Todd Michael's Reappointment as Research Professor

Committee: Satchin Panda (Chair)**,** Clodagh O'Shea and Joe Ecker

Summary

Todd joined the Salk Institute as a Research Professor in 2020 during the onset of the COVID-19 pandemic. His lab focuses on genome sequencing to explore plant diversity in function and architecture, studying plants with unique traits such as carnivorous and parasitic plants, minimal genomes (e.g., duckweed), diverse photosynthesis types (C3, C4, CAM), and specialized water-use efficiency (WUE) strategies. The team also investigates crops with extensive root systems and crop wild relatives (CWR) to understand genome organization and trait architecture.

At Salk, Todd contributes to the Harnessing Plants Initiative (HPI), focusing on breeding and engineering plants with larger, deeper roots to enhance carbon sequestration. His group's roles include (a) applying genome analysis tools to translate Arabidopsis findings to crop genomes, (b) standardizing crop genome resources for HPI scientists, and (c) developing tools like OrthoBrowser for comparative genomics and BLOOM for managing HPI's phenotypic and genotypic data.

Beyond HPI, Todd collaborates with multiple groups to advance genome and large-scale data analysis tools. His collaborations span diverse areas, including Drosophila research (with Kenta), protein structure analysis (with Dmitry), and others. Locally, Todd actively supports the San Diego Botanic Garden's efforts to leverage Southern California's medicinal plant collection. His work reflects a strong network of collaborators both within and outside the institute, fostering impactful research globally and in the local community.

Seminar

On October 9, 2024, at 10 a.m. in the Salk Auditorium, Todd delivered his scientific seminar titled "Beyond the Reference Genome." His presentation provided a comprehensive overview of his research within the Harnessing Plants Initiative (HPI), emphasizing tool development for his HPI colleagues and his broader interests in pangenomics. Todd highlighted his significant contributions to sequencing and annotating an unparalleled number of genomes, potentially setting a record at Salk.

He showcased how his work synthesizes knowledge from sequenced genomes, illustrating the nonrandom nature of haplotype rearrangements and gene evolution in relation to specific traits. Additionally, he advocated for the use of duckweed as a reference organism for photosynthesis research. The seminar was well-received, sparking engaging discussions and further interest in his innovative approaches.

Current and future research focus

Todd's passion lies in sequencing genomes and building pangenomes. As he states in his research statement "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." Along this line he has sequenced or assembled over 600 genomes in the last 4 years. As a next step towards engineering plants, he outlines several approaches including the use of CRISPR/CAS system for large deletions and replacements of plant genomes for desirable traits; such as deeper and larger roots for HPI. He also alludes to bottom-up approaches to build plant artificial chromosomes and deliver them into model plants.

Publications

Todd has numerous collaborations within and outside the institute and he has a relatively big lab. He has successfully leveraged this network to publish a large number of papers and preprints. He has listed 99 publications (excluding preprints) in his NCBI bibliography page. Since joining the Institute in 2020 he has co-authored 30 published manuscripts (including reviews). His CV lists an additional 36 preprints and 15 manuscripts in different stages of preparation, submission and review.

Current Lab Composition (13 full time personnel + 3 visiting scientists/exchange students)

Computational Scientist:	1
Bioinformatics Analyst -I:	2
Bioinformatics Analyst -II:	1
Postdoctoral Fellow:	5
Graduate Student:	1
Research Assistant:	2
Lab technician:	1
Visiting researchers/Exchange Student	3

Letters

Todd provided a list of ~20 letter writers, but all of them are his current or past collaborators. The committee requested letters from 7 outside evaluators (1 past collaborators). One declined to write because of personal family obligations and travel. 3 letters have been received and three have stated to return the letters by November 20th. All three letters have strongly recommended continuation of Todd's research professor position at Salk.

1. Dr. Elizabeth Kellogg
Robert E. King Distinguished Investigator
Donald Danforth Plant Science Center
ekellogg@danforthcenter.org

2. Ian R. Henderson
Professor of Genetics and Epigenetic

Cambridge University

3. Detlef Weigel
Director, Max Planck Institute

4. Rob Martienssen (will send by November 20th)
HHMI Investigator
William J Matheson Professor of Genomics and Plant Biology
Cold Spring Harbor Laboratory

5. Eric Lam (by November 12th)
Distinguished Professor
Department of Plant Biology
Rutgers, the State University of New Jersey

Funding

Todd was recruited to Salk as part of the HPI. According to the Institute guideline, the research professors are expected to fully fund their research program. Outside of HPI funding, he has secured a 3-year grant ($1.84M; 6/12022-5/31/2025) from Gates Foundation to study Cassava genome. His other two listed current funding are Hess Corporation, ($107,905, 01/01/2020-12/31/2024) and Harnessing the power of crop plant diversity for CO2 Removal on a Planetary Scale, Bezos Earth Fund, ($1.75M; 12/01/2020-11/30/2025).

There was no funding mentioned for his numerous collaborations on other plant genomes or non-plant genomes. It seems his continued appointment at Salk and maintaining a lab of 13 full time employees will depend on substantial funding from HPI. There was also no major significant collaborative publication with other HPI faculty on topics related to the HPI mission. Therefore, some input from HPI leadership about funding commitment to Todd's current and future research program will be helpful.

HPI Team Feedback

1) While I'm not available to weigh in on this matter at the moment, I would like to express my support for reappointing Todd.

2) *Q: Has Todd established and expanded an independent research program (including independent publishing and grant acquisition)?*
   A: Todd's research interests lie in uncovering the genomic basis for plant trait evolution, including agronomically important traits such as nitrogen uptake, water use, and metabolism. To do so, he has established an independent research program utilizing plants

with ‘unusual’ strategies for these traits, for example carnivorous plants or cannabis. Todd has been a pioneer in establishing ‘non-model’ plant species for molecular research. In order to move science forward and make meaningful discoveries, it is incredibly important to move beyond classical model systems. Todd is at the forefront for this, and his work is instrumental in accelerating research in non-model species (for example duck weed, which are the fastest-growing plants and thus highly relevant for carbon sequestration; or sea grasses, which are central to the health of our native ecosystems).

Q: Does Todd still provide a unique skill/technology that is needed for HPI that cannot be fulfilled in any other way?
A: Yes, absolutely. Todd is a world leader in genomics, particularly plant genomics. Todd and his lab develop a wealth of genomics tools and technologies that ensure HPI is at the forefront of science. Due to their complex nature (polyploidy, large genome size, repeats, …), the analysis of plant genomes is much more challenging than in other organisms, and requires substantial expertise. With Todd, we are fortunate to have a world-leading expert in the field of plant genomics in our team. His expertise is vital to HPI’s success, as the analysis of complex plant genomes (including pangenomes) of crops is required for (i) gene discovery responsible for traits of interest and (ii) genetic engineering of Salk Ideal plants. Importantly, Todd not only provides his scientific expertise to HPI, but also his leadership, vision, and strong network within academia and industry. I don’t see how his manyfold contributions to HPI can be fulfilled in any other way.

3) *Q: In the last 5 years has Todd contributed to Salk's research profile, provided technological expertise and met specialized scientific focuses?*
A: Todd has enabled a large component of HPI, which genome sequencing of species and varieties of HPI interest. He has also contributed to the analysis of this data. He has furthermore enabled the establishment of HPI cross-cutting tools and data management systems such as BLOOM. He has raised Salk’s research profile, provided lacking technological expertise and splayed a scientific focus of interspecies and cross-species genomics.

Q: Has he established and expanded an independent research program (including independent publishing and grant acquisition)?
A: He has brought his research program here and expended it. He has acquired independent funding and published independently. He is an independent established PI with high visibility. The only area he is underperforming is HPI publications. Despite enormous funding and efforts, most publications have yet to come. However, it is very likely that in 2025/2026 several important HPI related papers will be submitted.

Q: Does Todd still provide a unique skill/technology that is needed for HPI that cannot be fulfilled in any other way?
A: Todd is required for HPI's ambitious program, especially going in the future where we will expand even more into crop species. If he would leave, it is hard to imagine how to fill that gap - it would a detrimental blow to the HPI program.

4) *Q: In the last 5 years has Todd contributed to Salk's research profile, provided technological expertise and met specialized scientific focuses?*
A: Yes, he brings expertise in genome assembly (including pangenomes) and annotation that is not represented by other groups at Salk.

Q: Has he established and expanded an independent research program (including independent publishing and grant acquisition)?
A: Since joining the Salk, Todd has published many plant genome papers (in journals or BioRxiv). Many of these are collaborations outside of HPI, consistent with his high stature in the field. Related to HPI, he published a PanKmer paper in Bioinformatics in 2023, has a collaborative GWAS paper on BioRxiv: https://www.biorxiv.org/content/10.1101/2024.02.27.581071v1 and another collaborative paper in the final stages of a re-revision at Developmental Cell.

I don't have access to Todd's funding so cannot comment on his grants or their distribution between HPI and non-HPI activities within his group.

Q: Does Todd still provide a unique skill/technology that is needed for HPI that cannot be fulfilled in any other way?
A: Yes, Todd's work continues to enhance our ability to work across genomes and translate our findings from arabidopsis into crop plants as well as our ability to assess the effects of natural variation on traits of interest within various crop species of interest to the goals of HPI.

5) One member of HPI declined to provide their feedback

6) Awaiting feedback from 1 HPI member

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

2024-	**Adjunct Professor**, Department of Cell and Developmental Biology, School of Biological Sciences, and Center for Marine Biotechnology and Biomedicine, University of California, San Diego, La Jolla, CA.
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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33. Ding L, Macdonald HD, Smith HO, Hutchison Iii CA, Merryman C, **Michael TP**, Abramson BW, Kannan K, Liang J, Gill J, Gibson DG, Glass JI. Gross Chromosomal Rearrangements in *Kluyveromyces marxianus* Revealed by Illumina and Oxford Nanopore Sequencing. **Int J Mol Sci.** 2020 Sep 26;21(19):7112.

34. Minich JJ, Petrus S, Michael JD, **Michael TP**, Knight R, Allen EE. Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, Scomber japonicus. **mSphere**. 2020 May 20;5(3):e00401-20.

35. Liu J, Seetharam AS, Chougule K, Ou S, Swentowsky KW, Gent JI, Llaca V, Woodhouse MR, Manchanda N, Presting GG, Kudrna DA, Alabady M, Hirsch CN, Fengler KA, Ware D, **Michael TP**, Hufford MB, Dawe RK. Gapless assembly of maize chromosomes using long-read technologies. **Genome Biol**. 2020 May 20;21(1):121.

36. Poplawski SG, Garbett KA, McMahan RL, Kordasiewicz HB, Zhao H, Kennedy AJ, Goleva SB, Sanders TH, Motley ST, Swayze EE, Ecker DJ, Sweatt JD, **Michael TP**, Greer CB. An Antisense Oligonucleotide Leads to Suppressed Transcription of Hdac2

and Long-Term Memory Enhancement. **Mol Ther Nucleic Acids**. 2020 Mar 6;19:1399-1412.

37. MacKinnon KJ, Cole BJ, Yu C, Coomey JH, Hartwick NT, Remigereau MS, Duffy T, **Michael TP**, Kay SA, Hazen SP. Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation. **New Phytol**. 2020 Sep;227(6):1709-1724. doi: 10.1111/nph.16507. Epub 2020 Apr 1. PMID: 32112414.

38. VanBuren R, Man Wai C, Wang X, Pardo J, Yocca AE, Wang H, Chaluvadi SR, Han G, Bryant D, Edger PP, Messing J, Sorrells ME, Mockler TC, Bennetzen JL, **Michael TP**. Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. **Nat Commun**. 2020 Feb 14;11(1):884.

39. **Michael TP**, VanBuren R. Building near-complete plant genomes. **Curr Opin Plant Biol**. 2020 Apr;54:26-33. doi: 10.1016/j.pbi.2019.12.009. Epub 2020 Jan 22. PMID: 31981929.

40. Silva SR, Moraes AP, Penha HA, Julião MHM, Domingues DS, **Michael TP**, Miranda VFO, Varani AM. The Terrestrial Carnivorous Plant *Utricularia reniformis* Sheds Light on Environmental and Life-Form Genome Plasticity. **Int J Mol Sci**. 2019 Dec 18;21(1).

41. Silva SR, Pinheiro DG, Penha HA, Płachno BJ, **Michael TP**, Meer EJ, Miranda VFO, Varani AM. Intraspecific Variation within the *Utricularia amethystina* Species Morphotypes Based on Chloroplast Genomes. **Int J Mol Sci**. 2019 Dec 5;20(24).

42. Wai CM, Weise SE, Ozersky P, Mockler TC, **Michael TP***, VanBuren R*. Time of day and network reprogramming during drought induced CAM photosynthesis in *Sedum album*. **PLoS Genet**. 2019 Jun 14;15(6):e1008209. ***co-corresponding authors***

43. Chekan JR, McKinnie SMK, Moore ML, Poplawski SG, **Michael TP**, Moore BS. Scalable Biosynthesis of the Seaweed Neurochemical, Kainic Acid. **Angew Chem Int Ed Engl**. 2019 Jun 17;58(25):8454-8457.

44. Jupe F*, Rivkin AC*, **Michael TP***, Zander M*, Motley ST, Sandoval JP, Slotkin RK, Chen H, Castanon R, Nery JR, Ecker JR. The complex architecture and epigenomic impact of plant T-DNA insertions. **PLoS Genet**. 2019 Jan 18;15(1):e1007819. ***co-first authors***

45. Mower JP, Ma PF, Grewe F, Taylor A, **Michael TP**, VanBuren R, Qiu YL. Lycophyte plastid genomics: extreme variation in GC, gene and intron content and multiple inversions between a direct and inverted orientation of the rRNA repeat. **New Phytol**. 2018 Dec 17.

46. Hoang PNT*, **Michael TP***, Gilbert S, Chu P, Motley ST, Appenroth KJ, Schubert I, Lam E. Generating a high-confidence reference genome map of the Greater Duckweed by integration of cytogenomic, optical mapping, and Oxford Nanopore technologies. **Plant J**. 2018 Nov;96(3):670-684. ***co-first authors***

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50. VanBuren R, Wai CM, Ou S, Pardo J, Bryant D, Jiang N, Mockler TC, Edger P, **Michael TP**. Extreme haplotype variation in the desiccation-tolerant clubmoss *Selaginella lepidophylla*. **Nat Commun**. 2018 Jan 2;9(1):13.

51. Silva SR, **Michael TP**, Meer EJ, Pinheiro DG, Varani AM, Miranda VFO. Comparative genomic analysis of Genlisea (corkscrew plants-Lentibulariaceae) chloroplast genomes reveals an increasing loss of the ndh genes. **PLoS One**. 2018 Jan 2;13(1):e0190321. doi: 10.1371/journal.pone.0190321.

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

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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.

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

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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.

Ian R. Henderson
Professor of Genetics and Epigenetics

UNIVERSITY OF CAMBRIDGE

Department of Plant Sciences

22 October, 2024

Dear Salk Institute,

I am writing to provide my strongest recommendation for the reappointment of Dr. Todd Michael as Research Professor at the Salk Institute for Biological Studies

Dr. Michael is an exceptional scientist, leader, and academic, with a distinguished career in molecular and cellular biology, combined with his unparalleled expertise in plant genomics, that places him among the most accomplished scientists in this field. He has had particular impact in plant genomics, where he has been at the forefront of harnessing new sequencing technologies, including Oxford Nanopore Technologies, to generate the newest generation of complete telomere-to-telomere genomes, and increasingly pangenomes that capture genetic diversity within and between species. Dr. Michael combines this with a deep interest in plant biology, spanning photosynthesis, secondary metabolism and the circadian clock, and he uses functional genomics to probe and understand these traits. He has shown consistent creative and innovative research, for example, developing methods for reference-free pangenome GWAS, including tools such as PanKmer, which are unique in the field and highly timely as new genomic resources emerge.

I collaborated with Dr Michael to close the Arabidopsis centromere gaps for the first time. This work was inspired by breakthrough nanopore datasets that Dr Michael released as an early adopter of the technology. Dr Michael was instrumental in showing the potential of the data, and developing methods and approaches to quality control and achieve accurate and reliable genome assemblies of these highly repetitive chromosome regions. Dr Michael also brought expertise in optical mapping approaches to the project which provided critical orthogonal data to improve and test the genome assemblies. Dr Michael's experience, insight and collaborative spirit were central to the project and it was an honour and a pleasure to work with him.

Dr Michael's work spans an exceptional diversity of plant species, and his group have generated a remarkable number of datasets, including sequencing over 600 genomes from key crop species, in addition to delivering over 15 high quality T2T genomes, both in collaboration with other Salk researchers and with a very wide network of excellent plant scientists in the US and abroad. These data will serve as a rich resource for the entire field of plant genomics, in addition to driving research in Dr Michael's own group. A particularly exciting project is his recent study of the Cannabis pangenome, which is revealing new insights into regulation of the cannabinoid pathway. Aside from the fundamental interest into genetic and genomic architecture of secondary metabolism, this work also has significant biomedical relevance that Dr Michael is well placed to exploit due to his experience of industrial research. A further exciting project is the design and assembly of first generation plant artificial chromosomes, which has the potential to revolutionize crop improvement, focusing on Machantia and Wolffia duckweed model systems, the latter in which Dr Michael has been

prominent in driving forward. This will be visionary research and Dr Michael is excellently placed to achieve this using his cutting edge knowledge of both genomics and plant biology.

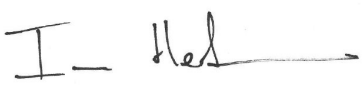
Dr. Michael's extensive experience across leading institutions—ranging from his current roles as a Research Professor at the Salk Institute for Biological Studies and Research Associate at the San Diego Botanical Garden, to his previous leadership positions at the J. Craig Venter Institute and Abbott Laboratories—demonstrates his ability to thrive in both academic and industry settings. Throughout his career, he has continually pushed the boundaries of scientific discovery, particularly in the areas of plant biology, genomics, and informatics. Dr Michael is a highly collaborative researcher and has nucleated and lead multiple international genomics initiatives and networks that have delivered wide ranging impact.

Dr. Michael's publication record is equally impressive, with 99 total publications, over 21,000 citations, and an H-index of 60. This not only underscores the depth of his research but also the widespread impact of his contributions to the scientific community. His work has significantly advanced our understanding of plant biology and continues to influence research globally. I have consistently been impressed by Dr. Michael's ability to lead cutting-edge research initiatives while also mentoring the next generation of scientists. His contributions to the field have been recognized with numerous prestigious awards, including the NIH Postdoctoral Fellowship, Monsanto Science Fellowship, and selection as one of Genome Technology's "Tomorrow's PIs," showcasing his forward-thinking vision and technical expertise.

Beyond his academic and research accomplishments, Dr. Michael is a collaborative leader and an exceptional mentor. He consistently demonstrates a rare combination of intellectual rigor, innovation, and scientific generosity. He is extremely well-respected by his peers, and his ability to foster collaboration across systems and countries has led to numerous successful interdisciplinary projects. His commitment to advancing scientific knowledge while supporting those around him makes him a truly exceptional colleague who it is a privilege to work with.

In conclusion, Dr. Michael is a highly distinguished scientist whose contributions to molecular biology and genomics have had a lasting impact on the field. He is an exemplary research leader and collaborator, and I give him my highest recommendation. I am confident that he will continue to excel and make significant contributions to the Salk research community, and more broadly both nationally and internationally, through his pioneering plant genomics research. He has my strongest recommendation.

Sincerely,



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DONALD DANFORTH
PLANT SCIENCE CENTER

November 4, 2024

Dr, Satchidananda Panda
Salk Institute for Biological Studies

Dear Dr. Panda,

I am happy to recommend Todd Michael for reappointment as Research Professor. I have been acquainted with Todd for some years and we have crossed paths at various meetings or when he was visiting colleagues here at the Danforth Center, but we have never collaborated.

From his CV, I see that Todd arrived at the Salk Institute in 2020, a year that was thoroughly disrupted for everyone in the world, and certainly in the US. Despite that unfortunate timing he has been highly productive and seems not to have slowed down at all, with 30 publications listed in the last five years (since Jan. 2020).

Todd is known nationally and internationally for his skill in genomics, particularly genome assembly and cross-species comparisons. This is an area where the tools for data acquisition change rapidly, requiring constant updating and improvement of analytical methods. His recent development of the tool PanKmer for analysis of pangenomes is a case in point (*Bioinformatics,* 2023). Pangenomes, summarizing the combined genome sequences of multiple members of a species or clade, are computationally challenging for eukaryotes with large complex genomes such as plants. Although its release is too recent to know if it will be widely applied, PanKmer is a valuable step toward making pangenome studies computationally tractable.

His paper on gapless assembly of maize chromosomes was another major step forward in methods development (*Genome Biology*, 2020). The sequencing technologies provided by PacBio, Oxford Nanopore, and BioNano together provide exceptional long-read data, but at the time that assembly was generated the tools for merging the data sets into chromosome-scale assemblies were just under development. The maize genome poses a particular challenge for any sequencing method because it contains long repetitive regions, particularly the sequences known as knobs, that are difficult to sequence and assemble (analogous to a jigsaw puzzle in which all the pieces are the same color). Producing an assembly in which some of the chromosomes were fully assembled without gaps was thus a major achievement and depended on a newly developed computational pipelines. This ability to combine the output of several sequencing methods also led to Todd's paper in *Science* (2021) that managed to sequence and assemble all five Arabidopsis centromeres, leading to novel insights about their structure and hints about details of their function and evolution.

Todd is also well known for his work on duckweeds, tiny aquatic flowering plants in the clade Lemnoideae of family Araceae. His team has published full genomes of multiple species in the subfamily, representing all genera. More importantly he has generated data on single cell DNA and RNA sequences, as well as methylation state. This is allowing him to understand the identity and developmental trajectory of every cell in the organism. The recent paper in *Genome*

DONALD DANFORTH
PLANT SCIENCE CENTER

Research (Denyer et al., 2024) computationally dissects gene expression for ca. 5600 cells of *Wolfia australiana*, and clusters them into functional and anatomical groups. A similar dataset was generated for *Lemna minuta* (*Plant Physiology*, 2022). These datasets are the first steps toward manipulating genes and gene expression to test hypotheses about gene function.

In addition to his work on tool development and creating resources for duckweed species, Todd has been involved in dozens of other genomic studies in systems as disparate as carnivorous plants (pitcher plants, bladderworts), mints, red algae, cannabis, cloves (*Syzygium*), cranberry and cassava. Given the diversity of his work, it is hard to identify the five most important publications. The methodological work will likely generate the most citations but the many genomic studies are foundational and each unlocks significant aspects of the biology of the system. His single-author paper in *Plant Physiology* (2022) on the conserved genomic location of circadian clock genes is thought provoking and the kind of paper only he could have written.

Todd is clearly a good collaborator. While he has a respectable number of papers where he is corresponding author or co-corresponding, he is middle author on many others, indicating that he is a sought-after and valued collaborator. The position as middle author is usually reserved for someone who brings a critical expertise to the project, which he has done extensively.

It is hard to compare Todd to "non-tenure track Research Professors in traditional universities", as requested in your cover letter. His background and experiences are far more diverse than those of most university professors, encompassing both private-sector and public-sector institutions. He has far more papers. His funding streams are varied and substantial indicating a truly creative mind that looks beyond the usual federal agencies. His publication record proves the efficacy of that approach. My own institution (the Donald Danforth Plant Science Center) is a free-standing non-profit research institution where none of the PIs are tenured and all have to generate robust self-funded programs. Collaboration is highly valued and team efforts are considered favorably. Based on his high level of expertise, productivity, and collaborative nature, Todd would easily receive a continued appointment here.

In summary, continuing Todd Michael's appointment should be an easy decision. He is an excellent scientist and a great asset to the Salk Institute.

Sincerely,

Elizabeth Kellogg

Dr. Elizabeth Kellogg
Robert E. King Distinguished Investigator
Donald Danforth Plant Science Center
ekellogg@danforthcenter.org

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FOR BIOLOGY TÜBINGEN

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Satchidananda Panda
Chair, Review Committee
The Salk Institute for Biological Studies

October 13, 2024

Dear Satchin, dear Members of the Review Committee,

You asked me to assist in the review of **Dr. Todd Michael** for his reappointment as Research Professor at the Salk. I note that I provided already a very positive letter for Todd's initial appointment five years ago. I also note that Todd and I have published together, mostly from Todd's time as a postdoc with Joanne Chory, but the last joint paper was in 2018. In addition to the written material provided, I had a chance to talk to Todd about some of his lab's effort when I visited the Salk this summer. My own lab has major efforts in pangenomics and GWAS, which aligns with Todd's work, and I am thus well qualified to comment on his achievements.

To recap, Todd had first a very productive PhD with Robertson McClung, followed by an even more productive postdoc with Joanne Chory, where he already showed his extraordinary talent for collaboration with others, teaming up specifically with another postdoc in the lab, Todd Mockler, with the two of them being key for moving the Chory lab into the genomic era. Todd's strong skills in genome-based studies were the foundation for his first independent research group at Rutgers University, where his ability to cross easily back and forth between wet lab biology and high-throughput genomics made him a highly sought-after collaborator all over the world. His taste for ever larger data sets eventually led him to accept positions in industry and then a private research institute, the J. Craig Venter Institute, where he became a pioneer in producing high-quality genome assemblies with long-read sequencing technology.

Since joining the Salk five years ago, Todd has continued to be at the forefront of generating high-quality genomes for a wide range of species. In addition, his lab has contributed to the generation of tools for the analysis of whole-genome collections. From his CV, it is clear that he is a leader for two important groups of emerging crops, *Cannabis* and duckweeds. It is also clear from his CV, as evidenced by joint papers and joint funding as well as a long list of invitations for seminars and conference talks, that many colleagues from all over the world seeks out collaborations with him, including reearchers from industry and large academic consortia.

From his CV, I did not get a complete sense of the size of Todd's lab at Salk, but was pleased to see that he has had 10 doctoral and postdoctoral researchers, mostly in genome informatics. It is difficult to know how widely the tools they are developing are/will be used, given that the development of tools for pangenome analysis is a very active area, with many

much large competing groups, but the ideas behind the tools Todd's group has been building are all excellent. More importantly, it is obvious that Todd has an absolutely essential and key role in the Harnessing Plant Initiative at Salk. Todd is a perfect complement for the efforts driven by Wolfgang Busch, who is an expert in plant phenotyping, but who has only limited experience in plant genomics. I was also very pleased to see that Todd collaborates with several other Salk faculty beyond the Harnessing Plant Initiative. One might criticize that Todd's efforts, as laid out in the description of his current research, are very broad, but since essentially all of them are collaborative efforts with others, either at the Salk or elsewhere, I do not see that as a concern.

In summary, Todd is a fantastic asset for Salk, and I am delighted to endorse his reappointment without any reservations.

Yours truly,

Detlef Weigel
Director, Max Planck Institute