

## Curriculum Vitae

**Yezhang Ding Ph.D.**

Lawrence Berkley National Laboratory  
Berkley, CA 94720

E-mail: [yezhangding@lbl.gov](mailto:yezhangding@lbl.gov); Phone: (+1) 806-773-2108

### 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. Selinene 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