

# Huazhong Agricultural University and University of Nebraska-Lincoln

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## Cooperative Plant Science Initiative



## Jim Alfano

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In 2000, Alfano joined the Center for Plant Science Innovation and the Department of Plant Pathology at the University of Nebraska where he went through the academic ranks to full professor. He is a distinguished Bessey Professor and is the Director of the Undergraduate Program in Microbiology. He is an expert in bacterial pathogenesis and plant immunity especially in regards to the type III secretion system and the effectors it injects into plant cells.

### Representative Publications

Guo M, Kim P, Li G, Elowsky CG, Alfano JR. A Bacterial Effector Co-opts Calmodulin to Target the Plant Microtubule Network. *Cell Host Microbe*. 2016 Jan 13;19(1):67-78. doi: 10.1016/j.chom.2015.12.007.

Nicaise V, Joe A, Jeong BR, Korneli C, Boutrot F, Westedt I, Staiger D, Alfano JR, Zipfel C. *Pseudomonas* HopU1 modulates plant immune receptor levels by blocking the interaction of their mRNAs with GRP7. *EMBO J*. 2013 Mar 6;32(5):701-12. doi: 10.1038/emboj.2013.15.

Fu ZQ, Guo M, Jeong BR, Tian F, Elthon TE, Cerny RL, Staiger D, Alfano JR. A type III effector ADP-ribosylates RNA-binding proteins and quells plant immunity. *Nature*. 2007 May 17;447(7142):284-8.

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## Ed Cahoon

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The Cahoon lab conducts basic and applied research on plant lipid metabolism. The goals of our research are to enhance the nutritional and industrial value of crop plants and to probe the synthesis and function of bioactive lipids including sphingolipids, tocotrienols, and carotenoids for nutritional biofortification and improved agronomic performance of crops. We also develop and adapt synthetic biology tools, such as genome editing and multi-gene assembly and

delivery, for crop improvement. My lab focuses primarily on *Arabidopsis* for basic research and camelina, soybean, and maize for translational studies.

### Representative Publications

Kimberlin AN, Han G, Luttgeharm KD, Chen M, Cahoon RE, Stone JM, Markham JE, Dunn TM, Cahoon EB (2016) ORM expression alters sphingolipid homeostasis and differentially affects ceramide synthase activities. *Plant Physiology* 172: 889-900.

Kimberlin AN, Majumder S, Han G, Chen M, Cahoon RE, Stone JM, Dunn TM, Cahoon EB (2013) *Arabidopsis* 56 amino acid serine palmitoyltransferase-interacting proteins stimulate sphingolipid synthesis, are essential, and affect mycotoxin sensitivity. *Plant Cell* 25: 4627-4639.

Cahoon EB, Hall SE, Ripp KG, Ganzke TS, Hitz WD, Coughlan SJ (2003) Metabolic redesign of vitamin E biosynthesis in plants for tocotrienol production and increased antioxidant content. *Nature Biotechnology* 21: 1082-1087.

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## Tom Clemente

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Clemente serves as the Manager of the Plant Transformation Core Research Facility (PTCRF), with research emphasis on introducing value-added and various input traits into crop plants.

### Representative Publications

Park H, Weier S, Razvi F, Peña PA, Sims NA, Lowell J, Hungate C, Kissinger K, Key G, Fraser P, Napier JA, Cahoon EB, Clemente TE. Towards the development of a sustainable soya bean-based feedstock for aquaculture. *Plant Biotechnol J*. 2016 Aug 6. doi: 10.1111/pbi.12608. [Epub ahead of print]

Park H, Graef G, Xu Y, Tenopir P, Clemente TE. Stacking of a stearyl-ACP thioesterase with a dual-silenced palmitoyl-ACP thioesterase and  $\Delta 12$  fatty acid desaturase in transgenic soybean. *Plant Biotechnol J*. 2014 Oct;12(8):1035-43. doi: 10.1111/pbi.12209.

Cook DE, Lee TG, Guo X, Melito S, Wang K, Bayless AM, Wang J, Hughes TJ, Willis DK, Clemente TE, Diers BW, Jiang J, Hudson ME, Bent AF. Copy number variation of multiple genes at Rhg1 mediates nematode resistance in soybean. *Science*. 2012 Nov 30;338(6111):1206-9. doi: 10.1126/science.1228746.

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## Steve Harris

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The primary focus of research in the Harris lab is to understand the regulation of hyphal morphogenesis and secretion in filamentous fungi. Diverse approaches are used to identify and functionally characterize genetic pathways that control cytoskeletal organization and vesicle trafficking. This includes investigating the roles of sphingolipids in these processes. Results are used to facilitate the engineering of fungal fermentation strains with enhanced productivity. In addition, the lab also studies the stress biology of extremophile fungi, with particular emphasis on the roles of light and fungal-algal interactions.

### Representative Publications

Si H, Rittenour WR, Harris SD. Roles of *Aspergillus nidulans* Cdc42/Rho GTPase regulators in hyphal morphogenesis and development. *Mycologia*. 2016 May-Jun;108(3):543-55. doi: 10.3852/15-232.

Rittenour WR, Harris SD. Glycosylphosphatidylinositol-anchored proteins in *Fusarium graminearum*: inventory, variability, and virulence. *PLoS One*. 2013 Nov 29;8(11):e81603. doi: 10.1371/journal.pone.0081603.

Si H, Rittenour WR, Xu K, Nicksarlian M, Calvo AM, Harris SD. Morphogenetic and developmental functions of the *Aspergillus nidulans* homologues of the yeast bud site selection proteins Bud4 and Axl2. *Mol Microbiol*. 2012 Jul;85(2):252-70. doi: 10.1111/j.1365-2958.2012.08108.x.

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## David Holding

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David Holding's research focuses on using functional genomics approaches to study maize and sorghum seed development from both basic and applied perspectives. The main focus is on the relationship between endosperm maturation and protein quality which has involved various ways to study modifier genes of the high-lysine, opaque-2 mutant. The lab has developed a large population of maize deletion mutants and an innovative mapping and candidate gene identification pipeline for studying kernel development as well as poorly defined vegetative processes such as mineral uptake. Holding is also interested in improving protein quality and digestibility in sorghum and is using gene editing approaches to manipulate kafirin family proteins which will be directly usable without lengthy regulatory processes.

### Representative Publications

Jia, S., Li, A., Morton, K., Avoles-Kianian, P., Kianian, S.F., Zhang, C., and Holding, D.R. (2016) A Population of Deletion Mutants and an Integrated Mapping and Exome-seq Pipeline for Gene Discovery in Maize. *G3: Genes, Genomes and Genetics*. g3.116.030528; Early Online June 3, 2016.

Morton, K., Jia, S., Zhang, C., and Holding, D.R. (2015) Proteomic profiling of maize opaque endosperm mutants reveals selective accumulation of lysine-enriched proteins. *Journal of Experimental Botany*. doi: 10.1093/jxb/erv532.

Yuan, L., Dou, Y., Kianian, S., Zhang, C. and Holding, D.R. (2014) Deletion mutagenesis identifies a haploinsufficient role for gamma-zein in opaque-2 endosperm modification. *Plant Physiol*. 164: 119-130.

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## David Hyten, Jr.

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My lab is focused on taking basic genetic and genomic discoveries in soybean and translating those discoveries into applied methods that can be used for the real-world improvement of soybean varieties.

### Representative Publications

Schmutz, ... Hyten, D.L. (24 of 41 authors), and Jackson, S.A. 2014. A reference genome for common bean and genome-wide analysis of dual domestications. *Nature Genetics*. 46:707-713.

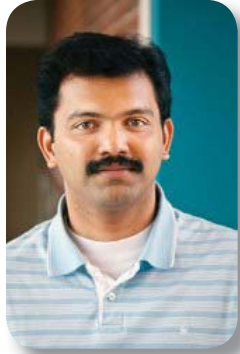
Bolon, Y.T., Hyten, D.L., Orf, J.H., Vance, C.P., and Muehlbauer, G.J. 2014. eQTL networks reveal complex genetic architecture in the immature soybean seed. *Plant Genome* 7:1.

Hwang, E.-Y., Song, Q., Jia, G., Specht, J.E., Hyten, D.L., Costa, J., Cregan, P.B. 2014. A genome-wide association study of seed protein and oil content in soybean. *BMC Genomics* 15:1.

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## Joe Louis

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Our research focuses on identifying the key components/genes/signaling mechanisms that are involved in modulating plant defenses upon insect herbivory and to understand the mechanisms by which insect salivary proteins/ effectors alter the plant defense responses. My teaching responsibilities include ENTO 409/809, “Insect Control by Host Plant Resistance” and ENTO 896, “Chemical Ecology of Insect-Plant Interactions”.

### Representative Publications

Varsani S, Basu S, Williams WP, Felton GW, Luthe DS and Louis J (2016). Intraplant communication in maize contributes to defense against insects. *Plant Signaling & Behavior*, 11: 8, e1212800.

Louis J, Basu S, Varsani S, Castano-Duque L, Jiang V, Williams WP, Felton GW and Luthe DS. (2015). Ethylene contributes to maize insect resistance1-mediated maize defense against the phloem-sap sucking corn leaf aphid. *Plant Physiology*, 169: 313-324.

Louis J, Peiffer M, Ray S, Luthe DS and Felton GW (2013). Host-specific salivary elicitor(s) of European Corn Borer (*Ostrinia nubilalis*) induce defenses in tomato and maize. *New Phytologist*, 199: 63-73.

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## Jeffrey Mower

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My lab is interested in the evolution of the mitochondrial and plastid genomes of vascular plants. Our research evaluates the evolutionary causes and organismal consequences of the genomic diversity in plant mitochondria and plastids. From a functional perspective, we are interested in generating novel types of cytoplasmic male sterility in crop plants such as crucifers to promote hybrid vigor.

### Representative Publications

Guo W, Grewe F, Fan W, Young GJ, Knoop V, Palmer JD, Mower JP. 2016. Ginkgo and Welwitschia mitogenomes reveal extreme contrasts in gymnosperm mitochondrial evolution. *Mol Biol Evol* 33:1448–1460.

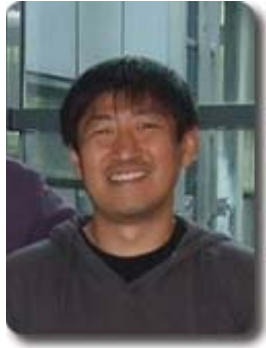
Zhu A, Guo W, Gupta S, Fan W, Mower JP. 2016. Evolutionary dynamics of the plastid inverted repeat: the effects of expansion, contraction, and loss on substitution rates. *New Phytol* 209:1747–1756.

Grewe F, Edger PP, Keren I, Sultan L, Pires JC, Ostersetzer-Biran O, Mower JP. 2014. Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of *Brassica oleracea*. *Mitochondrion* 19, 135–143.

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## Toshihiro Obata

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My research is focused on the regulation of plant primary metabolism in response to environmental inputs including abiotic stresses. Gas chromatography-mass spectrometry (GC-MS) based metabolomics and metabolic flux analyses are employed for dissecting the metabolic phenotypes. I am also interested in molecular mechanisms regulating a metabolic network with special focus on the functions of dynamic enzyme-enzyme interactions.

### Representative Publications

Obata T, Witt S, Lisek J, Palacios-Rojas N, Florez-Sarasa I, Yousfi S, Araus JL, Cairns JE, Fernie AR (2015) Metabolite profiles of maize leaves in drought, heat and combined stress field trials reveal the relationship between metabolism and grain yield. *Plant Physiol.* 169: 2665-2683.

Daloso DM, Müller K, Obata T, Florian A, Tohge T, Bottcher A, Riondet C, Bariat L, Carrari F, Nunes-Nesi A, Buchanan BB, Reichheld J-P, Araújo WL, Fernie AR (2015) Thioredoxin, a master regulator of the tricarboxylic acid cycle in plant mitochondria. *Proc. Natl. Acad. Sci.* 112: E1392-E1400.

Obata T, Fernie AR (2012) The use of metabolomics to dissect plant responses to abiotic stresses. *Cell Mol. Life Sci.* 69: 3225-3243.

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## Rebecca Roston

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Dr. Roston is studying the strategies some plant membranes use to avoid freezing damage during winter and unseasonal frosts, with the ultimate goal of engineering crop resistance to freezing. My lab also studies the formation and maintenance of the photosynthetic membranes in order to understand this process which is also essential to future plant engineering efforts.

### Representative Publications

Kelly AA, Kalisch B, Hölzl G, Schulze S, Thiele J, Melzer M, Roston RL, Benning C, Dörmann P. Synthesis and transfer of galactolipids in the chloroplast envelope membranes of *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 2016 Sep 20;113(38):10714-9. doi: 10.1073/pnas.1609184113.

Barnes AC, Benning C, Roston RL. Chloroplast Membrane Remodeling during Freezing Stress Is Accompanied by Cytoplasmic Acidification Activating SENSITIVE TO FREEZING2. *Plant Physiol.* 2016 Jul;171(3):2140-9. doi: 10.1104/pp.16.00286.

Roston RL, Wang K, Kuhn LA, Benning C. Structural determinants allowing transferase activity in SENSITIVE TO FREEZING 2, classified as a family I glycosyl hydrolase. *J Biol Chem.* 2014 Sep 19;289(38):26089-106. doi: 10.1074/jbc.M114.576694.

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## Daniel Schachtman

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The Schachtman lab is studying root growth and interactions with soil microbes. Currently we are working on understanding the key microbes that associate with plant roots. Who they are, what they do and how root exudates alter the microbes that thrive in the rhizosphere and endosphere. We have also been culturing microbes from agricultural fields of soy, corn and sorghum in addition to grasses from native grasslands to use for hypothesis testing.

In future we aim to extend the work to root phenotyping and the identification of genes that are responsible for heritable root traits. This research is new to my lab and we do not have recent publications on this topic. Older publications on related topics include work on mycorrhiza and nematodes.

### Representative Publications

Meister, R, Rajani, MS, Ruzicka, D., Schachtman, DP (2014) Challenges of modifying root traits in crops for agriculture. *Trends in Plant Science* 19: 779-788.

Larkan, N.J., Ruzicka, D.R., Edmonds-Tibbett, T., Durkin, J.M., Jackson, L.E., Smith, F.A., Schachtman, D.P., Smith, S.E, Barker, S.J. (2013) The reduced mycorrhizal colonisation (rmc) mutation of tomato disrupts five gene sequences including the CYCLOPS/IPD3 homologue. *Mycorrhiza* 7:573-584.

Marella, H, Nielsen, E, Schachtman, DP and Taylor C (2013) The amino acid permeases, AAP3 and AAP6, are involved in root-knot nematode parasitism of Arabidopsis. *Mol. Plant Microbe Interactions* 24:44 – 54.

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## James Schnable

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The Schnable lab focuses on understanding the link between genotype and phenotype using comparisons across groups of related species. To achieve this goal, we develop new computer vision based approaches for high throughput phenotyping, new methods to analyze multi-species RNA-seq experiments, and quantitative genetic methods to conduct integrated genome wide association studies using data from diversity panels of related species. These projects require diverse sets of expertise and

postdocs and graduate students in the Schnable lab work in close collaborations with computer scientists, engineers, and statisticians. Our current projects focus primarily on corn (maize), sorghum, and foxtail millet, as well as related wild grass species.

### Representative Publications

Walley JW, Sartor RC, Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, Schnable JC, Ecker JR, Briggs SP. (2016) “Integration of omic networks in a developmental atlas of maize.” *Science* doi: 10.1126/science.aag1125

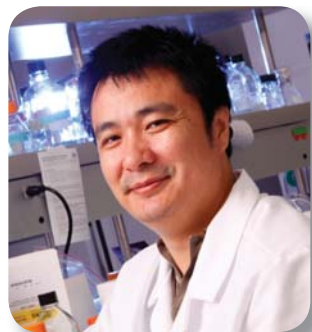
Ge Y, Bai G, Stoerger V, Schnable JC. (2016) “Temporal dynamics of maize plant growth, water use, and plant water content using automated high throughput RGB and hyperspectral imaging.” *Computers and Electronics in Agriculture* doi: 10.1016/j.compag.2016.07.028

Schnable JC, Springer NM, Freeling M. (2011) “Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss.” *PNAS* doi: 10.1073/pnas.1101368108

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## Bin Yu

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Our interest is to understand the mechanisms underlying the metabolism and function of non-coding RNAs that function as regulators of gene expression. We currently employ a combination of genetic, biochemical, cell biological, and genomic approaches to identify and characterize components involved in non-coding RNA metabolism and activity.

### Representative Publications

Liu, Y., Li, S., Chen, Y., Kimberlin, A.N., Cahoon, E.B. and Yu, B. (2016) snRNA 3' End Processing by a CPSF73-Containing Complex Essential for Development in Arabidopsis. *PLoS Biol*, 14, e1002571.

Ren, G., Xie, M., Zhang, S., Vinovskis, C., Chen, X. and Yu, B. (2014) Methylation protects microRNAs from an AGO1-associated activity that uridylyates 5' RNA fragments generated by AGO1 cleavage. *Proceedings of the National Academy of Sciences of the United States of America*, 111, 6365-6370.

Zhang, S., Xie, M., Ren, G. and Yu, B. (2013) CDC5, a DNA binding protein, positively regulates posttranscriptional processing and/or transcription of primary microRNA transcripts. *Proceedings of the National Academy of Sciences of the United States of America*, 110, 17588-17593.

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## Lirong Zeng

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My research focuses on the identification and characterization of genes and signal transduction pathways involved in plant immunity against microbial pathogens, particularly the roles and molecular mechanism by which the ubiquitination system regulates host defense responses in plants. Given that plant immunity is inextricably connected to plant development and environmental factors, my research also involves understanding the signaling crosstalk that orchestrates plant responses to different intrinsic and extrinsic signals. The long-term goal of our research is to elucidate and eventually manipulate for crop improvement the key molecular mechanisms that plants use to defend themselves against different biotic and abiotic stresses. To this end, a combination of cellular, molecular, biochemical, genetic, genomic and proteomic approaches will be employed to address relevant questions.

### Representative Publications

Mural R.V.\*, Liu Y.\*, Rosebrock T.R., Brady J.J., Hamera S., Connor R.A., Martin G.B., and Zeng, L. (2013). The Tomato Fni3 Lys63-Specific Ubiquitin-Conjugating Enzyme and Suv Ubiquitin E2 Variant Positively Regulate Plant Immunity. *Plant Cell*. 25: 3615-3631 (\*equal contribution).

Li W., Ahn I.-P., Ning Y., Park C.-H., Zeng L., Whitehill J.G.A., Lu H., Zhao Q., Ding B., Xie Q., Zhou J.-M., Dai L., and Wang G.-L. (2012). The U-Box/ARM E3 ligase PUB13 regulates cell death, defense, and flowering time in Arabidopsis. *Plant Physiol*. 159: 239-250.

Zeng L., Velásquez A.C., Munkvold K.R., Zhang J. and Martin G.B. (2011). A tomato LysM receptor-like kinase promotes immunity and its kinase activity is inhibited by AvrPtoB. *Plant J*. 69: 92-103.

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# Chi Zhang

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My research mainly focuses on Bioinformatics and Computational Systems Biology, with broad interests covering areas such as NGS high-throughput data analysis, omic-data integration, non-coding RNAs, protein structure and function prediction, and pathogen-host interactions, etc.

## Representative Publications

S. Jia, A. Li, K. Morton, P. Avoles-Kianian, S.F F. Kianian, Chi Zhang, D. Holding. A Population of Deletion Mutants and an Integrated Mapping and Exome-seq Pipeline for Gene Discovery in Maize. *G3* (2016); g3.116.030528; doi:10.1534/g3.116.030528.

Z. Wang, J.A. Casas-Mollano, J. Xu, J. M. Riethoven, Chi Zhang, H. Cerutti. Osmotic stress induces phosphorylation of histone H3 at threonine 3 in pericentromeric regions of *Arabidopsis thaliana*. *Proc Natl Acad Sci USA* (2015); 112 (27), 8487-8492.

Y. Dou, X. Guo, L. Yuan, D. Holding, Chi Zhang. Differential expression analysis in RNA-Seq by machine learning algorithm with local normalization. *BioMed Research International* (2015) Special Issue: Systems Biology Approaches to Mining High Throughput Biological Data.

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