinated petunias. *BMC Plant Biology*. 14(1): 307. doi: 10.1186/s12870-014-0307-2.
6. Lu P, **Wijeratne AJ**, Wang Z, Copenhaver GP, Ma H. 2014. Arabidopsis PTD Is Required for Type II Crossover Formation and Affects Recombination Frequency in Two Different Chromosomal Regions. *J Genet Genomics*. 41(3):165–75. doi: 10.1016/j.jgg.2014.02.001.
7. Nimmakayala P, Abburi VL, Bhandary A, Abburi L, Vajja VG, Reddy R, **Wijeratne AJ**, Tomason YR (n.d.). 2014. Use of VeraCode 384-plex assays for watermelon diversity analysis and integrated genetic map of watermelon with single nucleotide polymorphisms and simple sequence repeats. *Molecular Breeding*. 34(2):537–548.
8. Stewart LR, Teplier R, Todd J, Jones M, Cassone BJ, Wijeratne S, **Wijeratne AJ**, Redinbaugh M. 2014. Viruses in Maize and Johnsongrass in Southern Ohio. *Phytopathology*. 104(12): 1360–1369. doi: 10.1094/PHYTO-08-13-0221-R.
9. Jiang L*, **Wijeratne AJ***, Wijeratne S, Fraga M, Meulia T, Doohan D, Zhaohu L, Qu F. 2013. Profiling mRNAs of Two *Cuscuta* Species Reveals Possible Candidate Transcripts Shared by Parasitic Plants. *PLoS One*. 8(11): e81389. doi: 10.1371/journal.pone.0081389. (* Equal contributions)
10. Mamidala P, **Wijeratne AJ**, Wijeratne S, Poland T, Qazi SS, Doucet D, Cusson M, Beliveau C, Mittapalli O. 2013. Identification of Odor-Processing Genes in the Emerald Ash Borer, *Agilus planipennis*. *PLoS One*. 8(2): e56555. doi: 10.1371/journal.pone.0056555.
11. Lee S, Mian MR, McHale LK, Wang H, **Wijeratne AJ**, Sneller CH, Dorrance AE. 2013. Novel quantitative trait loci for partial resistance to *Phytophthora sojae* in soybean PI 398841. *Theor Appl Genet*. 126(4): 1121–1132. doi: 10.1007/s00122-013-2040-x.
12. DeLay B, Mamidala P, **Wijeratne AJ**, Wijeratne S, Mittapalli O, Wang J, Lamp W. 2012. Transcriptome analysis of the salivary glands of potato leafhopper, *Empoasca fabae*. *J Insect Physiol*. 58(12): 1626–1634.
13. Lu P, Han X, Qi J, Yang J, **Wijeratne AJ**, Li T, Ma H. 2012. Analysis of *Arabidopsis* genome-wide variations before and after meiosis and meiotic recombination by resequencing *Landsberg erecta* and all four products of a single meiosis. *Genome Res*. 22(3), 508–518. doi: 10.1101/gr.127522.111.
14. Mamidala P, **Wijeratne AJ**, Wijeratne S, Kornacker K, Sudhamalla B, Rivera-Vega LJ, Mittapalli O. 2012. RNA-Seq and molecular docking reveal multi-level pesticide resistance in the bed bug. *BMC Genomics*. 13(1): 6. doi: 10.1186/1471-2164-13-6.
15. Wang H, **Wijeratne AJ**, Wijeratne S, Lee S, Taylor CG, St Martin SK, Dorrance AE. 2012. Dissection of two soybean QTL conferring partial resistance to *Phytophthora sojae* through sequence and gene expression analysis. *BMC Genomics*. 13(1): 428. doi: 10.1186/1471-2164-13-428.

PUBLICATIONS – CONTINUED

16. Qi J, **Wijeratne AJ**, Tomsho LP, Hu Y, Schuster SC, Ma H. 2009. Characterization of meiotic crossovers and gene conversion by whole-genome sequencing in *Saccharomyces cerevisiae*. *BMC Genomics*. 10(1): 475. doi: 10.1186/1471-2164-10-475.
 17. **Wijeratne AJ**, Ma H. 2007. Genetic analyses of meiotic recombination in *Arabidopsis*. *J Integr Plant Biol*. 49(8): 1199–1207. (Review article)
 18. **Wijeratne AJ**, Zhang W, Sun Y, Liu W, Albert R, Zheng Z, Oppenheimer DG, Zhao D, Ma H. 2007. Differential gene expression in *Arabidopsis* wild-type and mutant anthers: insights into anther cell differentiation and regulatory networks. *Plant J*. 52(1): 14–29.
 19. **Wijeratne AJ**, Chen C, Zhang W, Timofejeva L, Ma H. 2006. The *Arabidopsis thaliana* PARTING DANCERS gene encoding a novel protein is required for normal meiotic homologous recombination. *Mol Biol Cell*. 17(3): 1331–1343.
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ADDENDUM

Skills and Techniques

Computational biology

- Expertise in
 - High performance computing
 - Programming in Python, R and bash scripts
 - High-throughput data analysis
 - RNA-seq analyses (De novo assembly, differential gene expression analyses, co-expression analysis)
 - Small RNA analyses (Computational prediction of novel miRNA and analyses of high-throughput data)
 - *De novo* assembly of genomic data
 - ChIP-seq analyses
- Computational finding of *cis*-regulatory elements
- Phylogenetic reconstructions (sequence alignments, building phylogenetic trees)

Software for high-throughput sequence data analysis:

Phylogenetic analysis

- MUSCLE (multiple sequence alignments)
- ClustIX (multiple sequence alignments)
- MEGA (phylogenetic trees)

De novo assembly software

- Velvet
- Rnnotator and Trinity pipelines (transcriptome)
- SOAP *de novo*

Guided assembly

- Mosaik (genome)
- Cufflink and cuffmerge (RNAseq)

Read mapping and search algorithms

- Tophat,
- Bowtie (short read mapping)
- BWA (short read mapping)

- GMAP (est mapping)
- Blast
- Blat
- Tophat (short read mapping)
- Lastz for 454 reads
- Mosaik aligner (Indel and SNP)

Sequence data quality control

- FASTXtoolkit (various manipulations of fastq and fasta files)
- FastQC (initial quality assessment of short reads)
- Cutadapt (removal of adapter sequences)

Differential gene expression

- Partek
- DESeq
- EdgeR
- Cuffcompare and cuffdiff

Annotation

- Blast2Go

SNP and indel analyses

- SAM tools (SNP calling from HT data and indel analysis)

Some of the custom scripts (examples)

- Python script to retrieve 5' and 3' ends from a cDNA file
- Automated RNAseq workflow that runs using a bash scrip to handle many samples

Python script to paralyze blast searches for many sequences

DNA and RNA techniques

- Sample preparation for Next Generations Sequencing for variety of applications (mRNAseq, DNAseq, ChIP-seq and small RNA sequencing)
- PCR genotyping (dCAPs, T-DNA genotyping)
- Semi qRT-PCR and qRT-PCR
- GUS array
- In situ hybridization
- Southern blot
- FACS analysis

Microscopy

- Immunofluorescence microscopy
- Confocal microscopy

Protein localization

- Immunolocalization
- In vivo protein localization
- Transient expression of recombinant proteins

Biochemistry

- Western blot
- *In vitro* transcription and translation
- Co-immunoprecipitation
- Recombinant protein expression and purification
- *In vitro* assay of recombinant protein and protein-protein interaction

Gene cloning

- Conventional cloning
- Cloning using Gateway technology
- Agrobacterium mediate gene transfer (stable and transient)
- Map based cloning