

Project No. and Title: NCCC307 Biochemistry and Genetics of Plant-Fungal Interactions

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Appendix: Publications

Alvarez-Escribano, I., Sasse, C., Bok, J. W., Na, H., Amirebrahimi, M., Lipzen, A., Schackwitz, W., Martin, J., Barry, K., Gutierrez, G., Cea-Sanchez, S., Marcos, A. T., Grigoriev, I. V., Keller, N. P., Braus, G. H., Canovas, D., 2019. Genome sequencing of evolved aspergilli populations reveals robust genomes, transversions in *A. flavus*, and sexual aberrancy in non-homologous end-joining mutants. *BMC Biol.* 17, 88.

Armaleo, D., Muller, O., Lutzoni, F., Andresson, O. S., Blanc, G., Bode, H. B., Collart, F. R., Dal Grande, F., Dietrich, F., Grigoriev, I. V., Joneson, S., Kuo, A., Larsen, P. E., Logsdon, J. M., Jr., Lopez, D., Martin, F., May, S. P., McDonald, T. R., Merchant, S. S., Miao, V., Morin, E., Oono, R., Pellegrini, M., Rubinstein, N., Sanchez-Puerta, M. V., Savelkoul, E., Schmitt, I., Slot, J. C., Soanes, D., Szovenyi, P., Talbot, N. J., Veneault-Fourrey, C., Xavier, B. B., 2019. The lichen symbiosis re-viewed through the genomes of *Cladonia grayi* and its algal partner *Asterochloris glomerata*. *BMC Genomics.* 20, 605.

Baccile, J. A., Le, H. H., Pfannenstiel, B. T., Bok, J. W., Gomez, C., Brandenburger, E., Hoffmeister, D., Keller, N. P., Schroeder, F. C., 2019. Diketopiperazine formation in fungi requires dedicated cyclization and thiolation domains. *Angew Chem Int Ed Engl.* 58, 14589-14593.

Boyce, G. R., Gluck-Thaler, E., Slot, J. C., Stajich, J. E., Davis, W. J., James, T. Y., Cooley, J. R., Panaccione, D. G., Eilenberg, J., De Fine Licht, H. H., Macias, A. M., Berger, M. C., Wickert, K. L., Stauder, C. M., Spahr, E. J., Maust, M. D., Metheny, A. M., Simon, C., Kritsky, G., Hodge, K. T., Humber, R. A., Gullion, T., Short, D. P. G., Kijimoto, T., Mozgai, D., Arguedas, N., Kasson, M. T., 2019. Psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens. *Fungal Ecol.* 41, 147-164.

- Brown, D. W., Villani, A., Susca, A., Moretti, A., Hao, G., Kim, H. S., Proctor, R. H., McCormick, S. P., 2020. Gain and loss of a transcription factor that regulates late trichothecene biosynthetic pathway genes in *Fusarium*. *Fungal Genet Biol.* 136, 103317.
- Caesar, L. K., Kelleher, N. L., Keller, N. P., 2020a. In the fungus where it happens: History and future propelling *Aspergillus nidulans* as the archetype of natural products research. *Fungal Genet Biol.* 144, 103477.
- Caesar, L. K., Robey, M. T., Swyers, M., Islam, M. N., Ye, R., Vagadia, P. P., Schiltz, G. E., Thomas, P. M., Wu, C. C., Kelleher, N. L., Keller, N. P., Bok, J. W., 2020b. Heterologous expression of the unusual terreazepine biosynthetic gene cluster reveals a promising approach for identifying new chemical scaffolds. *mBio.* 11.
- Chen, Y., Kistler, H. C., Ma, Z., 2019. *Fusarium graminearum* trichothecene mycotoxins: biosynthesis, regulation, and management. *Annu Rev Phytopathol.* 57, 15-39.
- Clare, S. J., Wyatt, N. A., Brueggeman, R. S., Friesen, T. L., 2020. Research advances in the *Pyrenophora teres*-barley interaction. *Mol Plant Pathol.* 21, 272-288.
- Drott, M. T., Satterlee, T. R., Skerker, J. M., Pfannenstiel, B. T., Glass, N. L., Keller, N. P., Milgroom, M. G., 2020. The Frequency of Sex: population genomics reveals differences in recombination and population structure of the aflatoxin-producing fungus *Aspergillus flavus*. *mBio.* 11.
- Essarioui, A., LeBlanc, N., Otto-Hanson, L., Schlatter, D. C., Kistler, H. C., Kinkel, L. L., 2020. Inhibitory and nutrient use phenotypes among coexisting *Fusarium* and *Streptomyces* populations suggest local coevolutionary interactions in soil. *Environ Microbiol.* 22, 976-985.
- Farinas, C., Gluck-Thaler, E., Slot, J. C., Peduto Hand, F., 2019. Whole-genome sequence of the *Phlox* powdery mildew pathogen *Golovinomyces magnicellulatus* strain FPH2017-1. *Microbiol Resour Announc.* 8.
- Farinas, C., Jourdan, P. S., Paul, P. A., Slot, J. C., Daughtrey, M. L., Ganeshan, V. D., Baysal-Gurel, F., Hand, F. P., 2020. *Phlox* species show quantitative and qualitative resistance to a population of powdery mildew isolates from the eastern United States. *Phytopathology.* 110, 1410-1418.

- Faris, J. D., Friesen, T. L., 2020. Plant genes hijacked by necrotrophic fungal pathogens. *Curr Opin Plant Biol.* 56, 74-80.
- Faris, J. D., Overlander, M. E., Kariyawasam, G. K., Carter, A., Xu, S. S., Liu, Z., 2020. Identification of a major dominant gene for race-nonspecific tan spot resistance in wild emmer wheat. *Theor Appl Genet.* 133, 829-841.
- Frawley, D., Greco, C., Oakley, B., Alhussain, M. M., Fleming, A. B., Keller, N. P., Bayram, O., 2020. The tetrameric pheromone module SteC-MkkB-MpkB-SteD regulates asexual sporulation, sclerotia formation and aflatoxin production in *Aspergillus flavus*. *Cell Microbiol.* 22, e13192.
- Galagedara, N., Liu, Y., Fiedler, J., Shi, G., Chiao, S., Xu, S. S., Faris, J. D., Li, X., Liu, Z., 2020. Genome-wide association mapping of tan spot resistance in a worldwide collection of durum wheat. *Theor Appl Genet.* 133, 2227-2237.
- Gluck-Thaler, E., Haridas, S., Binder, M., Grigoriev, I. V., Crous, P. W., Spatafora, J. W., Bushley, K., Slot, J. C., 2020. The architecture of metabolism maximizes biosynthetic diversity in the largest class of fungi. *Mol Biol Evol.* 37, 2838-2856.
- Greco, C., Keller, N. P., Rokas, A., 2019a. Unearthing fungal chemodiversity and prospects for drug discovery. *Curr Opin Microbiol.* 51, 22-29.
- Greco, C., Pfannenstiel, B. T., Liu, J. C., Keller, N. P., 2019b. Depsipeptide aspergillins revealed by chromatin reader protein deletion. *Chem. Biol.* 14, 1121-1128.
- Guo, J., Shi, G., Kalil, A., Friskop, A., Elias, E., Xu, S. S., Faris, J. D., Liu, Z., 2020. *Pyrenophora tritici-repentis* Race 4 isolates cause disease on tetraploid wheat. *Phytopathology.* PHYTO05200179R.
- Hafez, M., Gourlie, R., Despins, T., Turkington, K., Friesen, T. L., Aboukhaddour, R., 2020. *Parastagonospora nodorum* and related species in western Canada: genetic variability and effector genes. *Phytopathology.*
- Jiang, C., Cao, S., Wang, Z., Xu, H., Liang, J., Liu, H., Wang, G., Ding, M., Wang, Q., Gong, C., Feng, C., Hao, C., Xu, J. R., 2019. An expanded subfamily of G-protein-coupled receptor

- genes in *Fusarium graminearum* required for wheat infection. *Nat Microbiol.* 4, 1582-1591.
- Jiang, C., Hei, R., Yang, Y., Zhang, S., Wang, Q., Wang, W., Zhang, Q., Yan, M., Zhu, G., Huang, P., Liu, H., Xu, J. R., 2020. An orphan protein of *Fusarium graminearum* modulates host immunity by mediating proteasomal degradation of TaSnRK1alpha. *Nat Commun.* 11, 4382.
- Jurick, W. M., Peng, H., Beard, H. S., Garrett, W. M., Lichtner, F. J., Luciano-Rosario, D., Macarisin, O., Liu, Y., Peter, K. A., Gaskins, V. L., Yang, T., Mowery, J., Bauchan, G., Keller, N. P., Cooper, B., 2020. Blistering1 nodulates *Penicillium expansum* virulence via vesicle-mediated protein secretion. *Mol Cell Proteomics.* 19, 344-361.
- Kim, H. S., Lohmar, J. M., Busman, M., Brown, D. W., Naumann, T. A., Divon, H. H., Uhlig, S., Proctor, R. H., 2020. Identification and distribution of gene clusters required for synthesis of sphingolipid metabolism inhibitors in diverse species of the filamentous fungus *Fusarium*. *BMC Genomics.* 21, 510.
- Kim, W., Cavinder, B., Proctor, R. H., O'Donnell, K., Townsend, J. P., Trail, F., 2019. Comparative Genomics and Transcriptomics During Sexual Development Gives Insight Into the Life History of the Cosmopolitan Fungus *Fusarium neocosmosporiellum*. *Front Microbiol.* 10, 1247.
- Lai, X., Qi, A., Liu, Y., Mendoza, L., Liu, Z., Lin, Z., Khan, M. F. R., 2020. Evaluating Inoculation Methods to Infect Sugar Beet with *Fusarium oxysporum f. betae* and *F. secorum*. *Plant Dis.* 104, 1312-1317.
- Lan, H., Wu, L., Sun, R., Keller, N. P., Yang, K., Ye, L., He, S., Zhang, F., Wang, S., 2019. The HosA Histone Deacetylase Regulates Aflatoxin Biosynthesis Through Direct Regulation of Aflatoxin Cluster Genes. *Mol Plant Microbe Interact.* 32, 1210-1228.
- Li, G., Qi, X., Sun, G., Rocha, R. O., Segal, L. M., Downey, K. S., Wright, J. D., Wilson, R. A., 2020. Terminating rice innate immunity induction requires a network of antagonistic and redox-responsive E3 ubiquitin ligases targeting a fungal sirtuin. *New Phytol.* 226, 523-540.

- Li, X., Fan, Z., Yan, M., Qu, J., Xu, J. R., Jin, Q., 2019. Spontaneous mutations in FgSAD1 suppress the growth defect of the Fgprp4 mutant by affecting tri-snRNP stability and its docking in *Fusarium graminearum*. *Environ Microbiol.* 21, 4488-4503.
- Liang, X., Cao, M., Li, S., Kong, Y., Rollins, J. A., Zhang, R., Sun, G., 2020. Highly Contiguous Genome Resource of *Colletotrichum fructicola* Generated Using Long-Read Sequencing. *Mol Plant Microbe Interact.* 33, 790-793.
- Liu, X., Jiang, Y., He, D., Fang, X., Xu, J., Lee, Y. W., Keller, N. P., Shi, J., 2020a. Copper Tolerance Mediated by FgAceA and FgCrpA in *Fusarium graminearum*. *Front Microbiol.* 11, 1392.
- Liu, Y., Salsman, E., Wang, R., Galagedara, N., Zhang, Q., Fiedler, J. D., Liu, Z., Xu, S., Faris, J. D., Li, X., 2020b. Meta-QTL analysis of tan spot resistance in wheat. *Theor Appl Genet.* 133, 2363-2375.
- Liu, Y., Zhang, Q., Salsman, E., Fiedler, J. D., Hegstad, J. B., Liu, Z., Faris, J. D., Xu, S. S., Li, X., 2020c. QTL mapping of resistance to tan spot induced by race 2 of *Pyrenophora tritici-repentis* in tetraploid wheat. *Theor Appl Genet.* 133, 433-442.
- Liu, Z., Jian, Y., Chen, Y., Kistler, H. C., He, P., Ma, Z., Yin, Y., 2019. A phosphorylated transcription factor regulates sterol biosynthesis in *Fusarium graminearum*. *Nat Commun.* 10, 1228.
- Longley, R., Noel, Z. A., Benucci, G. M. N., Chilvers, M. I., Trail, F., Bonito, G., 2020. Crop Management Impacts the Soybean (*Glycine max*) Microbiome. *Front Microbiol.* 11, 1116.
- Luciano-Rosario, D., Keller, N. P., Jurick, W. M., 2020. *Penicillium expansum*: biology, omics, and management tools for a global postharvest pathogen causing blue mould of pome fruit. *Mol Plant Pathol.* 21, 1391-1404.
- Lyu, H. N., Liu, H. W., Keller, N. P., Yin, W. B., 2020. Harnessing diverse transcriptional regulators for natural product discovery in fungi. *Nat Prod Rep.* 37, 6-16.
- Ma, L. J., Xu, J. R., 2019. Shuffling effector genes through mini-chromosomes. *PLoS Genet.* 15, e1008345.

- Mcculloch, M., Nuckles, E. M., Vaillancourt, L. J., Ward-Gauthier, N. A., 2020a. Use of telomere fingerprinting to identify *Colletotrichum fioriniae* clones and application to cross-infection studies in Kentucky mixed-fruit orchards. 110. 7.
- McCulloch, M. J., Edwards, S., Inocencio, H., Machado, F., Nuckles, E., Farman, M., Ward Gauthier, N. A., Vaillancourt, L., 2020b. Diversity and cross-infection potential of *Colletotrichum* causing fruit rots in mixed-fruit orchards in Kentucky. Plant Dis.
- McCulloch, M. J., Gauthier, N. W., Vaillancourt, L. J., 2020c. First Report of Bitter Rot of Apple Caused by a *Colletotrichum* sp. in the *C. kahawae* Clade in Kentucky. Plant Dis. 104.
- McDonald, M. C., Taranto, A. P., Hill, E., Schwessinger, B., Liu, Z., Simpfendorfer, S., Milgate, A., Solomon, P. S., 2019. Transposon-Mediated Horizontal Transfer of the Host-Specific Virulence Protein ToxA between Three Fungal Wheat Pathogens. mBio. 10.
- Niu, M., Keller, N. P., 2019. Co-opting oxylipin signals in microbial disease. Cell Microbiol. 21, e13025.
- O'Mara, S. P., Broz, K., Boenisch, M., Zhong, Z., Dong, Y., Kistler, H. C., 2020. The *Fusarium graminearum* t-SNARE Sso2 Is Involved in Growth, Defense, and DON Accumulation and Virulence. Mol Plant Microbe Interact. 33, 888-901.
- Peng, Z., Hu, Y., Zhang, J., Huguet-Tapia, J. C., Block, A. K., Park, S., Sapkota, S., Liu, Z., Liu, S., White, F. F., 2019. *Xanthomonas translucens* commandeers the host rate-limiting step in ABA biosynthesis for disease susceptibility. Proc Natl Acad Sci U S A. 116, 20938-20946.
- Peters Haugrud, A. R., Zhang, Z., Richards, J. K., Friesen, T. L., Faris, J. D., 2019. Genetics of Variable Disease Expression Conferred by Inverse Gene-For-Gene Interactions in the Wheat-*Parastagonospora nodorum* Pathosystem. Plant Physiol. 180, 420-434.
- Raffa, N., Keller, N. P., 2019. A call to arms: Mustering secondary metabolites for success and survival of an opportunistic pathogen. PLoS Pathog. 15, e1007606.

- Raffa, N., Osherov, N., Keller, N. P., 2019. Copper Utilization, Regulation, and Acquisition by *Aspergillus fumigatus*. *Int J Mol Sci.* 20.
- Ren, J., Li, C., Gao, C., Xu, J. R., Jiang, C., Wang, G., 2019. Deletion of FgHOG1 Is Suppressive to the mgv1 Mutant by Stimulating Gpmk1 Activation and Avoiding Intracellular Turgor Elevation in *Fusarium graminearum*. *Front Microbiol.* 10, 1073.
- Rhoades, N. A., Harvey, A. M., Samarajeewa, D. A., Svedberg, J., Yusifov, A., Abusharekh, A., Manitchotpisit, P., Brown, D. W., Sharp, K. J., Rehard, D. G., Peters, J., Ostolaza-Maldonado, X., Stephenson, J., Shiu, P. K. T., Johannesson, H., Hammond, T. M., 2019. Identification of rfk-1, a Meiotic Driver Undergoing RNA Editing in *Neurospora*. *Genetics.* 212, 93-110.
- Richards, J. K., Stukenbrock, E. H., Carpenter, J., Liu, Z., Cowger, C., Faris, J. D., Friesen, T. L., 2019. Local adaptation drives the diversification of effectors in the fungal wheat pathogen *Parastagonospora nodorum* in the United States. *PLoS Genet.* 15, e1008223.
- Rocha, R. O., Elowsky, C., Pham, N. T. T., Wilson, R. A., 2020. Spermine-mediated tight sealing of the *Magnaporthe oryzae* appressorial pore-rice leaf surface interface. *Nat Microbiol.*
- Rocha, R. O., Wilson, R. A., 2020. *Magnaporthe oryzae* nucleoside diphosphate kinase is required for metabolic homeostasis and redox-mediated host innate immunity suppression. *Mol Microbiol.*
- Roossinck, M. J., 2019. Viruses in the phytobiome. *Curr Opin Virol.* 37, 72-76.
- Rush, T. A., Puech-Pages, V., Bascaules, A., Jargeat, P., Maillet, F., Haouy, A., Maes, A. Q., Carriel, C. C., Khokhani, D., Keller-Pearson, M., Tannous, J., Cope, K. R., Garcia, K., Maeda, J., Johnson, C., Kleven, B., Choudhury, Q. J., Labbe, J., Swift, C., O'Malley, M. A., Bok, J. W., Cottaz, S., Fort, S., Poinot, V., Sussman, M. R., Lefort, C., Nett, J., Keller, N. P., Becard, G., Ane, J. M., 2020. Lipo-chitooligosaccharides as regulatory signals of fungal growth and development. *Nat Commun.* 11, 3897.
- Safari, M., Ferrari, M. J., Roossinck, M. J., 2019. Manipulation of Aphid Behavior by a Persistent Plant Virus. *J Virol.* 93.

- Schoen, T. J., Rosowski, E. E., Knox, B. P., Bennin, D., Keller, N. P., Huttenlocher, A., 2019. Neutrophil phagocyte oxidase activity controls invasive fungal growth and inflammation in zebrafish. *J Cell Sci.* 133.
- Sharma, J. S., Zhang, Q., Rouse, M. N., Klindworth, D. L., Friesen, T. L., Long, Y., Olivera, P. D., Jin, Y., McClean, P. E., Xu, S. S., Faris, J. D., 2019. Mapping and characterization of two stem rust resistance genes derived from cultivated emmer wheat accession PI 193883. *Theor Appl Genet.* 132, 3177-3189.
- Slot, J. C., Gluck-Thaler, E., 2019. Metabolic gene clusters, fungal diversity, and the generation of accessory functions. *Curr Opin Genet Dev.* 58-59, 17-24.
- Staples, R., LaDuca, R. L., Roze, L. V., Laivenieks, M., Linz, J. E., Beaudry, R., Fryday, A., Schillmiller, A. L., Koptina, A. V., Smith, B., Trail, F., 2020. Structure and Chemical Analysis of Major Specialized Metabolites Produced by the Lichen *Evernia prunastri*. *Chem Biodivers.* 17, e1900465.
- Sun, G., Qi, X., Wilson, R. A., 2019. A Feed-Forward Subnetwork Emerging from Integrated TOR- and cAMP/PKA-Signaling Architecture Reinforces *Magnaporthe oryzae* Appressorium Morphogenesis. *Mol Plant Microbe Interact.* 32, 593-607.
- Tamang, P., Richards, J. K., Alhashal, A., Sharma Poudel, R., Horsley, R. D., Friesen, T. L., Brueggeman, R. S., 2019. Mapping of barley susceptibility/resistance QTL against spot form net blotch caused by *Pyrenophora teres f. maculata* using RIL populations. *Theor Appl Genet.* 132, 1953-1963.
- Tannous, J., Barda, O., Luciano-Rosario, D., Prusky, D. B., Sionov, E., Keller, N. P., 2020. New Insight Into Pathogenicity and Secondary Metabolism of the Plant Pathogen *Penicillium expansum* Through Deletion of the Epigenetic Reader SntB. *Front Microbiol.* 11, 610.
- Thapa, V., Roossinck, M. J., 2019. Determinants of Coinfection in the Mycoviruses. *Front Cell Infect Microbiol.* 9, 169.
- Venkatesh, N., Keller, N. P., 2019. Mycotoxins in Conversation With Bacteria and Fungi. *Front Microbiol.* 10, 403.

- Villani, A., Proctor, R. H., Kim, H. S., Brown, D. W., Logrieco, A. F., Amatulli, M. T., Moretti, A., Susca, A., 2019. Variation in secondary metabolite production potential in the *Fusarium incarnatum-equiseti* species complex revealed by comparative analysis of 13 genomes. *BMC Genomics*. 20, 314.
- Wang, B., Yu, H., Jia, Y., Dong, Q., Steinberg, C., Alabouvette, C., Edel-Hermann, V., Kistler, H. C., Ye, K., Ma, L. J., Guo, L., 2020a. Chromosome-Scale Genome Assembly of *Fusarium oxysporum* Strain Fo47, a Fungal Endophyte and Biocontrol Agent. *Mol Plant Microbe Interact*. 33, 1108-1111.
- Wang, H., Chen, D., Li, C., Tian, N., Zhang, J., Xu, J. R., Wang, C., 2019a. Stage-specific functional relationships between Tub1 and Tub2 beta-tubulins in the wheat scab fungus *Fusarium graminearum*. *Fungal Genet Biol*. 132, 103251.
- Wang, Q., Sun, M., Zhang, Y., Song, Z., Zhang, S., Zhang, Q., Xu, J. R., Liu, H., 2020b. Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. *Mol Plant Pathol*. 21, 330-348.
- Wang, Y., Wei, X., Bian, Z., Wei, J., Xu, J. R., 2020c. Coregulation of dimorphism and symbiosis by cyclic AMP signaling in the lichenized fungus *Umbilicaria muhlenbergii*. *Proc Natl Acad Sci U S A*. 117, 23847-23858.
- Wang, Y. W., Hess, J., Slot, J. C., Pringle, A., 2020d. De novo gene birth, horizontal gene transfer and gene duplication as sources of new gene families associated with the origin of symbiosis in *Amanita*. *Genome Biol Evol*.
- Wang, Z., Lopez-Giraldez, F., Wang, J., Trail, F., Townsend, J. P., 2019b. Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of *Chaetomium globosum*. *mBio*. 10.
- Wang, Z., Ma, T., Huang, Y., Wang, J., Chen, Y., Kistler, H. C., Ma, Z., Yin, Y., 2019c. A fungal ABC transporter FgAtm1 regulates iron homeostasis via the transcription factor cascade FgAreA-HapX. *PLoS Pathog*. 15, e1007791.
- Wang, Z., Miguel-Rojas, C., Lopez-Giraldez, F., Yarden, O., Trail, F., Townsend, J. P., 2019d. Metabolism and Development during Conidial Germination in Response to a

Carbon-Nitrogen-Rich Synthetic or a Natural Source of Nutrition in *Neurospora crassa*. mBio. 10.

- Wilson, R. A., Fernandez, J., Rocha, R. O., Marroquin-Guzman, M., Wright, J. D., 2019. Genetic evidence for *Magnaporthe oryzae* vitamin B3 acquisition from rice cells. Microbiolog. 165, 1198-1202.
- Wolff, P. B., Nielsen, M. L., Slot, J. C., Andersen, L. N., Petersen, L. M., Isbrandt, T., Holm, D. K., Mortensen, U. H., Nodvig, C. S., Larsen, T. O., Hoof, J. B., 2020. Acurin A, a novel hybrid compound, biosynthesized by individually translated PKS- and NRPS-encoding genes in *Aspergillus aculeatus*. Fungal Genet Biol. 139, 103378.
- Wyatt, N. A., Richards, J. K., Brueggeman, R. S., Friesen, T. L., 2020. A Comparative Genomic Analysis of the Barley Pathogen *Pyrenophora teres f. teres* Identifies Subtelomeric Regions as Drivers of Virulence. Mol Plant Microbe Interact. 33, 173-188.
- Yin, J., Hao, C., Niu, G., Wang, W., Wang, G., Xiang, P., Xu, J. R., Zhang, X., 2020. FgPal1 regulates morphogenesis and pathogenesis in *Fusarium graminearum*. Environ Microbiol.
- Zhang, W., Zhu, X., Zhang, M., Shi, G., Liu, Z., Cai, X., 2019. Chromosome engineering-mediated introgression and molecular mapping of novel *Aegilops speltoides*-derived resistance genes for tan spot and *Septoria nodorum* blotch diseases in wheat. Theor Appl Genet. 132, 2605-2614.
- Zhang, Y., Dai, Y., Huang, Y., Wang, K., Lu, P., Xu, H., Xu, J. R., Liu, H., 2020a. The SR-protein FgSrp2 regulates vegetative growth, sexual reproduction and pre-mRNA processing by interacting with FgSrp1 in *Fusarium graminearum*. Curr Genet. 66, 607-619.
- Zhang, Y., Yang, H., Turra, D., Zhou, S., Ayhan, D. H., DeIulio, G. A., Guo, L., Broz, K., Wiederhold, N., Coleman, J. J., Donnell, K. O., Youngster, I., McAdam, A. J., Savinov, S., Shea, T., Young, S., Zeng, Q., Rep, M., Pearlman, E., Schwartz, D. C., Di Pietro, A., Kistler, H. C., Ma, L. J., 2020b. The genome of opportunistic fungal pathogen *Fusarium oxysporum* carries a unique set of lineage-specific chromosomes. Commun Biol. 3, 50.

Zhang, Y., Zhang, J., Vanderpool, D., Smith, J. A., Rollins, J. A., 2020c. Genomic and transcriptomic insights into *Raffaelea lauricola* pathogenesis. BMC Genomics. 21, 570.

Zhu, G., Yu, G., Zhang, X., Liu, J., Zhang, Y., Rollins, J. A., Li, J., Pan, H., 2019. The Formaldehyde Dehydrogenase SsFdh1 Is Regulated by and Functionally Cooperates with the GATA Transcription Factor SsNsd1 in *Sclerotinia sclerotiorum*. mSystems. 4.