

## Curriculum Vitae

**Yezhang Ding Ph.D.**

Lawrence Berkley National Laboratory  
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### EDUCATION

- 2014 Ph.D. Microbiology and Cell Science, University of Florida, USA

### RESEARCH EXPERIENCE

#### Project Scientist

Lawrence Berkley National Laboratory, Berkeley

2020.12 - Current

- Understanding and uncovering plant specialized metabolism in plant microbiome interactions;

#### Post-Doctoral Scholar

University of California, San Diego

2015.6 - 2020.11

- Focused on uncovering plant secondary metabolism, characterizing genes for biosynthesis of plant small molecules, exploring biological functions of small molecules in plant microbe interactions, and understanding plant defense signaling and disease resistance mechanisms with integrated multidisciplinary approaches;
- Explored regulation of plant specialized metabolism;
- Led two research collaboration involved eight researchers from UC-Davis, USDA-ARS, Max Planck Institute for Chemical Ecology (Germany) and UC-San Diego (funded by the NSF and USDA PBI, respectively);
- Participated in five collaborative projects led by Cornell University, UC-Davis, Max Planck Institute for Chemical Ecology (Germany), Cold Spring Harbor Laboratory, USDA-ARS, and University of Cologne (Germany).

#### Visiting Scientist

University of California, Davis, CA

2016.7 - 2016.8

- Performed *in vitro* and *in vivo* characterization of P450s in plant specialized metabolism

#### Post-Doctoral Research Associate

University of Florida, Gainesville, FL

2014.9 - 2015.5

- Studied the promoter regulation of *NPR1*, an important defense gene in *Arabidopsis*;
- Explored the mechanism(s) underlying plant defense priming.

#### Graduate Research

Microbiology and Cell Science, University of Florida, Gainesville, FL

2010.1 - 2014.8

- Employed forward and reverse genetic approaches to identify components involved in the salicylic acid biosynthesis/signaling pathway in *Arabidopsis*;
- Elucidated the interaction between biotic stress (SA signaling) and abiotic stress (ABA signaling) in plant immune response;

- Performed a study entitled “Overexpression of Elongator genes enhances plant disease resistance”.

**Research Assistant (Oil Crop Breeding)**  
Texas Tech University, Lubbock, TX

2009.1 - 2009.7

- Performed data collection for oil crop field trials;

## TEACHING EXPERIENCE

### Teaching Assistant

- 2013 Teaching Assistant, Advanced Biology of Microorganisms laboratory, MCB3020 section 310; and MCB3020 section 4G10, University of Florida;
- 2012 Teaching Assistant, Basic Biology of Microorganisms Laboratory, MCB2000L section 1025, and Advanced Biology of Microorganisms Laboratory, MCB3020 Section 3029, University of Florida;

**Lecturer** 2005-2008, “General Genetics”, Nanjing Agricultural University, China;

## MENTORING

### Undergraduate:

- 2018-2020, Evan Saldivar, UC San Diego;
- 2017, Edward Runey, UC San Diego;
- 2016, Josie Tran, UC San Diego;
- 2012-2013, Danjela Shaholli, University of Florida;
- 2010-2011, Deepak Sathyanarayan, University of Florida;

### Visiting Ph.D. candidate student:

- 2018 - 2020 Mengxi Wu (Visiting Ph.D. candidate student from Sichuan Agricultural University, China), UC San Diego;

## RESEARCH TECHNIQUE PROFICIENCY

- **Molecular Biology:** Nucleic acid isolation, recombinant DNA technologies; RACE-PCR; CRISPR/cas9 genome editing; heterologous protein expression and purification; Western blot; enzyme activity assays; site-directed mutagenesis; gene expression analysis (qPCR and RNAseq analysis); confocal microscopy; cell culture and transformation; antimicrobial assays; engineering of metabolic pathways in *E. coli*, *N. benthamiana* and yeast; and many others;
- **Analytical Biochemistry Techniques:** Analyzing small molecules with HPLC, GC-FID, GC-MS (Agilent), and LC-MS/MS; Both targeted and untargeted metabolomic analysis; Purification of small natural products for NMR analysis, etc.
- **Quantitative Genetics:** Genome-wide association studies, linkage analysis, map-based gene cloning, molecular marker-assisted selection (MAS), etc.
- **Bioinformatics:** Basic R programming and familiarity with many software packages for data processing and statistical analysis;

## INVITED PEER REVIEWER

*Plant Physiology, Phytochemistry* (3), *Frontiers in Plant Science* (5), *PLoS One* (5), *Plant Cell Reports, Planta* (2), *Plant Disease* (6), *Molecular Plant Pathology* (2), *Physiological and Molecular Plant Pathology* (5), *Euphytica* (2), *American Journal of Plant Science*.

## PROFESSIONAL MEMBERSHIPS

- American Society of Plant Biologists (ASPB);
- Phytochemical Society of North America (PSNA);

## PATENTS

- “Use of Elongator Genes to Improve Plant Disease Resistance”.  
Mou Z, **Ding Y**, Folta KM, Zhang X.
- WO 2017011462 A1, 2017 (Worldwide);
- US20180371490A1, 2018 (USA)

## SELECTED INVITED TALKS

1. 2020 62th Annual Maize Genetics Conference, Sheraton Kona, Hawaii, USA;
2. 2019 American Society of Plant Biologists, San Jose, CA, USA;
3. 2018 57th Annual Meeting of the Phytochemical Society of North America. San Luis Potosi, Mexico;
4. 2016 55th Annual Meeting of the Phytochemical Society of North America, Davis, CA, USA;

## SELECTED POSTER PRESENTATIONS

1. 2019 61th Annual Maize Genetics Conference (2019), St. Louis, MO, USA;
2. 2017 59th Annual Maize Genetics Conference (2017), St. Louis, MO, USA;
3. 2016 Plant Volatiles Gordon Research Conference, Ventura, CA, USA;
4. 2016 Food & Fuel for the 21st Century, San Diego, CA, USA;

## MANUSCRIPTS UNDER PREPARATION

1. **Ding Y**, Saldivar E, Huaffaker A, Schmelz EA. Convergent evolution on terpenoid metabolism contributes to plant defense against biotic stress. Under preparation

## PUBLICATIONS

### In 2022

1. **Ding Y\***, Wu M\*, Christensen S, Huffaker A, Schmelz EA. Discovery of a noncanonical cyclase in plants defines a key biosynthetic branch point between jasmonate and death acid pathways. *Nature Plants*, submitting (\*contributed equally)
2. Förster C, Handrick V, **Ding Y**, Nakamura Y, Paetz C, Schneider B, Castro-Falcón G, Hughes CC, Luck K, Kunert G, Huffaker A, Gershenzon J, Schmelz EA, Köllner TG.

Biosynthesis and antifungal activity of fungus-induced O-methylated flavonoids in maize. *Plant Physiology*, 2022, 188: 167-190

### In 2021

3. **Ding Y**, Northen TR, Khalil AS, Huffaker A, Schmelz EA. Getting back to the grass roots: harnessing specialized metabolites for improved crop stress resilience. *Current Opinion in Biotechnology*, 2021, 70: 174–186

### In 2020

4. **Ding Y**, Weckwerth PR, Poretsky E, Murphy KM, Sims J, Saldivar E, Christensen SA, Char SN, Yang B, Tong AD, Shen Z, Kremling KA, Buckler ES, Kono T, Nelson DR, Bohlmann J, Bakker MG, Vaughan MM, Khalil AS, Betsiashvili M, Dressano K, Köllner TG, Briggs SP, Zerbe P, Schmelz EA, Huffaker A. Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. *Nature Plants*, 2020, 6: 1375-1388
5. **Ding Y\***, Dommel MR\*, Wang C, Li Q, Zhao Q, Zhang X, Dai S, Mou Z. Full induction of NPR1 is required for basal immunity but not for systemic acquired resistance in *Arabidopsis thaliana*. *Frontiers in Plant Science*, 2020, 11: 1455
6. Wu Q, Xu F, Liu L, Char SN, **Ding Y**, Schmelz EA, Yang B, Jackson D. The maize heterotrimeric G-protein  $\beta$  subunit controls shoot meristem development and immune responses. *Proceedings of the National Academy of Sciences USA*, 2020, 117: 1799-1805

### In 2019

7. **Ding Y**, Murphy KM, Poretsky E, Mafu S, Yang B, Char SN, Christensen S, Saldivar E, Wu M, Wang Q, Ji L, Dr. Schmitz R, Kremling K, Buckler E, Shen Z, Briggs S, Bohlmann J, Sher A, CastroFalcon G, Hughes C, Huffaker A, Zerbe P, Schmelz EA. Multiple genes recruited from hormone pathways partition maize diterpenoid defences. *Nature Plants*, 2019, 5: 1043-1056
8. Wang S, Chen Z, Tian L, **Ding Y**, Zhang J, Zhou J, Liu P, Chen Y, Wu L. Comparative proteomics combined with analyses of transgenic plants reveal ZmREM 1.3 mediates maize resistance to southern corn rust. *Plant Biotechnology Journal*, 2019, 17: 2153-2168
9. Zhou S, Zhang YK, Kremling KA, **Ding Y**, Bennett JS, Bae JS, Kim DK, Ackerman HH, Kolomiets MV, Schmelz EA, Schroeder FC, Buckler ES, Jander G. Ethylene signaling regulates natural variation in the abundance of antifungal acetylated diferuloylsucroses and *Fusarium graminearum* resistance in maize seedling roots. *New Phytologist*, 2019, 221: 2096-2111

### In 2018

10. Mafu S\*, **Ding Y\***, Murphy KM, Yaacoobi O, Addison JB, Wang Q, Shen Z, Briggs SP, Bohlmann J, Castro-Falcón G, Hughes CC, Betsiashvili M, Huffaker A, Schmelz EA, Zerbe P. Discovery, biosynthesis and stress-related accumulation of dolabradiene-derived defenses in maize. *Plant Physiology*, 2018, 176: 2677-2690 (\*contributed equally)

11. Murphy KM, Ma LT, **Ding Y**, Schmelz EA, Zerbe P. Functional characterization of two class II diterpene synthases indicates additional specialized diterpenoid pathways in maize (*Zea mays*). *Frontiers in Plant Science*, 2018, 9: 1542
12. Ziemann S, van der Linde K, Lahrmann U, Acar B, Kaschani F, Colby T, Kaiser M, **Ding Y**, Schmelz EA, Huffaker A, Holton N, Zipfel C, Doehlemann G. An apoplastic peptide activates salicylic acid signaling in maize. *Nature Plants*, 2018, 4: 172-180

#### In 2017

13. **Ding Y**, Huffaker A, Köllner TG, Weckwerth P, Robert CAM, Spencer JL, Lipka AE, Schmelz EA. Seline volatiles are essential precursors for maize defense promoting fungal pathogen resistance. *Plant Physiology*, 2017, 175: 1455-1468

#### In 2016

14. **Ding Y**, Dommel M, Mou Z. Abscisic acid promotes proteasome-mediated degradation of the transcription coactivator NPR1 in *Arabidopsis thaliana*. *The Plant Journal*, 2016, 86: 20-34
15. An C\*, **Ding Y\***, Zhang X, Wang C, Mou Z. Elongator plays a positive role in exogenous nicotinamide adenine dinucleotide-induced defense responses in *Arabidopsis*. *Molecular Plant-Microbe Interactions*, 2016, 29: 396-404 (\*contributed equally)

#### In 2015

16. **Ding Y**, Mou Z. Elongator and its epigenetic role in plant development and responses to abiotic and biotic stresses. *Frontiers in Plant Science*, 2015, 6: 296
17. **Ding Y**, Shaholli D, Mou Z. A large-scale genetic screen for mutants with altered salicylic acid accumulation in *Arabidopsis*. *Frontiers in Plant Science*, 2015, 5: 763
18. Wang C, **Ding Y**, Yao J, Zhang Y, Sun Y, Colee J, Mou Z. *Arabidopsis* Elongator subunit 2 positively contributes to resistance to the necrotrophic fungal pathogens *Botrytis cinerea* and *Alternaria brassicicola*. *The Plant Journal*, 2015, 83: 1019-1033

#### Before 2015

19. Wang P, Zhu Y, Song X, Cao Z, **Ding Y**, Liu B, Zhu X, Wang S, Guo W, Zhang T. Inheritance of long staple fiber quality traits of *G. barbadense* in *G. hirsutum* background using CSILs. *Theoretical and Applied Genetics*, 2012, 124: 1415-1428
20. Song L, Guo W, Qin H, **Ding Y**, Zhang T. Genetic analysis and molecular validation of chromosome assignment for fuzzless genes *N1* and *n2* in cotton. *Journal of Nanjing Agricultural University*, 2010, 33: 12-18
21. Marek G, Carver R, **Ding Y**, Sathyanarayan D, Zhang X, Mou Z. A high-throughput method for isolation of salicylic acid metabolic mutants. *Plant Methods*, 2010, 6: 21
22. Chen D, **Ding Y**, Guo W, Zhang T. Molecular mapping of genic male-sterile genes *ms<sub>15</sub>*, *ms<sub>5</sub>* and *ms<sub>6</sub>* in tetraploid cotton. *Plant Breeding*, 2009, 128: 193-198

23. Chen D, **Ding Y**, Guo W, Zhang T. Molecular cloning and characterization of a flower-specific class III peroxidase gene in *G. hirsutum*. *Molecular Biology Report*, 2009, 36: 461-469
24. Ma X, **Ding Y**, Jiang F, Zhu X, Guo W, Zhou B, Zhang T. Quantitative genetic analysis of asiatic cotton major quality. *Journal of Plant Genetic Resources*, 2008, 9: 212-216
25. Ma X, **Ding Y**, Zhou B, Guo W, Lu Y, Zhu X, Zhang T. QTL mapping in A-genome diploid Asiatic cotton and their congruence analysis with AD-genome tetraploid cotton in *Gossypium*. *Journal of Genetics and Genomics*, 2008, 35: 751-762
26. Wu S, Wang H, Li F, Chen T, Zhang J, Jiang Y, **Ding Y**, Guo W, Zhang T. Enhanced agrobacterium-mediated transformation of embryogenic calli of upland cotton via efficient selection and timely subculture of somatic embryos. *Plant Molecular Biology Reporter*, 2008, 26: 174-185
27. Wang P, **Ding Y**, Lu Q, Guo W, Zhang T. Development of *Gossypium barbadense* chromosome segment substitution lines in the genetic standard line TM-1 of *Gossypium hirsutum*. *Chinese Science Bulletin*, 2008, 53: 1512-1517
28. **Ding Y**, Zhang T. Development and utilization of the new germplasm of transgenic *Bt* + *GNA* insect-resistant cotton with high lint percentage. *Molecular Plant Breeding*, 2008, 12: 1-6
29. **Ding Y**, Guo W, Zhang T. Genetic analysis of two mutants of fiber in *Gossypium hirsutum*. *Cotton Science*, 2007, 19: 17-20
30. Dong C, **Ding Y**, Guo W, Zhang T. Fine mapping of the dominant glandless Gene  $Gf^2$  in sea-island cotton (*Gossypium barbadense* L.). *Chinese Science Bulletin*, 2007, 52: 3105-3109
31. Guo W, Zhang T, **Ding Y**, Zhu Y, Shen X, Zhu Z. Molecular marker assisted selection and pyramiding of two QTLs for fiber strength in upland cotton. *Journal of Genetics and Genomics*, 2005, 32: 1275-1285



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Dear UCR Department of Botany and Plant Sciences, Metabolomics of Adaptive Responses  
Assistant Professor search committee,

In my role as a faculty mentor, it is with my strongest endorsement and opinion that Dr. Yezhang Ding be considered as an outstanding applicant for an assistant professor position in plant metabolomics of adaptive responses. I have been engaged in research surrounding numerous aspects of plant immune responses to insects and pathogens for 25 years (>100 research papers, h-index=59). Dr. Yezhang Ding first came to my new laboratory at UCSD in May of 2015. A major research goal was to leverage maize mapping populations to uncover causal genes and endogenous pathways critical for the production of specialized metabolites with antifungal and signaling roles. Yezhang played an essential role in maize physiological assays and field management of the first large root metabolite mapping trial in 2015. Yezhang's efforts led to the discovery of  $\beta$ -costic acid in maize and the only  $\beta$ -selinene synthase cloned in any organism (PMID: 28931629). The work involved large scale cloning of gene variants from different inbred lines, use of metabolite led Genome Wide Association Studies (mGWAS), *in vitro* enzyme assays, and demonstration of biological function using both pharmacological antifungal assays and near isogenic line (NIL) bioassays with and without functional genes. A second major push of Dr. Yezhang Ding was to understand protective antifungal maize diterpenoids, namely the kauralexin biosynthetic pathway. To do this Yezhang had to first work to define competing branched biosynthetic pathways and ultimately contributed to the discovery of dolabradiene-based defenses, termed dolabraloxins (PMID: 29475898). Yezhang's careful analyses of mutants, root response assays and purification of novel endogenous defenses provided essential contributions to the effort enabling discovery of new antibiotic pathways. Using bioinformatics, transcriptomics, proteomics, large-scale genetic mapping, mutant analyses, and heterologous gene expression, Yezhang then defined and proved *in planta* the entire 5 step kauralexin pathway accounting for multiple hormone and defense genes with redundant catalytic functions. The herculean effort entitled was published in Nature Plants (PMID: 31527844). Of direct human relevance was Yezhang's discovery and enzymatic characterization of a plant steroid 5 $\alpha$  reductase closely related human SRD5A3 (type-3; PMID: 17986282) that has been associated with cancer. His efforts represent the single most in depth and systematic study by my laboratory to date. In a much larger team effort with the laboratory of Dr. Alisa Huffaker, Yezhang pushed to define the first 10 genes of the isoprenoid-based zealexin pathway (Zx) that critically controls pathogen resistance. Extreme diversity, gene duplications, multiple pathway interactions and the complexity of 17 related antibiotics elucidated made this project a true challenge to define on a genome wide level. Working with Huffaker lab members, Yezhang had the single largest role in completing this second monumental effort in Nature Plants (PMID: 33106639). Yezhang further drove other key discoveries in many published collaborative efforts and has been spectacular in his interactions with my colleagues.

As a final direction, a long-term interest has been to discover unique biosynthetic enzymes regulating the production of "jasmonate-like" 9-lipoxygenase derived cyclopentenones such as 10-oxo-11 phytoenoic acid (10-OPEA). Our published data is consistent with 10-OPEA as a concentration dependent signal with cell protective roles at low levels and cell death-inducing activity at high levels. Using genetic mapping Yezhang discovered a novel non-canonical family of 9-allene oxide cyclases (9-AOC) in present in all grain crops now proven with gene synthesis and enzyme assays via heterologous expression. Maize death acids have measurable conceptual and structural similarities to prostaglandins in humans. Using isogenic knock out lines, Yezhang confirmed a number of predicted phenotypes to conclusively demonstrate the biological roles *in planta*. Yezhang is leading this near-term submission at Nature Plants. This direction alone is likely to cause great interest in plant oxidative stress protection, cell death and pathogen protection mediated by defined specialized metabolites. While remaining a partial research direction of my lab, Yezhang and I are discussing aspects of this oxylipin research worthy of expanding on after obtaining well-deserved principle investigator position. In all projects Yezhang focused on understanding plant genetics, biochemistry, and specialized metabolites that underly complex microbiome interactions. A few of Yezhang's approaches are detailed in his recent invited review (PMID: 34129999, Curr. Opin. Biotechnol.).

Some of Yezhang's strengths are tirelessness, fearlessness, a solid understanding of complexities surrounding genetic mapping, and the rapid leveraging of multi-omics to narrow mapping candidates for final proof in functional molecular studies. The research accomplishments described above partly speak to the drive, creativity and productivity of Dr. Yezhang Ding. Yezhang is among the most talented and effective molecular biologists I know and has a true passion for leveraging genetic variation, bioinformatics and chemistry to connect previously unknown genes and small molecules to key biological functions in the field. Yezhang has overcome many obstacles to get this far. Having obtained a Masters degree and enjoyable research position at Nanjing Agricultural University (China), Yezhang decided to take a harder path and push himself to learn English during a Plant Microbiology Ph.D. in the U.S. I worked on the University of Florida campus for 15 years and knew his PhD advisor Dr. Zhonglin Mou personally. Yezhang had an extremely productive time in the Mou lab as a Ph.D. student. Encouraged by his efforts, I offered Yezhang a postdoc position at UCSD. During this time, Yezhang has continually sought to improve and expand his research, writing, mentoring and public speaking skills. Yezhang has made admirable efforts in mentoring and guiding undergraduate student researchers such as my honors thesis student Evan Saldivar (now a Stanford PhD student with Dr. Sue Rhee) and visiting PhD student Mengxi Wu. Following Yezhang's leadership, Evan and Mengxi worked countless evenings and weekends driven by shared excitement and personal passion for research discovery. Simply stated, I could not be more pleased with the effort and commitment to mentorship that Yezhang has demonstrated these past few years. Yezhang seeks his own research program and has worked tirelessly his entire life to earn the opportunity to contribute to science. I believe Yezhang would take this same approach to teaching undergraduate classes and similarly inspire the best in others. Yezhang has driven a considerable portion of my UCSD research program and I don't think I could have located a harder working, more motivated or more effective scientist to work with. The vast number of responsibilities I asked Yezhang to take on have provided him with considerable training for the realities associated with being a professor. Yezhang's CV accurately reflects his ability not only to drive key collaborations and but also successfully lead and complete large-scale systematic discovery efforts. Please do not hesitate to contact me directly (work: 858-534-3946, home: 352-514-4718) if I can be of further assistance in speaking to the qualifications and qualities of Dr. Yezhang Ding that make him an outstanding candidate for your position that seeks new talent capable of efficiently elucidating plant metabolic pathways that impact key traits.

Sincerely, 