GAURAV MOGHE

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LAB GOALS

Plants make hundreds of thousands of compounds, many of which are important for humanity. Unfortunately, <5% of these compounds can be identified, and in most species, their biosynthetic pathways and enzymes are poorly described. This creates roadblocks in breeding/engineering crops for better stress resilience and in drug and agrochemical discovery. To illuminate this "black box" of phytochemical diversity, my lab seeks to (i) develop computational approaches for better parsing this diversity, (ii) characterize the evolutionary and biosynthetic mechanisms that generate this diversity and (iii) identify how we can use this diversity for human endeavors. We work with several model systems such as tomato, sweet potato, Poaceae crops and Euphorbias implementing diverse techniques such as genomics, molecular biochemistry, mass spectrometry, computational biology, and field work.

SUMMARY OF RESEARCH

Assistant Professor | Cornell University | Plant Biology Section | 2017- current
- **Project 1:** Predicting the functions of enzyme family members, using BAHD acyltransferases – involved in lignin, anthocyanin, polyamine, wax and secondary metabolite production – as models. Work involves developing computational pipelines for predictive biology and validating functions using enzyme assays and protein structure analysis.
- **Project 2:** Identifying genetic basis of resin glycosides in sweet potato. We have characterized remarkable diversity of resin glycoside acylsugars in Convolvulaceae family species. We are currently identifying biosynthetic enzymes and plan to screen sweet potato germplasm for resin glycoside traits to identify breeding accessions and molecular targets.
- **Project 3:** Developing tools to rapidly analyze metabolomic datasets and identify relevant signals. We have performed such analysis in *Brachypodium distachyon* – a model C3 species related to rice and other C4 Poaceae crops. Integrative analysis with transcriptome data is helping identify novel targets for heat shock resilience and association with arbuscular mycorrhizal fungi (AMFs).
- **Project 4:** Characterizing associations between sweet potato, their carotenoids and apocarotenoids, and AMFs. Unraveling the biochemistry of sweet potato-AMF interactions can help devise new molecular strategies for abiotic stress resilience.
- Developed open-source tools and pipelines in Python for analysis of untargeted metabolomics data (https://metapathwaymap.solgenomics.net/), integration of metabolomic-transcriptomic datasets (ongoing) and for gene function prediction using phylogenomic and enzyme activity datasets (GitHub). The latter pipeline provided a 3X improvement in functional predictions of enzyme family members, enabling faster downstream experimental validation.
- As a session co-chair, collaborated with leaders of the Uniprot, Gene Ontology Consortium, NCBI, PathwayTools, KBase and other databases for a workshop on resolving the bottleneck of protein function annotation in organismal genomes. This led to a whitepaper in the journal Databases and a call for additional funding to the National Science Foundation.
- Developed the "Concepts and Techniques in Computational Biology" and "Introduction to Machine Learning for Plant Scientists" courses for advanced students
- Mentored 25 students including 2 postdocs, 1 lab technician and 3 graduate students

- Since 2017, published/submitted 22 papers in journals such as PNAS, The Plant Journal, Molecular Biology and Evolution, Genome Biology and Evolution, Horticulture Research, Current Opinions in Plant Biology and Annual Reviews in Plant Biology.
- Recipient of the 2018 Early Career Award by the American Society of Plant Biologists for exceptional creativity in early career research

Postdoctoral Research Associate | Michigan State University | Robert Last Lab | Department of Biochemistry and Molecular Biology | 2013-2017
- **Project:** Identifying genes and pathway evolution of a plant defense metabolite class called acylsugars. Developed transient gene silencing strategies through elaborate silencing construct design, phylogenomic and mass spectrometric analysis to study metabolic and pathway diversity.
- Study revealed that the whole pathway had reorganized over 50 million years of the Solanaceae (tomato) family evolution, and generated novel hypotheses that were pursued by students who came after me.

Graduate Research Assistant | Michigan State University | Shin-Han Shiu Lab | Genetics Program | Quantitative Biology Dual Degree Program | 2007-2013
- Characterizing evolution of duplicate genes and origin of novel genes in plant genomes
- **Project:** Performing genome assembly and annotation of the wild radish genomes. Used the annotated genes to study how duplicate genes diversify in function. Used SVM to predict whether duplicated genes would be deleted or retained over time, by compiling over 55 features for each gene from sequence, expression, network and evolutionary conservation data.
- Contributed to development of a ML algorithm to predict whether a gene knockout would cause lethality.
- Analyzed dozens of very early RNA-seq datasets (36-bp/50-bp) to determine extent of intergenic transcription and led identification of candidate intergenic transcripts with possible functional significance. Performed strand-specific RNA-seq using very early library protocols.

LIST OF APPENDICES

Appendix 1: Appointments, Education, Honors
Appendix 2: Research accomplishments
Appendix 3: Teaching and mentoring
Appendix 4: Leadership and service

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APPOINTMENTS

Assistant Professor (2017-current)
  Plant Biology Section, School of Integrative Plant Sciences, Cornell University
  Member, Plant Breeding and Genetics Section
  Faculty Fellow, Cornell Atkinson Center for Sustainability
  Faculty Mentor, TW Turner Mentoring Program
  Member, Computational Biology Field, Cornell University
  Member, Chemistry-Biology Interface Training Program
Postdoctoral Research Associate (2013-2017)
  Dept. of Biochemistry and Molecular Biology, Michigan State University, USA
Lecturer, Masters Course in Bioanalytical Sciences (2006-2007)
  Dept. of Bioanalytical Sciences, Ramnarain Ruia College, University of Mumbai, India

EDUCATIONAL BACKGROUND

Doctor of Philosophy, Genetics and Quantitative Biology (2007-2013)
  Dept. of Plant Biology, Michigan State University, USA
Master of Science, Biochemistry (2004-2006)
  Dept. of Biochemistry, The Maharaja Sayajirao University of Baroda, India
Bachelor of Science, Microbiology and Biotechnology (2001-2004)
  Dept. of Microbiology, Ramnarain Ruia College, University of Mumbai, India

AWARDS AND HONORS

- 2023   Arthur J. Neish Young Investigator Award, Phytochemical Society of North America
- 2018   Early Career Award, The American Society of Plant Biologists
- 2017   BMB Postdoctoral Independent Career Potential Award, MSU
- 2016   13th Annual Solanaceae Meeting Travel Award (Speaker)
- 2016   Gordon Research Seminar on Plant Molecular Biology Speaker Award
- 2013   Outstanding Genetics Graduate Student Award, MSU
- 2013   Dissertation Completion and Continuation Fellowships, MSU
- 2009   Research Fellowship, Quantitative Biology Program, MSU
- 2008   Research Fellowship, Gene Expression in Development and Disease, MSU
- 2006   Research Fellowship, Council for Scientific and Industrial Research (CSIR), India
         (similar in scope to NSF Graduate Research Fellowship)

Awards and Honors for trainees
- 2022   Elizabeth Mahood, American Society of Plant Biologists Travel Award
- 2021   Mohammad Irfan (postdoc), Cornell Atkinson Center Postdoctoral Small Grant
- 2021   Se Jin Park (undergraduate student), Finalist, Undergraduate Research – Plant Sciences
- 2021   Elizabeth Mahood (graduate student), Best Oral Talk, Botany: Phytochemistry Section
- 2021   Elizabeth Mahood (graduate student), USDA Predoctoral Fellowship
- 2020   Elizabeth Mahood (graduate student), Third Prize, Cornell Institute for Digital Ag. Hackathon
- 2018   Lars Kruse (postdoc), German DFG Postdoctoral Fellowship

PEER-REVIEWED PUBLICATIONS

*Squiggly underlines indicate Moghe Lab members. * Corresponding author*

1. Elizabeth Mahood, Alexandra Bennett, Karyn Komatsu, Lars Kruse, Vincent Lau, Maryam Rahmati Ishka, Yulin Jiang, Armando Bravo, Katherine Louie, Benjamin Bowen, Katherine Louie, Maria Harrison, Nicholas Provart, Olena Vatamaniuk, Gaurav Moghe* (2023, in press) Information theory and machine learning illuminate large-scale metabolomic responses of Brachypodium distachyon to environmental change. ***The Plant Journal*** doi: 10.1111/tpj.16160
   o Selected as a Research Highlight (pending)

2. Gaurav Moghe*, Mohammad Irfan, Bhaswati Sarmah (2023) Dangerous sugars: structural diversity and functional significance of acylsugar-like defense compounds in flowering plants. ***Current Opinion in Plant Biology*** doi: 10.1016/j.pbi.2023.102348

3. Arielle Johnson, Yuanzheng Yue, Sarah Carey, Se Jin Park, Lars Kruse, Ashley Bao, Asher Pasha, Alex Harkess, Nicholas Provart, Gaurav Moghe*, Margaret Frank* (2023) Chromosome-level genome assembly of *Euphorbia peplus*, a model system for plant latex, reveals that relative lack of Ty3 transposons contributed to its small genome size. ***Genome Biology and Evolution*** doi: 10.1093/gbe/evad018
   o * Co-corresponding authors

4. Lars Kruse, Jason Chobirko, Ben Fehr, Gaurav Moghe* (2023) Phylogenomic analyses across land plants reveals motifs and co-expression patterns useful for functional prediction in the plant BAHD acyltransferase family. ***Frontiers in Plant Science*** doi: 10.3389/fpls.2023.1067613

5. Gaurav Moghe, Lars Kruse, Maike Peterson, Federico Scossa, Alisdair Fernie, Emmanuel Gacquerel, John C. D'Auria* (accepted, 2023 issue) BAHD Company – the ever-expanding roles of the BAHD acyltransferase gene family in plants. ***Annual Reviews in Plant Biology***

6. Gaurav Moghe, Susan Strickler (pre-print) metaPathwayMap: A tool to predict metabolic pathway neighborhoods from structural classes of untargeted metabolomics peaks. ***bioRxiv*** (pre-print only), doi: 10.1101/2022.03.15.484337

7. V. de Crecy-Lagard et al (55 authors) (2022) A roadmap for the functional annotation of protein families: a community perspective ***Database*** doi: 10.1093/database/baac062

8. Lars Kruse, Austin Weigle, Mohammad Irfan, Jesus Martinez-Gomez, Jason Chobirko, Jason Schaffer, Alexandra Bennettt, Joe Jez, Chelsea Specht, Diwakar Shukla, Gaurav Moghe* (2022) Orthology-based analysis helps map evolutionary diversification and predict substrate class use of BAHD acyltransferases ***The Plant Journal*** doi: 10.1111/tpj.15902

9. Lars Kruse, Alexandra Bennett, Elizabeth Mahood, Elena Lazarus, Se Jin Park, Frank Schroeder, Gaurav Moghe* (2021) Illuminating the lineage-specific diversification of resin glycoside acylsugars in the morning glory (Convolvulaceae) family using computational metabolomics ***Horticulture Research*** doi: 10.1093/hr/uhab079

10. Honglin Feng, Lucia Acosta-Gamboa, Lars Kruse, Alba Ruth Nava Fereira, Sara Shakir, Hongxing Xu, Garry Sunter, Michael Gore, Gaurav Moghe, Georg Jander (2021) Acylsugars protect *Nicotiana benthamiana* against insect herbivory and dessication. ***Plant Molecular Biology*** doi: 10.1007/s11103-021-01191-3

11. Alexandra Bennett, Elizabeth Mahood, Kai Fan, Gaurav Moghe* (2021) Untargeted metabolomics of purple and orange-fleshed sweet potatoes reveals a large structural diversity of anthocyanins and flavonoids ***Scientific Reports*** 11:16408 doi: 10.1038/s41598-021-95901-y
    o SIPS faculty team up for sweet potato improvement

12. Arielle Johnson, Gaurav Moghe, Margaret Frank (2021) Growing a glue factory: Open questions in laticifer cell biology. ***Current Opinion in Plant Biology*** 64:102096. doi: 10.1016/j.pbi.2021.102096

13. Mohammad Irfan, Benjamin Chavez, Paride Rizzo, John D'Auria, Gaurav Moghe* (2021) Evolution-aided engineering of plant specialized metabolism ***aBiotech*** doi: 10.1007/s42994-021-00052-3

14. Jacob Landis, Christopher Miller, Amanda Broz, Alexandra Bennett, Robert Last, Patricia Bedinger, Gaurav Moghe* (2021) Migration through a major Andean ecogeographic disruption as a driver of genetic and phenotypic diversity in a wild tomato species ***Molecular Biology and Evolution*** 38(8): 3202-3219 doi: 10.1093/molbev/msab092

15. Elizabeth Mahood, Lars Kruse, Gaurav Moghe* (2020) Machine learning: A powerful tool for gene function prediction in plants ***Applications in Plant Sciences*** e11376 doi: 10.1002/aps3.11376

16. Shayne Wierbowski, Tommy Vo, Pascal Falter-Braun, Timothy Jobe, Lars Kruse, Xiaomu Wei, Jin Liang, Michael Meyer, Nurten Akturk, Christen Rivera-Erick, Nicolas Cordero, Mauricio Paramo, Elnur Shayhidin, Marta Bertolotti, Nathaniel Tippens, Kazi Akther, Rita Sharma, Yuichi Katayose, Kourosh Salehi-Ashtiani, Pamela Ronald, Joseph Ecker, Peter Schweitzer, Shoshi Kikuchi, Hiroshi Mizuno, David Hill, Marc Vidal, Gaurav Moghe, Susan McCouch, Haiyuan Yu (2020) ***Proceedings of the National Academy of Sciences*** A massively parallel barcoded sequencing pipeline to generate the first single colony ORFeome and high-quality protein-protein interaction interactome for rice. doi: 10.1073/pnas.1918068117

17. Stacey Smith, Ruthie Angelovici, Karolina Heyduk, Hiroshi Maeda, Gaurav Moghe, Chris Pires, Joshua Widhalm, Jennifer Wisecaver (2019) The renaissance of comparative biochemistry. ***American Journal of Botany***, 106(1): 3-13 doi: 10.1002/ajb2.1216

18. Gaurav Moghe* and Lars Kruse (2018) The study of plant specialized metabolism: Challenges and prospects in the genomics era ***American Journal of Botany***, 105(6): 1-4 doi:10.1002/ajb2.1101

19. Gaurav Moghe and Stacey Smith (2018) The push and pull of plant specialized metabolism underlies a long-standing, colorful mystery. ***New Phytologist***, 217(2) doi: 10.1111/nph.14914

PUBLICATIONS RESULTING FROM PRE-FACULTY WORK

1. Bryan Leong, Steven Hurney, Paul Fiesel, TM Anthony, Gaurav Moghe, A Daniel Jones, Robert Last (2022) Identification of BAHD acyltransferases associated with acylinositol biosynthesis in *Solanum quitoense* (naranjilla) ***Plant Direct*** doi: 10.1002/pld3.415

2. Bryan Leong, Steven Hurney, Paul Fiesel, <u>Gaurav Moghe</u>, A. Daniel Jones, Robert Last (2020) Specialized Metabolism in a Nonmodel Nightshade: Trichome Acylinositol Biosynthesis ***Plant Physiology***, 183(3): 915-924 doi: 10.1104/pp.20.00276

3. John Lloyd, Megan Bowman, Christina Azodi, <u>Gaurav Moghe</u>, Kevin Childs, Shin-Han Shiu (2019) Evolutionary characteristics of intergenic transcribed regions indicate widespread noisy transcription in the Poaceae. ***Scientific Reports***, 9, 12122 doi: 10.1038/s41598-019-47797-y

4. Haiyang Xu, <u>Gaurav Moghe</u>, Krystle Wiegert-Rininger, Anthony Schilmiller, Cornelius Barry, Robert Last, Eran Pichersky (2018) Identification of dehydrogenases involved in the biosynthesis of the monoterpene moiety of pyrethrin ***Plant Physiology*** doi: 10.1104/pp.17.01330

5. <u>Gaurav Moghe</u>, Bryan Leong, Steven Hurney, A. Daniel Jones, Robert Last (2017) Evolutionary routes to biochemical innovation revealed by integrative analysis of a plant-defense related specialized metabolic pathway. ***eLife,*** 6:e28468
   - New study sheds light on mysterious plant compounds. *Cornell Chronicle*
   - Tomatoes' crystal ball reveals evolutionary secrets. *MSU Today*
   - Tomato hair holds clues to evolution. *Futurity*

6. Pengxiang Fan, <u>Gaurav Moghe</u>, Robert Last (2016) Comparative biochemistry and *In Vitro* pathway reconstruction as powerful partners in studies of metabolic diversity. ***Methods in Enzymology***, Synthetic Biology and Metabolic Engineering in Plants and Microbes Part A. vol. 575. (Book chapter)

7. <u>Gaurav Moghe</u>, Robert Last (2015) Something old, something new: Conserved enzymes and the evolution of novelty in plant specialized metabolism. ***Plant Physiology***, 169 (3):1512-1523
   - The genesis of plant languages: How plants evolve new metabolic pathways from existing ones. *Invited article, Atlas of Science*

8. Melissa Lehti-Shiu, Sahra Uygun, <u>Gaurav Moghe</u>, David Hufnagel, Hannah Jasicki, Vivian Fang et al. (2015) Molecular evidence for functional divergence and decay of a transcription factor derived from whole genome duplication in *Arabidopsis thaliana*. ***Plant Physiology***, 168(4):1712-1734

9. Jing Ning, <u>Gaurav Moghe</u>, Bryan Leong, Jeongwoon Kim, Itai Ofner et al. (2015) A feedback insensitive isopropylmalate synthase affects acylsugar composition in cultivated and wild tomato. ***Plant Physiology,*** 169)3:1821-1835

10. John Lloyd, Alexander Seddon, <u>Gaurav Moghe</u>, Matthew Simenc, Shin-Han Shiu (2015) Characteristics of plant essential genes allow for within-and between-species prediction of lethal mutant phenotypes. ***The Plant Cell***, 27(8):2133-2147

11. Anthony Schilmiller, <u>Gaurav Moghe</u>, Pengxiang Fan, Banibrata Ghosh, Jing Ning, A. Daniel Jones, Robert Last (2015) Functionally divergent alleles and duplicated loci encoding an acyltransferase contribute to acylsugar metabolite diversity in *Solanum* trichomes. ***The Plant Cell***, 27(4):1002-1017

12. <u>Gaurav Moghe</u>, David Hufnagel, Haibao Tang, Yongli Xiao, Christopher Town, Ian Dworkin et al. (2014) Consequences of whole genome triplication as revealed by comparative genomic analyses of the wild radish *Raphanus raphanistrum* and three other Brassicaceae species, ***The Plant Cell***, 26(5):1925-1937.
   - Featured as a Research Highlight in Nature Reviews Genetics (July 2014), doi:10.1038/nrg3774

13. <u>Gaurav Moghe</u>, Shin-Han Shiu (2014) The causes and molecular consequences of polyploidy in flowering plants. ***Annals of the New York Academy of Sciences,*** 1320: 16-34

14. Michael Campbell, MeiYee Law, Carson Holt, Joshua Stein, <u>Gaurav Moghe</u>, David Hufnagel, et al. (2014) MAKER-P: a tool-kit for the rapid creation, management, and quality control of plant genome annotations. ***Plant Physiology***, 164 (2): 513-524

15. <u>Gaurav Moghe</u>, Melissa Lehti-Shiu, Alexander Seddon, Shan Yin, Yani Chen, Piyada Juntawong, et al. (2013) Characteristics and significance of intergenic polyA transcription in *Arabidopsis thaliana*. ***Plant Physiology***, 161(1):210-224

16. Rebecca Davidson*, Malali Gowda*, <u>Gaurav Moghe</u>, Haining Lin, Brieanne Vaillancourt, Shin-Han Shiu et al. (2012) Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. ***The Plant Journal***, 71(3):492-502.

17. Haining Lin, <u>Gaurav Moghe</u>, Shu Ouyang, Shin-Han Shiu, Xun Gu, C. Robin Buell (2010) Comparative analyses reveal distinct sets of lineage-specific genes within *Arabidopsis thaliana*. ***BMC Evolutionary Biology***, 10:41.

RESEARCH SEMINARS PRESENTED

1. ***Upcoming invited 2023:*** *University of Missouri-Columbia (March), Gordon Research Conference, Barcelona (June), Botany (July), ASPB (August)*
2. ***University of Toronto – Scarborough (Nov 2022)***
3. Predictive analysis of plant metabolomes and metabolic enzymes (***Zhejiang U., China, Nov 2022***)
4. Predictive analysis of plant metabolomes and metabolic enzymes ***Purdue University (Sep 2022)***
5. ***Phytochemical Society of North America (July 2022)***
6. Uncovering the phytochemical diversity in the Convolvulaceae family using computational metabolomics. ***Convolvulaceae Seminar Series (June 2022)***
7. Challenges of functional propagation in plant enzyme families. ***NSF-sponsored workshop on protein function annotation, Orlando (Feb 2022)***.
8. Using Information theory and machine learning to analyze plant metabolomes ***Plant and Animal Genome Conference XXIX (Jan 2022, conference cancelled due to Covid)***
9. Enzyme families and the evolution of plant metabolic diversity ***Iowa State University (Sep 2021)***
10. Evolution of the diversity of defensive sugar metabolites in the morning glory (Convolvulaceae) family ***Botany 2021, colloquium on Phytochemistry***
11. Evolution of the diversity of defensive sugar metabolites in Solanaceae and Convolvulaceae ***Solanaceae Seminar Series*** (virtual seminar; January 2021)
12. Classification of lipids and other compounds into structural categories using supervised machine learning. ***American Society of Plant Biologists annual meeting*** (2020)
13. Emergence of innovation in plant metabolism ***University of California – San Diego*** (virtual seminar; May 2020)
14. Dissecting the structure and evolution of plant metabolic networks using a multi-disciplinary toolbox ***Rutgers University, New Brunswick*** (Jan 2020)
15. High-value metabolites in sweet potato ***Empire State Producers Expo***, Syracuse, NY (Jan 2020)
16. Chipping away at plant metabolic complexity using a multi-disciplinary toolbox ***University of Nebraska - Lincoln Plant Sciences annual symposium*** (Oct 2019)
17. The emergence of novelty in plant specialized metabolism. ***American Society of Plant Biologists Annual Meeting (Presidential Session)*** (July 2019)
18. Plant metabolic diversity: Evolution and Applications. ***Plant Breeding and Genetics Section, Cornell University*** (Feb 2019)

19. The evolution of novelty in plant metabolism. ***Plant Biology Department, University of Massachusetts – Amherst*** (Oct 2018)
20. Teasing apart the complexity of plant metabolic networks using integrative approaches. ***Computational Biology field, Cornell University*** (2018)
21. All in the family: The emergence of biochemical novelty in plant specialized metabolism. ***Boyce Thompson Institute annual symposium*** (2017)
22. Acylsugar biosynthesis and the evolutionary dynamics of specialized metabolic pathways. ***Cold Spring Harbor Plant Biotechnology symposium*** (2017)

TALKS (PRE-FACULTY)

1. Phylogenetics meets biochemistry: Unraveling plant specialized metabolism using multi-omic strategies. ***Cornell University*** (2017)
2. Comparative biochemical genomics of Solanaceae acylsugars illustrates the mechanisms of evolutionary diversification in plant specialized metabolism. ***13th Annual Solanaceae Conference, UC-Davis*** (2016)
3. The emergence of biological complexity: An investigation of acylsugar biosynthesis using comparative biochemical genomics*. **Gordon Research Seminar on Plant Molecular Biology**, **Holderness School*** (2016)
4. All in the family: The origins and evolution of acylsugar biosynthesis in Solanaceae. ***PRL Tuesday noon seminar, MSU BEACON seminar*** (2016)
5. High-throughput approaches and the study of natural metabolic variation in plants. ***iCER NextGen talks, MSU*** (2015)
6. Plant molecular evolution in the genomics era: How omic strategies can inform evolutionary studies of biological phenomena. ***Indian Institute of Science, Education & Research (IISER), Pune, India*** (2015)
7. An early look at the genome of wild radish *Raphanus raphanistrum* genome. ***iCER NextGen talks, MSU*** (2012)
8. Insights into genome evolution post-polyploidization in Brassicaceae using the newly sequenced genome of Wild Radish *(Raphanus raphanistrum)*. ***American Society of Plant Biology Conference, Austin, TX*** (2012), ***MSU-BEACON Centre*** (2013)
9. Characteristics and significance of intergenic polyA transcripts in *Arabidopsis thaliana*. ***Great Lakes Bioinformatics Conference, Ann Arbor, MI*** (2012)
10. Intergenic Dark Matter transcripts: Insights from the analyses of the *Arabidopsis thaliana* transcriptome. ***Genetics Retreat*, MSU*** (2011)
11. Discovery and analyses of novel RNA genes in *Arabidopsis thaliana.* ***Genetics Forum, MSU*** (2010), ***Society for Molecular Biology and Evolution Conference, Iowa City*** (2009)

APPENDIX 3: TEACHING AND MENTORING

COURSES TAUGHT

- **PLBIO 4000/6000: Concepts and techniques in computational biology (Spring 2019-); 4 credits**
    - Contains the following course content comprising theory lectures and hands-on exercises:
    - Module 1: Unix, HPC, Python, Introduction to Docker/GitHub/MySQL
    - Module 2: Local/global alignment, BLAST, phylogenetic reconstruction, orthology analysis
    - Module 3: Genome assembly using Illumina, PacBio, HiC, RNA-seq reference based (HISAT2) and denovo (Trinity) assembly, differential expression analysis using edgeR
    - Module 4: Hidden Markov Models, motif analysis, network reconstruction concepts, Gene Ontology analysis, protein structure prediction and docking
    - Module 5: Machine learning, supervised/unsupervised methods, Scikit-learn, PyCaret, WEKA, deep learning concepts
    - Module 6: Student projects
- **PLSCI 7202: Applications of machine learning to plant sciences (Fall 2020-2022); 8 lectures/year**
    - https://github.com/moghelab/ml-teaching-plsci7202
    - Contains concept lectures and hands-on exercises conducted in Jupyter Notebook using above Python libraries
    - Examples include predicting appropriate crop plantings using soil nutrition and weather features, whether mushrooms are edible/poisonous based on their morphological features, whether gene mutation is lethal/not lethal based on its sequence, expression and network features
- PLBIO 6410: Introduction to LC-MS: Data acquisition and analysis (Fall 2018-); 2 lectures/year
- PLBIO 7410: Introduction to research literature in plant biology (Spring 2018-); 1 lecture/year
- Guest lecture: BTRY 4950: Gene Expression Clustering: Methodological considerations (2019)

Pre-faculty:
- TA, Theories and Practices in Bioinformatics (Dept. of Plant Biology, MSU, 2011, 2013)
- Guest lecture: Differential expression analysis using edgeR (Cold Spring Harbor Laboratories, 2013)
- TA, Frontiers in Plant Sciences (Cold Spring Harbor Laboratories, 2010, 2013)
- Guest lecture: Introduction to Python Programming (Theories and Practices in Bioinformatics, 2011)
- TA, Fundamental Genetics (Dept. of Zoology, MSU, 2009)
- Instructor, Masters in Bioanalytical Sciences (Ramnarain Ruia College, Mumbai, 2006)

MENTORING

As faculty:
- Mentored postdoctoral researchers (2), graduate students (2.5), rotating graduate students (6), lab technicians (1), undergraduate students (8), visitors (6) on various research projects. Some of these students successfully applied and received Cornell and federal grants. At least three of these students were first-generation students taking their early steps into the scientific world.
- Over 30 students from CALS and CAS, through the BIO Advising program (2018-2021) and the Plant Science major mentoring program.

- Mentored two REU students from STEM under-represented sections, both of whom contributed significantly to be authors on publications.
- On dissertation committees of ten graduate students.

Pre-faculty:
- Mentored graduate students (2), undergraduates (6) and high school students (2).

APPENDIX 4: LEADERSHIP AND SERVICE

COMMITTEES AND ORGANIZATIONS

External:
1. Elected President, Phytochemical Section of the Botanical Society of America (2022-2024)
2. Co-founder, PhytochemTalks – a biweekly online seminar series organized on behalf of the BSA Phytochemistry section and more recently, PSNA. The goal of this series is to highlight early career plant biochemists including graduate students, postdocs and early career faculty. So far, over 2 dozen scientists from North America and Europe have spoken at this well-attended forum.
3. Co-founder (with Stacey Smith), Botanical Society of America Phytochemistry section (2020, 2021). This section aims to bring together scientists with phytochemical interests at the Botany meeting and beyond, through organization of symposia, colloquia, workshops, travel awards and off-conference meetings such as the PhytochemTalks. Through this forum, we aim to create a networking and presentation opportunity for grad students and postdocs attending the Botany meeting.
4. Co-organizer of Botany 2023 symposium "Standing your ground: Understanding plant defense from molecules to morphology"
5. Co-organizer (with Rob Raguso) of a Botany 2021 colloquium "Phytochemistry: From atoms to ecosystems"
6. *Ex-officio* member, ASPB Early Career Award Committee (2019)

At Cornell:
1. Lead PI and co-organizer of Cornell-Weill Cornell symposium on "*Drug discovery from nature's metabolites*" planned May 2023.
2. Member, Graduate students admissions committee (2020, 2021)
3. Member, Synthetic Plant Biology faculty search committee (2019)
4. Member, Cornell Institute of Biotechnology Metabolomics Advisory Board (2017-)
5. Faculty co-founder, Cornell Ents Club (monthly plant biology journal club)

Pre-faculty:
- Member, Biochemistry Department Awards Committee (2015)
- President of Genetics Student Organization (2012)
- Member of Genetics Director Search Committee (2012), Genetics Program Executive Committee (2012), Genetics Student Organization (2011), Genetics Admissions Committee (2010)
- Representative for Dean's Student Advisory Council and Faculty Advisory Council (2011)

JOURNAL EDITORSHIP AND PEER REVIEW

- Review Editor, Frontiers in Plant Sciences, Section: Plant Metabolism and Chemodiversity (2021-)
- Editorial Board, Plant Direct (2017-)
- Manuscript review – PNAS, Science Advances, eLife, Nature Plants, Plant Physiology, Molecular Biology and Evolution, New Phytologist, PLoS ONE, BMC Genomics, BMC Evolutionary Biology, Gene, Frontiers in Plant Sciences, 3Biotech, Ecology and Evolution, Phytochemistry, Molecular Phylogenetics and Evolution
- Grant review – National Science Foundation, France ANR, Estonian Research Council