

UCDAVIS

DEPARTMENT OF PLANT SCIENCES

Assistant Professor of Evolutionary Biology

Department of Biological Sciences

University of Arkansas

Dear members of the search committee,

My name is Jordan Dowell, and I am a USDA National Institute of Food and Agriculture (NIFA) postdoctoral fellow in the Department of Plant Sciences at the University of California, Davis. I am applying for the Assistant Professor of Host-Pathogen Interactions position in the Department of Biological Sciences at the University of Arkansas. While I am early in my career, I started building my independent program on day one of graduate school. In addition, I understand what it takes to build a successful program from the ground up and with limited resources. I have been an integral part of starting two labs, one of my Ph.D. advisor Chase Mason and a close collaborator Dr. Eric Goolsby. In this capacity, I had to consider developing long and short-term projects to build a successful program while considering the logistics of obtaining the tools, space, and labor necessary to complete projects in the short pre-tenure timeline. Thus, first-hand experiences and open dialogs have prepared me for many of the rigors of starting a lab. Further, **I will bring transferable funds of \$150,000 as early as August 2023** to start my program.

As a broadly trained chemical ecologist and comparative biochemist, my research spans a variety of empirical, theoretical, and computational approaches. I integrate tools from diverse fields, including biochemistry, physiology, machine learning, toxicology, and molecular biology spanning scales from multi-organismal to synthetic cellular interactions. Integrating my expertise in leveraging remote sensing, analytical chemistry, and machine learning for metabolomics and developing noninvasive phenotyping tools will expand the Department of Biological Sciences' strong interdisciplinary focus. In addition, metabolomics and the analysis of small organic molecules is an uncommon skill invaluable among industries from food science and forensics to biotechnology and biomedical science. For my dissertation, I assessed trait genetic architecture of metabolomic and physiological variation in an association mapping population of cultivated Sunflower (*Helianthus annuus*), identified evidence of recent breeding practices, and uncovered genomic links to potential novel self-incompatibility proteins commonly found across eudicots. Further, I combined remote sensing and analytical chemistry methods to develop a noninvasive phenotyping tool that predicts herbivore-induced responses across the genus *Helianthus* with ~95% accuracy. In addition, I characterized volatile organic compounds(VOCs) present across the genus in various herbivory contexts to understand the evolution of inducible defenses. Finally, I chose to expand this work and develop molecular biology skillsets in my current postdoc. Currently, I am using integrative approaches from ecotoxicology, molecular, and synthetic biology to study the direct and indirect effects of volatile plant chemicals used for information transfer on a common fungal pathogen's (*Botrytis cinerea*) life history traits and their underlying genetic architecture while furthering our understanding of the common chemicals used for information transfer across eudicots.

I am excited at the potential to build interdisciplinary collaborations with the stellar faculty of the Department of Biological Sciences and across the University. Apart from potential collaborations with other plant-, fungi-, or insect-associated labs, I see many other potential collaborations integrating my program's approaches to understanding chemical diversity and metabolic investment. For instance, for faculty working with bacteria, we can find synergy by identifying metabolic vulnerabilities in individual strains for drug discovery, in bacterial communities to identify functionally important taxa, or examine metabolites involved with biofilm production or quorum sensing. On the other end of the tree of life, vertebrate metabolic systems have very few unique metabolites not found in plants or fungi, making easy extensions of my program's protocols useful for faculty interested in organic molecule and aerosol impacts on metabolism, health, or biomarker discovery. In summary, there are very few labs across chemistry, computer science, and life sciences where I have yet to find an idea or two for collaboration. In fact, developing collaborative ideas is my greatest joy in science.

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I have mentored over sixty undergraduate and graduate students throughout my career, leading to several independent, integrative, and fundable lines of inquiry that I am excited to bring to the University of Arkansas. As an educator and mentor, I prioritize the mentorship of others. In addition, I have expanded diversity, equity, and inclusion initiatives at every institution I have been affiliated. Finally, I leverage my own personal lens as a queer African American cis-male and rely on published works in biology education research to make data-driven decisions on developing interventions and refining existing infrastructure. In fostering change, it is advantageous to leverage existing infrastructure rather than create new programs with little initial cultural capital or exposure. As a University of Arkansas faculty member, I want to continue my efforts to expand the recruitment and especially the retainment of marginalized researchers. In addition, more broadly, I want to continue serving the community and opening doors for people who can't see them yet.

I have a strong record of collaboration, obtaining extramural research funding, and fiercely independent research productivity. I have used my time as a graduate student and postdoctoral fellow to develop a diverse program that continues to grow. I am excited to interact with the faculty at the University of Arkansas to create synergistic avenues of research. Thank you for your consideration and contributions to education and research excellence.

With best regards,
Jordan Dowell, Ph.D.
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University of California, Davis
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As a chemical ecologist and comparative biochemist, I am especially interested in understanding the evolution of chemical diversity and the effects of chemical diversity on organismal interactions across spatial and temporal scales. As nature's prime organic chemists, plants produce diverse chemicals (metabolites) to deter and attract beneficial organisms, ease abiotic stress, and communicate within and among species. Producing metabolites to mediate biotic and abiotic interactions requires nutrient investment, often at the expense of growth or reproduction. For instance, photosynthesis, specifically the assimilation of CO₂ into organic molecules, is a fundamental ecosystem process. Assimilated carbon can be invested into more nutrient-acquiring tissues to increase photosynthesis(e.g., growth) or reproduction to promote fitness.

However, plants live in dynamic, stressful environments. As a result, plants face an inherent physiological trade-off between investment in specialized metabolites that mediate biotic and abiotic stress versus investment in growth or reproduction to ensure individual or population survival. However, ‘tradeoffs’ suggest that investment in specialized metabolites has no role in growth or reproduction, but as with most biological concepts, ‘it depends.’ For instance, volatile organic compounds (VOCs) attract and direct pollinators, increasing fitness, and can communicate herbivore damage within and among individuals to prime induced defense pathways. In trying to go from ‘it depends’ to ‘under these set of circumstances’, my program asks, **“How do multifunctional metabolites fit into evolutionary and ecological hypotheses,” and more simply, “How many metabolites are multifunctional !?”**

Traditional cell-signaling and chemical ecology hypotheses assert that single molecules are responsible for these induced responses. However, in VOC-induced responses in plants and fungi, qualitative and quantitative variation in VOCs blends have a larger impact than any single VOC in inducing plant responses, suggesting signal synergism. As VOCs are structurally constrained, synergism may have developed due to similarity in physiochemical properties. Further, maintaining synergistic signaling may allow for metered responses using conserved protein receptors, while shifting cues may help conceal plants from organisms with more canalized sensory perception, like animals. Thus, selection by pests and pathogens may drive changes in cues more directly than cellular receptors, leading to increased diversity of signaling molecules compared to receptor proteins.

In addition to signaling, VOCs act directly and indirectly. For instance, cis-3-Hexen-1-ol (the smell of fresh-cut grass) is widely distributed across the plant kingdom and can induce acquired pest and pathogen resistance across many plant species. In addition, this VOC directly inhibits the sporulation and growth of a common host-generalist fungal pathogen, *Botrytis cinerea*. However, in the broader scale of host-pathogen interactions, there are no definitive studies or models delineating the impacts of maintaining detoxification mechanisms and, simultaneously, retaining the ability to interpret host-infochemicals on pathogen phenotypic and genetic diversity.

To answer these questions and ultimately ask more, I combine integrative, multi-omic approaches with natural and life history to take an organism-centered approach. My program has three primary foci: **(1)**Developing theoretical and empirical models of the evolutionary ecology of plant VOC-mediated interactions, **(2)** Identifying the relationships between the evolution of phytochemical diversity and physiological tradeoffs, **(3)** Testing the direct and indirect effects of plant VOC-mediated interactions in plant-pathogen systems, and **(4)** Developing statistical frameworks to assess chemical diversity and models of chemically-mediated cellular and species-level interactions.

My USDA NIFA fellowship will fund portions of this work as a transferable standard grant as early as August 2023(\$150,000 remaining).

Focus 1: VOC-induced responses among individuals within a species have reduced effectiveness as populations' genetic and physical distance increase, but we observe a high efficacy of VOC-induced responses among distantly related species. My lab will identify biotic and abiotic factors contributing to shifts in the efficacy of VOC-induced responses across evolutionary scales. I hypothesize that selection and genetic drift impact the transition from plant 'communication' as a function of self-recognition towards 'eavesdropping, manipulation, or mutually beneficial communication' mediated by ecological interactions, including physiological tradeoffs, niche partitioning, biotic stress intensity, and reproductive viability. To test my hypotheses, we will conduct cross-species experiments in lab and field settings using multi-omic approaches with nine species of the annual clade of *Helianthus* (Sunflower), which vary in hybridization success and ecological niche, native to all ecoregions of the continental U.S. I have assessed physiological variation, constitutive and herbivory-induced VOCs, and developed a noninvasive tool to assess induced responses across the genus in real-time. From these experiments, the explanatory power of factors affecting VOC-induced responses expands our understanding of the interaction between community assembly and evolutionary processes. Further, including transcriptomics to understand the regulation of VOCs and identify plant receptors (none of which have been identified or hypothesized!) will lead to novel avenues of signaling research of interest to NSF, USDA, and NIH.

Focus 2: Developing evolutionary models requires understanding the regulation of trait variation and inheritance. My lab will test how offspring from chemotypically and physiologically distinct parents vary compared to transcriptomic and genomic predictions. In addition, we will examine how hybridization and introgression alter patterns of metabolite profiles and physiological variation with experimental crosses. The comprehensive examination of the inheritance of phenotypic variation across the genus will develop novel hypotheses that my lab can test more broadly in other species of economic and ecological importance to NSF, USDA, and DOE. In my previous genome-wide association study(GWAS) in cultivated Sunflowers, I found that lines selected for increases in absolute fitness (e.g., total seed yield) are associated with leaves with high photosynthetic capacity and reduced concentration of specialized metabolites in comparison to lines selected for fitness stability (stress tolerance) associated with leaves with lower photosynthetic capacity and higher concentrations of specialized metabolites. In addition, several linkage blocks were associated with both physiology and specialized metabolism. These data point towards pleiotropy or selective sweeps underlying observed phenotypic variation.

Focus 3: Assessing direct and indirect impacts on fitness requires delineating effects across generations. My undergraduates and I are conducting a multi-generational toxicological GWAS of VOC effects on fitness-related traits in *Botrytis cinerea*. In addition, we are testing the impacts of VOC exposure(to host and/or pathogen) on the infection success of new tissue. Using and expanding this data, my lab will test how multifunctional metabolites, mixture toxicity, and host-induced responses can affect pathogen genetic diversity and life history evolution. As my lab continues, simulations will be combined with further data on isolate-level competition, nutritional dynamics, and microbiome composition to produce and test novel hypotheses about the evolutionary ecology of host-pathogen interactions in the context of multifunctional host-infochemicals (VOCs).

Focus 4: As we continue to develop new questions concerning the evolutionary ecology of complex traits, our methods also need to develop. Like individual species, metabolites are non-independent entities. Thus in examining metabolomic data, we need to account for variation due to shared biosynthetic properties accurately, as well we can exploit autocorrelation for synthetic biology. To understand the explanatory power of canonical and non-canonical biosynthesis, I developed a statistical method to assess the phenotypic integration (complex patterns of covariation among functionally related

traits) of metabolite profiles, given an unknown pathway using the empirical three-dimensional physiochemical properties of observed metabolites. To integrate my previous work into synthetic approaches to assess physiological tradeoffs, I am incorporating process-based models of metabolism to assess energetic investment in various pathways and the integration of metabolism. My undergraduates and I are examining how pathogen infections alter carbon and nutrient investment by *Arabidopsis thaliana* into specialized metabolism. In tandem, we are modeling investment by the fungal pathogen *B. cinerea* into specialized metabolism during infections. By incorporating transcriptomic data, we are developing proxy measures of metabolism and identifying reactions associated with susceptibility or virulence.

Specifically, I will use these models to explore the evolution of metabolic flux and energetic investment in specialized metabolic products based on simulated nutrient requirements necessary for production, leveraging publicly available transcriptomic datasets. In addition, as single-cell transcriptomic data becomes more available, we will apply these pipelines to assess cellular physiological tradeoffs and explore how the metabolism of organs is coordinated. Further, as most studies examine physiological tradeoffs in the context of carbon, nitrogen, or water acquisition, My lab will expand the field by exploring alternative physiological tradeoffs in the context of various macro and micronutrients through simulation and follow-up empirical validation.

In brief, I am excited to bring my program to MSU. I envision my lab as an interdisciplinary training ground to support an array of scientists while considering diverse extramural funding sources. For agricultural funding sources, Sunflower is one of the world's most important drought-resilient oilseed crops, making my program's discoveries directly translatable to agriculture. In addition, many VOCs are terpenes, bioactive molecules with anti-microbial and anti-cancer therapeutic applications. In food science, terpenes drive scent and flavor, making the products of this research essential to the growing brewing and floriculture industries. While these research foci represent a portion of my program, I am eager to engage with the department to develop new collaborations with new questions and within my program's core projects.

Dr. Kaye Whitehead, a professor at Loyola University Maryland, once told me that taking up space as a Black individual in a predominantly white space is a radical political act. Nevertheless, it is one's prerogative to use that space and knowledge gained to position oneself as a public intellectual and be authentic in engaging with systems that may be hostile. According to the National Science Foundation, as of 2019, ~1% of the Life Sciences tenure-track professoriate is Black or African American, with similar percentages for doctoral students and recipients in the U.S.A. With many Black professors concentrated at Historically Black Colleges and Universities, many public university students complete their education without gaining instruction from a Black Life Scientist. I am one such student.

As the first Black Ph.D. within the Department of Biology at one of the largest universities in the U.S.A. by enrollment(University of Central Florida) in a field that is historically hostile towards people of color, I have faced more than my fair share of hardships from socioeconomic to institutional racism and discrimination. I have taken up the advice of Dr. Whitehead as a call to action. Although my experiences only provide a personal lens for formulating ideas on how to combat issues of equity and inclusion, apart from diversity representation. Given my privileged position as a scholar, researcher, and educator, I have taken it as my duty to not just excel in my studies and research but to engage with others authentically and rely on my skills to make data-driven decisions.

To increase representation in science and public policy, I prioritize the mentorship of others. In my mentorship, I rely heavily on published works on biology undergraduate education. Works such as Thompson and Jensen-Ryan^[3] have inspired me to be aware of cultural capital when interacting with a large group of undergraduate mentees. At an individual level, I have used the strategies put forth by Le et al.^[1] to foster 'science identity' development and help students name aspects of science that align with their developing 'scientific identities.' Learning not just to navigate the academy's hidden curriculum but to communicate scientific findings within a community that has historically been actively hostile towards people of color (e.g., eugenics and apartheid ecology) can be a significant challenge to preserving one's value in their identity. In supporting a scientific identity and fostering positive development, I believe it is essential to be aware of mentee responsibilities outside the lab. I develop individual projects for students that work with their schedules supplying a unique undergraduate research experience that, from my experience, is rarely observed.

As of 2022, I have mentored over 65 undergraduates in varying capacities, most of whom are from marginalized and/or underrepresented groups. Many of these students have continued in science at various levels (e.g., graduate school, private industry, government, and non-profit work), focused on diversifying the face of science while increasing representation. My leadership style focuses on supplying a space where one does not have to fundamentally change themselves to succeed. Instead, I encourage my students to draw from their firsthand experiences to communicate their research, from making MEMEs of their honor theses to developing their thesis defense presentations in ways that people important to them would grasp the concepts. By being authentic and promoting authenticity, I have helped my students support their identity and interest in science without compromising their identity in exchange for academic success.

A survey by the National Science Foundation reported that U.S.-born Black individuals, regardless of sex, have the lowest enrollments in Life Science doctoral programs. In addition, low enrollment factors are further compounded by the highest attrition rates compared to other underrepresented groups^[2]. Current hypotheses postulate a lack of role models as the culprit, which is similar in many other sciences^[2]. As education is the lens through which I primarily look at equity and inclusion, exposure to potential mentors through diversity initiatives is valuable. As such, another colleague and I gained funding for a college-level initiative (UCF College of Science Visiting Scholars). This initiative supplies funding to bring in historically excluded scholars from every department in the college for research seminars, and social events focused on providing undergraduate and graduate students

with opportunities to foster authentic interdisciplinary mentorship. As a part of my next steps, I would like to develop a similar program at U of A.

As a student and postdoc, I have interacted with several diversity centers and found them incredibly useful. Integrating campus diversity centers into department-level and college-level initiatives is an easy way to increase exposure and recruit students. For example, a straightforward implementation to expand exposure to underrepresented groups on campus is to start a department email for lab positions and funding opportunities. The diversity centers can then distribute these opportunities to their lists of students. During my postdoc, I took a similar initiative to hire three work-study positions. In less than a week, I had an applicant pool of over a hundred qualified applicants that fit one or more of NSF's diversity categories.

In supporting U of A's equity and inclusion initiatives, I would love to extend the REU programs by reapplying for funding and developing a **Plant and Microbial Biology** specific REU. Further, I would like to integrate REUs across campus to develop collaborative spaces with individuals working across systems to foster a diverse interdisciplinary cohort of researchers and expose individuals to intersecting areas of science. In expanding these programs, I would like to develop a set of meetings during the program to read works on undergraduate and graduate education. Using primary literature to center conversations of equity and inclusion will further develop these students as interdisciplinary scientists. Specifically, statistically many of these particular students will have very few peers or mentors with similar life experiences. Having students read and discuss research on people with similar life experiences serves as a way to bridge the gap in mentorship until the diversity of STEM researchers catches up. In addition, I would like to link these students with industry mentors or incorporate industry mentorship into the grant submission, as several USDA initiatives have multi-mentor programs in mind. I personally have many industry connections across small(23andme, Running Tide, Pestscope, etc.) and large companies(Bayer, Syngenta, Corteva, etc.) and Non-governmental organizations (Bill and Melinda Gates Foundation, United Negro College Fund, etc.) that would be great places to start.

My most impactful contribution to diversity, equity, and inclusion, would be through the implementation of my class, Scientific Racism: a historical perspective. I envision this as a graduate or upper-division undergraduate class where we discuss significant impacts and implementations of 'scientific' findings. I think of this course as being a more intense ethics course where we contextualize current and historically controversial ideas while expanding on their impacts on systemic inequities seen today. My course would be an excellent opportunity to allow students to take extra time and really sit and think about their impacts on communities now and into the future.

In the long term, I want to further reach out to the community at multiple levels. One of the most critical turning points in my life happened when I walked around the mall as a middle schooler. In Las Vegas, magnet high schools typically set up posters once a year and discuss their programs. This experience was the first time someone told me I could positively impact my community, and science was a way to do it. While malls do not have the same foot traffic as they did when I was a kid, I would love to develop a similar outreach program with the **Department of Biological Sciences**. Specifically, hosting graduate and undergraduate poster sessions at various public spaces outside the University to encourage community engagement. In addition, the first museum I ever visited was The Las Vegas Natural History Museum. After my Ph.D., I took some time to walk through the halls and remember how important this place was to me as a child. I would love to work alongside people in other departments to make an area in a local museum, like the **Fayetteville Local History Museum**, focused on discoveries from people who grew up in the **Fayetteville or broader Arkansas** community. A community exhibit is a great way to expose young community members to diverse scientists from their neighborhoods.

In conclusion, ensuring that all students, regardless of background, are fully prepared and able to gain meaningful experiences from education and research is critical to ensuring the development of a well-informed citizenry and maximizing the importance of education in securing gainful employment.

References: [1]Le PT, Doughty L, Thompson AN, Hartley LM. 2019. Investigating Undergraduate Biology Students' Science Identity Production (EL Dolan, Ed.). *CBE—Life Sciences Education* 18: ar50. [2]Okahana H, Klein C, Allum J, Sowell R. 2018. STEM Doctoral Completion of Underrepresented Minority Students: Challenges and Opportunities for Improving Participation in the Doctoral Workforce. *Innovative Higher Education* 43: 237–255. [3]Thompson JJ, Jensen-Ryan D. 2018. Becoming a "science person": Faculty recognition and the development of cultural capital in the context of undergraduate biology research. *CBE Life Sciences Education* 17.

In today's world, we have access to the world's thoughts twenty-four hours a day, seven days a week. Now more than ever, it is vital to teach our students essential concepts and equip them with basic skills to apply scientific reasoning to both analysis of the natural world and everyday life. This skill set includes basic training in scientific skepticism to dissect claims and evaluate their validity based on available data. In addition, we must equip students with statistical literacy. The ability to understand the scientific process and interpret the validity of scientific claims requires an appreciation for a wide variety of statistical concepts, many of which are beyond the scope of introductory undergraduate statistics courses. Unfortunately, statistical illiteracy is pervasive, even in professions requiring advanced degrees (e.g., medicine, pharmacy, and law). The potential reasons for statistical illiteracy are varied but often stem from a lack of motivating factors or a student's belief that they are not a "math person." Contrary to these misconceptions, statistics is a handy tool for everyone and can be intuitive and accessible when portrayed in a tangible, interactive, and applied framework.

Equally important across the sciences, fluency in one or programming languages empowers students to control how they learn new concepts, analyze data, and even create new ideas. For many beginning graduate and undergraduate students, learning a programming language can seem impossible and directly antithetical to why they wanted to get into life sciences in the first place. Unfortunately, in computer science departments, introductory coding courses are often intended as the first step of a multi-year sequence. However, time is a limited resource for both undergraduate and graduate students. A more practical approach is to develop specialized traditional or short courses taught within life science departments. Semester-long course themes could cover, for example, working with a command interface and scripting, statistical computing, and high-performance cluster computing. These courses are stand-alone and non-redundant, so students can take multiple courses as needed. Such courses also provide exceptional opportunities for graduate students to integrate their research (e.g., potentially adding a thesis chapter) or even develop novel publishable works resulting from course-long projects. For instance, one of the central chapters of my dissertation came from projects in courses like this.

Integrating statistical computing into graduate and advanced undergraduate courses is invaluable. R is freely available on all platforms, completely open-source, and provides a real-time interface to demonstrate virtually any statistical concept. By incorporating R into coursework, students can examine concepts at a basic level to understand how and why concepts work. In addition, computer simulations can demonstrate concepts under various scenarios, where students can assess the sensitivity of a concept to violations of assumptions.

Further, incorporating R-based simulations negates the need for cost-prohibitive software to show processes like genetic drift and selection. In addition, many journals now require raw data to be provided alongside publications for fully reproducible analyses, tables, and figures. Freely available data presents an unprecedented opportunity for incorporating primary literature into the classroom. On the one hand, given only background information, methodology for data collection, and raw data, students can collaborate and decide for themselves the most appropriate statistical analyses and further perform them. Additionally, in developing individual projects, students can take data from papers that interest them increasing the diversity of potential projects and reinforcing students' 'scientific identities.'

Significant works in biology education research stress the importance of the 'scientific identity' in retaining marginalized groups in life sciences. 'Scientific identity' posits seeing oneself as a valid part of the scientific community helps instill a sense of belonging, which supplies further intrinsic motivation to succeed. In developing courses, I stress identity development through course-based research experiences. For example, in my Ph.D., I designed the lab proportion of a new plant genomics and biochemistry

course, where I initially developed an integrated lab that would allow students to use metabolomics to test hypotheses. However, with the COVID-19 pandemic, this course had to be moved 100% online. I incorporated basic R programming skills, statistical computing, and freely available data to facilitate this class. During the semester, we centered discussions on biochemical pathways in meaningful ways that incorporated students' interests. This experience culminated with students generating questions about specific pathways and leveraging available genomic and phenotypic data to test specific hypotheses. I believe presenting research, communicating, and engaging with peers throughout the semester helps build the 'scientific identity.'

Statement on mentorship

In training mentees, I view mentees from my group, regardless of where their career takes them, as leaders. As a mentor, it is my job to facilitate that development. Candid conversations about management strategies and encouraging mentees to take different management/leadership courses are invaluable in learning to lead a team. One of the most influential courses I took as an undergraduate or graduate student was bar management. In this course, I learned budgeting, leadership styles, how to have difficult conversations with employees, and further how to develop training systems that support and produce competent workers efficiently. While seemingly unrelated, fostering the development of transferable skills is invaluable. It is important to note that not every mentor is suitable for every mentee. For instance, I stress the importance of independence and interdisciplinary ability. Specifically, an essential skill I want mentees that leave my group to have is the ability to move into new systems and ask further questions. We constantly have to acclimate to new systems and integrate new knowledge in industry and academia. So, solid skills to ease transitions are crucial to excel across fields.

When approaching new systems or questions, I stress a 'first principles' approach. My process includes breaking down existing problems in the context of generalized theories, such as energy conservation. By initially focusing on 'simple' generalizable ideas, we can begin to ask about nuances or question dogma within fields. Specifically, a dogma my group works on is signaling. Traditional signaling research points to one signal to one receptor, and in predator-prey interactions, the red queen hypothesis is a general evolutionary concept that can be applied. The red queen hypothesis states that species must constantly adapt to survive when pitted against an ever-evolving opposing species. For example, prey signals and receptors change based on selection by the predator. From observations of signal synergism, we begin to ask about the nuances of the hypothesis. Signal synergism, or the maintenance of multiple signaling molecules that can produce complex responses and shift in relative use and abundance based on single selection targets of predators, can be applied to many systems and questions. An analogous situation is choosing startup products to invest in from social media 'likes'. Instead of only focusing on which product has the most 'likes', one can diversify investment over many products and shift relative investment based on which product has the most 'likes' at a given time. The application of generalizable hypotheses to new systems is a skill set I seek not just to incorporate into my mentorship but into my teaching as well. While these values may not be suitable for every student, I think straightforward communication is key to ensuring both mentor and mentee are good fits. Lastly, as mentors, we should always question our abilities and methodologies. Thus I view my continued training and development as critical to ensuring my lab and classroom run smoothly and produce successful leaders in science.

EDUCATION

PhD	University of Central Florida, Integrative Biology Dissertation: Running Title: "Volatile metabolomic dynamics of the annual clade of <i>Helianthus</i> " Advisors: Chase Mason (chair), Pedro Quintana-Ascencio (vice-chair)	2021
MS	University of Nevada, Las Vegas, Ecology & Evolutionary Biology Thesis: "Landscape scale: inter- and intraspecific variation in plant interactions along a stress gradient in the sheep mountain range of Nevada" Advisor: Dale Devitt	2019
BS	University of Nevada, Las Vegas, Ecology & Evolutionary Biology	2014

GRANTS, HONORS AND AWARDS

Identifying furanocoumarin alternative biotic resistance mechanisms among U.S. celery germplasm	2022
• \$90,000 External grant (pending) • PI's: Jordan Dowell , Celine Caseys, Daniel Kliebenstein	
USDA, National Institute of Food and Agriculture: Agriculture and Food Research Initiative Postdoctoral Fellowship	2021-Present
• \$225,000 external fellowship (\$150,000 transferable funds August 2023) • Direct and indirect effects of conserved and lineage-specific volatile organic compounds among eudicots for control of <i>Botrytis cinerea</i>	
Florida Education Fund Dissertation Fellowship	2020-2021
• \$12,000 External Fellowship	
Private Funding, Sponsor: Massey services, Inc.	2020-2021
• \$140,900 Private funding (Allocation to Dowell: \$9,500) • PI, Swaminathan Rajaraman Co-PI, B. Sharanowski • Initiative to develop novel nano-sensors for pest management.	
University of Washington's Statistical Genetics Summer Institute Scholarship	2020
• \$900 External Workshop Scholarship	
Bill and Melinda Gates Foundation	2019
• \$1,000 External travel award • Institute for Teaching and Mentoring: Compact for Faculty Diversity	
University of Central Florida, Biology Graduate Student Association	2019
• \$300 Internal travel award	
University of Central Florida, Biology Department	2019

- \$250 Internal travel award

Bill and Melinda Gates Foundation Millennium Graduate Fellow 2015-2020

- \$175,000 External Fellowship

University of Central Florida's Doctoral Conference Support 2017

- \$4,300 Internal Grant

University of Nevada, Las Vegas: Graduate and Professional Society 2016

- \$1,000 Internal Research Grant

Bill and Melinda Gates Foundation 2016

- \$1,000 External travel award
- Institute for Teaching and Mentoring: Compact for Faculty Diversity

Bill and Melinda Gates Foundation Millennium Undergraduate 2009-2014

- \$150,000 External Scholarship

Silver State Millennium Foundation Scholarship 2009-2011

- \$2,500 External Scholarship

PUBLICATIONS

*Journal Publications (*undergraduate authors)*

- **Dowell, J.A.**, *Clark, E.J., *Pliakas, T.P., Mandel J.R., Burke, J.M., Donovan, L.A., and Mason, C.M., 2019, “Genome wide association mapping of floral traits in cultivated sunflower (*Helianthus annuus*),” *Journal of Heredity*, 110:3 275-286
<https://doi.org/10.1007/s00049-020-00322-4>
- **Dowell, J. A.** and Mason, C. M., 2020, “Correlation in plant volatile metabolites: physiochemical properties as a proxy for enzymatic pathways as an alternative biosynthetically informed metric,” *Chemoecology*. <https://doi.org/10.1007/s00049-020-00322-4>
- *De La Pascua, D. R., *Smith-Winterscheidt, C., **Dowell, J. A.**, Goolsby, E. W., and Mason, C. M., 2020, “Evolutionary trade-offs in the chemical defense of floral and fruit tissues across genus *Cornus*,” *American Journal of Botany* 107(9): 1260– 1273.
<https://doi.org/10.1002/ajb2.1540>
- Stahlhut, K.N., **Dowell, J.A.**, Temme, A.A., Burke, J. M., Goolsby, E. W., Mason, C. M., 2021, ”Genetic control of arbuscular mycorrhizal colonization by *Rhizophagus intraradices* in *Helianthus annuus* (L.).” *Mycorrhiza* **31**, 723–734.
<https://doi.org/10.1007/s00572-021-01050-5>

(in-press)

- Bahmani K, *Robinson A, Majumder S, *LaVardera A, **Dowell J**, Goolsby E, Mason C, “Broad diversity in monoterpane-sesquiterpene balance across wild sunflowers: implications of leaf and floral volatiles for biotic interactions”

(in-revision)

- **Dowell J.**, Bowsher A., *Jamshad A., *Shah R., Burke J., Donovan L., Mason M., “Historic breeding practices contribute to germplasm divergence in leaf specialized metabolism and ecophysiology in cultivated sunflower (*Helianthus annuus*).” (American Journal of Botany)
- Ridenbaugh, R., **Dowell J.**, Goolsby E., Sharanowski., “The effects of plant phytochemistry on parasitoid (Hymenoptera: Braconidae) niche breadth.” (Ecology and Evolution)
- Bahmani K., *Giguere M., **Dowell J.**, Mason C., “Germplasm Diversity of Sunflower Volatile Terpenoid Profiles Across Vegetative and Reproductive Organs”

(in-review)

- **Dowell J.**, Mason C. “Candidate pathway and genome-wide association approaches reveal alternative genetic architectures of carotenoid content in cultivated sunflower (*Helianthus annuus*).”

(in-prep)

- **Dowell J.**, *Jowais J., Mason C. “Species-specific herbivore-induced responses across the genus *Helianthus*.”
- *Valdiviezo M., **Dowell J.**, Goolsby E., Mason C. “Validation and optimization of hyperspectral reflectance analysis-based predictive models for the determination of plant functional traits in *Cornus*, *Rhododendron*, and *Salix*.”

Selected conference Oral/Poster Presentations

- **Dowell, J. A.**, “Isolate specific effects of *Botrytis cinerea* on the expression of biosynthetic enzymes in *Arabidopsis thaliana*”, Fungal Genetics Society 2022
- **Dowell, J. A.**, “Evolution & diversification of plant-plant communication: An intermediate hypothesis”, Plant Biology 2020
- **Dowell, J. A.**, Mason, C. M. “Correlation in plant volatile metabolites: physiochemical properties as a proxy for enzymatic pathways and an alternative metric of biosynthetic constraint”, Botany 2020, ABSTRACT ID-576
- *De La Pascua, D. R., *Smith-Winterscheidt, C., **Dowell, J. A.**, Goolsby, E. W., Mason, C. M., S., “Evolutionary trade-offs in the chemical defense of floral and fruit tissues across genus *Cornus*”, Botany 2020, ABSTRACT ID-166
- *Stahlhut, K., **Dowell, J. A.**, Temme, A., Burke, J., Goolsby, E., Mason, C. M., “Genetic control of arbuscular mycorrhizal colonization in *Helianthus annuus*”, Botany 2020 ABSTRACT ID-137
- *Stahlhut, K., **Dowell, J. A.**, Mason, C. M., “Genetic control of mycorrhizal colonization in *Helianthus annuus*”, Botany 2019, ABSTRACT ID-469

- *Davis, R., **Dowell, J. A.**, and Mason, C. M., “Describing Photosynthetic Diversity in Cultivated Sunflower,” Botany 2019, ABSTRACT ID-385
- *Valdiviezo, M. I., **Dowell, J. A.**, and Mason, C. M., “Comparing Leaf Reflectance Analysis Prediction Models Based on Dried Whole Leaf Tissue against Dried Ground Tissue”, Botany 2019, ABSTRACT ID-766.
- **Dowell, J. A.**, and Mason, C. M., “An evolutionarily relevant definition of ‘Eavesdropping’ and ‘Communication,’ International Society of chemical ecology, 2019
- **Dowell, J. A.** and Mason, C. M., “Impacts of physical chemistry on biosynthetic constraints of plant volatile profiles,” International Society of chemical ecology, 2019
- **Dowell, J.A.**, *Clark, E.J., *Pliakas, T.P., Mandel J.R., Burke, J.M., Donovan, L.A., and Mason, C.M., “Genome-wide association mapping of floral traits in cultivated sunflower (*Helianthus annuus*),” Botany, 2018, ABSTRACT ID-295.

WORKSHOPS AND INVITED LECTURES

- **Lecture**, “Can you really have it all? Growth-defense tradeoffs in plant-pathogen interactions,” University of California Davis, Plant Pathology department, Postdoctoral fellow seminar series. 2022.
- **Lecture**, “Leveraging hyperspectral reflectance to assess volatile organic compound(VOC) mediated induced responses across the genus *Helianthus*,” American Chemical Society Fall 2022, Early Career Symposium: Deciphering plant-insect-microorganism signals for sustainable crop protection. 2022.
- **Lecture**, “Evolution & diversification of plant-plant communication: An intermediate hypothesis,” Plant Biology 2020, MAC Symposium 3: Evo-Devo 2020: Case Studies in Diversity. 2020
- **Lecture**, “The language of life: chemically mediated interactions in plant ecology & evolution,” Niagara University, Early career researcher diversity seminar series, 2019.
- **Workshop**, “Comparative plant metabolomics & Bayesian hierachal clustering analysis,” University of Central Florida, Department of Biology, 2019.
- **Lecture**, “Sassy sages and gossiping goldenrods: recent advances in plant volatile communication,” Florida Native Plant Society, Florida Native Plant Month, 2019.
- **Lecture**, “Volatile metabolomics of the annual clade of *Helianthus*,” University of Central Florida, Department of Biology, 2019.
- **Workshop**, “Comparative analytical techniques in Plant Metabolomics,” University of Central Florida, Department of Biology, 2019.
- **Lecture**, “Sassy sages and gossiping goldenrods: recent advances in plant volatile communication,” Florida Native Plant Society, Tarflower Chapter, 2019.

- **Workshop**, “Introduction to Random Forest models,” University of Central Florida’s Biology Graduate Student Association data science seminar, 2018.
- **Lecture**, “Landscape Scale: inter-and intraspecific variation in plant interactions along a stress gradient in the sheep mountain range,” University of Nevada, Las Vegas, Graduate Student Seminar series, 2017.

TEACHING EXPERIENCE

University of Central Florida Teaching Assistant , Department of Biology	2019-2020
• Advisor: Eric Goolsby	
• Plant Genomics & Biochemistry, Ran an original lab during a pandemic of a joint graduate and undergraduate course. This course consisted of 23 total students, all of which produced individual projects integrating publicly available multi-omic data to answer questions concerning plant genomics and biochemistry.	
University of Central Florida Curriculum Development Assistant , Department of Biology	2019-2020
• Advisor: Eric Goolsby	
• Plant Genomics & Biochemistry, development of instructional materials and laboratories for a new joint graduate and undergraduate course. Assorted topics include chromatography (liquid, gas, & capillary electrophoresis), mass spectrometry, untargeted & targeted metabolomics, metabolic pathway modeling, and machine learning in metabolomics & genomics.	
University of Nevada, Las Vegas Graduate Teaching Assistant , Department of Biology	2015-2017
• Principles of Modern Biology II Lab, an undergraduate laboratory course averaging 60 students per semester, covering the following topics: organismal biology, ecological/evolutionary patterns, and processes.	
Bodies: The Exhibition , Las Vegas, NV Educational Director	2012-2015
• Development of instructional materials for docents and educational outreach materials for assorted topics, including anatomy, physiology, and new developments in the field of medicine and comparative anatomy. During my tenure museum, average foot traffic was ~300-600 people per day with a docent staff of 15 individuals.	

COURSES PREPARED TO TEACH

- **Currently in the 2022-2023 catalog**
(Most easily implemented)
 - Undergraduate
 - **Plant Biology**, Microbial Fermentation, Principles of Plant Pathology, **Evolutionary Biology**, General Ecology, Taxonomy of Flowering Plants, Dendrology, Food Microbiology, Plant Disease Control, Dynamic Models in Biology, Genomics and Bioinformatics, Ecological Genomics, **Physiological Ecology**, Population Ecology, **Plant Ecology**, **Biometry**, Community and Ecosystem Ecology,

- Graduate
 - Taxonomy of Flowering Plants, Food Microbiology, Dendrology, **Practical Programming for Biologists**, Dynamic Models in Biology, Genomics and Bioinformatics, Ecological Genomics, Comparative Botany, Principles of Evolution, **Physiological Ecology**, Population Ecology, **Plant Ecology**, **Biochemical Genetics**, **Biometry**, **Science Communication**,
- New classes I could offer depending on need and interest
(Most easily implemented)
 - Undergraduate
 - Agricultural Biotechnology and Public Policy, Hemp Biology and Chemistry, **Chemical Ecology**, Community Ecology, **Comparative Biochemistry**, **Ecotoxicology**, Ethnobotany, Evolution of Agriculture, Feeding the Planet: Influences on the Global Food Supply, Forensic Botany, Fungal Systematics, **Host-pathogen Interactions**, Integrative Pest-management, Introduction to Experimental Design, Introduction to Plant Breeding, Introduction to Plant Pathology, Introduction to Science Communicaiton, Malting and Brewing Science, **Medicinal Botany**, Mycology, **Plant-biotic Interactions**, Natural Products Extraction & Analysis, Phylogenomics, **Plant Genomics and Biochemistry**, Plant Growth & Development, Principles & Practices of Plant Propagation, **Programming for Biologists**, **Quantative and Population Genomics**, **Science and Society**, Science of Flavor, **Scientific Racism: a Historical Perspective**, Sustainability & Agroecosystem Management, **Systems Biology**, Taxonomy & Ecology of Environmental Plant Families, and Wine Production and Microbiology
 - Graduate
 - Advanced Topics in Specialized Metabolism, Biochemistry and Molecular Biology of Plant-Microbe Interactions, Hemp Biology and Chemistry, **Chemical Ecology**, Community Ecology, **Comparative Biochemistry**, **Ecotoxicology**, Forensic Botany, Fungal Genetics, **High-dimensional Statistics for Biologists**, Host-pathogen Interactions, Machine Learning for Biological Data, **Metabolic Modeling: from Individuals to Systems**, **Metabolomics**, Methods for Complex Comparative Genomics, Mycology, Natural Products Extraction & Analysis, Phenomics, Phylogenomics, **Physicochemical and Environmental Plant Physiology**, **Plant Genomics and Biochemistry**, Plant Pathology, **Population and Quantitative Genomics**, **Programming for Biologists and Introduction to High Performance Computing**, Remote Sensing/Image Analysis for Biologists, Research-team Leadership and Management, **Scientific Racism: a Historical Perspective**, **Statistical Rethinking: Bayesian Statistics for Biologist**, and **Systems Biology**

MENTORSHIP EXPERIENCE

Undergraduate Honors Student Committee Service

- Ana Robinson, “Role of polyploidy in leaf functional trait and secondary metabolite evolution across *Helianthus*,” 2019-2020
- Isaac Valdiviezo, “Comparing Leaf Reflectance Analysis Prediction Models Based on Dried Whole Leaf Tissue against Dried Ground Tissue”, 2019-2020
- Mari Irving, “Developmental Effects of Terpenes on *Vanessa cardui* at Varying Temperatures”, 2019-2020
- Katie Stahlhut, “Genetic control of mycorrhizal colonization in *Helianthus annuus*”, 2019-2020
- Danielle De La Pascua, “Reproductive defense trade-offs in the fruits and flowers of the genus *Cornus*”, 2018-2019
- Rayner Seavey, “The Hyperaccumulation of Zinc in Sunflowers and its Effect on Disease Resistance”, 2018-2019
- Rebekah Davis, “Capillary Electrophoresis buffer optimization for plant tissue analysis”, 2018-2019
- Jessica Jowais, “Comparison of secondary metabolite response to *Vanessa cardui* across the genus *Helianthus*”, 2017-2018

Selection of undergraduate research mentees and their projects

- **University of California, Davis**
 - Carina Caccobaci
 - Machine learning approaches to measuring lesion size across species in images with complex backgrounds
 - Jarell Mangsat
 - Expanded the *Botrytis*-eudicot pathosystem to include nine new species and collected preliminary disease phenotype data
 - Angela Gao
 - Effects of *in vitro* diet complexity on *Botrytis* virulence over successive generations
 - Lori Pradhan
 - Leveraging genome-scale metabolic models to explore the evolution of metabolic complexity and specialized metabolite investment across the genus *Botrytis*
 - Minh Tran
 - Development of live cell assays for longitudinal phenotyping of *Botrytis* in liquid culture
 - Samantha Lenao

- Leveraging deep-learning approaches to assess variation in selective sweep history across the genus *Helianthus*
- Xiaoqing Zheng
 - Simulation of protein-protein interaction of potential cultivated sunflower self-incompatibility proteins
- Julia Cook
 - Leveraging genome-scale metabolic models to explore the investment in specialized metabolites by *Botrytis cinerea* during infection of *Arabidopsis thaliana*
- Melanie Madrigal
 - Genome-wide association of the effects of plant infochemicals on the growth rate of *Botrytis cinerea*.
- **University of Central Florida**
 - Gillian Gomer
 - Genome-wide association of Sulfur metabolism in *Helianthus annuus*
 - Abigail Tripka
 - Impacts of common terpenoids on growth and establishment of host-generalist plant fungal pathogens
 - Austin Hart
 - Genome-wide association of vegetative growth rate in *Helianthus annuus*
 - Logan Walck
 - Developed machine learning hyperspectral reflectance models to detect and differentiate D- & L- malate in complex solutions for indirect phenotyping of Crassulacean acid metabolism(CAM) photosynthesis
 - Juliana Wall
 - Smells like family to me! Population structure correlates of corolla terpenoid variation
 - Kaley Haff
 - Save the Bracts for Last: Comparison of flowering time & terpenoid variation in cultivated *Helianthus*
 - Linsey Plyler
 - Assessed terpenoid diversity of *Rhododendron* leaves using GC-MS
 - Bree-Alexandra Donley
 - Look & Smell Pretty? Correlates of petal carotenoid content & terpenoid variation in cultivated *Helianthus*
 - Dasiell Desravines

- Contributed to the method development of GC-MS protocols to assess volatile organic compound variation across plant tissue types
- Group projects
 - Development of computer vision tools to assess allometric growth in cultivated *Helianthus annuus*.
 - Sergio Solano, Kyra Paris, Nicholas Cooke,
 - Development of non-invasive methods to phenotype CAM photosynthesis in real-time
 - Danielle Waugh, Kristine Vu, Madison Worsfold, Gabriela Wasif
- **University of Nevada, Las Vegas**
 - Group project
 - Assessment of plant spatial patterns in the Desert National Wildlife Refuge
 - Jordan Afaga, Young Kang, Shannon Zayas, Luisa Najera, Jacob James Nogra, Richard Van

NON-DEGREE SEEKING RESEARCH EXPERIENCE

Postdoctoral Associate , University of California, Davis	2021-2022
Advisor: Daniel Kliebenstein; Leveraging multi-omic network approaches to explore the evolution of specialized metabolism and biotic-interactions between <i>Botrytis cinerea</i> (a plant fungal pathogen) and 16 eudicots species.	
Research Associate , University of Nevada, Reno-Cooperative Extension	2017
Advisor: Tammara Wynne Development of outreach-focused experiments concerning domesticated <i>Solanum lycopersicum</i> production in the Mojave Desert.	
Research Associate , University of Nevada, Las Vegas	2017
Advisors: Lorenzo Apodaca and Dale Devitt Development and implementation of image analysis-based methods of xylem flow dynamics in urban horticulture trees. Implementation of multidimensional kriging of climate data concerning the ambient effects of photovoltaic power plants on native shrublands.	
Restoration Ecology Intern , Great Basin Institute, Nevada, Las Vegas	2015
Advisor: Russell Lee Nasrallah Improvement of highly visible and ecologically important state and national park resources by controlling exotic plants, maintaining hiking trails, and providing an educational resource for park visitors. (Great Basin National Park, Lake Mead National Recreation Area, Spring Mountain Ranch State Park, Desert National Wildlife Refuge, and Pahranagat National Wildlife Refuge).	
Undergraduate Research Assistant , University of Nevada, Las Vegas	2012-2013
Advisors: Tereza Jezkova and Javier Rodriguez Elucidation of phylogeographic and population structure in Mona and Virgin Island Boas, <i>Chilabothrus monensis</i> (<i>Epicrates monensis</i>).	

PROFESSIONAL SERVICE

One Garden fellow invited lecture series	2022-present
<ul style="list-style-type: none"> ● Two live seminars: <ul style="list-style-type: none"> ○ “Do plants have something to say?” ○ Food Futures: Could new plants solve a food crisis? <ul style="list-style-type: none"> ■ Link: https://onegarden.com/fellow/dr-jordan-dowell ○ 10,000+ viewers per talk across the Americas, Africa, Asia, and Europe 	
Botanical Society of America's Publications Committee member	2021-2023
<ul style="list-style-type: none"> ● Includes APPS, <i>Plant Science Bulletin</i>, and <i>American Journal of Botany</i> 	
Reviewing Editor for <i>Applications in Plant Sciences (APPS)</i>	2020-2022
UCF College of Science Visiting Scholars program	2020-Reoccurring
<ul style="list-style-type: none"> ● \$32,000 per year Internal funding allocation ● Co-author Ian Will ● Initiative to supply funding to bring in historically underrepresented scholars to give research seminars and supply a mentorship opportunity for historically underrepresented undergraduate and graduate students. 	
American Society of Plant Biology panel member; “Interested in Graduate School”	2020
<ul style="list-style-type: none"> ● Answered questions concerning graduate school funding and career options for an audience of ~100 undergraduate participants. 	
Consultant for SEE Turtles organization BIPOC scholarship fund	2020-2023
<ul style="list-style-type: none"> ● Supplied guidance on barriers for BIPOC engaging in field programs and developed a funding schema to house and pay students. 	
Reviewer	
<ul style="list-style-type: none"> ● Oikos, Journal of Chemical Ecology, Chemoecology, Plant Cell, American Journal of Botany, Applications in Plant Sciences 	
Biology Graduate Student Association	
<ul style="list-style-type: none"> ● President, University of Central Florida, ● Secretary, University of Central Florida, 	2019-2021 2018-2019
UCF's Biology Integrated Orlando Training and Enrichment Camp	2018
<ul style="list-style-type: none"> ● Plant Science coordinator ● Developed and taught a weeklong curriculum of plant science focused experiments on engaging over 30 high school students from the surrounding Orlando metropolitan area in current research techniques, such as genomics and metabolomics. 	
Botanical Society of America Graduate School Career Panel (UCF Chapter)	2019-2021
<ul style="list-style-type: none"> ● Answered questions concerning graduate school funding and career options for an audience of 50 undergraduate participants. 	
Plants Beyond Limits Conference	
<ul style="list-style-type: none"> ● Graduate Student Coordinator, University of Central Florida, 	2017

- Initiated, organized, and funded the first student-led conference of Plants Beyond Limits at UCF with ~500 attendees, 20 speakers, and 15 submitted posters from graduate students and postdocs

REFERENCES

- **Daniel Kliebenstein,**
 - **Professor in the Department of Plant Sciences at the University of California, Davis**
 - Email
 - kliebenstein@ucdavis.edu
 - Relationship
 - Dr. Kliebenstein is my current postdoctoral mentor
- **Chase Mason, Ph. D.**
 - **Assistant Professor in the Department of Biology at the University of Central Florida**
 - Email
 - chase.mason@ucf.edu
 - Relationship
 - Dr. Mason is my major advisor for my doctoral studies.
- **Eric Goolsby, Ph. D.**
 - **Assistant Professor in the Department of Biology at the University of Central Florida**
 - Email
 - Eric.goolsby@ucf.edu
 - Relationship
 - Dr. Goolsby was a member of my doctoral committee, with whom I have several ongoing collaborations both in research and education.
- **Laurence Von Kalm, Ph. D.**
 - **Associate Professor & Associate Chair in the Department of Biology at the University of Central Florida**
 - Email:
 - Laurence.vonkalm@ucf.edu
 - Relationship
 - During my tenure as president and secretary of the University of Central Florida's Biology Graduate Student Association I have worked hand in hand with Dr. Von Kalm on issues concerning graduate student wellbeing, education, and departmental policy.



The Cost of Gossip: Growth-Defense Tradeoffs & Multifunctional Traits

Jordan Dowell, Ph.D.



Perceive

Process

Persist



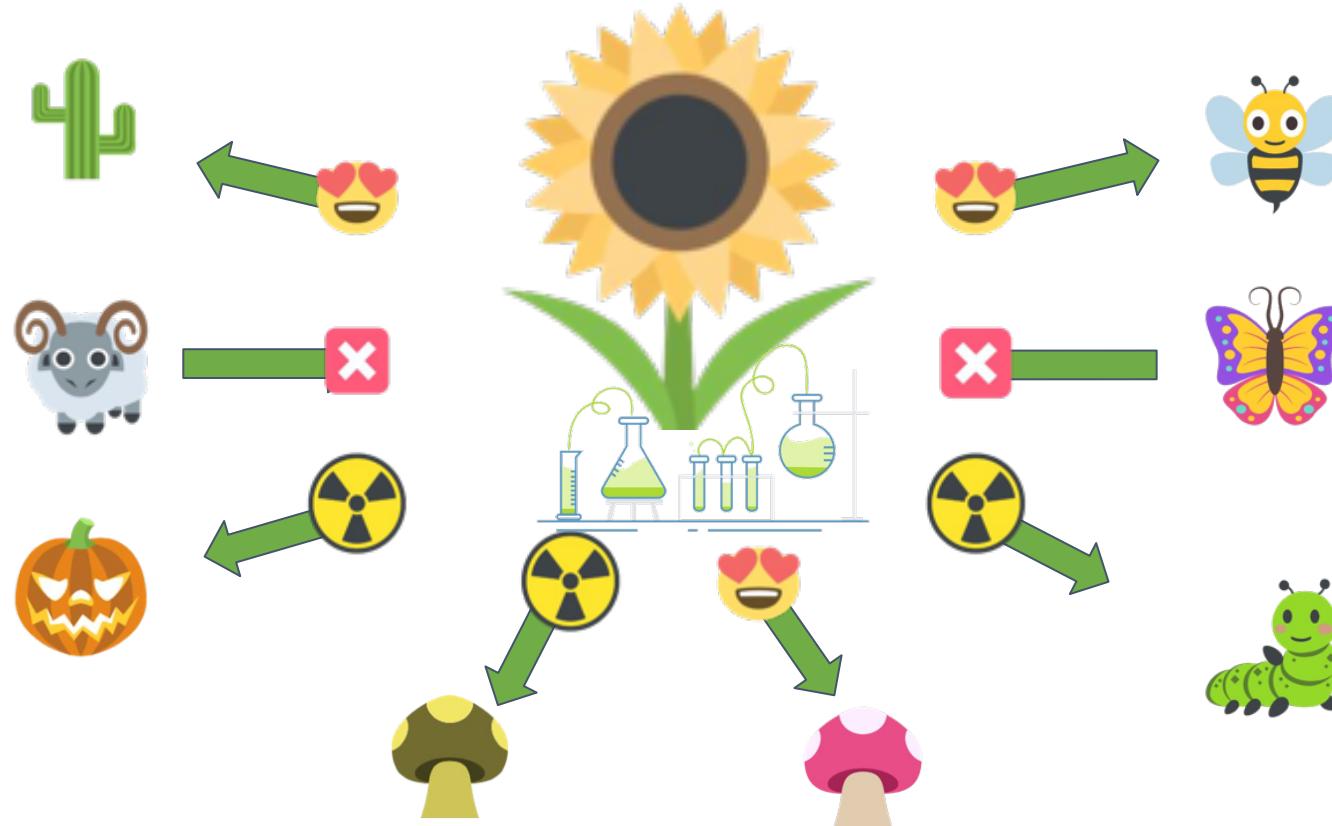


Chemically-mediated interactions



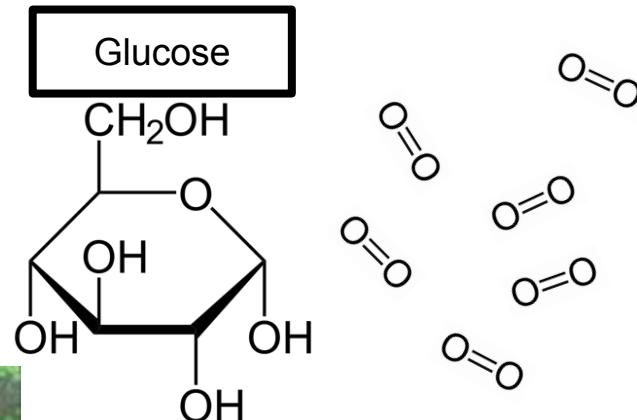
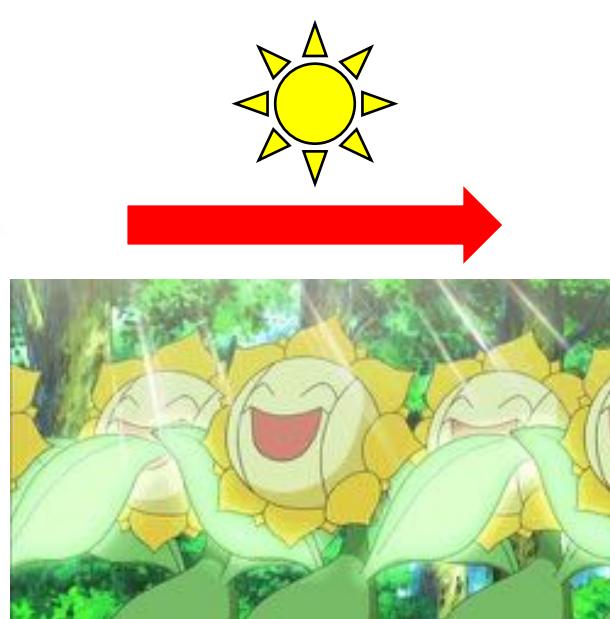
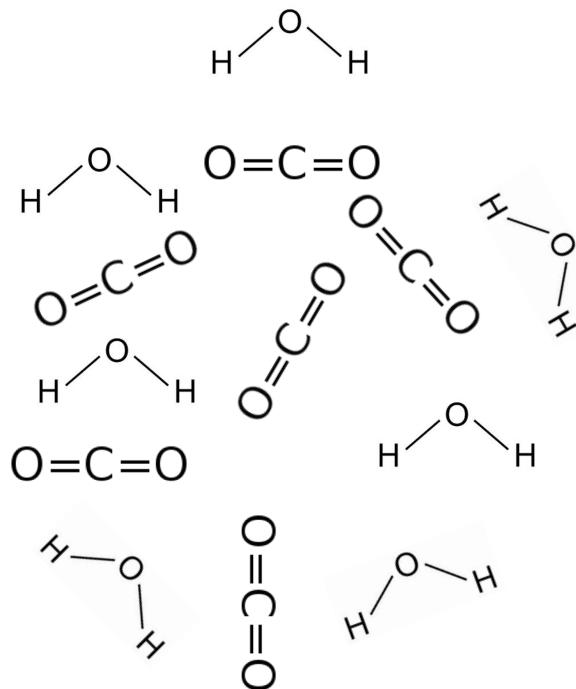


Chemically-mediated interactions



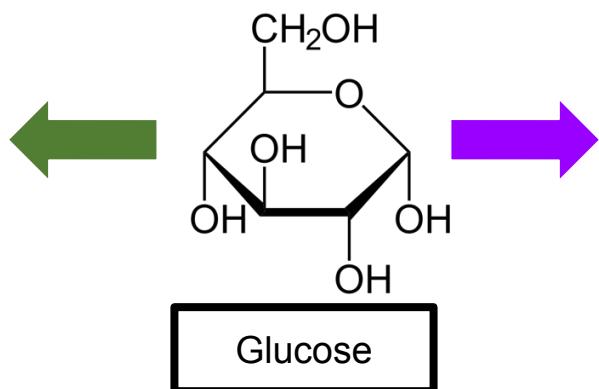
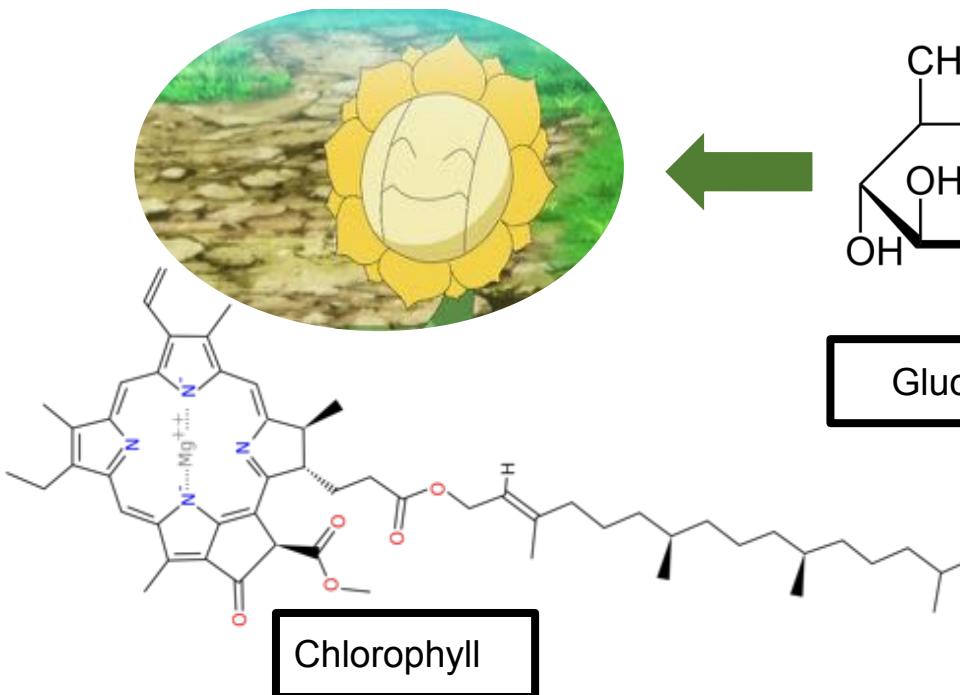


Photosynthesis



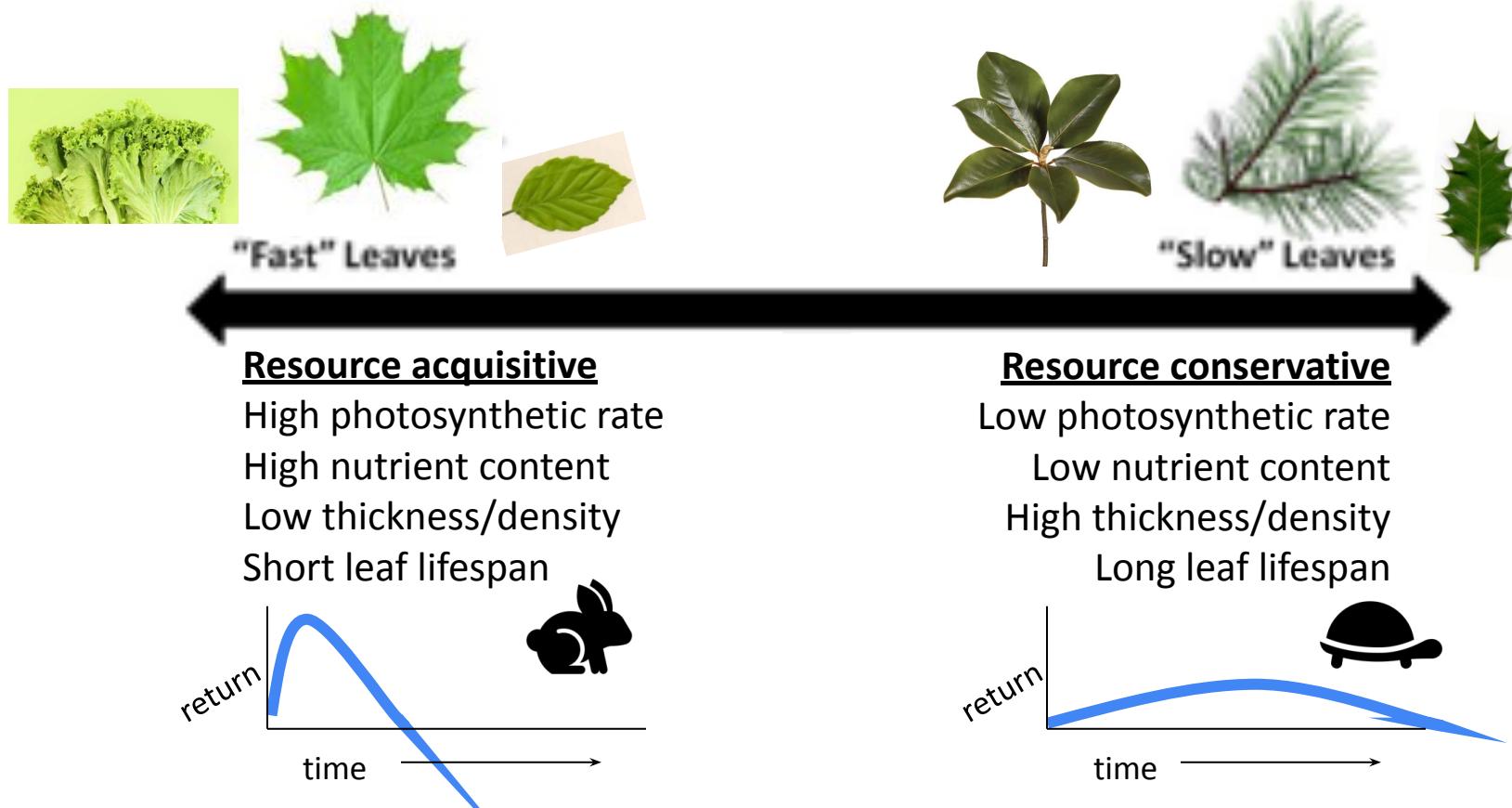


Photosynthesis



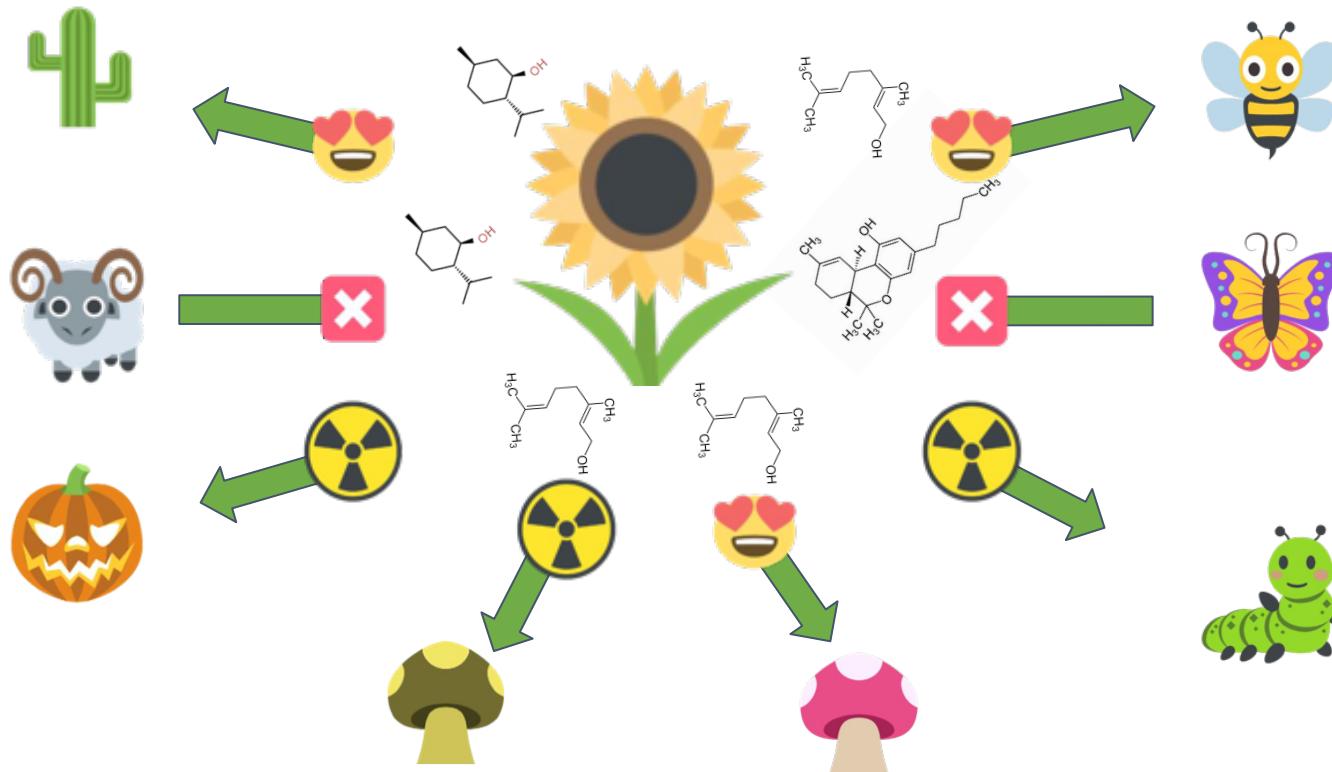


Leaf economic spectrum





Multifunctional metabolites





Central question

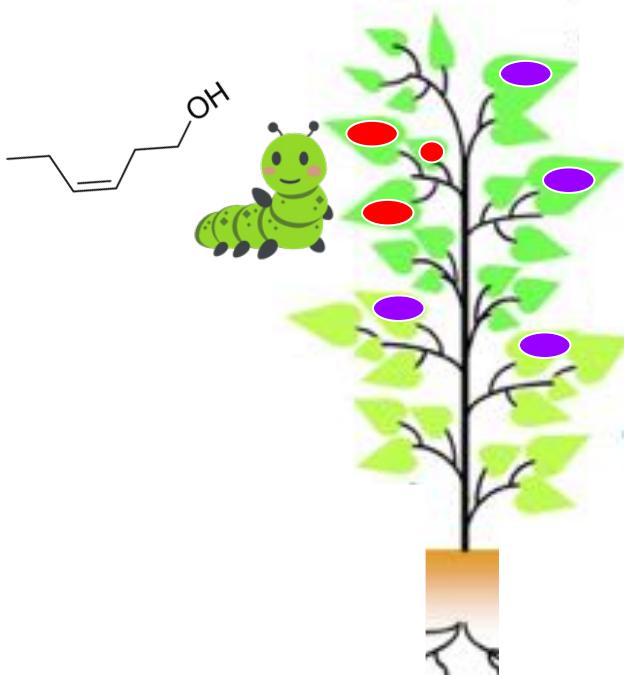
How do multifunctional metabolites fit into evolutionary and ecological hypotheses?



Part 3: Volatile organic compound (VOC) impacts on pathogen genetic diversity and physiology



Plant-plant communication

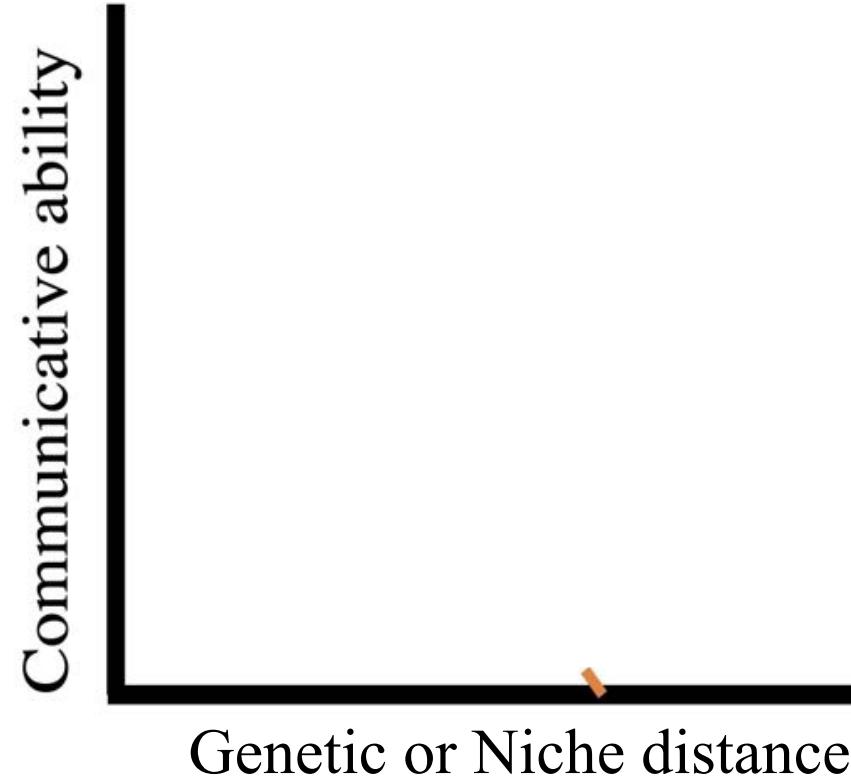




Plant-plant communication

Communication ability

- Ability of the receiver to mitigate a stress compared to a 'naive' state

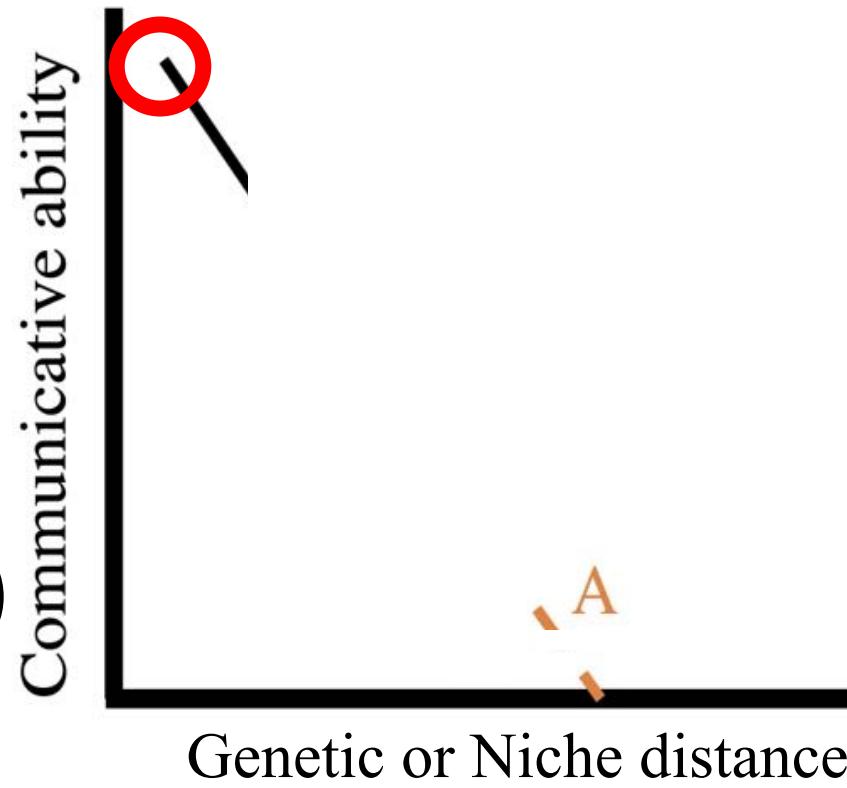
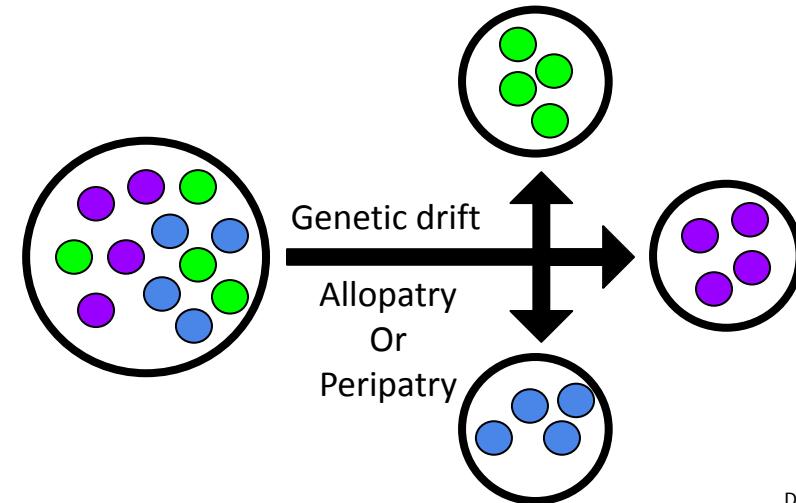




Plant-plant communication

Communication ability

- Ability of the receiver to mitigate a stress compared to a 'naive' state

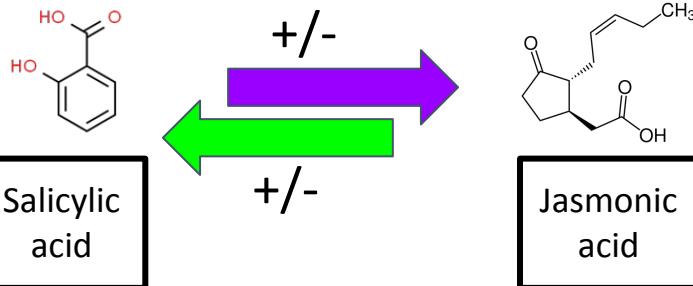


Plant-plant communication

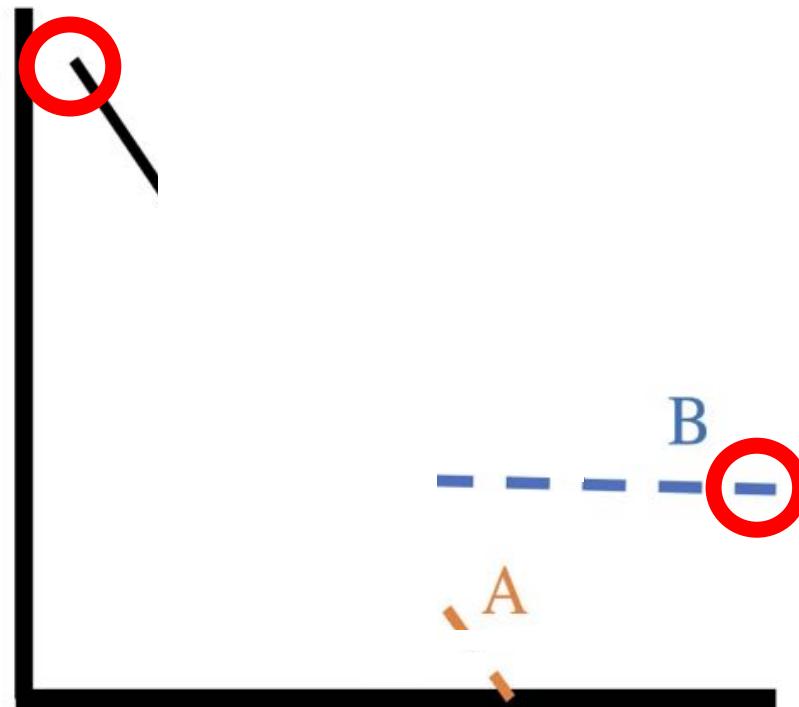
Communication ability

- Ability of the receiver to mitigate a stress compared to a ‘naive’ state

Conserved pest/pathogen signaling



Communicative ability



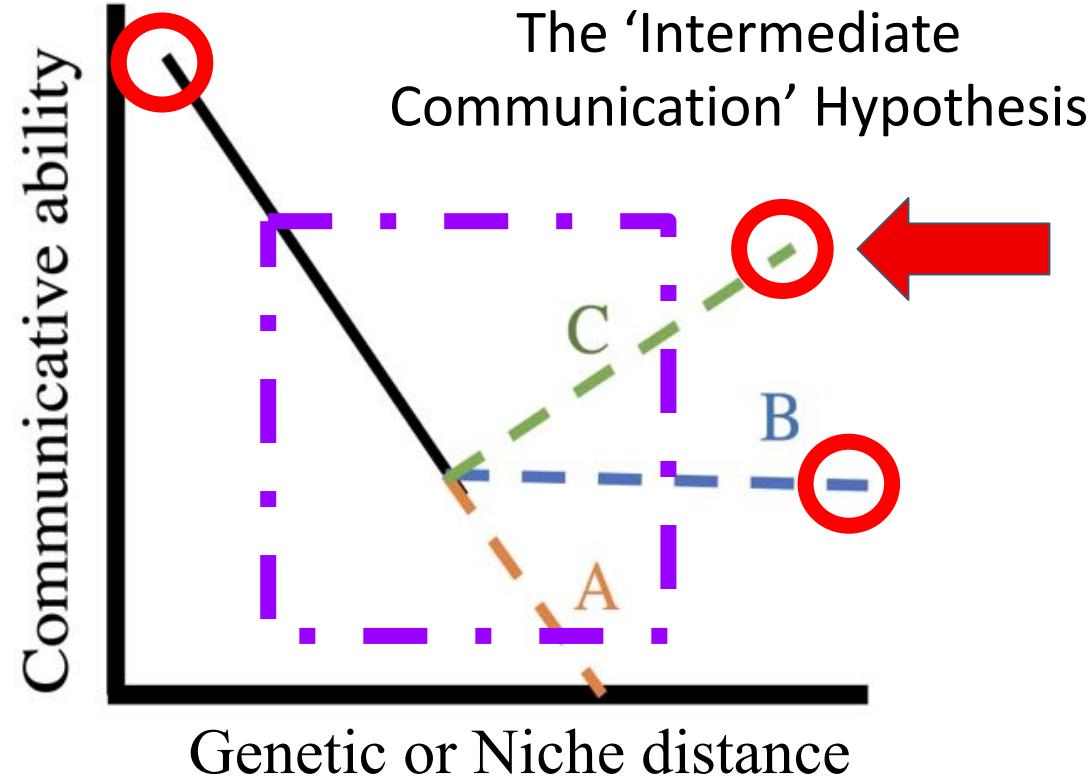
Genetic or Niche distance



Plant-plant communication

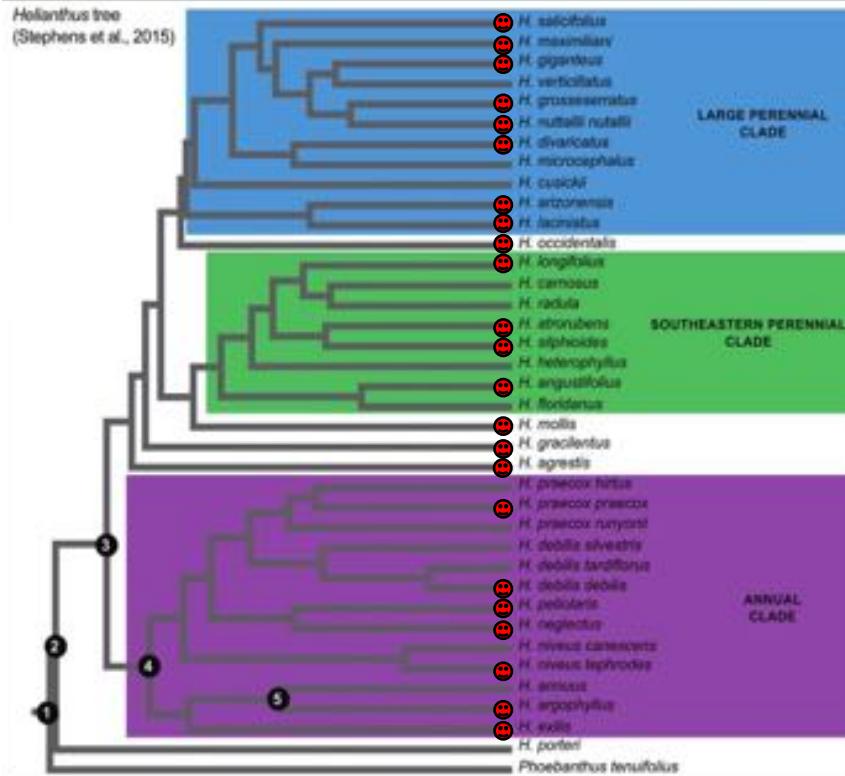
Communication ability

- Ability of the receiver to mitigate a stress compared to a 'naive' state





The genus *Helianthus*



Species used in this study 😊





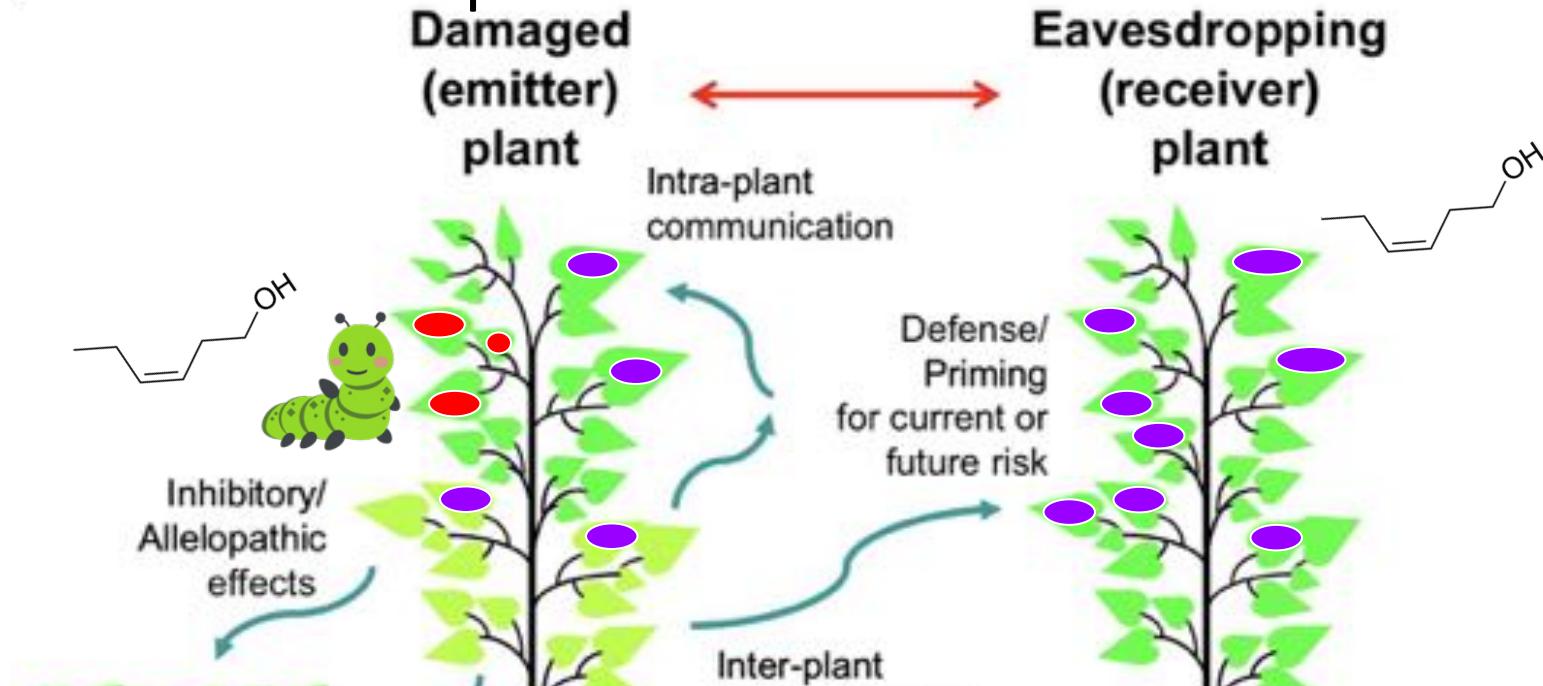
Volatile organic compound (VOC)-mediated interactions across the genus *Helianthus*

Questions:

- 1) How prevalent are airborne plant-plant communication responses across the genus *Helianthus*?
- 2) Are there common signals of plant-plant communication responses across the genus?



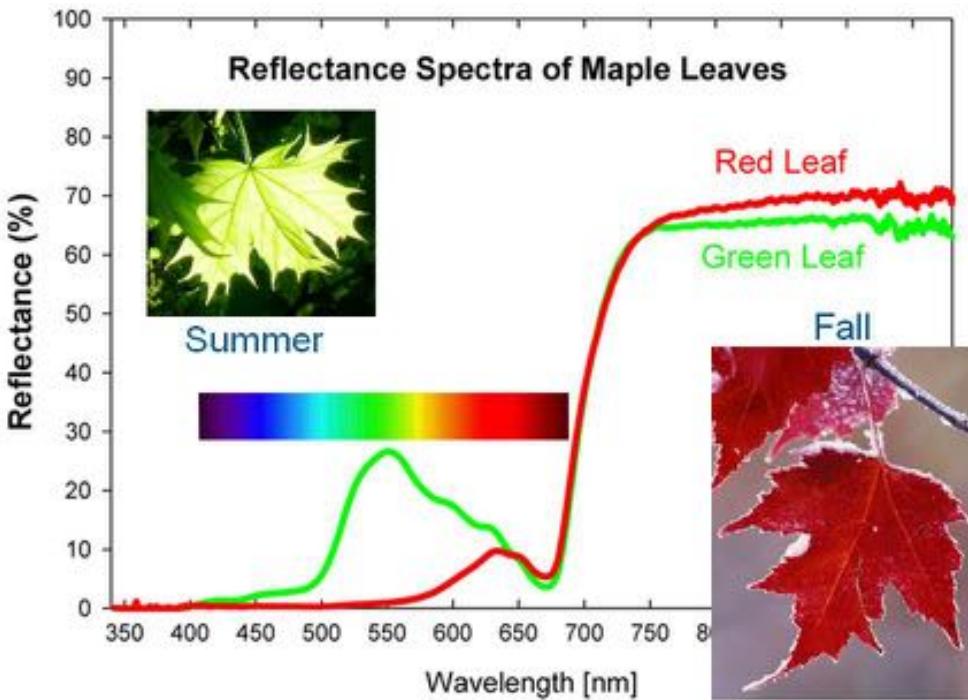
Plant-plant communication



Problem: VOC collection and analysis is not feasible at scale



Hyperspectral reflectance



Spectroscopy (remote sensing) is commonly used to assess biochemical and physiological variation *in planta*



Experimental layout



Positive pressure provides low volume
unidirectional airflow

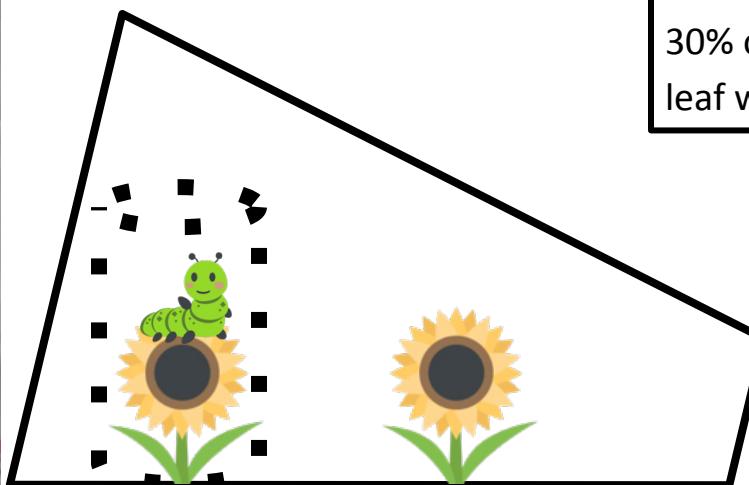


Vanessa cardui
'Painted lady butterfly'
(generalist herbivore)





Experimental layout

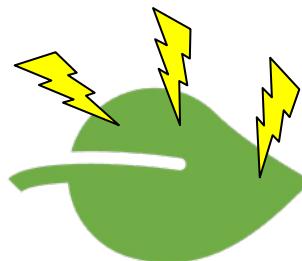


Herbivory & VOC exposure treatments lasted 24-48 hours depending on when 30% of leaf area of at least 1 leaf was eaten





Experimental layout



Experimental Steps

1. 20 scans at 3 locations on each leaf location recording 190-2500nm by 0.3nm
2. Leaf samples flash frozen and stored at -80°C
3. Analyzed homogenized tissue with SPME GC-MS



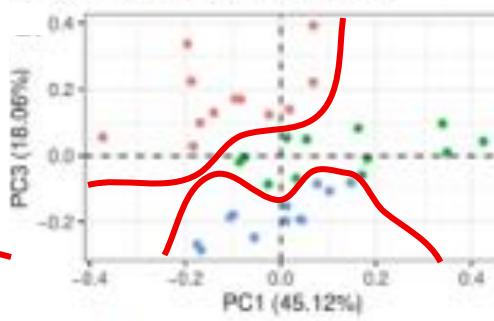
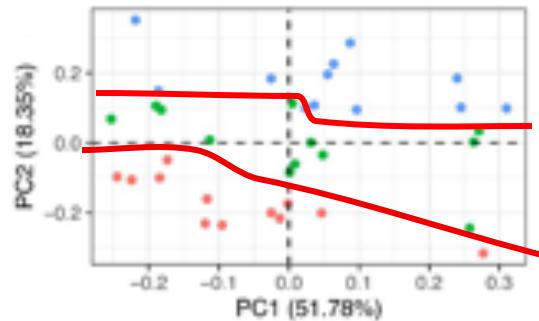


Species-specific reflectance

Treatment • Control • Herbivore-induced • Volatile-induced



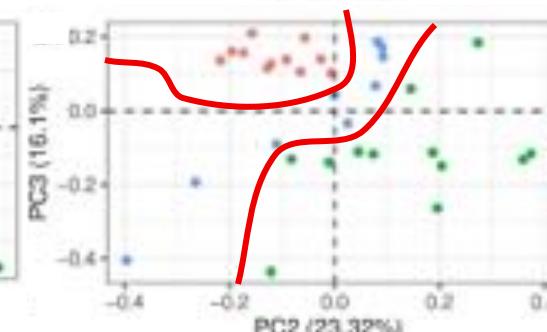
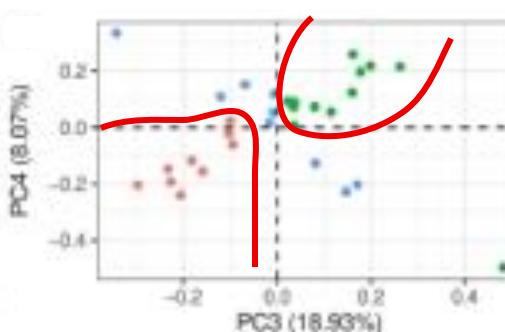
H. divaricatus



H. nuttallii



H. gracilentus

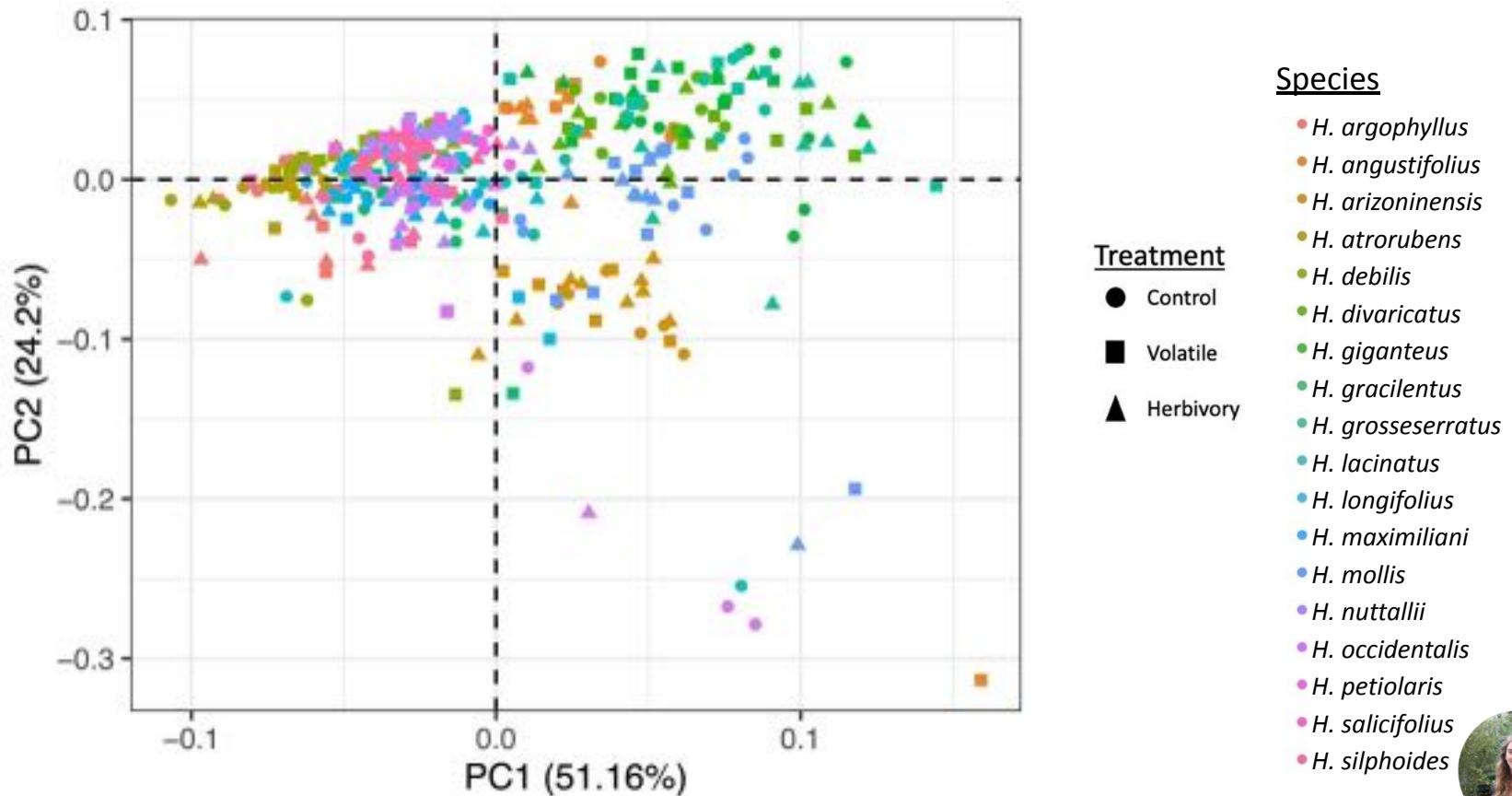


H. maximiliani





Genus-wide reflectance





Independent test data

Analyses performed with support vector regression trained using 10x-cross validation

		Predicted		
		Control	Herbivore-induction	Volatile-induction
Observed	Accuracy 95.21%	48	0	0
	Control	48	0	0
	Herbivore-induction	1	47	2
Volatile induction	Control	48	0	0
	Herbivore-induction	1	47	2
Volatile induction	Control	48	0	0
	Herbivore-induction	1	47	2
		2	2	44

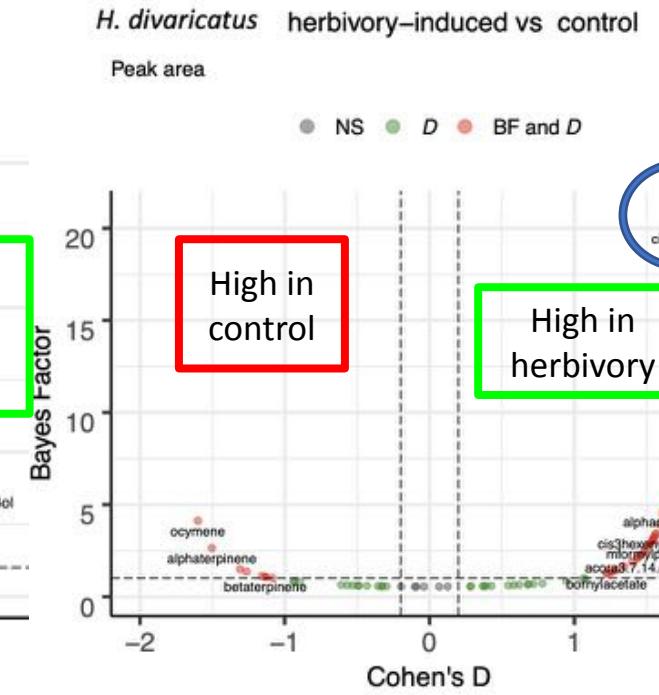
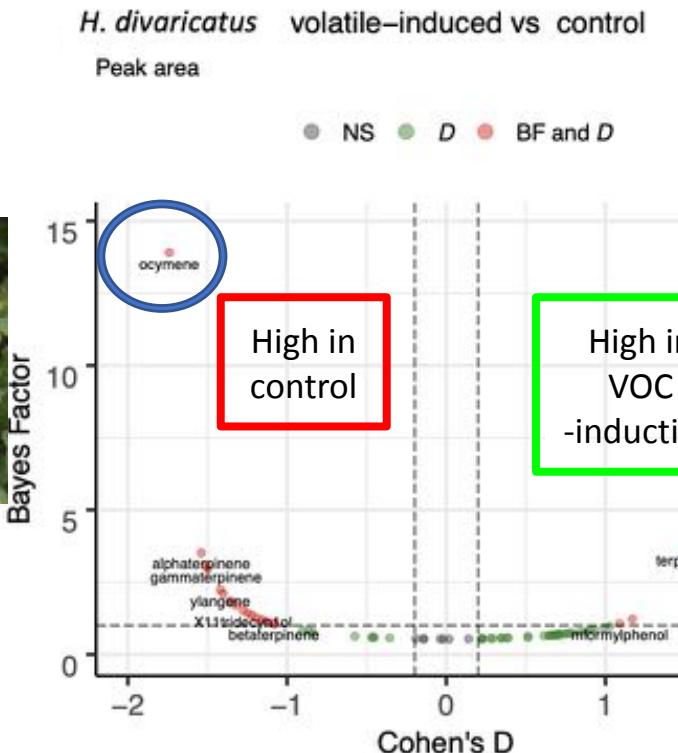




Species-specific chemical responses



H. divaricatus

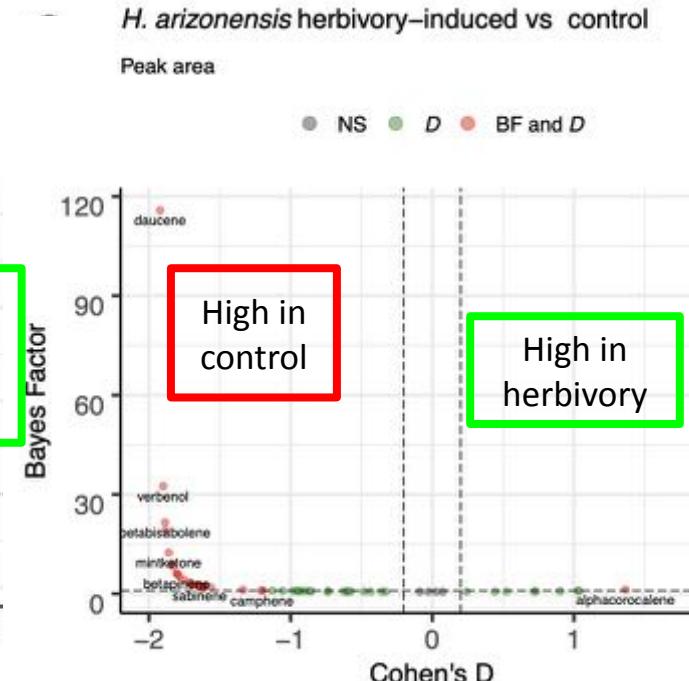
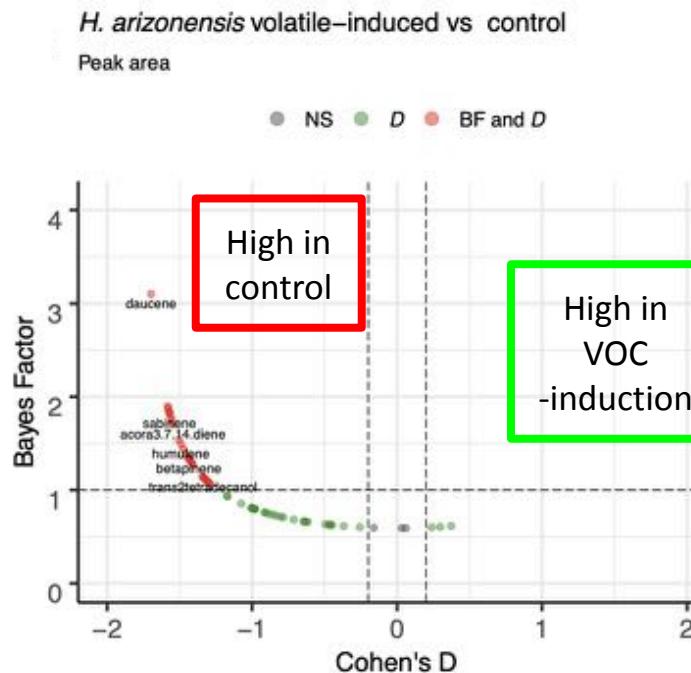




Species-specific chemical responses



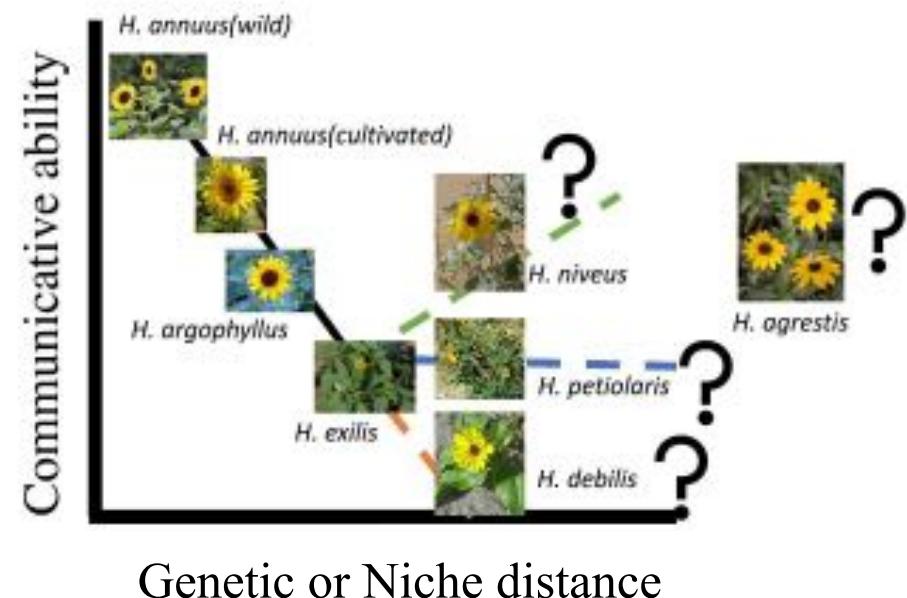
H. arizonicensis



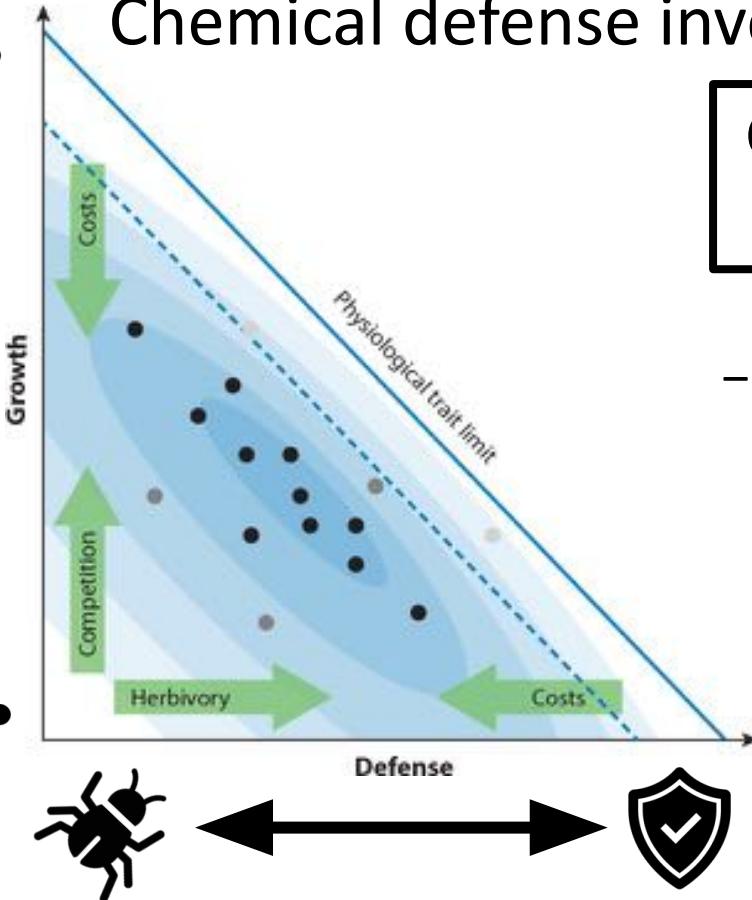


Summary

1. VOC diversity across *Helianthus* in the context of herbivory is highly species specific
2. We can noninvasively predict herbivory status across wild relatives of cultivated sunflower



Genetic or Niche distance



Chemical defense investment

Genotype-phenotype
relationship?

Can't "have it all"
– no fast growth with high defense





Cultivated sunflower as a model system





Sunflower hybrid breeding

Faster generation time



Self-pollination



Pollen-sterility maintainer
(cytoplasmic pollen-sterility)

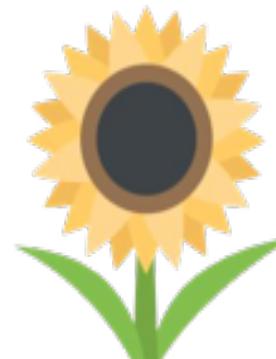
Slower generation time



Self-pollination



Fertility restorer



Consumer F1-hybrid

Bias among hybrid crops in using
pollen-sterility maintainer lines for new
line production via introgression or
genetic modification



Sunflower Association Mapping Panel (SAM Panel)

- 288 cultivated lines representing an estimated 90% of allelic diversity within the USDA and INRA germplasm repositories.
Mean date of introduction = $1990 \pm 7\text{yr}$ (SD)
- Multiple genetic maps, most recently full-genome resequencing data available for 261 lines, resulting in ~1.4 million SNP map (~3.6 Gb genome)
- Handy “Core 12” set of lines representing ~half of allelic diversity within USDA + INRA germplasm



Theor Appl Genet (2011) 123:693–704
DOI 10.1007/s00122-011-1649-3

ORIGINAL PAPER

Genetic diversity and population structure in cultivated sunflower and a comparison to its wild progenitor, *Helianthus annuus* L.

J. R. Mandel · J. M. Dechaine · L. F. Marek ·
J. M. Burke





Growth defense tradeoffs in cultivated Sunflower

Questions:

- 1) Does crop sunflower exhibit tradeoffs between chemical defense and ecophysiology?
- 2) What is the underlying genetic architecture of the relationship between ecophysiology and chemical defense investment?
- 3) Are genes associated with reproductive biology in physical linkage with genes underlying phenotypic diversity

Sunflower Association Mapping Panel (SAM Panel)

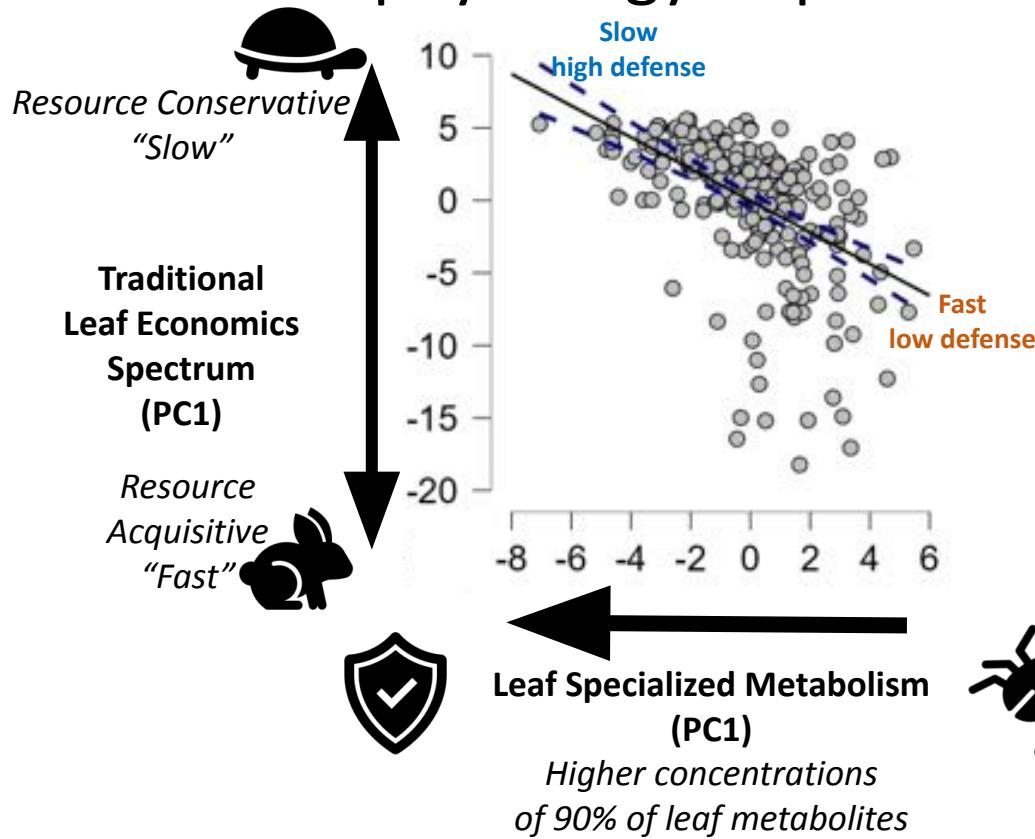
The most recently fully expanded leaf pairs were phenotyped for:

- Ecophysiology traits
 - leaf area, water and chlorophyll content, etc.
- Specialized metabolites
 - Methanol extracts of fresh leaves were analyzed with high performance liquid chromatography





Leaf ecophysiology + specialized metabolism



Negative correlation between leaf economic strategy and overall specialized metabolite concentrations ($R^2=0.25$) among cultivated sunflower lines



“Faster” strategy is associated with older breeding targets (1950s) for total seed yield opposed to recent targets (1990s) of yield stability



For leaf economics (PC1), Fertility-restorers are on average “**faster**” than pollen-sterility maintainers effect size $d=0.09$ (Bayes Factor=51)



Leaf ecophysiology

Small



Large

PC2 – leaf size (20%)

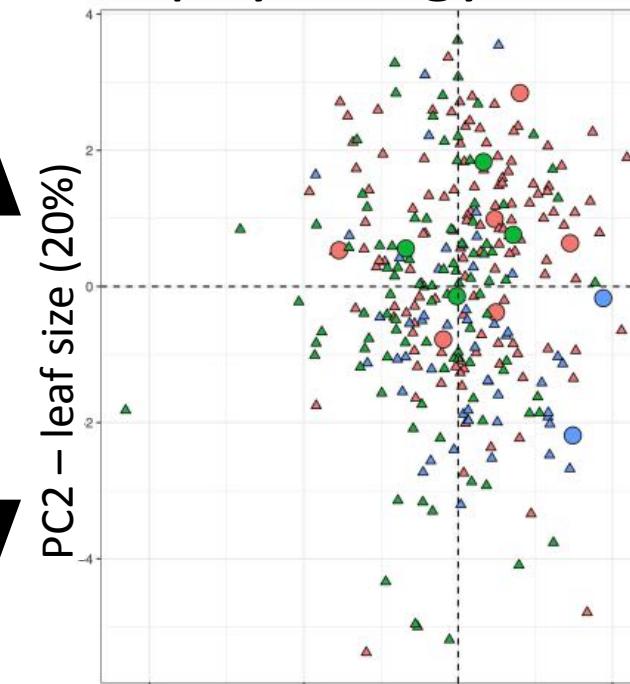
PC1 – leaf economics (35%)



Resource Acquisitive
“Fast”



Resource Conservative
“Slow”



Core 12

- Lines representing 50% of allelic diversity

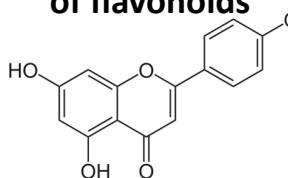
- △ Non-core lines

Breeding group

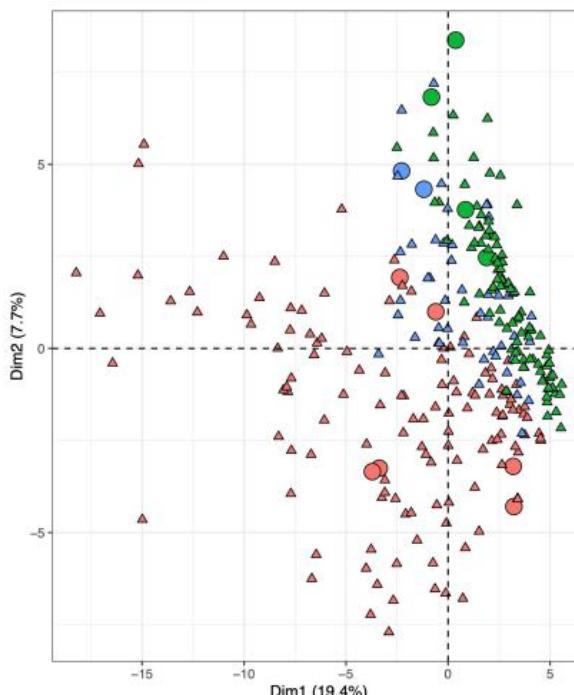
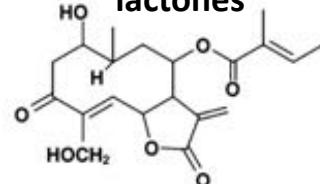
- Pollen-sterility maintainers
- Fertility restorers
- Unknown

Leaf specialized metabolism (nonvolatile-HPLC)

Higher relative concentrations of flavonoids



Higher relative concentrations of sesquiterpene lactones



PC1 (19.4%)

Higher concentrations of 90% of metabolites

Core 12

○ Lines representing 50% of allelic diversity

△ Non-core lines

Breeding group

● Pollen-sterility maintainers

● Fertility restorers

● Unknown

The 1990s were the first major investment by the US government into Sunflower breeding

Globally first time on a large scale Sunflower is bred in areas with its natural enemies

Pollen-sterility maintainers on average have a **higher** concentration of specialized metabolites (BF>1000)

Pollen-sterility maintainers on average have **higher** relative concentrations of sesquiterpene lactones(BF>1000)

Asteraceae

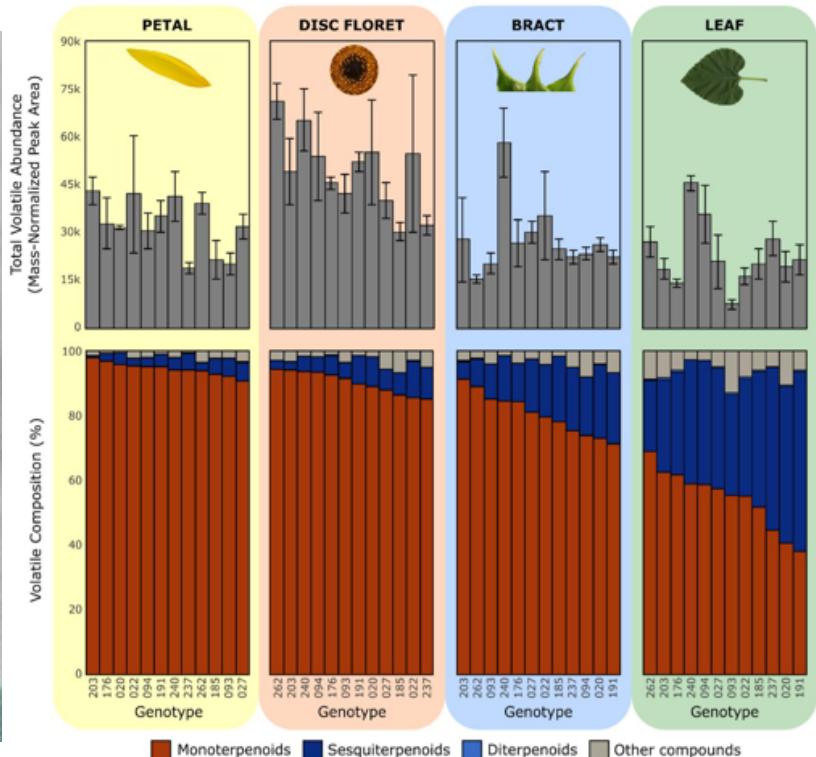
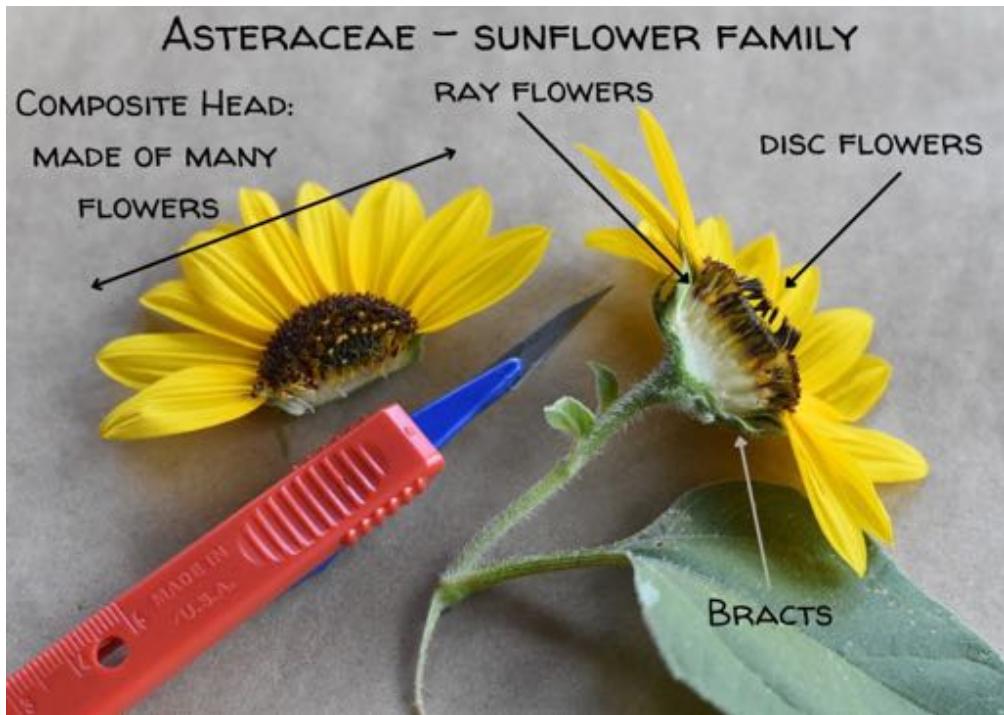


Photo credit: Philosophy Flowers & Team Flower

72

Genome-wide association

Linear mixed model

$$y = \mathbf{1}_n \mu + X\beta + u + \varepsilon.$$

$$u \sim MVN_n(0, \sigma_b^2 \tau^{-1} K),$$

$$\varepsilon \sim MVN_n(0, \tau^{-1} I_n),$$

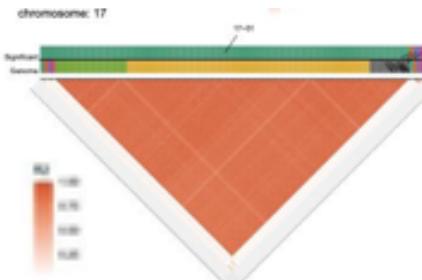
$$\beta_i \sim N\left(0, \frac{\sigma_b^2}{p\tau}\right)$$

- ~1.4 million SNPs across the ~3.6 Gb genome
- Identifying SNPs and linkage regions associated with traits and trait composites



Genome-wide association

Chromosome 17-01	
RT 8.81-UNK	+
Aspect ratio	-
Dry mass	+
LES PC1	-
LES PC2	-
Unique Metabolites PC1	+
Common Metabolites PC1	-
Chlorophyll content (area basis)	-
Circularity	-
Lamina density	-
Leaf area	+
Perimeter	+
Total flavonoids	+
Water content	+
RT 3.3-UNK	-
RT 3.77-UNK	+
RT 4.05-HCA	+
RT 4.6-UNK	+
RT 5.28-UNK	-
RT 7.1-HCA	-
RT 7.28-HCA	-
RT 7.58-UNK	-
RT 7.93-	-
Polyacetylene	
RT 8.11-UNK	-



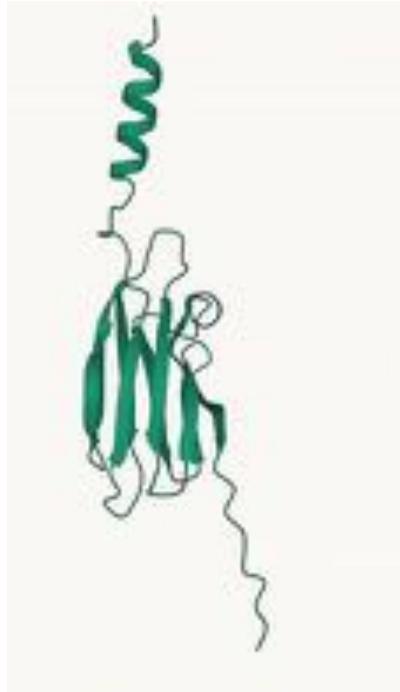
Very few enzymes
Many transcription factors
Many genes related to cell wall production
No genes associated with the maintenance of hybrid breeding systems

Questions

- What kinds of genes are in these multi-trait associated regions that are not found in other regions associated with a single trait or no traits?
- Why do we not find more enzymatic variants?



Self-compatibility protein homologs



Self-compatibility protein homolog

*AlphaFold simulation

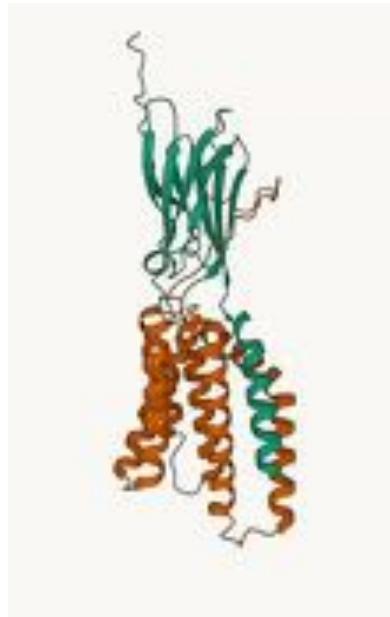


Papaver rhoeas (Flanders poppy)

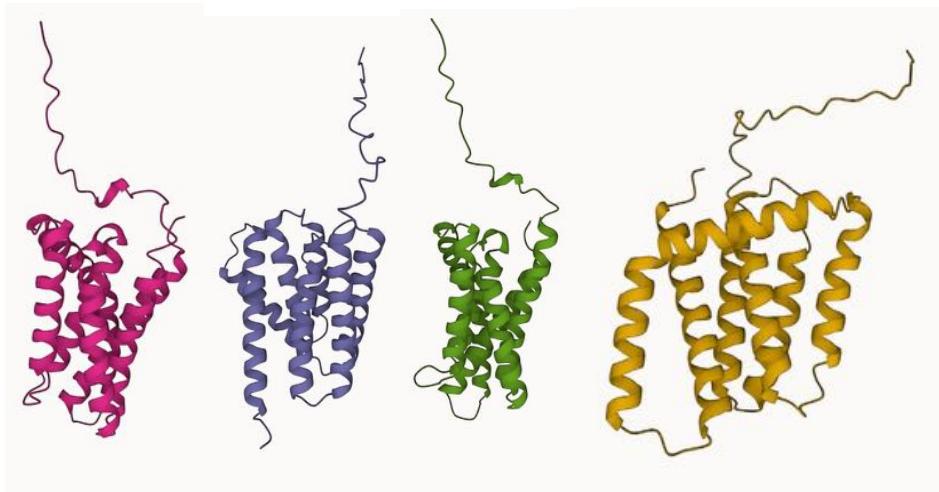
Confer quantitative self-incompatibility in Poppy, similar to observations of yield traits in cultivated sunflower

Transgenic studies demonstrate conservation of downstream molecular mechanisms in *Arabidopsis thaliana*

Self-compatibility protein homologs



Poppy receptor



*AlphaFold simulation



Genome-wide association

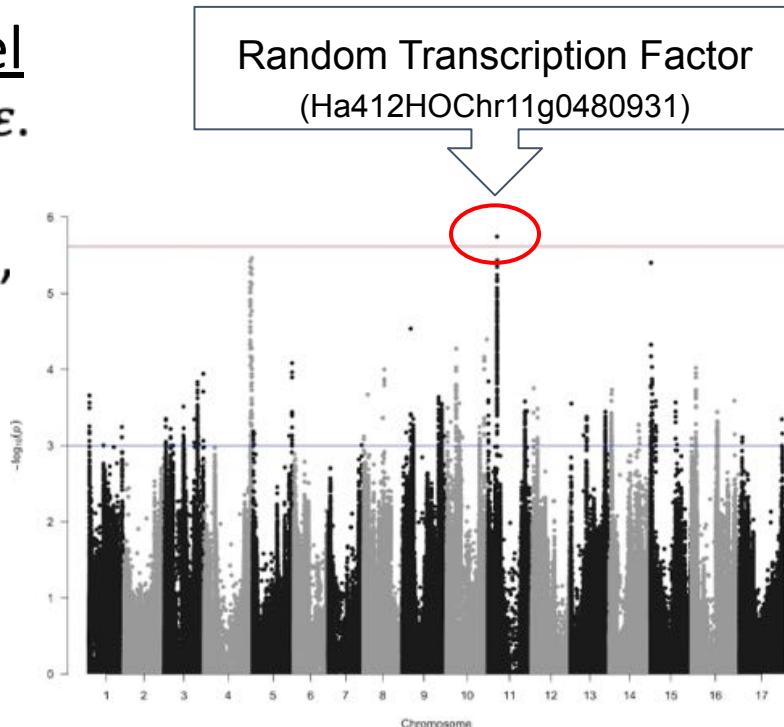
Linear mixed model

$$y = 1_n \mu + X\beta + u + \varepsilon.$$

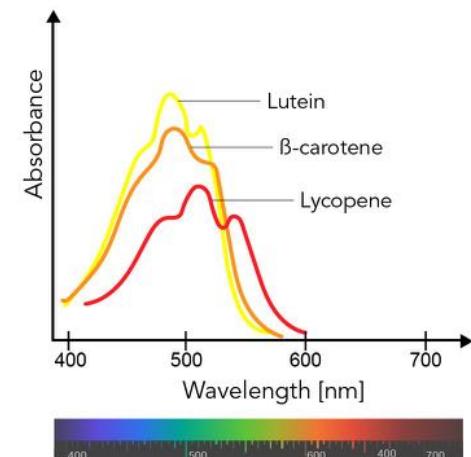
$$u \sim MVN_n(0, \sigma_b^2 \tau^{-1} K),$$

$$\varepsilon \sim MVN_n(0, \tau^{-1} I_n),$$

$$\beta_i \sim N\left(0, \frac{\sigma_b^2}{p\tau}\right)$$



GWAS of Carotenoid Content



Linear mixed model

$$y = 1_n \mu + X\beta + u + \varepsilon.$$

$$u \sim MVN_n(0, \sigma_b^2 \tau^{-1} K),$$

$$\varepsilon \sim MVN_n(0, \tau^{-1} I_n),$$

$$\beta_i \sim N\left(0, \frac{\sigma_b^2}{p\tau}\right)$$

Bayesian Sparse linear Mixed model

$$y = 1_n \mu + X\tilde{\beta} + u + \varepsilon.$$

$$u \sim MVN_n(0, \sigma_b^2 \tau^{-1} K),$$

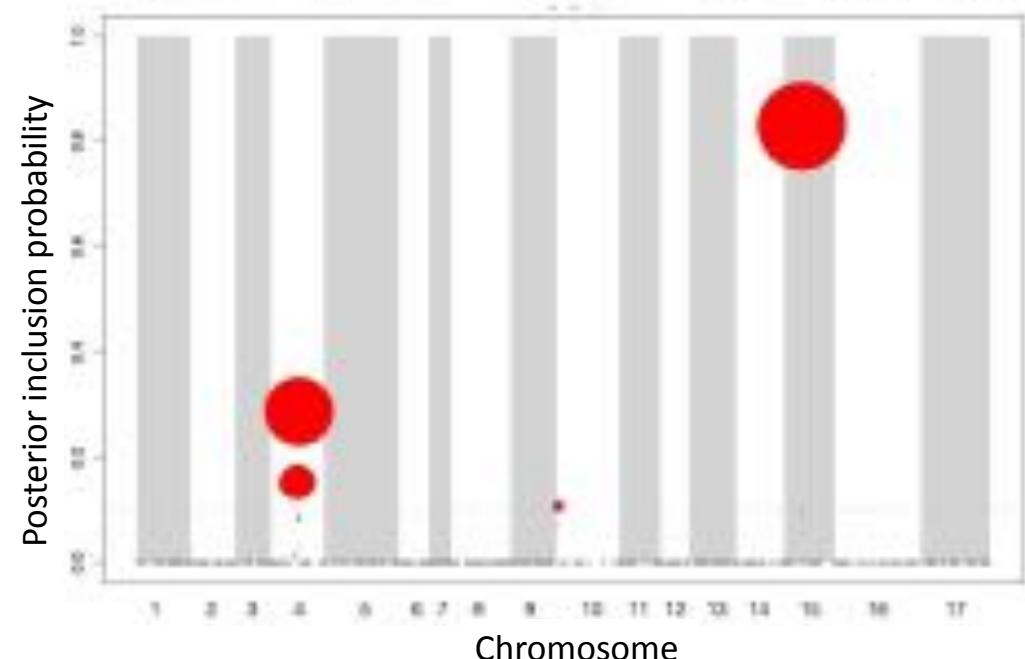
$$\varepsilon \sim MVN_n(0, \tau^{-1} I_n),$$

$$\beta_i \sim \pi N\left(0, \frac{\sigma_a^2 + \sigma_b^2}{p\tau}\right) + (1 - \pi)N\left(0, \frac{\sigma_b^2}{p\tau}\right)$$



Effect

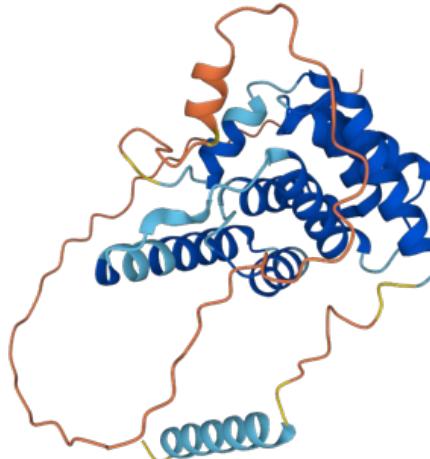
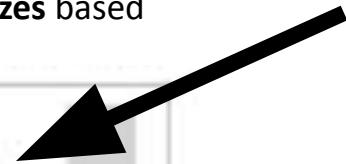
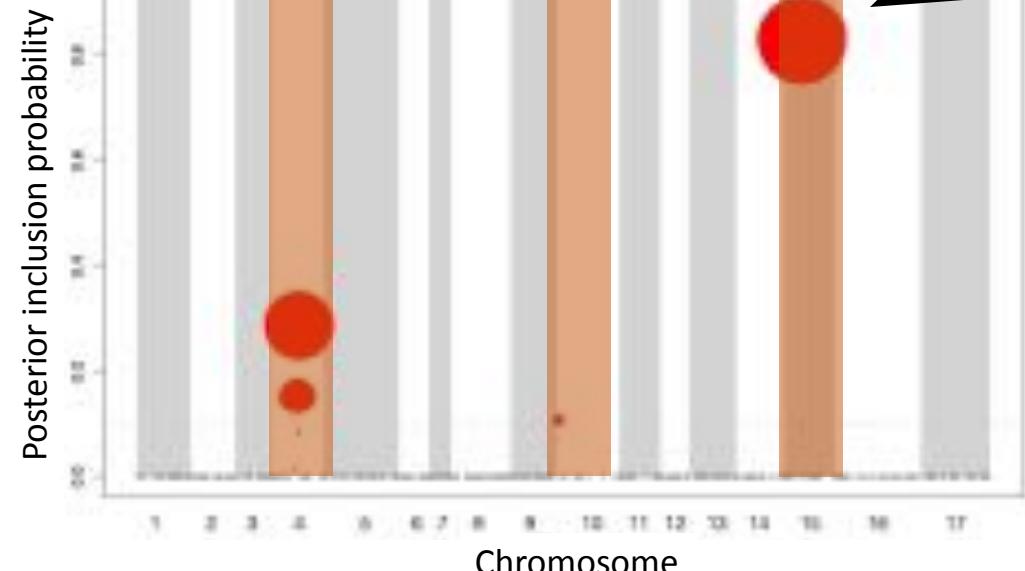
BSLMM of SNPs with the **bottom 1% of effect sizes** based
on a traditional linear mixed model





Effect

BSLMM of SNPs with the **bottom 1% of effect sizes** based
on a traditional linear mixed model



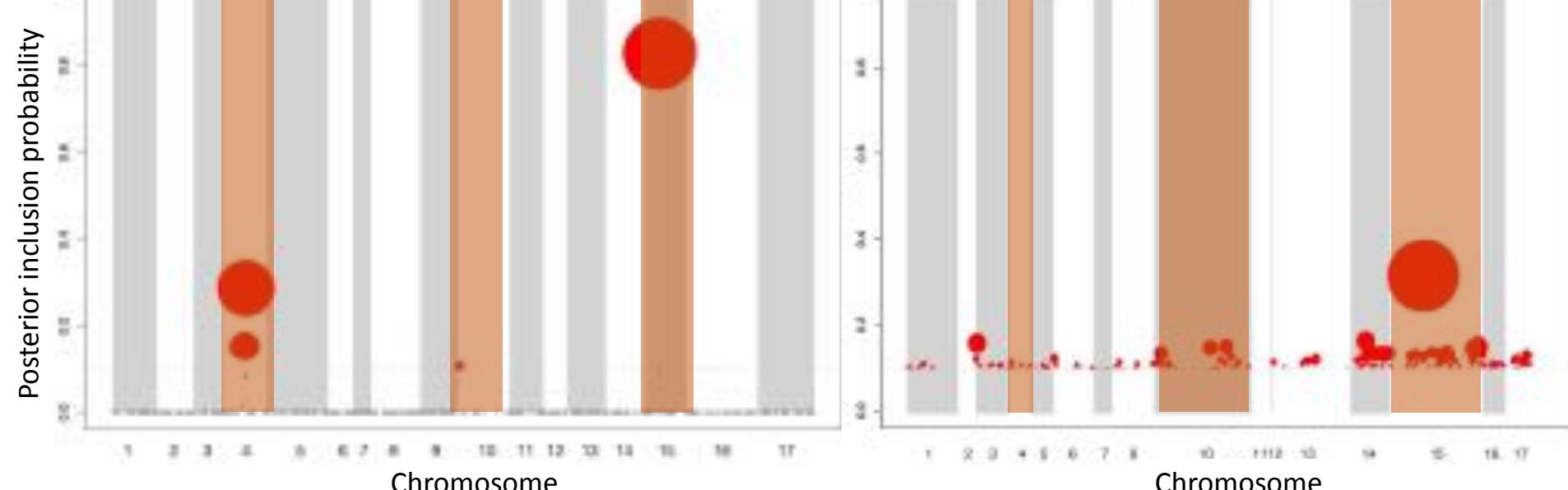
Photosystem I assembly factor PSA3—
Cooperates with PYG7 to promote the stable
assembly of PSI in the thylakoid membrane



Effect

BSLMM of SNPs with the **bottom 1% of effect sizes** based on a traditional linear mixed model

BSLMM of SNPs within the Carotenoid pathway



—Regions identified previously in the population or independently in biparental crosses

Growth-Defense Trade-off!

Beta-carotene Isomerase associated with variation in carotenoid content

Potential trade off between Carlactones & Xanthophyll cycle



•Carotenoids

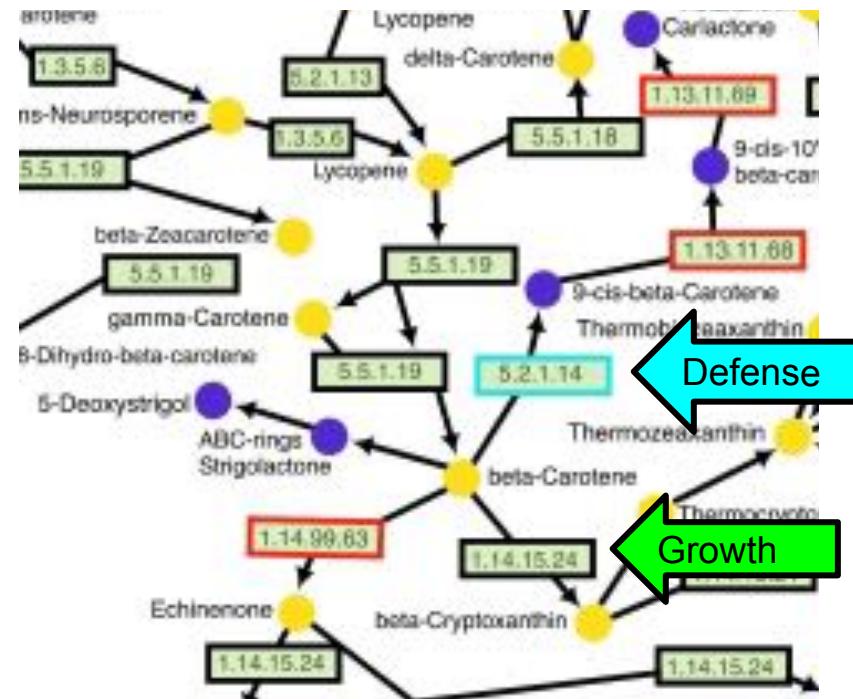


●—Specialized metabolite precursors

Growth-Defense Trade-off!

Beta-carotene Isomerase associated with variation in carotenoid content

Potential trade off between Carlactones & Xanthophyll cycle



—Carotenoids

—Specialized metabolite precursors



Summary

Many genomic regions associated with ecophysiology and chemical diversity are colocated

Biologically informed association models provide novel insight

Pollen-sterility maintainer

more resource-conservative leaves
higher conc. of metabolites
more SQTLs relative to flavonoids

Fertility restorer

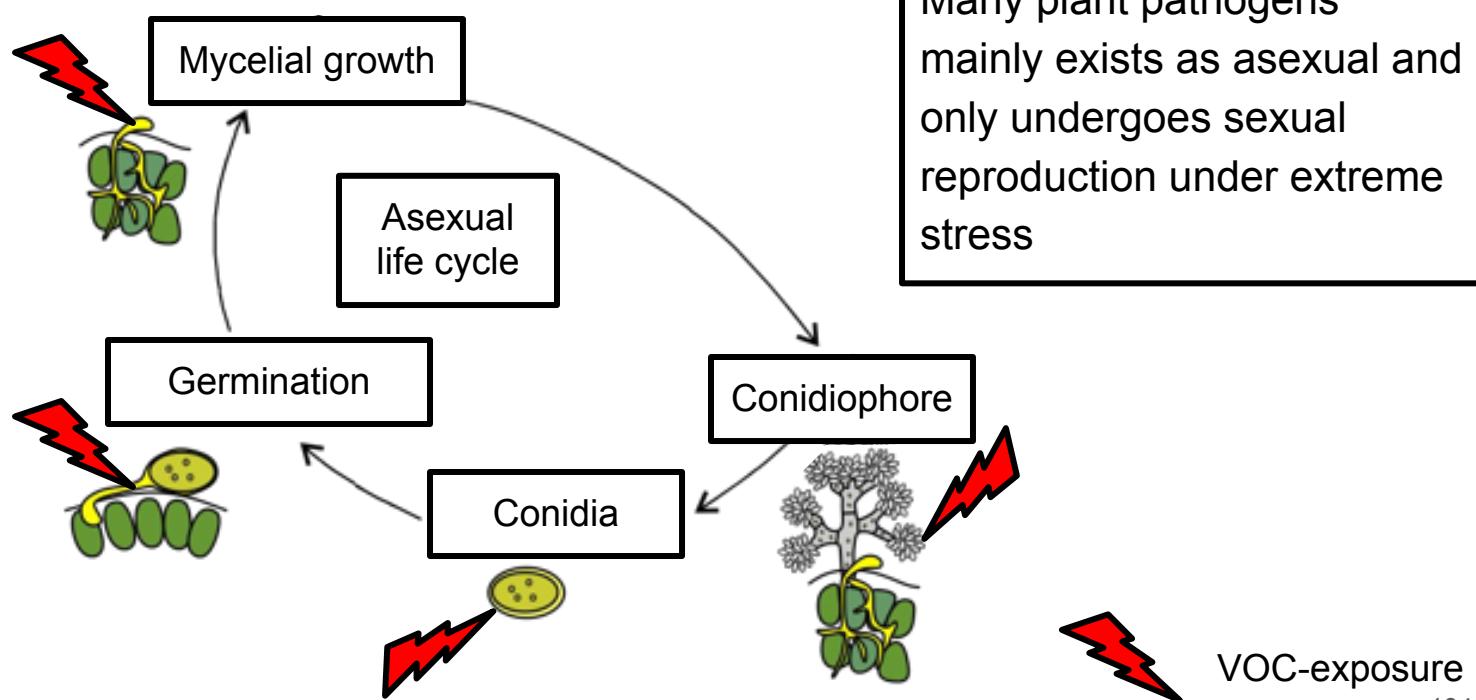
more resource-acquisitive leaves
lower conc. of metabolites
more flavonoids relative to SQTLs







Host-pathogen interactions





Kliebenstein lab developed
an association mapping
population of 96 isolates



Botrytis cinerea

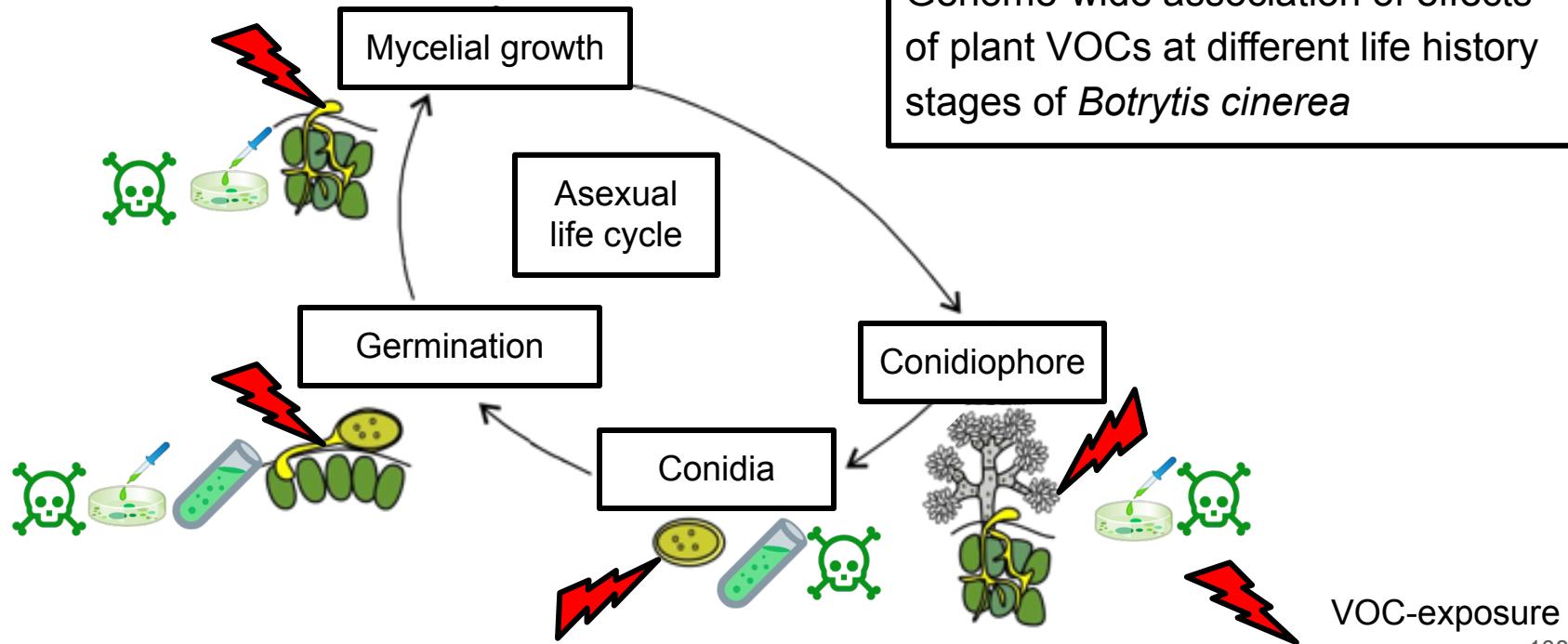


Volatile organic compound (VOC) impacts on pathogen genetic diversity and physiology

Questions:

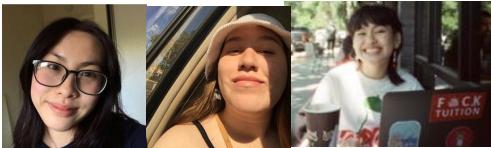
- 1) What are the direct and indirect effects of plant VOCs and host infochemicals on pathogen populations

- 2) How do nutritional status and metabolism mediate host-pathogen interactions?





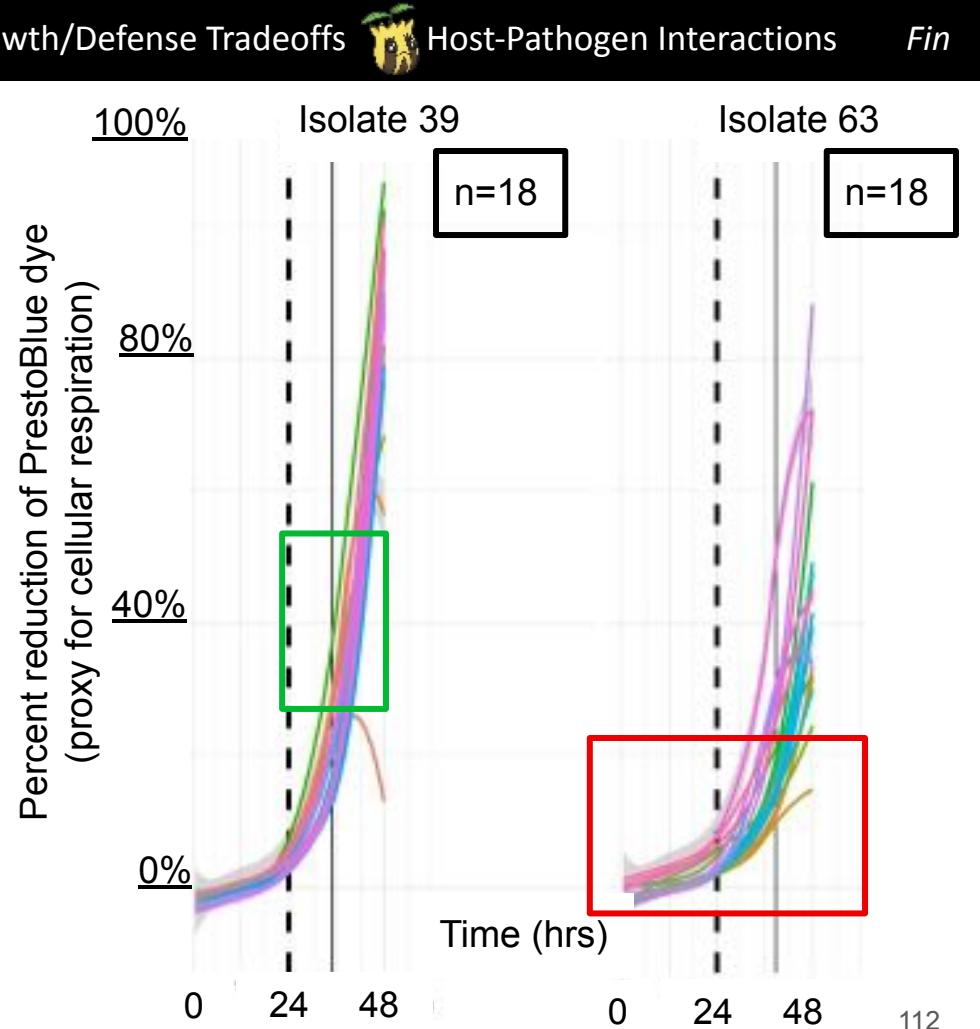
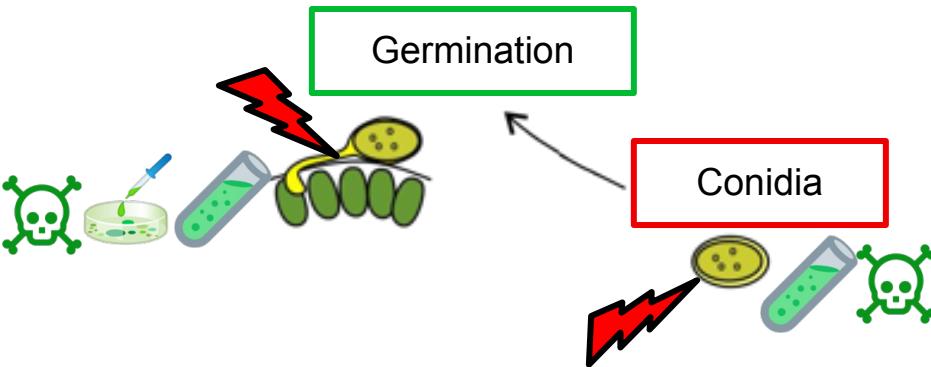
Toxicology



Two isolates exposed to 500 μ M linalool

Dashed line indicates 24hrs post inoculation

Solid line indicates time at which genotype average reaches of 20% reduction of PrestoBlue dye

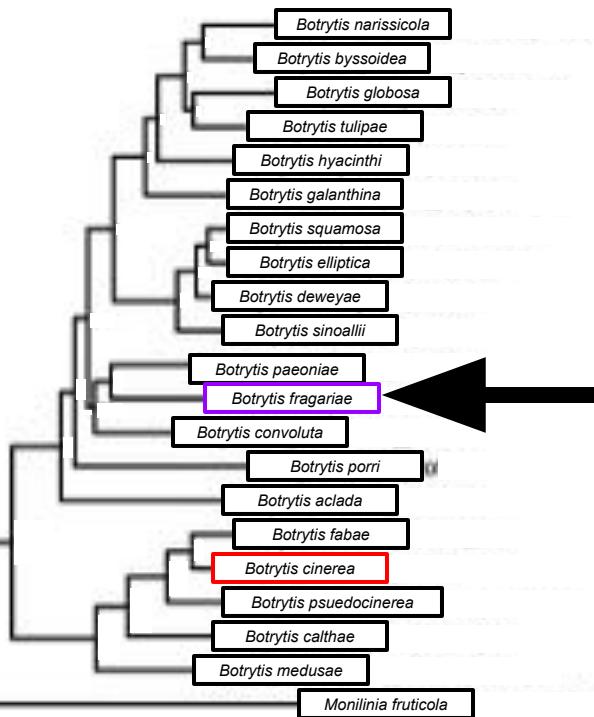




Botrytis phylogenomics



Maximum likelihood tree of ~5,000 single-copy orthologs
All nodes supported with greater than 99% bootstrap support



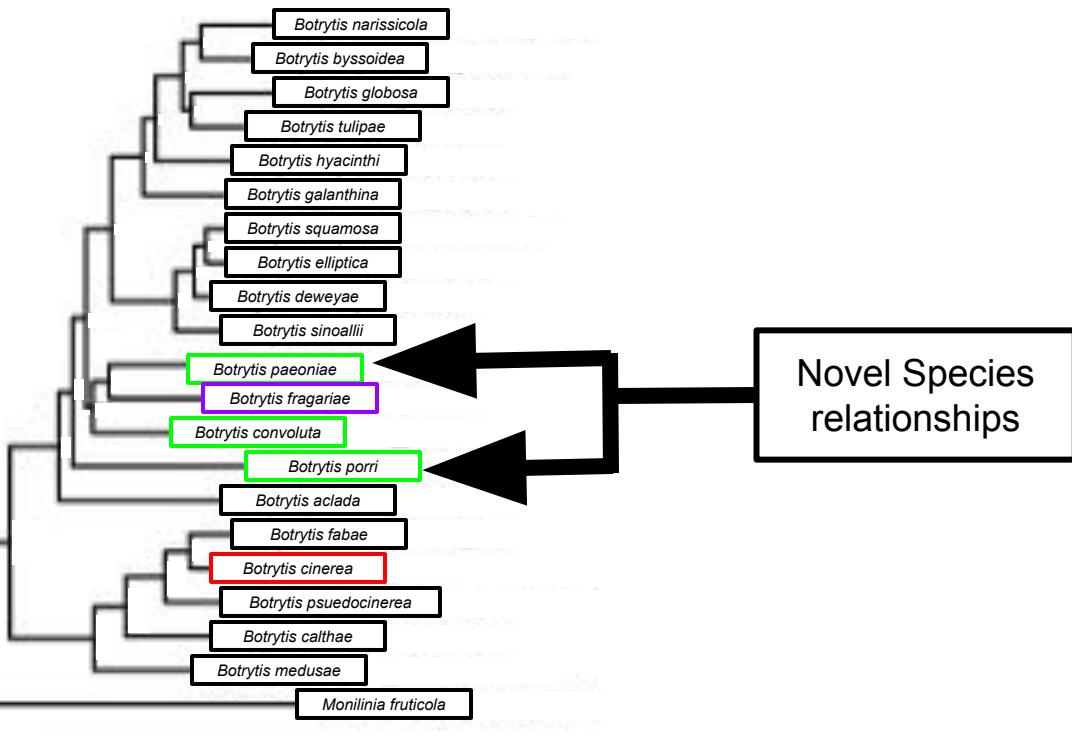
New Species incorporated



Botrytis phylogenomics



Maximum likelihood tree of ~5,000 single-copy orthologs
All nodes supported with greater than 99% bootstrap support

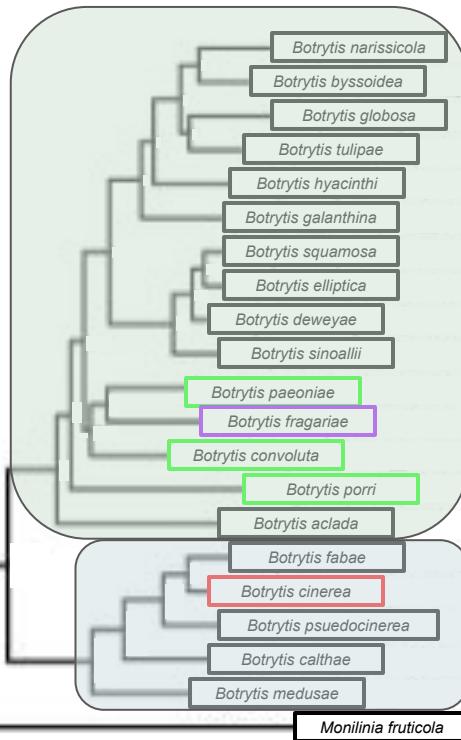




Botrytis phylogenomics



Maximum likelihood tree of ~5,000 single-copy orthologs
All nodes supported with greater than 99% bootstrap support



Clade 2
floral monocot
semi-specialists

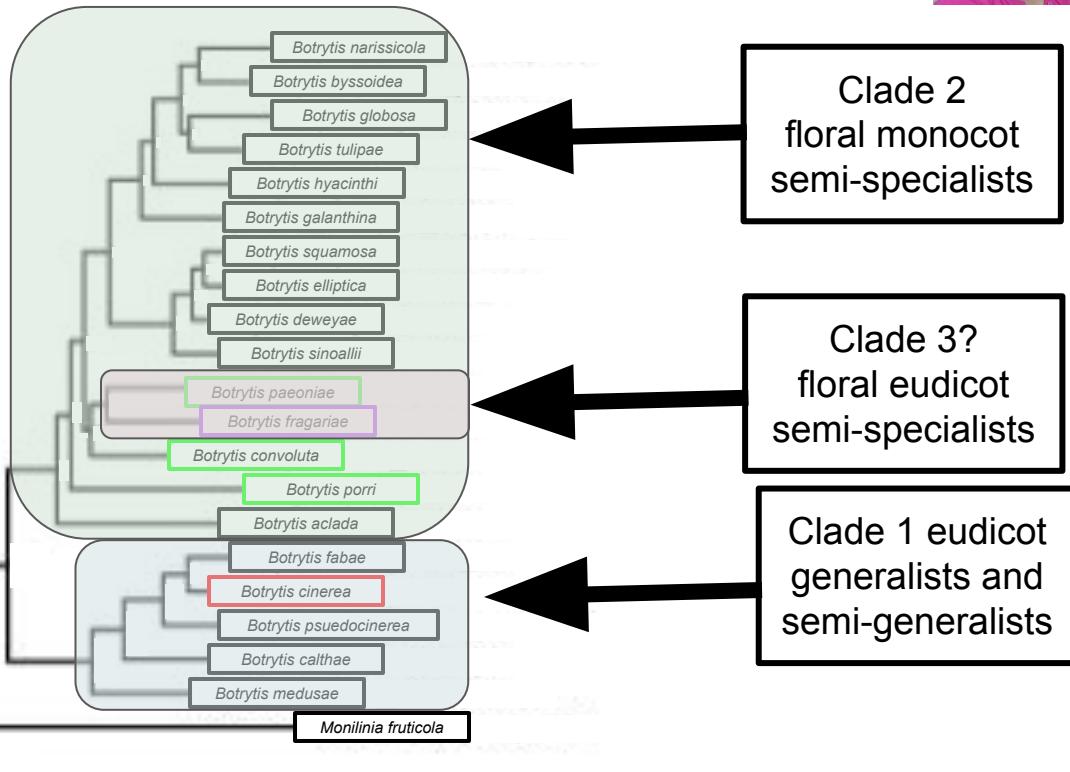
Clade 1 eudicot
generalists and
semi-generalists



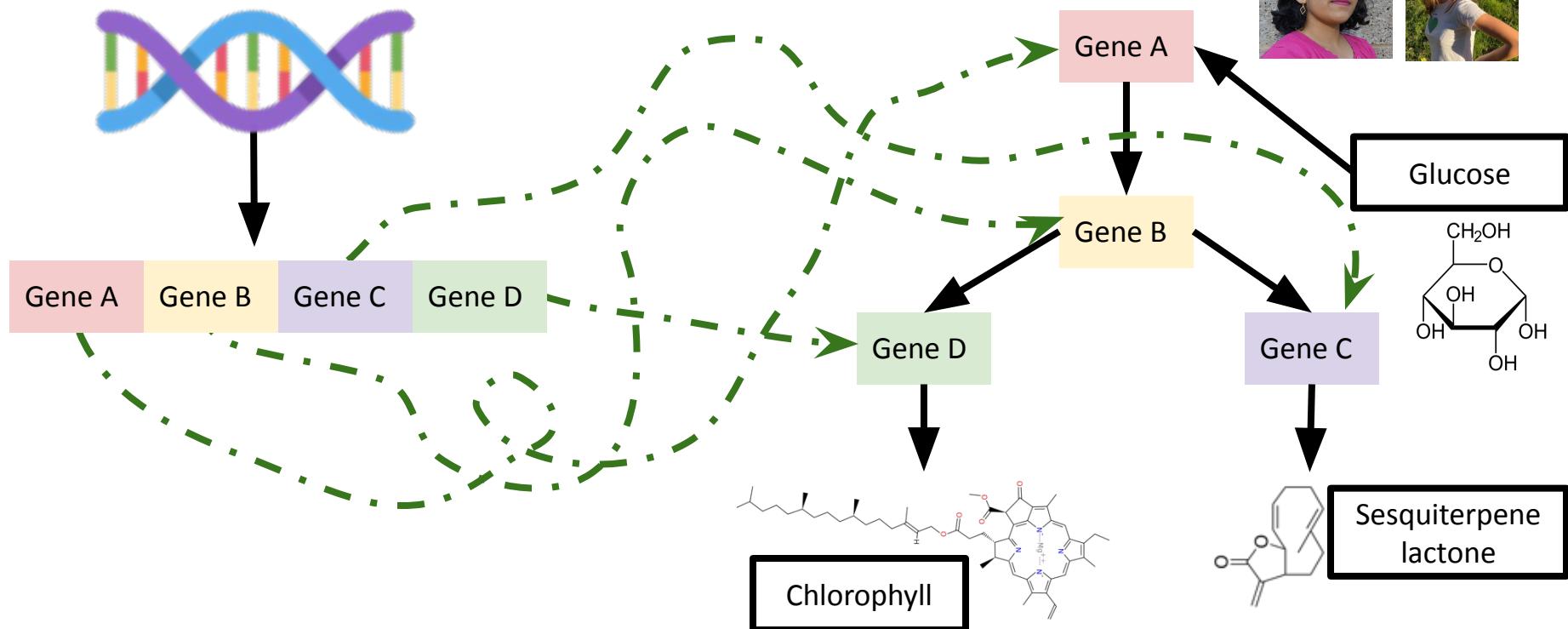
Botrytis phylogenomics



Maximum likelihood tree of ~5,000 single-copy orthologs
All nodes supported with greater than 99% bootstrap support



Genome-scale metabolic models

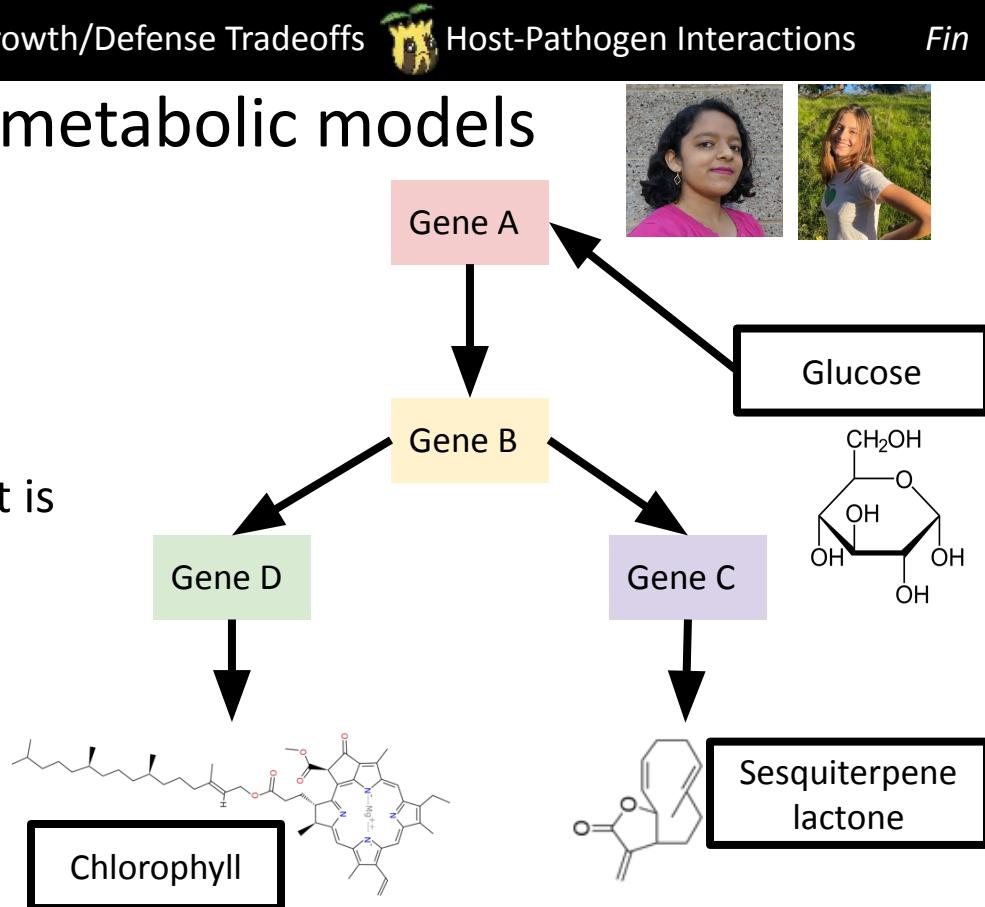




Genome-scale metabolic models

Question:

Given all potential nutrient needs what is the maximum growth rate?

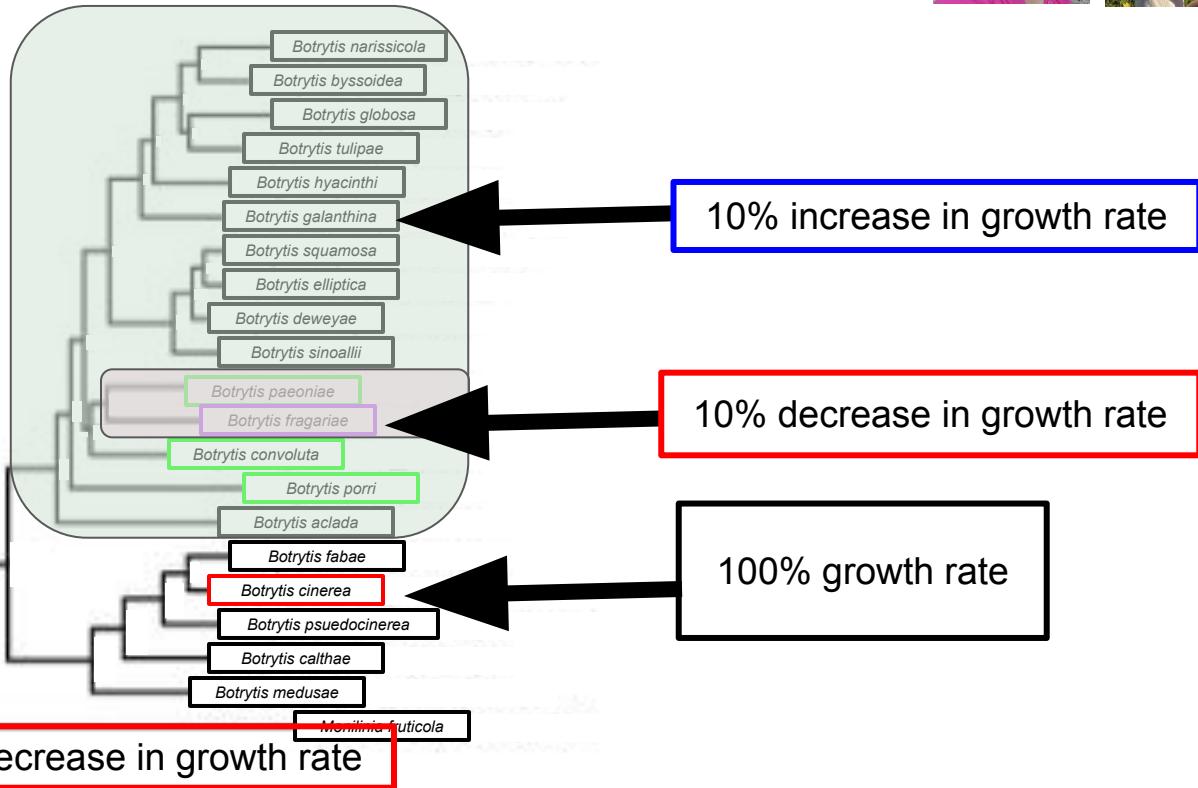




Metabolic flux across *Botrytis*



Maximum likelihood tree of ~5,000 single-copy orthologs
All nodes supported with greater than 99% bootstrap support





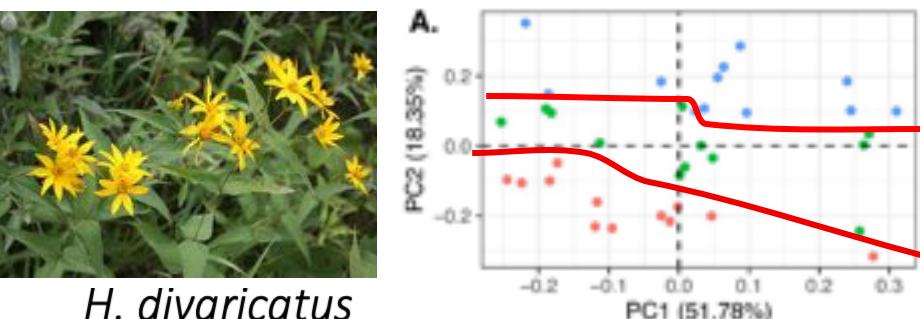
Take homes

Part 1:

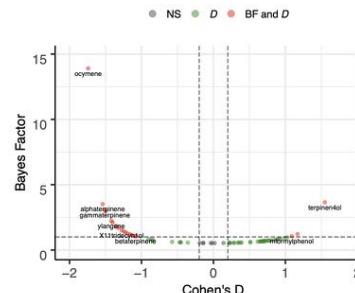
- Changes in VOCs in the context of herbivory are species specific across *Helianthus*
- Reflectance can be used to predict herbivory context noninvasively across *Helianthus*



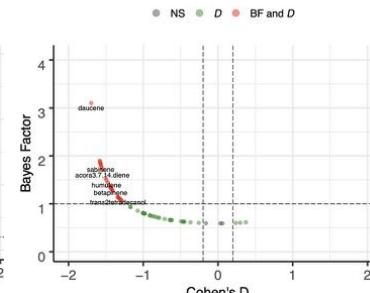
H. divaricatus



A *H. divaricatus* volatile-induced vs control
Peak area



A *H. arizonensis* volatile-induced vs control
Peak area

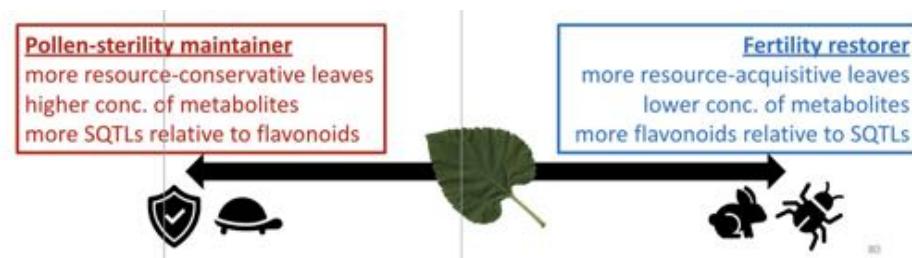
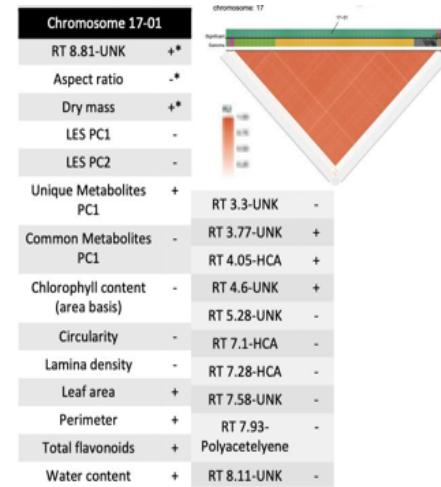




Take homes

Part 2:

- In crop Sunflower breeding practices have contributed to phenotypic divergence
- The genetic architecture of ecophysiology and chemical diversity in crop sunflower colocalizes
- Biologically informed models provide expanded insight

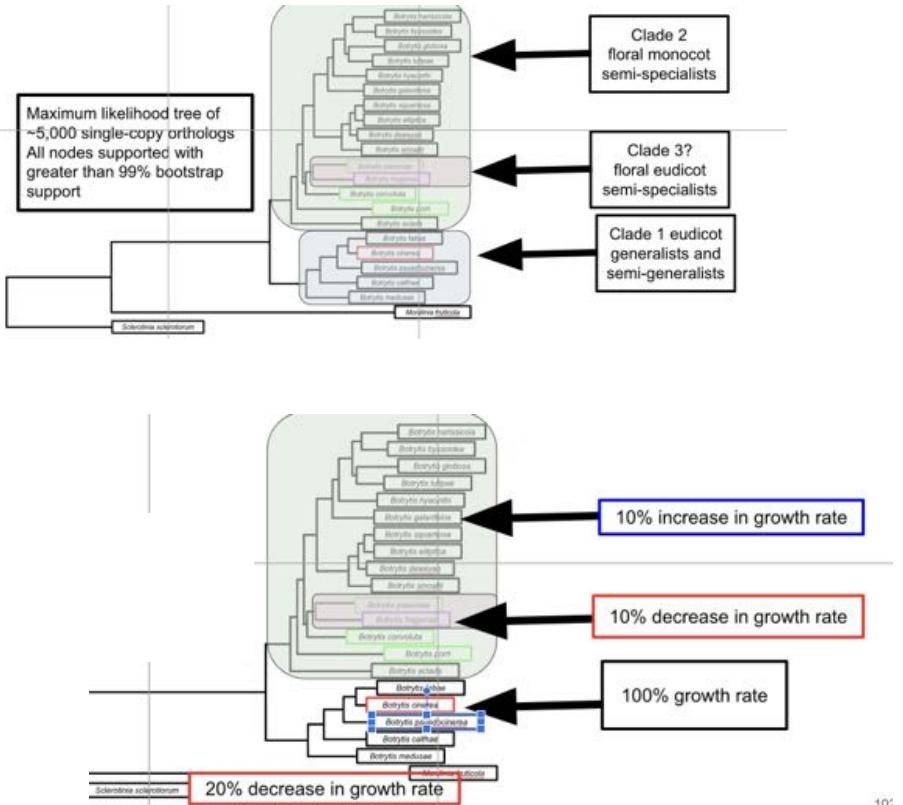




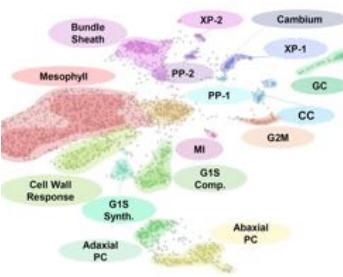
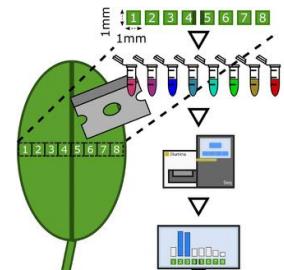
Take homes

Part 3:

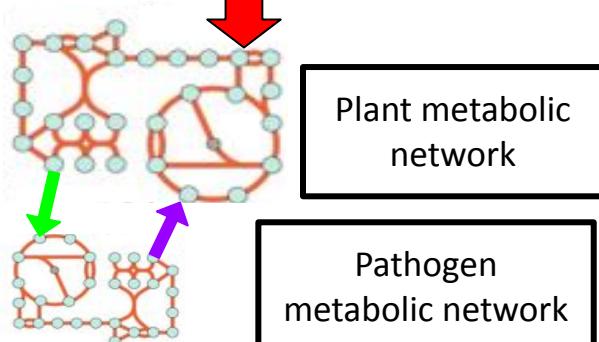
- Phylogenomics of *Botrytis* indicates new relationships associated with differences in pathogenicity and simulated growth



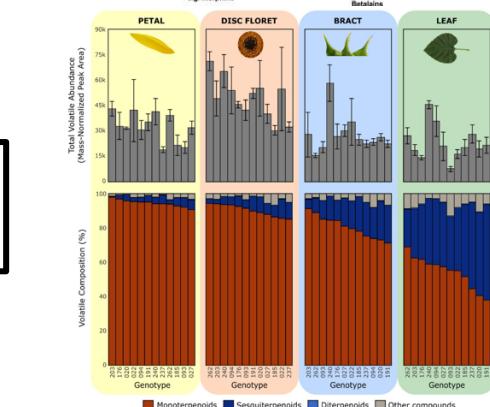
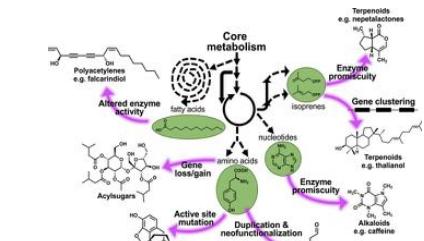
Future directions



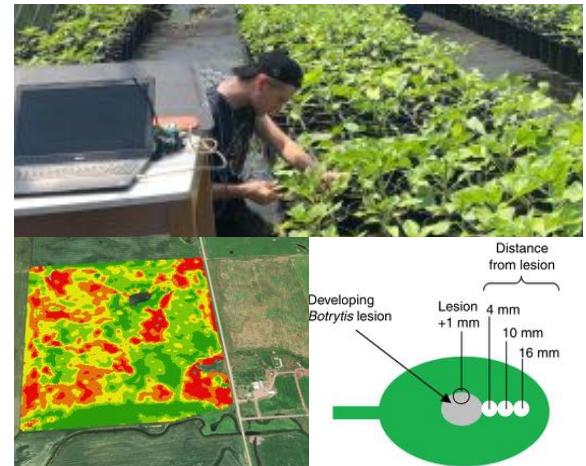
Spatial & single-cell transcriptomics
& Phylotranscriptomics



Metabolic flux & cellular physiological tradeoffs in host-pathogen interactions



Evolution and genetic architecture of multifunctional metabolites & metabolic flux



Developing real-time models of metabolism and induced defense

Soltis, Nicole E, Celine Caseys, Wei Zhang, Jason A Corwin, Susanna Atwell, and Daniel J Kliebenstein. *Genetics* 215, 1:253–66.

Kliebenstein, D. J., H. C. Rowe, and K. J. Denby. 2005. *The Plant Journal: For Cell and Molecular Biology* 44: 25–36.

Zhang, Wei et al., Jason A Corwin, Daniel Harrison Copeland, Julie Feuerer, Robert Esthbaugh, David E Cook, Suzi Atwell, and Daniel J

Kliebenstein. *Elife* 8:e44279.

Giolai, M., Verweij, W., Lister, A. et al. Spatially resolved transcriptomics reveals plant host responses to pathogens. *Plant Methods* 15, 114 (2019).

<https://doi.org/10.1186/s13007-019-0498-5>

Rubén Tenorio Berrio, et al.; Single-cell transcriptomics sheds light on the identity and metabolism of developing leaf cells, *Plant Physiology*,

Bahmani K, *Giguere M, Dowell J, Mason C, "Germplasm Diversity of Sunflower Volatile Terpenoid Profiles Across Vegetative and Reproductive Organs" (in-revision)

Bahmani K, *Robinson A, Majumder S, *LaVardera A, Dowell J, Goolsby E, Mason C, "Broad diversity in monoterpane-sesquiterpene balance across wild sunflowers: implications of leaf and floral volatiles for biotic interactions"

Collaborators

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- John Burke (UGA)
- Lisa Donovan (UGA)
- Jennifer Mandel (UTM)
- Keivan Bahmani (UCF)
- Alan Bowsher (UGA)*
- Andries Temme(UGA)
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- Minh Tran
- Sam Lenao
- Xiaoqing Zeng
- Melanie Madrigal
- Jaisy Huang
- Jessica Jowais
- Isaac Valdiviezo
- Rebekah Davis
- Jarell Mangsat
- Carina Caccobaci
- Ana Robinson



BILL & MELINDA
GATES foundation

THE
Fred C. Gloeckner
FOUNDATION, INC.



We are almost done I promise!

Production of specialized metabolites & chemical defenses



Ecological and evolutionary drivers of chemical diversity



Impacts of multifunctional metabolites on plant-biotic interactions



Development of new tools & methodologies

