Current research activities and future research plans, Todd P. Michael, PhD

What are plant genome architectural features that control important traits? Plants are fundamental to human survival, providing us with essential resources such as food, fuel, and fiber as well as medicine. Beyond their critical role in capturing carbon dioxide through photosynthesis and converting it into complex carbon compounds, plants perform an astonishing array of biochemical processes that humans sometimes struggle to replicate. Moreover, plants adapted to thrive in nearly every ecological niche, extracting and concentrating essential elements while playing a central role in maintaining and stabilizing ecosystems. At the heart of these remarkable capabilities lies an unparalleled diversity of plant genomes, which represent the most complex and varied on Earth. Plant genomes span several orders of magnitude in size and exhibit a wide array of ploidies and chromosome numbers. This diversity reflects plants' extraordinary ability to evolve through genome mixing, reorganization, and restructuring to exploit their local environment. Recent advances in both sequencing technologies as well as computational approaches have made it possible to create phased, haplotype-resolved, telomere-to-telomere (T2T) assemblies for even the most complex genomes such as those displaying autopolyploidy and aneuploidy, which are common in economically important crops. The Michael lab focuses on plants that display unique morphological or lifestyle characteristics (carnivorous, parasitic), minimal genomes (duckweed), different types of photosynthesis (C3, C4, and CAM), unique water use efficiency (WUE) strategies, crops with larger root systems and crop wild relatives (CWR), to better understand plant genome organization and trait architecture. We are developing reference-free pan-genome methods for integration into genome-wide selection studies (GWAS) and genomic selection paradigms to link population-level phenotypes to gene networks underlying environmental response and growth traits. The long-term goal of the lab is to leverage learnings from these genomes to design plants using both top-down and bottom-up engineering approaches.

IARPA and Pangenome tools: When I joined the Salk Institute in April 2020, San Diego had just entered lockdown, and the Institute was closed due to the COVID-19 pandemic. Prior to joining Salk, my group had been collaborating with the Intelligence Advanced Research Projects Activity (IARPA) to design software tools to detect engineered organisms. We participated in a meeting in Washington, D.C., where various groups were given early access to COVID-19 data to assess whether the virus was engineered. This event brought significant attention to our pipeline, which was adopted by several agencies. We subsequently refined our program called PanKmer for eukaryotic genomes, and based on benchmarking and community feedback, it is one of the most efficient pangenome tool available[1].

Harnessing Plants Initiative (HPI): One of the reasons I moved my lab over to the Salk was to join the HPI effort to breed and engineer plants with larger, deeper roots to draw down more carbon into the soil. My group's initial role in the HPI program was to utilize our genome analysis tools and expertise to translate discoveries made in the model plant *Arabidopsis* to crop genomes that would enable HPI to scale to the acreage needed to impact global carbon dioxide levels. We deployed a consistent set of crop genomes to unify the HPI discovery scientists (https://resources.michael.salk.edu/), which we later generalized into a tool called OrthoBrowser that any group can use to translate discoveries across model and crop genomes[2]. We also developed a data management platform called BLOOM to enable access to all of the HPI phenotypic and genotypic data (https://bloom.salk.edu/), which has been transformative in terms of increasing the pace of discovery, unifying access to data types and ensuring the discoveries made in HPI are captured.

Pangenome enabled Genome Wide Association Studies (GWAS): HPI received a funding boost when Jeff Bezos contacted Joanne about using plants to fight climate change and we proposed to discover root traits directly in crops with a pangenome enable GWAS approach. Under this effort, we sequenced over 600 genomes for Soybean, Soybean relatives, Pennycress, Sorghum, Maize (corn), Alfalfa, Canola, and Zostera (Seagrass). We further augmented PanKmer[1] with additional funding from the Bill and Melinda Gates Foundation (BMGF) to enable the use of pangenomes in breeding efforts. Additional tools we deployed are PanDots[3] that enables rapid visual identification of structural variations (SVs) across plangenomes, telomnum that identifies telomere sequence length from genomes sequenced with long read technologies[4], and LoopViz that enables rapid validation of sub-cloning products using the handheld Oxford Nanopore Technologies (ONT) MinION sequencer[5].

Salk collaborations: My lab's unique expertise and tools are critical to the collaborations within HPI as well as with other Salk faculty. One example in HPI is the genomes and tools we developed are used in conjunction with the root phenotyping and single cell expression from the Busch lab to conduct GWAS in Soybean, Alfalfa and Sorghum. In Soybean, we leveraged these tools in collaboration with the University of Missouri to identify 54 potential deep rooted gene leads[6]. In addition to collaborating with Salk faculty on HPI projects, several collaborations with other Salk faculty have been developing: Kenta on the Sweat Bee transcriptome, Dmitry on the plant BAF complex, Jan on telomeres (his lab has helped us with telomere assays), and Joe Ecker on developing duckweed as a model system[7,8].

Sequencing and Analyzing Genomes: Since joining the Salk the lab has collaborated to publish over 15 plant genomes[7,9–23], several coral and macroalgae genomes for biochemical discovery[24,25], and fish genomes for sample preservation studies[26]. In multiple genome sequencing efforts we leveraged the power of long read sequencing to discover regions of genomes previously unassimilable such as disease resistance loci in plants[14,16,18,21], biosynthesis clusters in plants and corals[9,25], features of plant genome architecture like complete centromeres and polyploidy[10–12,19,22], and unique biological adaptations like plants using Crassulacean Acid Metabolism (CAM) photosynthesis to exploit underwater environments[15]. A significant achievement was the completion of the centromeres in a T2T Arabidopsis assembly in collaboration with Ian Henderson and Mike Schatz[19].

***Future Pangenome efforts*:** A primary focus of the lab is to build pangenomes with hundreds to thousands of haplotypes to discover plant genome architecture features important for engineering and breeding. We recently finished the Cannabis pangenome in collaboration with the company Oregon CBD, who donated PacBio sequenced genomes to my lab to leverage our pangenome tools and expertise[27]. The pangenome exposed the extensive presence/absence (PAV) and SVs associated with the cannabinoid pathway suggesting novel ways of modulating the fatty synthesis pathway. The lab is also funded by BMGF to build pangenomes and tools to sync up with breeding efforts in the economically important "root tuber banana" (RTB) crops cassava, yam and banana in collaboration with Ed Buckler at Carnell. Finally, for HPI in collaboration with Wolfgang's lab, we are also building matched pangenomes/phenomes in Soybean, Sorghum, Alfalfa, and Canola to discover networks governing larger, deeper roots.

Future research, building the in silico plant: The ultimate goal of our lab is to uncover the fundamental principles that govern plant genome architecture and apply these insights both *in silico* and in the lab to design and engineer the next generation of plants. To achieve this, we are pursuing three complementary approaches: First, we are building comprehensive datasets to model plant development across its entire lifecycle in the field. Second, we are developing the fast-growing, minimal-genome duckweed *Wolffia* as a whole-plant discovery system. Third, we are designing and implementing Plant Artificial Chromosomes (PACs). Together, these strategies will not only culminate in the creation of an *in silico* plant but will also provide tools for transformative plant genome architecture discoveries.

***Time of day developmental sampling*:** My lab has demonstrated that, across plant species, most if not all genes are expressed in a time-of-day (TOD) manner, ensuring that biological processes align with daily environmental conditions[28–30]. By analyzing hundreds of high-quality plant genomes, we discovered that this global orchestration of biological activity is rooted in the architecture of plant genomes[31,32]. While genes are generally thought to be randomly arranged in eukaryotes, aside from certain biosynthetic gene clusters, we found that genes regulating TOD biology are non-randomly organized. Furthermore, these TOD gene networks rewire throughout the growing season, reflecting the plant's transition from vegetative to reproductive stages[33]. My lab is currently designing experiments to track TOD gene expression across developmental stages in the field, both at the bulk tissue and single-cell levels, to create datasets for modeling plant behavior over its lifecycle. Beyond providing a foundation for these models, the datasets will also allow us to address a longstanding question in plant biology: the mechanistic basis of hybrid vigor[34].

***Duckweed as synthetic biology chassis*:** Before *Arabidopsis* became the primary model plant, duckweed was widely used in research, and we are working to re-establish it as a powerful model for basic, applied, and synthetic biology studies[35–37]. We have published genomes from each duckweed genus (covering multiple species)[7,20–22,38] and discovered a unique epigenetic system that enables duckweed genomes incredible sexual and architectural flexibility[22,39,40], specific cell types that carry out important biology[8,20], and novel ways they interact with their biotic as well as abiotic environments[41,42]. We have selected *Wolffia australiana* as a synthetic biology chassis due to its tiny size (comparable to a pinhead), rapid doubling time (less than a day), and minimal, non-redundant gene set[36]. Recently, we took the next step in developing *Wolffia* by defining all its cell types according to their TOD expression patterns[7,8]. We are now advancing this work by developing cell-specific CRISPR-Cas9 screens to pinpoint gene function in this minimal cell and gene system.

***Plant Artificial Chromosomes (PACs)*:** We are deploying "top-down" engineering methods such as CRISPR CAS9 to disrupt genes, make large deletions and directly replace genes/regions to engineer plants with larger and deeper roots for HPI[43]. However, "bottom-up" methods such as building PACs and installing them into plant cells would be transformative. There are three significant challenges to achieve the design and deployment of a PAC: first, building the PAC and neo-centromere, which we tackled by extending a flexible cloning system[5]; second, identification a plant ideal for a proof-of-concept, which we found in the model liverwort *Marchantia polymorpha*; and third, a method to deliver a complete chromosome, which is our current focus with several collaborators. The PACs will facilitate discovery of gene function in a combinatorial setting as well as providing a novel approach to build plants with larger roots.

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APPOINTMENTS

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2022-	**Research Associate**, San Diego Botanical Garden, Encinitas, CA.
2020-	**Research Professor**, Salk Institute for Biological Studies, La Jolla, CA.
2017-2020	**Professor and Director of Informatics**, J. Craig Venter Institute, La Jolla, CA.
2013-2017	**Director**, Genomics, Abbott Laboratories, Carlsbad, CA.
2009-2013	**Head,** The Genome Analysis Center, Monsanto Company, St. Louis, MO.
2008-2010	**Member**, The Cancer Institute of New Jersey, New Brunswick, NJ.
2008-2010	**Visiting Scholar**, The Simons Center for Systems Biology, Institute of Advanced Study, Princeton, NJ.
2007-2009	**Head**, Waksman Genomics Laboratory, Waksman Institute for Microbiology, Piscataway, NJ.
2007-2010	**Assistant Professor**, Waksman Institute for Microbiology and Department of Plant Biology and Pathology, Rutgers, The State University of New Jersey, New Brunswick, NJ.
2003-2007	**Postdoctoral Fellow**, Salk Institute for Biological Studies, La Jolla, CA. Advisor: Joanne Chory.

EDUCATION

2002	**Dartmouth College**, Hanover, NH, *Ph.D.* Molecular and Cellular Biology. Advisor: C. Robertson McClung.
1996	**University of Virginia**, Charlottesville, VA, *B.A.* Biology. Advisor: Michael Timko.

HONORS AND AWARDS

2016	Research Fellow, Volwiler Society, Abbott Laboratories
2011	Associate Fellow, Monsanto Science Fellows Society
2008	Tomorrow's PIs: Genome Technology's special year. Genome Technology
2003-2007	NIH Postdoctoral Fellowship, The Salk Institute, La Jolla, CA
2003	Hannah Croasdale Award for Outstanding Graduate Work
1998-1999	Graduate Associate in the College of Arts and Sciences
1995	Teaching Assistant, Introduction to Biology
1993-1994	Van der Poel Scholarship
1992-1994	Dean's Award for Excellence
1992	Phi Eta Sigma National Honor Society

PUBLICATIONS

99 Total publications, 21,353 citations, H-Index **60**, i10-index **93**
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FLOWERING LOCUS T mediate natural variation in flowering responses of *Arabidopsis thaliana*. **Genetics**. 2009 Oct;183(2):723-32.

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85. Zdepski A, Wang W, Priest HD, Ali F, Alam M, Mockler TC, **Michael TP**. Conserved Daily Transcriptional Programs in Carica papaya. **Trop Plant Biol**. 2008 Dec;1(3-4):236-245.

86. Loudet O, **Michael TP**, Burger BT, Le Metté C, Mockler TC, Weigel D, Chory J. A zinc knuckle protein that negatively controls morning-specific growth in Arabidopsis thaliana. **Proc Natl Acad Sci U S A**. 2008 Nov 4;105(44):17193-8.

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90. **Michael TP***, Mockler TC*, Breton G*, McEntee C, Byer A, Trout JD, Hazen SP, Shen R, Priest HD, Sullivan CM, Givan SA, Yanovsky M, Hong F, Kay SA, Chory J. Network discovery pipeline elucidates conserved time-of-day-specific cis-regulatory modules. **PLoS Genet**. 2008 Feb;4(2):e14. ***co-*first *authors***

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PREPRINTS (36)

1. Hartwick, Nolan T, and Todd P Michael. "OrthoBrowser: Gene Family Analysis and Visualization." bioRxiv (2024): 2024.08.27.609986. In review ***Bioinformatics***.

2. Grayson, Natalie et al "A widespread metabolic gene cluster family in metazoans" Research Square (2024): https://doi.org/10.21203/rs.3.rs-4859447/v1. In review ***Nature Chemical Biology***.

3. Lynch, Ryan C. et al "Domesticated cannabinoid synthases amid a wild mosaic cannabis pangenome." bioRxiv (2024): 2024.05.21.595196. In revision ***Nature***.

4. Kitony, Justine K. et al "Chromosome-level baobab (Adansonia digitata) genome illuminates its evolutionary insights." bioRxiv (2024): 2024.04.14.589434. In revision ***Nature Communications***.

5. Colt, Kelly et al "Telomere Length in Plants Estimated with Long Read Sequencing." bioRxiv (2024): 2024.03.27.586973. In revision ***Plant Physiology***.

6. Sun, Ying et al "Genome-Wide Association Study Reveals Influence of Cell-specific Gene Networks on Soybean Root System Architecture." bioRxiv (2024): 2024.02.27.581071.

7. Ernst, Evan et al "The genomes and epigenomes of aquatic plants (Lemnaceae) promote triploid hybridization and clonal reproduction." bioRxiv (2023): 2023.08.02.551673.

8. Aylward, Anthony J. et al "PanKmer: k-mer based and reference-free pangenome analysis." bioRxiv (2023): 2023.03.31.535143. Published ***Bioinformatics***.

9. Saul, Franziska et al "Subgenome dominance shapes novel gene evolution in the decaploid pitcher plant Nepenthes gracilis." bioRxiv (2023): 2023.06.14.544965. Published ***Nature Plants***.

10. Garfinkel, Andrea R. et al "Genetic Mapping of SNP Markers and Candidate Genes Associated with Day-Neutral Flowering in Cannabis sativa L." bioRxiv (2023): 2023.04.17.537043.

11. Minich, Jeremiah J et al "Generating high quality reference genomes from field collected specimens by optimizing preservation." bioRxiv (2023): 2023.03.10.532097. Published ***Communications Biology***.

12. Acosta, Kenneth et al "Optimization of molecular methods for detection and quantification of specific duckweed-bacteria interactions." bioRxiv (2023): 2023.01.04.522651. Published ***Plants***.

13. Pasaribu, Buntora et al "Genomics of turions from the Greater Duckweed reveal its pathways for dormancy and reemergence strategy." bioRxiv (2022): 2022.12.24.521731. Published ***New Phytologist***.

14. Michael, Todd P.. "Time of day analysis over a field grown developmental time course in rice." bioRxiv (2022): 2022.11.30.518604. Published ***Plants***.

15. Snoeck, Simon et al "Evolutionary gain and loss of a plant pattern-recognition receptor for HAMP recognition." bioRxiv (2022): 2022.03.30.484633. Published ***ELife***.

16. Minich, Jeremiah et al "Fish microbiomes 101: disentangling the rules governing marine fish mucosal microbiomes across 101 species." bioRxiv (2022): 2022.03.07.483203. Published ***Nature Communications***.

17. Michael, Todd P.. "Core circadian clock and light signaling genes brought into genetic linkage across the green lineage." bioRxiv (2021): 2021.11.02.466975. Published special issue on circadian clocks in ***Plant Physiology*** with the cover.

18. Voorhies, Mark et al "Chromosome-level genome assembly of a human fungal pathogen reveals synteny among geographically distinct species." bioRxiv (2021): 2021.07.13.452254. Published ***mBio***.

19. Kawash, Joseph et al "Contrasting a reference cranberry genome to a crop wild relative provides insights into adaptation, domestication, and breeding." bioRxiv (2021): 2021.06.27.450096. Published ***PLoS One***.

20. Mansfeld, Ben N. et al "Large structural variations in the haplotype-resolved African cassava genome." bioRxiv (2021): 2021.06.25.450005. Published ***Plant Journal***.

21. Wickell, David et al "Underwater CAM photosynthesis elucidated by Isoetes genome." bioRxiv (2021): 2021.06.09.447806. Published ***Nature Communications***.

22. Abramson, Bradley W. et al "Single nuclei transcriptome of the Lesser Duckweed Lemna minuta reveals cell trajectories for an entire plant." bioRxiv (2021): 2021.06.03.446947. Published in the plant single cell issue ***Plant Physiology***.

23. Naish, Matthew et al "The genetic and epigenetic landscape of the Arabidopsis centromeres." bioRxiv (2021): 2021.05.30.446350. Published ***Science***.

24. Lensink, Mariele et al "LoopViz: A uLoop Assembly Clone Verification Tool for Nanopore Sequencing Reads." bioRxiv (2021): 2021.02.01.427927.

25. Harkess, Alex et al "Unusual predominance of maintenance DNA methylation in Spirodela polyrhiza." bioRxiv (2020): 2020.12.03.410332. Published ***G3***.

26. Sutton, Granger et al "A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes." bioRxiv (2020): 2020.06.11.147629. Published ***F1000Res***.

27. Michael, Todd P. et al "Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme minimization with un-gated plant growth." bioRxiv (2020): 2020.03.31.018291. Published ***Genome Research***.

28. Harkess, Alex et al "A new Spirodela polyrhiza genome and proteome reveal a conserved chromosomal structure with high abundances of proteins favoring energy production." bioRxiv (2020): 2020.01.23.909457. Published ***Journal of Experimental Biology***.

29. Liu, Jianing et al "Gapless assembly of maize chromosomes using long read technologies." bioRxiv (2020): 2020.01.14.906230. Published ***Genome Biology***.

30. MacKinnon, Kirk J-M. et al "Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation." bioRxiv (2019): 762021. Published ***New Phytologist***.

31. Poplawski, Shane G. et al "An antisense oligonucleotide leads to suppressed transcriptional elongation of Hdac2 and long-term memory enhancement." bioRxiv (2019): 618116. Published ***Molecular Therapeutic Nucleic Acids***.

32. Minich, Jeremiah J et al "Temporal, environmental, and biological drivers of the mucosal microbiome in a wild marine fish, Scomber japonicus." bioRxiv (2019): 721555. Published ***mSphere***.

33. VanBuren, Robert et al "Exceptional subgenome stability and functional divergence in allotetraploid teff, the primary cereal crop in Ethiopia." bioRxiv (2019): 580720. Published ***Nature Communications***.

34. Grassa, Christopher J. et al "A complete Cannabis chromosome assembly and adaptive admixture for elevated cannabidiol (CBD) content." bioRxiv (2018): 458083. Published ***New Phytologist***.

35. Jupe, Florian et al "The complex architecture and epigenomic impact of plant T-DNA insertions." bioRxiv (2018): 282772. Published ***PLoS Genetics***.

36. Michael, Todd P. et al "High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell." bioRxiv (2017): 149997. Published ***Nature Communications***.

PUBLICATIONS IN PROCESS (***15 manuscripts***; in prep, in review, in revision, in print)

1. Hartwick, Nolan T, and Todd P Michael. OrthoBrowser: Gene Family Analysis and Visualization. **In review *Bioinformatics*. BioRxiv.**

2. Ryan C. Lynch, Lillian K. Padgitt-Cobb, Andrea R. Garfinkel, Brian J. Knaus, Nolan T. Hartwick, Nicholas Allsing, Anthony Aylward, Allen Mamerto, Justine K. Kitony, Kelly Colt, Emily R. Murray, Tiffany Duong, Aaron Trippe, Seth Crawford, Kelly Vining, **Todd P. Michael**. Domesticated cannabinoid synthases amid a wild mosaic cannabis pangenome. **In revision *Nature*. BioRxiv**.

3. Justine K. Kitony, Kelly Colt, Bradley W. Abramson, Nolan T. Hartwick, Semar Petrus, Emadeldin H. E. Konozy, Nisa Karimi, Levi Yant and **Todd P. Michael.** Chromosome-level baobab (*Adansonia digitata*) genome illuminates its evolutionary insights. **In revision *Nature Communications*. BioRxiv.**

4. J. Antonio Baeza, Jeremiah J. Minish, **Todd P. Michael**. Assembly of mitochondrial genomes using nanopore long-read technology in three sea chubs (Teleostei: Kyphosidae). **In revision *Molecular Ecology Resources***.

5. Gary C. Longo, Jeremiah J. Minich, Nicholas Allsing, Kelsey James, Ella S. Adams-Herrmann, Wes Larson, Nolan Hartwick, Tiffany Duong, Barbara Muhling, **Todd P. Michael**, and Matthew T. Craig. Crossing the Pacific: Genomics Reveals the Presence of Japanese Sardine (*Sardinops melanosticta*) in the California Current Large Marine Ecosystem. **In revision *Molecular Ecology***.

6. **Todd P. Michael**. Can a plant biologist fix a thermostat? **In review *New Phytologist***.

7. Natalie E. Grayson, Paul D. Scesa, Malia L. Moore, Jean-Baptiste Ledoux, Jessica Gomez-Garrido, Tyler Alioto, **Todd P. Michael**, Immo Burkhardt, Eric W. Schmidt, Bradley S. Moore. A widespread natural product gene cluster family to briarane diterpenoids in coral animals. **In review *Nature Chemical Biology*. Research Square**.

8. Jeremiah J. Minich, Nicholas Allsing, M. Omar Din, Michael J. Tisza, Kenneth Maleta, Daniel McDonald, Nolan Hartwick, Allen Mamerto, Caitriona Brennan, Lauren Hansen, Justin Shaffer, Emily R. Murray, Rob Knight, Kevin Stephenson, Mark J. Manary, and **Todd P. Michael**. Culture-independent meta-pangenomics enabled by long-read metagenomics reveals novel associations with pediatric undernutrition. **Submitted *Cell***.

9. Caroline A. Dowling, **Todd P. Michael**, Paul F. McCabe, Susanne Schilling and Rainer Melzer. FT-like genes in Cannabis and hops: sex specific expression and copy-number variation may explain flowering time variation. **Submitted *G3*.**

10. Michael Mudgett, Bradley Abramson, Xinhua Dai, Ruofan Kang, Ethan Young, **Todd P. Michael**, Yunde Zhao. Gene targeting in Arabidopsis through one-armed homology-directed repair. **Submitted *Plant and Cell Physiology***.

11. Sarah B. Carey, Joshua S. Havill, Laramie M. Akozbek, Philip C. Bentz, Austin Osmanski, John T. Lovell, Lillian Padgitt-Cobb, Ryan Lynch, Nicholas Allsing, Leo Orozco, Haley Hale, Hannah Mueller, Zachary Meharg, John McKay, Rafael Guerrero, Daniela Vergara, Nolan Kane, **Todd P. Michael**, Gary J. Muehlbauer, and Alex Harkess. The evolution of heteromorphic sex chromosomes in plants. **In preparation *Nature***.

12. Ashot Papikian, Rachel Rattner-Norris, Jenni Kao, Neil Hauser, Nicholas Allsing, Allen Mamerto, Nolan T. Hartwick, **Todd P. Michael**. Targeted deletions of large syntenic regions in *Arabidopsis thaliana*. **In preparation *PNAS*.**

13. Emily R. Murray, Jeremiah J. Minich, Jocelyn Saxton, Marie de Gracia, Nathaniel Eck, Nicholas Allsing, Justine Kitony, Eric Allen, **Todd P. Michael**, Nadia Shakoor. Soil depth determines the microbial communities in *Sorghum bicolor* fields. **In preparation *ISME*.**

14. **Todd P. Michael**, Nolan Hartwick, Kelly Colt, Philip Ozersky, Emily Carroll, Robert VanBuren, Marie de Gracia Coquerel, Boubacar Gano, Nathaniel Eck, Jessica Adams, Getu Duguma, Nigel Taylor, Ndjido Kane, Mame Codou, Victor A. Albert, Todd C. Mockler, Nadia Shakoor. The fonio *(Digitaria exilis)* genome unveils agronomic potential for a West African orphan crop. **In preparation *Nature Communications* special issue on orphan crops.**

15. Bradley W. Abramson, Phuong T.N. Hoang, Buntora Pasaribu, Evan Ernst, Luca Braglia, Semar Petrus, Tram N.B. Tran, Jörg Fuchs, Veit Schubert, Nolan Hartwick, Megan Wang, Mariele Lensink, Kelly Colt, Manuela Bog, Sowjanya Sree, Laura Morello, Klaus-J. Appenroth, Ingo Schubert, Robert A. Martienssen, Eric Lam, **Todd P. Michael**. The Lemna super pangenome reveals a history of polyploidy**. In preparation *Plant Physiology*.**

BOOK CHAPTERS (3)

1. Slovin J. and **Michael TP**. Strawberry Structural and Functional Genomics, In: Genetics, Genomics and Breeding of Berries, Folta K and Chittaranjan K. eds., CRC Press, 162-188, 2011.

2. Zdepski A, Debnath SC, Howell A, Polashock J, Oudemans P, Vorsa N and **Michael TP**. Cranberry. In: Genetics, Genomics and Breeding of Berries, Folta K and Chittaranjan K. eds., CRC Press, 41-60, 2011.

3. McClung CR, Salomé PA, **Michael TP**. The Arabidopsis Circadian System. 2002. The Arabidopsis Book, eds. C.R. Somerville and E.M. Meyerowitz, American Society of Plant Biologists, Rockville, MD, doi/10.1199/tab.0009, http://www.aspb.org/publications/arabidopsis/.

PATENT APPLICATIONS (3)

D Ecker, ST Motely, JC Hannis, LG Krieg, **TP Michael**, DD Duncan, SG Poplawski, and TN Chiesl. Modified nucleic acids for nanopore analysis. US20180164280 A1.

D Ecker, **TP Michael**, LL Cummins, MW Eshoo, ST Motely, DM Chou. Alterations of neurological gene expression by synthetic piRNAs and by alteration of piRNA function. US20140275216 A1.

O Loudet, **TP Michael**, D Weigel, J Chory. 2009. ZINC KNUCKLE PROTEINS. US20120017335 A1.

INVITED TALKS

Colorado State University, Fort Collins, CO, Aug 8, 2024.
University of California, Davis (UCD), Davis, CA, April 12, 2024.
University of California, San Diego (UCSD, San Diego, CA, April 5, 2024.
Ellen Potter Research Symposium, San Diego CA, Mar 20, 2024.
Nanopore Day, San Diego, CA, Feb 29, 2024.
Medicinal Plant Conference, San Diego, CA Feb 27, 2024.
Plant and Animal Genome, San Diego, CA, Jan 13/16, 2024.
Scripps Institute of Oceanography, La Jolla, CA, Nov 17, 2023.
U.S. Canola Research Conference, St. Louis, MO, Oct 30, 2023.
University of Washington, Seattle, WA, May 9, 2023.
SD Sequencing Road Show, La Jolla, CA, March 9, 2023.
University of California, San Diego (UCSD), La Jolla, CA, Jan 1, 2023.
Plant and Animal Genome, San Diego, CA, Jan 13, 2023.
University of Toronto, Toronto, Canada, December 12, 2022.
Danforth Center for Plant Science, St. Louis, MO, December 6, 2022.
Plant Physiology Webinar, online, Oct 18, 2022.
ViTech, San Diego, CA, Sept 22, 2022.
NextGen Cassava Meeting, online, Sept 9, 2022.
Canadian Federation of Agriculture, online, July 20, 2022.
San Diego Botanical Garden, San Diego, CA, June 6, 2002.
6th International Conference Duckweed Research, Gatersleben, Germany May 31, 2022.
Salk Science and Music, La Jolla, CA, April 24, 2022.
Finish Museum of Natural History, online, Mar 9, 2022.
Plant and Animal Genome XXIV, San Diego, CA, Jan 10, 2022 (canceled).
Michigan State University, online, October 26, 2021.
University of Illinois, online, August 25, 2021.
San Diego Natural History Museum, online, April 20, 2021.
London Calling, Oxford Nanopore, Online, June 18, 2020.
The Scripps Research Institute (TSRI), La Jolla, CA, Mar 5, 2020.
Plant and Animal Genome XXVIII, San Diego, CA, Jan 12, 2020.

São Paulo State University, Jaboticabal, SP, Brazil, Dec 12, 2019.
Nanopore Community Meeting, New York, NY Dec 5, 2019.
5th **ICDRA Conference,** Weizmann Institute, Israel, September 11, 2019.
University of Georgia, Athens, GA, April 19, 2019**.**
Mexico City, Mexico, April 4, 2019**.**
Nanyang Technological University, Singapore, Jan 22, 2019.
Plant and Animal Genome XXVII, San Diego, CA, Jan 12, 2019.
Nanopore Community Meeting, San Francisco, CA Nov 29, 2018.
Front Line Genomics, Webinar, Nov 8, 2018.
Negative Emissions Conference, Canberra, Australia, Oct 31, 2018.
University of Washington, Seattle, WA, Oct 9, 2018.
London Calling, Oxford Nanopore, London, May 24, 2018.
NAFKI Challenge, Ocean Memory, Djerassi, Woodland, CA, March 7, 2018.
Plant and Animal Genome XXVI, San Diego, CA, Jan 17, 2018.
TSRI, La Jolla, CA, Jan 12, 2018.
Central University of Kerala, Kerala, India, October 25, 2017.
NAS workshop, Friday Harbor, WA, September 20, 2017.
UCSD, San Diego, CA, September 15, 2017.
Plant and Animal Genome XXII, San Diego, CA, Jan 12, 2016.
Illumina Users Meeting, San Diego, CA, Dec 1, 2015.
Plant and Animal Genome XXI, San Diego, CA, Jan 13, 2013.
Crop Wild Relatives, Asilomar, CA, Dec 11, 2012.
University of Illinois, Urban, IL, Sept 19, 2012.
Mascoma Corporation, Lebanon, NH, June, 2012.
Advances in Genome Biology and Technology, Marco Island, FL, Feb 16, 2012.
Plant and Animal Genome XX, San Diego, CA, Jan 16, 2012.
Plant genomes & biotechnology: from genes to networks, Cold Spring Harbor, NY, Nov 30, 2011.
Genotype to Phenotype, Banbury Meeting, Cold Spring Harbor, NY, Oct 19, 2011.
International Botanical Congress, Melbourne, Australia, July 23, 2011.
Botany 2011, St. Louis, MO, July 10, 2011.
Tree Biotechnology 2011, Arraial D'Aduja, Bahia, Brazil, June 26, 2011.
2011 In Vitro Biology Meeting, Raleigh, NC, June 4, 2011.
6th Annual Sequencing, Finishing and Analysis of the Future Meeting, Santa Fe, NM, June 1, 2011.
NSF Workshop: The Future of Plant Genome Sequencing and Analysis, Banbury Meeting, Cold Spring Harbor, NY, May 18, 2011.
The Donald Danforth Plant Science Center, St. Louis, MO, May 11, 2011.
New Mexico Bioinformatics and Science Symposium, Santa Fe, NM, March 24, 2011.
Washington University, St. Louis, MO, October 15, 2010.
LIFE Technology SOLiD Users Meeting, Sao Paulo, Brazil, September 9, 2010.
Plant and Animal Genome, San Diego, CA, January 12, 2010.
Aquatic plants Banbury Meeting, Cold Spring Harbor, NY, October 18, 2009.
Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China, June 16, 2009.
Guangxi University, Nanning, Guangxi, China, June 16, 2009.
Guangxi Academy of Sciences, Nanning, Guangxi, China, June 15, 2009.
Beijing Institute of Genomics, Beijing, China, June 12, 2009.

Tianjin Institute of Industrial Biotechnology, Chinese Academy of Science, Tianjin, China, June 11, 2009.
Shenzen-Hong Kong Institute of Infectious Disease, Shenzen, Guangdong, China, June 10, 2009.
Peking University, Beijing, China, June 9, 2009.
University of Mogi da Cruzes, Mogi da Cruzes, Sao Paulo, Brazil, May 25, 2009.
University of Sao Paulo, Sao Paulo, Sao Paulo, Brazil, May 22, 2009.
XXXVIII Annual Meeting of Brazilian Society of Biochemistry and Molecular Biology, Aguas de Lindoia, Sao Paulo, Brazil, May 17, 2009.
University of Maryland, College Park, MD, April 4, 2009.
Genetic Epidemiology Meeting, Cancer Institute of New Jersey, Institute of Advanced Studies, Princeton, NJ, March 18, 2009.
Institute of Advanced Studies, Princeton, NJ, March 9, 2009.
Applied Biosystems SOLiD Asian Pacific Users Meeting, Kuala Lumpar, Malaysia, March 4-6, 2009.
University of Adelaide, Adelaide, Australia, February 27, 2009.
University of South Whales, Sydney Australia, February 26, 2009.
Victor Chang Research Institute, Sydney Australia, February 26, 2009.
Columbia University, New York, NY, January 21, 2008.
Rockefeller University, New York, NY, December 17, 2008.
Duke University, Durham, NC, Department of Biology, December 11, 2008.
North Carolina Biotechnology Center, December 11, 2008.
National Institutes of Health, Bethesda, MD, December 10, 2008.
University of Michigan, Ann Arbor, MI, 2008.
Biosystems SOLiD System North American Users Meeting, San Francisco, CA, 2008.
Brookhaven National Laboratory, Brookhaven, NY, 2007.
New York Botanical Garden, New York, NY, 2007.
16th International Conference on Arabidopsis Research. Madison, WI, 2005.
Salk Science Day, Salk Institute for Biological Studies, La Jolla, CA, 2005.
University of Chicago, Department of Biology Seminar, Chicago, IL, 2004.
Molecular and Cellular Biology Retreat, Dartmouth College, Hanover, NH, 2000.
7th Meeting of the Society for Research on Biological Rhythms. Amelia Island, FL, 2000.

TEACHING

University of California, San Diego, CA (UCSD):
Plant Systems Biology (Fall 2018; Spring 2020; Spring 2021; Spring 2022; Spring 2023; Winter 2024): graduate course; one lecture on genome sequencing and assembly.
Marine Biotechnology (Spring 2018; Fall 2019; Spring 2020; Spring 2022; Winter 2024): graduate course; one lecture on genome sequencing and assembly.

Rutgers University, New Brunswick, NJ:
Bioinformatics (Spring 2009); undergraduate and graduate course; designed curriculum; 20 students, **30 lectures**, computer-based classroom; basics of bioinformatic scripting languages (perl, python, ruby) and using unix/linux based programs to handle large biological datasets.
Topics in Computational Biology (Fall 2008); graduate course; **one lecture** on next generation sequencing and sequence assembly**.**
Genomes (Fall 2008); undergraduate course; **two lectures** on advanced genome analysis and plant genome structure.

Advanced Plant Genetics (Fall 2008); graduate course in the plant graduate program; **two lectures** covering quantitative trait and association mapping.

MENTORED STUDENTS

Salk Institute for Biological Studies (8 postdocs, 2 grad student, 6 undergrads, 9 high school students)

Postdoctoral Fellows**:** Brad Abramson (single cell); Ying Sun (soy genomics); Abigail Cannon (seagrass ecology); Jeremiah Minich (fish genomics); Ryan Lynch (genome informatics); Justine Kitony (genome informatics); Lillian Padgett-Cobb (genome informatics); Heidi Chen (genome informatics).

Grad students: Malia Moore (SIO, seagrass genomics; co-advised with Eric Allen); Emily Murray (SIO, seagrass genomics).

Undergraduate: JD Trout (UCLA), Amanda Byer (UC San Diego), Saba Parsa (UC Berkley), Rachel Sperling (Stanford), Debbie Fiegero (Florida State University), Kavi Patel-Jhawar (UCSD).

High School: Jawon Lee (Torrey Pines HS, UC Berkley), Connor McIntee (SFC HS, MIT), Cristina Littler (SFC HS, Stanford); Ty Maag (SFC HS, Dartmouth); Zhan Ren (High Tech HS); DeAnne Scott; Isela Ordonez; Chris Tong, Jadon Pandian.

JCVI (1 postdoc, 2 undergrad)

Postdoctoral Fellows: Brad Abramson (Synthetic Biology).

Undergraduate advisees: Conner Smith (UCSD), Marielle Lensink (Point Loma University).

Abbott (2 postdocs, 2 undergrads)

Postdoctoral Fellows: Elliott Meer (Genomics), Shane Poplawski (Genomics).

Rutgers University (3 postdocs, 4 graduate students, 19 undergrads, 3 high school students)

Postdoctoral Fellows: Kerry Lutz (Assistant Professor, Farmingdale State College), Ana Faigon, Dave Sidote.

Graduate Students: Wenqin Wang (Plant Biology), Ariella Sasson (Computational Biology), Anna Zdepski (Plant Biology), Adel Dayarian (Physics).

Undergraduate advisees: Michael Boemo (Aresty RA), Dibyo Roy (Aresty RA), Russel Pepe (Aresty RA), Nicole Sroczynski (Plant Biology), Jason Krychiw (Algal Biology), Andrew Khazanovich (Bioinformatics), Lisa Cohen (Genetics), Daniel Pfister (Bioinformatics), Faraz Ali (Bioinformatics), Rick Swain (Molecular Biology), Meryl William (Physics), Ami Patel (Biology), Justyna Marcinow (Molecular Biology), Gajendra Patel (Biology), Dasean Brown (Biographics), Lauren Theis (Biographics), Collette Brown (RISE Summer Student, Johnson C. Smith University, Biology), Cynthia Anyanwu (RISE Summer Student, Georgetown University, Mathematics), Emily Nowiki (RISE summer student, The College of New Jersey, bioinformatics).

High School: Chris Marion, Ira Herniter, Sherry Prasad.

Thesis Committee: Tengbo Huang (Plant Biology), Chokchai Kittiwongwattana (Plant Biology), Laura Cortesse (Plant Biology), Craig Harvey (Toxicology).

Dartmouth College (7 undergrads)

Undergraduate advisees: Emily Sharp ’05; OmoLara Olowoyeye ’04; Taylor Spencer ’03; Petra Halsema ’03; Hannah Yu ’02; James Colligan ’02; Olga Kulinets ’01.

ACADEMIC SERVICE

***Ad hoc* grant reviewer**: NSF and USDA.

NSF panel member: Plant Fungal and Microbial Developmental Mechanisms, 2008-2009.

Manuscript reviewer: PNAS (ad hoc and invited editor), Bioinformatics, Plant Molecular Biology, Plant Physiology, The American Naturalist, Plant Cell, Science, PLoS Biology, PLoS ONE, RNA, Science, Nature Biotechnology, Nature Communications and Nature Genetics.

Board Member: Rutgers Energy Institute, 2007-2009.

Admissions Committee: Rutgers RISE (Undergraduate Research in Science and Engineering), 2008-2009.

Graduate admissions committee: Computational Biology and Molecular Biophysics Graduate Program, 2007-2009.

Duckweed and Cannabis Workshop organizer: Plant and Animal Genome (PAG) Conference, 2017-2023.

Funding

PI, The Cassava Pangenome, Bill and Melinda Gates Foundation, 06/01/22-05/31/25, $1,839.698. The goal of this work is to develop software to construct pangenomes with a specific focus on cassava.

coPI, Carbon Removal on a Planetary Scale (CRoPS) & Coastal Plant Restoration (CPR), Hess Corporation, 01/01/2020-12/31/2024, $107,905. The goal of this work is to analyze the genome of Typha (cattail) for genes in the suberin pathway.

coPI, Harnessing the power of crop plant diversity for CO2 Removal on a Planetary Scale, Bezos Earth Fund, 12/01/2020-11/30/2025, $1,750,000. The goal of this work is to identify gene networks associated with deeper root growth from large surveys of variation in soy, canola, rice and sorghum.

Past Funding

PI, DARPA, “SELECT: Selecting Elite-performers with Longitudinal Epigenomic Characterization and Tracking.” 1 yr, 04/01/18-04/01/19. $618,174.

PI, DARPA, “E3: Environmental Exposure Epigenomics.” 1 yr, 04/01/18-04/01/19. $320,207.

PI, DARPA, “Sequence specific DNA methylation to modulate gene expression.” 2 yrs $2,729,407.

PI, DARPA, “Predicting contagiousness of influenza infection prior to symptom display,” 2 yrs, $2,909,122.

PI, DARPA, “Epigenetic alterations to achieve a sustained biological response.” 3yrs $17,252,290.

PI, Illumina, The Greater Good Initiative, “African Baobab Tree (*Adansonia digitata*) Genome Sequencing,” 2 yrs, $50,000.

PI, NSF, “Arabidopsis 2010: Daily adaptation of transcriptional programs,” 3 yrs, $1,807,858; declined to move to Monsanto.

PI, USDA, “Sequencing the Cranberry genome,” 1 yr, $62,000.

PI, NJCCR, “Next Generation sequencing core for cancer research in NJ,” 1 yr, $505,810.

PI, DOE-JGI CSP2009, “Genome sequencing of the duckweed *Spirodela polyrhiza*: a biofuels, bioremediation and carbon cycling crop.” No money associated with this award.

PI, Busch Biomedical Grant, “*de novo* short read sequencing,” 2 yrs, $50,000.

coPI, CRoPS (CO2 Removal on a Planetary Scale) program, TED Audacious, 07/01/19-06/30/2024, $109,000. The goal of this work is to identify syntenic orthologs between Arabidopsis and crops of interest.

coPI, IARPA, “A Tiered, Multi-Disciplinary Approach to Identifying Engineered Organisms.” 3.5 yrs, 07/03/18 – 12/03/21. $5,184,131. Noblis is the prime.

coPI, DARPA, “iTAB: Investigating Training Associated Blast.” 2 yrs, 01/01/18-12/31/19, $225,164.

coPI, DARPA, “PECAN.” $11,000,000 with $1,238,945 to Dr. Michael. Leidos is the prime.

coPI, DARPA, ““LEAP: Learning through Electrical Augmentation of Plasticity” 4 yrs, $2,788,190 to Dr. Michael.

coPI, DOE, “The Brachypodium ENCODE Project – from sequence to function: Predicting physiological responses in grasses to facilitate engineering of biofuel crops,” 3 yrs, $1,498,585.

coPI, DOE-JGI CSP2017, “A Complete-Sequence Population for Pan-Genome Analysis of Sorghum.” No money associated with this award.

coPI, DOE-JGI CSP2014, “From sequence to function: Predicting physiological responses in Brachypodium to facilitate engineering of biofuel crops.” No money associated with this award.

coPI, UNESP, “Genomics and transcriptomics of *Utricularia reniformis* (Lentibulariaceae): An evolutive and functional approach.”

coPI, NSF, “IGERT: Solutions for Renewable and Sustainable Fuel in the 21st Century,” 5 yrs, $3,198,175.

coPI, DOE-USDA, “A universal genome array and transcriptome atlas for *Brachypodium distachyon*,” 4 yrs, $1,435,278.

coPI, DOE-JGI CSP2009, “Resequencing diverse genotypes of *Brachypodium distachyon*, a tractable model grass species.” No money associated with this award.

coPI, DOE-JGI CSP2007, “Genome sequencing of *Brachypodium distachyon*, a model for energy crops and temperate grasses.” No money associated with this award.

Senior Personnel, NSF “Comparative Genomic Analysis of Diurnal and Circadian Gene Expression Regulation,” 3yrs, $1,192,225.