

# Jason E. Stajich

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## Education

2006–2009 Postdoctoral training, University of California, Berkeley, CA. Mentor: Dr. John W Taylor  
2001–2006 Ph.D. in Genetics and Genomics, Duke University, Durham, NC. Advisor: Dr. Fred S Dietrich  
1995–1999 B.S. in Computer Science, Duke University, Durham, NC

## Academic appointments:

2017– Professor  
2014–2017 Associate Professor (with tenure)  
2009–2014 Assistant Professor  
Dept of Plant Pathology & Microbiology. University of California Riverside.  
2006–2009 Postdoctoral Research Fellow. Miller Institute for Basic Research.  
Dept of Plant and Microbial Biology, University of California Berkeley.

## Honors and Awards:

2017 Whetzel-Westcott-Dimock Special Lecturer, Cornell University  
2015 Kavli Fellow, Kavli Frontiers of Science  
2014 C. J. Alexopoulos Prize, Mycological Society for America  
2006–2009 Miller Institute for Basic Research in Science, Postdoctoral Research Fellowship  
2003–2006 National Science Foundation, Graduate Research Fellowship

## Publications: (Listed in reverse chronological order.)

### Peer Reviewed Publications

1. Kirkland, T. N., Muszewska, A., and **Stajich**, J. E. 2018. Analysis of transposable elements in *Coccidioides* species. *Journal of fungi (Basel, Switzerland)* 4. doi:10.3390/jof4010013.
2. Leonard, G., Labarre, A., Milner, D. S., Monier, A., Soanes, D., Wideman, J. G., Maguire, F., Stevens, S., Sain, D., Grau-Bové, X., Sebé-Pedrós, A., **Stajich**, J. E., Paszkiewicz, K., Brown, M. W., Hall, N., Wickstead, B., and Richards, T. A. 2018. Comparative genomic analysis of the 'pseudofungus' *Hyphochytrium catenoides*. *Open biology* 8. doi:10.1098/rsob.170184.
3. Beaudet, D., Chen, E. C. H., Mathieu, S., Yildirim, G., Ndikumana, S., Yolande, D., Séuin, S., Farinelli, L., **Stajich**, J. E., and Corradi, N. 2017. Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. *DNA Research* doi:10.1093/dnares/dsx051.
4. Lu, L., Chen, J., Robb, S. M. C., Okumoto, Y., **Stajich**, J. E., and Wessler, S. R. 2017. Tracking the genome-wide outcomes of a transposable element burst over decades of amplification. *Proceedings of the National Academy of Sciences of the United States of America* 114:E10550–E10559. doi: 10.1073/pnas.1716459114.
5. Na, F., Carrillo, J. D., Mayorquin, J. S., Ndinga-Muniania, C., **Stajich**, J. E., Stouthamer, R., Huang, Y.-T., Lin, Y.-T., Chen, C.-Y., and Eskalen, A. 2017. Two novel fungal symbionts *Fusarium kuroshium* sp. nov. and *Graphium kuroshium* sp. nov. of kuroshio shot hole borer (*Euwallacea* sp. nr. *forficatus*) cause fusarium dieback on woody host species in california. *Plant Disease In Press*. doi:10.1094/PDIS-07-17-1042-RE.

6. Aryal, S. K., Carter-House, D., **Stajich**, J. E., and Dillman, A. R. 2017. Microbial associates of the southern mole cricket (*Scapteriscus borellii*) are highly pathogenic. *Journal of invertebrate pathology* 150:54–62. doi:10.1016/j.jip.2017.09.008.
7. Park, S.-Y., Scranton, M. A., **Stajich**, J. E., Yee, A., and Walling, L. L. 2017. Chlorophyte aspartyl aminopeptidases: Ancient origins, expanded families, new locations, and secondary functions. *PloS one* 12:e0185492. doi:10.1371/journal.pone.0185492.
8. Torres-Cruz, T. J., Billingsley Tobias, T. L., Almatruk, M., Hesse, C. N., Kuske, C. R., Desirò, A., Benucci, G. M. N., Bonito, G., **Stajich**, J. E., Dunlap, C., Arnold, A. E., and Porras-Alfaro, A. 2017. *Bifiguratus adelaidae*, gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. *Mycologia* 109:363–378. doi:10.1080/00275514.2017.1364958.
9. Sinha, S., Flibotte, S., Neira, M., Formby, S., Plemenitaš, A., Cimerman, N. G., Lenassi, M., Gostinčar, C., **Stajich**, J. E., and Nislow, C. 2017. Insight into the recent genome duplication of the halophilic yeast *Hortaea werneckii*: combining an improved genome with gene expression and chromatin structure. *G3: Genes|Genomes|Genetics* 7(7):2015–2022. doi:10.1534/g3.117.040691.
10. Mondo, S. J., Dannebaum, R. O., Kuo, R. C., Louie, K. B., Bewick, A. J., LaButti, K., Haridas, S., Kuo, A., Salamov, A., Ahrendt, S. R., Lau, R., Bowen, B. P., Lipzen, A., Sullivan, W., Andreopoulos, B. B., Clum, A., Lindquist, E., Daum, C., Northen, T. R., Kunde-Ramamoorthy, G., Schmitz, R. J., Gryganskyi, A., Culley, D., Magnuson, J., James, T. Y., O'Malley, M. A., **Stajich**, J. E., Spatafora, J. W., Visel, A., and Grigoriev, I. V. 2017. Widespread adenine N6-methylation of active genes in fungi. *Nature Genetics* 49:964–968. doi:10.1038/ng.3859.
11. Ahrendt, S. R., Medina, E. M., Chia-en, A. C., and **Stajich**, J. E. 2017. Exploring the binding properties and structural stability of an opsin in the chytrid *Spizellomyces punctatus* using comparative and molecular modeling. *PeerJ* 5:e3206. doi:10.7717/peerj.3206.
12. Nguyen, T. A., Cissé, O. H., Yun Wong, J., Zheng, P., Hewitt, D., Nowrousian, M., **Stajich**, J. E., and Jedd, G. 2017. Innovation and constraint leading to complex multicellularity in the Ascomycota. *Nature Communications* 8:14444. doi:10.1038/ncomms14444.
13. Chen, J., Wrightsman, T., Wessler, S. R., and **Stajich**, J. E. 2017. RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. *PeerJ* 5:e2942. doi:10.7717/peerj.2942.
14. Spatafora, J. W., Chang, Y., Benny, G. L., Lazarus, K., Smith, M. E., Berbee, M. L., Bonito, G., Corradi, N., Grigoriev, I., Gryganskyi, A., James, T. Y., O'Donnell, K., Roberson, R. W., Taylor, T. N., Uehling, J., Vilgalys, R., White, M. M., and **Stajich**, J. E. 2016. A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. *Mycologia* 108:1028–1046. doi:10.3852/16-042.
15. Short, D. P., O'Donnell, K., **Stajich**, J. E., Hulcr, J., Kijimoto, T., Berger, M. C., Macias, A. M., Spahr, E. J., Bateman, C. C., Eskalen, A., et al. 2017. PCR multiplexes discriminate *Fusarium* symbionts of invasive *Euwallacea* ambrosia beetles that inflict damage on numerous tree species throughout the United States. *Plant Disease* 101(1):233–240. doi:10.1094/PDIS-07-16-1046-RE.
16. Castanera, R., López-Varas, L., Borgognone, A., LaButti, K., Lapidus, A., Schmutz, J., Grimwood, J., Pérez, G., Pisabarro, A. G., Grigoriev, I. V., **Stajich**, J. E., and Ramírez, L. 2016. Transposable elements versus the fungal genome: Impact on whole-genome architecture and transcriptional profiles. *PLoS Genet* 12(6):e1006108. doi:10.1371/journal.pgen.1006108.
17. Lee, M. J., Geller, A. M., Bamford, N. C., Liu, H., Gravelat, F., Snarr, B. D., Le Mauff, F., Chabot, J., Ralph, B., Ostapska, H., Lehoux, M., Cerone, R. P., Baptisa, S. D., Vinogradov, E., **Stajich**, J. E., Filler, S. G., Howell, P. L., and Sheppard, D. C. 2016. Deacetylation of fungal exopolysaccharide mediates adhesion and biofilm formation. *mBio* 7(2):e00252–16. doi:10.1128/mBio.00252-16.
18. de Man, T. J. B., **Stajich**, J. E., Kubicek, C. P., Teiling, C., Chenthamara, K., Atanasova, L., Druzhinina, I. S., Levenkova, N., Birnbaum, S. S. L., Barribeau, S. M., Bozick, B. A., Suen, G.,

- Currie, C. R., and Gerardo, N. M. 2016. Small genome of the fungus *Escovopsis weberi*, a specialized disease agent of ant agriculture. *Proc Natl Acad Sci U S A* 113(13):3567–3572. doi:10.1073/pnas.1518501113.
19. U'Ren, J. M., Miadlikowska, J., Zimmerman, N. B., Lutzoni, F., **Stajich**, J. E., and Arnold, A. E. 2016. Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). *Mol Phylogenet Evol* 98:210–232. doi:10.1016/j.ympev.2016.02.010.
  20. Pieuchot, L., Lai, J., Loh, R. A., Leong, F. Y., Chiam, K.-H., **Stajich**, J. E., and Jedd, G. 2015. Cellular subcompartments through cytoplasmic streaming. *Dev Cell* 34(4):410–420. doi:10.1016/j.devcel.2015.07.017.
  21. Wang, Y., Smith, K. M., Freitag, M., and **Stajich**, J. E. 2015. Endogenous small RNA mediates meiotic silencing of a novel DNA transposon. *G3: Genes|Genomes|Genetics* 5(10):g3.115.017921. doi:10.1534/g3.115.017921.
  22. Liu, P. and **Stajich**, J. E. 2015. Characterization of the Carbohydrate Binding Module 18 gene family in the amphibian pathogen *Batrachochytrium dendrobatidis*. *Fungal Genet Biol* 77:31–39. doi:10.1016/j.fgb.2015.03.003.
  23. Willger, S. D., Liu, Z., Olarte, R. A., Adamo, M. E., **Stajich**, J. E., Myers, L. C., Kettenbach, A. N., and Hogan, D. A. 2015. Analysis of the *Candida albicans* phosphoproteome. *Eukaryot Cell* 14(5):474–485. doi:10.1128/EC.00011-15.
  24. Collins, R. A., **Stajich**, J. E., Field, D. J., Olive, J. E., and DeAbreu, D. M. 2015. The low information content of *Neurospora* splicing signals: implications for RNA splicing and intron origin. *RNA* 21(5):997–1004. doi:10.1261/rna.047985.114.
  25. Mélida, H., Sain, D., **Stajich**, J. E., and Bulone, V. 2015. Deciphering the uniqueness of mucoromycotina cell walls by combining biochemical and phylogenomic approaches. *Environmental Microbiology* 17(5):1649–62. doi:10.1111/1462-2920.12601.
  26. Teixeira, M. M., de Almeida, L. G., Kubitschek-Barreira, P., Alves, F. L., Kioshima, E. S., Abadio, A. K., Fernandes, L., Derengowski, L. S., Ferreira, K. S., Souza, R. C., Ruiz, J. C., de Andrade, N. C., Paes, H. C., Nicola, A. M., Albuquerque, P., Gerber, A. L., Martins, V. P., Peconick, L. D., Neto, A. V., Chaucanez, C. B., Silva, P. A., Cunha, O. L., de Oliveira, F. F., Dos Santos, T. C., Barros, A. L., Soares, M. A., de Oliveira, L. M., Marini, M. M., Villalobos-Duno, H., Cunha, M. M., de Hoog, S., da Silveira, J. F., Henrissat, B., Niño-Vega, G. A., Cisalpino, P. S., Mora-Montes, H. M., Almeida, S. R., **Stajich**, J. E., Lopes-Bezerra, L. M., Vasconcelos, A. T., and Felipe, M. S. 2014. Comparative genomics of the major fungal agents of human and animal Sporotrichosis: *Sporothrix schenckii* and *Sporothrix brasiliensis*. *BMC Genomics* 15:943. doi:10.1186/1471-2164-15-943.
  27. Ouyang, S., Park, G., Atamian, H. S., Han, C. S., **Stajich**, J. E., Kaloshian, I., and Borkovich, K. A. 2014. Regulation of innate immunity to the fungal pathogen *Fusarium oxysporum* by microRNAs in tomato. *PLoS Path* 10(10):e1004464. doi:10.1371/journal.ppat.1004464.
  28. Inglis, D. O., Skrzypek, M. S., Liaw, E., Moktali, V., Sherlock, G., and **Stajich**, J. E. 2014. Literature-based gene curation and proposed genetic nomenclature for *Cryptococcus*. *Eukaryot Cell* 13(7):878–883. doi:10.1128/EC.00083-14.
  29. Treseder, K. K., Maltz, M. R., Hawkins, B. A., Fierer, N., **Stajich**, J. E., and McGuire, K. L. 2014. Evolutionary histories of soil fungi are reflected in their large-scale biogeography. *Ecol Lett* 17(9):1086–1093. doi:10.1111/ele.12311.
  30. Janbon, G., Ormerod, K. L., Paulet, D., Byrnes, E. J., 3rd, Yadav, V., Chatterjee, G., Mullapudi, N., Hon, C.-C., Billmyre, R. B., Brunel, F., Bahn, Y.-S., Chen, W., Chen, Y., Chow, E. W. L., Coppée, J.-Y., Floyd-Averette, A., Gaillardin, C., Gerik, K. J., Goldberg, J., Gonzalez-Hilarion, S., Gujja, S., Hamlin, J. L., Hsueh, Y.-P., Ianiri, G., Jones, S., Kodira, C. D., Kozubowski, L., Lam, W., Marra, M., Mesner, L. D., Mieczkowski, P. A., Moyrand, F., Nielsen, K., Proux, C., Rossignol, T., Schein,

- J. E., Sun, S., Wollschlaeger, C., Wood, I. A., Zeng, Q., Neuveglise, C., Newlon, C. S., Perfect, J. R., Lodge, J. K., Idnurm, A., **Stajich**, J. E., Kronstad, J. W., Sanyal, K., Heitman, J., Fraser, J. A., Cuomo, C. A., and Dietrich, F. S. 2014. Analysis of the genome and transcriptome of *Cryptococcus neoformans* var. *grubii* reveals complex RNA expression and microevolution leading to virulence attenuation. *PLoS Genet* 10(4):e1004261. doi:10.1371/journal.pgen.1004261.
31. Sachs, J. L., Skophammer, R. G., Bansal, N., and **Stajich**, J. E. 2014. Evolutionary origins and diversification of proteobacterial mutualists. *Proc Biol Sci* 281(1775):20132146. doi:10.1098/rspb.2013.2146.
  32. Traeger, S., Altegoer, F., Freitag, M., Gabaldon, T., Kempken, F., Kumar, A., Marcet-Houben, M., Pöggeler, S., **Stajich**, J. E., and Nowrousian, M. 2013. The genome and development-dependent transcriptome of *Pyronema confluens*: a window into fungal evolution. *PLoS Genetics* 9(9):e1003820. doi:10.1371/journal.pgen.1003820.
  33. Gryganskyi, A. P., Humber, R. A., **Stajich**, J. E., Mullens, B., Anishchenko, I. M., and Vilgalys, R. 2013. Sequential utilization of hosts from different fly families by genetically distinct, sympatric populations within the *Entomophthora muscae* species complex. *PLoS One* 8(8):e71168. doi:10.1371/journal.pone.0071168.
  34. Gioti, A., **Stajich**, J. E., and Johannesson, H. 2013. *Neurospora* and the dead-end hypothesis: genomic consequences of selfing in the model genus. *Evolution* 67(12):3600–3616. doi:10.1111/evo.12206.
  35. James, T. Y., Pelin, A., Bonen, L., Ahrendt, S., Sain, D., Corradi, N., and **Stajich**, J. E. 2013. Shared signatures of parasitism and phylogenomics unite Cryptomycota and Microsporidia. *Curr Biol* 23(16):1548–1553. doi:10.1016/j.cub.2013.06.057.
  36. Rosenblum, E. B., James, T. Y., Zamudio, K. R., Poorten, T. J., Ilut, D., Rodriguez, D., Eastman, J. M., Richards-Hrdlicka, K., Joneson, S., Jenkinson, T. S., Longcore, J. E., Parra Olea, G., Toledo, L. F., Arellano, M. L., Medina, E. M., Restrepo, S., Flechas, S. V., Berger, L., Briggs, C. J., and **Stajich**, J. E. 2013. Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. *Proc Natl Acad Sci U S A* 110(23):9385–9390. doi:10.1073/pnas.1300130110.
  37. Robb, S. M. C., Lu, L., Valencia, E., Burnette, J. M., 3rd, Okumoto, Y., Wessler, S. R., and **Stajich**, J. E. 2013. The use of RelocaTE and unassembled short reads to produce high-resolution snapshots of transposable element generated diversity in rice. *G3: Genes|Genomes|Genetics* 3(6):949–57. doi:10.1534/g3.112.005348.
  38. Jamieson, K., Rountree, M. R., Lewis, Z. A., **Stajich**, J. E., and Selker, E. U. 2013. Regional control of histone H3 lysine 27 methylation in *Neurospora*. *Proc Natl Acad Sci U S A* 110(15):6027–6032. doi:10.1073/pnas.1303750110.
  39. Cheng, C. K., Au, C. H., Wilke, S. K., **Stajich**, J. E., Zolan, M. E., Pukkila, P. J., and Kwan, H. S. 2013. 5'-serial analysis of gene expression studies reveal a transcriptomic switch during fruiting body development in *Coprinopsis cinerea*. *BMC Genomics* 14(1):195. doi:10.1186/1471-2164-14-195.
  40. Gioti, A., Nystedt, B., Li, W., Xu, J., Andersson, A., Averette, A. F., Münch, K., Wang, X., Kappauf, C., Kingsbury, J. M., Kraak, B., Walker, L. A., Johansson, H. J., Holm, T., Lehtiö, J., **Stajich**, J. E., Mieczkowski, P., Kahmann, R., Kennell, J. C., Cardenas, M. E., Lundeborg, J., Saunders, C. W., Boekhout, T., Dawson, T. L., Munro, C. A., de Groot, P. W. J., Butler, G., Heitman, J., and Scheynius, A. 2013. Genomic insights into the atopic eczema-associated skin commensal yeast *Malassezia sympodialis*. *MBio* 4(1):e00572–e00512. doi:10.1128/mBio.00572-12.
  41. Nygren, K., Wallberg, A., Samils, N., **Stajich**, J. E., Townsend, J. P., Karlsson, M., and Johannesson, H. 2012. Analyses of expressed sequence tags in *Neurospora* reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. *BMC Evol Biol* 12:229. doi:10.1186/1471-2148-12-229.

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43. Gioti, A., Mushegian, A. A., Strandberg, R., **Stajich**, J. E., and Johannesson, H. 2012. Unidirectional evolutionary transitions in fungal mating systems and the role of transposable elements. *Mol Biol Evol* 29(10):3215–3226. doi:10.1093/molbev/mss132.
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45. Joneson, S., **Stajich**, J. E., Shiu, S.-H., and Rosenblum, E. B. 2011. Genomic transition to pathogenicity in chytrid fungi. *PLoS Pathog* 7(11):e1002338. doi:10.1371/journal.ppat.1002338.
46. Ellison, C. E., **Stajich**, J. E., Jacobson, D. J., Natvig, D. O., Lapidus, A., Foster, B., Aerts, A., Riley, R., Lindquist, E. A., Grigoriev, I. V., and Taylor, J. W. 2011. Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus *Neurospora tetrasperma*. *Genetics* 189(1):55–69. doi:10.1534/genetics.111.130690.
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48. Burns, C., **Stajich**, J. E., Rechtsteiner, A., Hanlon, S. E., Wilke, S. K., Palmerini, H. J., Savytskyy, O. P., Gathman, A. C., Lilly, W. W., Lieb, J. D., Zolan, M. E., and Pukkila, P. J. 2010. Analysis of the basidiomycete *Coprinopsis cinerea* reveals conservation of the core meiotic expression program over half a billion years of evolution. *PLoS Genetics* 6(9):e1001135. doi:10.1371/journal.pgen.1001135.
49. Smith, K. M., Sancar, G., Dekhang, R., Sullivan, C. M., Li, S., Tag, A. G., Sancar, C., Bredeweg, E. L., Priest, H. D., McCormick, R. F., Thomas, T. L., Carrington, J. C., **Stajich**, J. E., Bell-Pedersen, D., Brunner, M., and Freitag, M. 2010. Transcription factors in light and circadian clock signaling networks revealed by genomewide mapping of direct targets for Neurospora White Collar Complex. *Eukaryot Cell* 9(10):1549–1556. doi:10.1128/EC.00154-10.
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51. Strandberg, R., Nygren, K., Menkis, A., James, T. Y., Wik, L., **Stajich**, J. E., and Johannesson, H. 2010. Conflict between reproductive gene trees and species phylogeny among outcrossing members of the filamentous ascomycete genus *Neurospora*. *Fungal Genetics & Biology* 11(7):869–878. doi:10.1016/j.fgb.2010.06.008.
52. Ohm, R. A., de Jong, J. F., Lugones, L. G., Aerts, A., Kothe, E., **Stajich**, J. E., de Vries, R. P., Record, E., Levasseur, A., Baker, S. E., Bartholomew, K. A., Coutinho, P. M., Fowler, T. J., Gathman, A. C., Lombard, V., Henrissat, B., Knabe, N., Kües, U., Lilly, W. W., Lindquist, E., Lucas, S., Magnuson, J. K., Piumi, F., Raudaskoski, M., Salamov, A., Schmutz, J., Schwarze, F. W., vanKuyk, P. A.,

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#### Submitted Manuscripts and Preprints

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## Books and Book Chapters

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## Meeting and Technical Reports

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5. Lapp, H., Bala, S., Balhoff, J., Bouck, A., Goto, N., Holder, M., Holland, R., Holloway, A., Katayama, T., Lewis, P. O., Mackey, A. J., Osborne, B. I., Piel, W. H., Kosakovsky Pond, S. L., Poon, A., Qiu, W., **Stajich**, J. E., Stoltzfus, A., Thierer, T., Vilella, A. J., Vos, R. A., Zmasek, C., Zwickl, D., and Vision, T. J. 2007. The 2006 NESCent Phyloinformatics Hackathon: A field report. *Evolutionary Bioinformatics Online* 3:357–366.

### Commentaries and Book Reviews

1. **Stajich**, J. E. 2016. Fungal Evolution: *Mucor* and *Phycomyces* see double. *Curr Biol* 26(16):R775–R777. doi:10.1016/j.cub.2016.06.049.
2. **Stajich**, J. E. 2011. Review of cellular and molecular biology of filamentous fungi. *The Quarterly Review of Biology* 86(1):59–59. doi:10.1086/658451. Book Review.
3. **Stajich**, J. E. 2009. Review of bioinformatics, Volume I: Data, Sequence Analysis and Evolution; Volume II: Structure, Function and Applications. *The Quarterly Review of Biology* 84(3):284–285. doi:10.1086/644662. Book Review.

### Essays

1. **Stajich**, J. E. 2014. Top 5 real wolves of wall street. <http://nautil.us/issue/10/mergers--acquisitions/top-5-real-wolves-of-wall-street>. "Moldy Monopolies" and "Creepy Crawly Conglomerate" in the "Mergers & Acquisitions" issue.

### Software and other Products

BioPerl - <http://bioperl.org> - Core developer  
 Github <http://github.com/hyphal-tip> - individual projects  
 Github <http://github.com/stajichlab> - lab projects  
 Github <http://github.com/1KFG> - 1000 Fungal genomes project  
 Github <http://github.com/zygolife> - ZyGoLife NSF project and associated phylogenomics  
 Website: <http://1000.fungalgenomes.org> - 1KFG project  
 Website: <http://zygolife.org> - NSF Zygolife  
 Website: <http://dynamiterice.org> - NSF Rice Transposable Element project  
 Website: <http://fungalgenomes.org/blog> - "The Hyphal Tip" A Blog I write about Fungal Genomics  
 Website & Database (Collaboration): <http://fungidb.org>

### Grant Support:

#### Ongoing support

- |           |  |
|-----------|--|
| 2011-2016 | W.M. Keck Foundation. \$1M (No Cost Extension thru 2018)<br>"New Active Transposable Elements for Mosquito Genetics."<br>Role: Co-I. PI: SR Wessler (UC Riverside). Co-I: P Atkinson (UC Riverside).   |
| 2011-2017 | National Science Foundation. Plant Genome - IOS-1027542. \$4.9M (No Cost Extension thru 2019)<br>"CPGS: Genome-wide impact of <i>mPing</i> transposition on rice phenotypic diversity."<br>Role: Co-I. PI: SR Wessler (UC Riverside).<br><a href="http://dynamiterice.org">http://dynamiterice.org</a> |

2015-2018 National Science Foundation. GO Life DEB-1441715. \$714k (\$2.5M total award)  
 “Collaborative Research: The Zygomycetes Genealogy of Life (ZyGoLife)- the conundrum of Kingdom Fungi”  
 Role: PI. Collaborative linked award with 3 other PIs and 12 collaborating labs: J Spatafora (Oregon State), TY James (U Michigan), R Robertson (Arizona State)  
<http://zygolife.org>

2016-2019 National Science Foundation. DEB-1557110. \$317k (\$709k total award)  
 “Collaborative Research: Phylogenomics and evolutionary history of the anaerobic fungal group, Neocallimastigomycota”  
 Role: PI. Collaborative linked award PI: N Youssef (Oklahoma State)

2017-2020 Univ of California-Office of the President, MRPI. \$105k (\$1.7M total award)  
 “UC Valley Fever Research Initiative”  
 Role: Co-PI. PI: Anita Sil (UCSF) and Co-PIs at UC Berkeley, UCMerced, UC San Diego

2017-2020 National Institutes of Health. R01-AI127548-01A1  
 “Evolved Heterogeneity contributes to chronic fungal lung infections”  
 Role: Senior Personnel. PI: D Hogan (Dartmouth)

2017-2020 National Institutes of Health. R01-AI130128-01A1  
 “Evolution of *Aspergillus fumigatus* virulence”  
 Role: Senior Personnel. PI: RA Cramer, Jr (Dartmouth)

#### **Completed support**

2010-2013 Burroughs Wellcome Fund. \$500k  
 “FungiDB: A Pan Fungal Genome Database”.  
 Role: Co-I. PI: DS Roos (U Pennsylvania)

2011-2012 UC Riverside, Chancellor’s Strategic Investment Funds. \$25k  
 “Coelomomyces Genomics for Mosquito Vector Control”  
 Role: Co-I. PI: B Federici. Co-I: A Ray (UC Riverside)

2013-2014 UC Riverside, Office of Research Strategic Investment Funds. \$50k  
 “High-throughput synthetic biology for natural products discovery”  
 Role: Co-I. PI: K Borkovich. Co-I: C Larive (UC Riverside)

2013-2014 National Institutes of Health - 1-R03-AI105636-01. \$168k  
 “Annotation of *Cryptococcus* genomes by comprehensive curation of published literature”  
 Role: PI. Co-I G Sherlock (Stanford)

2011-2014 Alfred P. Sloan Foundation. \$750k  
 “MoBe DAC: A data coordinating center for the Sloan Indoor Environment Metagenomic Project - Fungal resources”.  
 Role: PI. Linked grants with F Meyer (U Chicago/ANL), R Knight (U Colorado), M Sogin (Marine Biological Lab).

2014-2015 National Science Foundation. DBI-1429826. \$548k  
 “MRI: Acquisition of a Big Data Compute Cluster for Interdisciplinary Research” Role: Co PI. PI T Girke. Co-Is J Bailey-Serres, M Allen, and S Lonardi (UCR)

2014-2017 National Institutes of Health - 1-R01-GM108492-01.  
 “Dynamics of bacterial-fungal interactions in chronic lung infections”  
 Role: Co-I. PI: D Hogan (Dartmouth)

#### **Service**

##### **University and Departmental**

2017– Director & Admissions Advisor, Microbiology Graduate Program  
 2017– Graduate Council  
 2015–2016 Director & Admissions Advisor, Microbiology Graduate Program  
 2014–2015 Graduate Advisor, Microbiology Graduate Program

### **Editorial Boards**

2018–	Associate Editor, Genetics
2018–	Associate Editor, Mycologia
2016–	Editorial Board, Current Opinion in Microbiology
2015–	Associate Editor, Microbial Genomics
2014–	Associate Editor, Fungal Genetics & Biology
2013,2015	Guest Associate Editor, PLoS Genetics
2013	Guest Associate Editor, Mycologia
2011–2016	Faculty Member in Microbial Genetics & Genomics, Faculty of 1000
2010–2015	Editorial Board, Eukaryotic Cell.
2009–2016	Section Editor, PLoS One.
2007–2016	Academic Editor, PLoS One.

### **Professional Service**

2018-2020	Co-Vice Chair (2018) and Co-Chair (2020) of Cellular and Molecular Fungal Biology, Gordon Research Conference
2014–2018	Neurospora Policy Committee, Co-Organized 2016 Neurospora conference
2013–2019	Fungal Genetics Policy Committee
2012–2017	Scientific advisory board, Plant Microbe Interactions - DOE Science Focus Area, Oak Ridge National Laboratory
2012–2018	Scientific advisory board, WormBase
2012–2015	Scientific advisory board, Ensembl Genomes
2010–2012	Councilor for Genetics & Molecular Biology, Mycological Society of America
2009–2010	Advisory Board for Genomic Encyclopedia of Fungi, Joint Genome Institute, US Department of Energy.
2009–2010	Pan-Fungal Database Steering Committee for Burroughs Wellcome Fund.
2007–2009	Scientific advisory board NSF Computer Science Education Revitalization (PI Owen Astrachan, Duke University)
2005–2008	Scientific advisory committee Information Technology and Computing infrastructure, National Center for Evolutionary Synthesis (NESCent).
2005–2011	President and Board Member [2005–2014], Open Bioinformatics Foundation <a href="http://www.open-bio.org/">http://www.open-bio.org/</a>
2001–	Co-Project leader, BioPerl. <a href="http://www.bioperl.org/">http://www.bioperl.org/</a>

### **Membership in Professional Societies:**

2002–	International Society for Computational Biology
2004–	Society for Molecular Biology and Evolution
2007–	American Society for Microbiology
2004–	Genetics Society of America
2007–	Mycological Society of America
2001–	BioPerl developed. Co-Project leader (2001-2012).
2002–	Open Bioinformatics Foundation

### **Graduate Students:**

2009–13	PhD student, Divya Sain. Genetics, Genomics, & Bioinformatics. Currently: Bioinformatics Scientist at Ambry Genetics.
2010–12	MS student, Yi (Zoe) Zhu. Genetics, Genomics, & Bioinformatics. Currently: Biostatistician at Biostatistical Consulting Inc.
2014	MS student, Elizabeth Holmes, Plant Pathology & Microbiology
2010–14	PhD student, Yizhou Wang. Plant Biology. Currently: Research Bioinformati-

cian at Cedars Sinai.  
 2011–15 PhD student, Steven Ahrendt. Genetics, Genomics, & Bioinformatics. Currently: Postdoc at UC Berkeley/LBNL & DOE Joint Genome Institute.  
 2015– PhD Student, Sawyer Masonjones. Genetics, Genomics, & Bioinformatics  
 2015– PhD Student, Nuttapom Pombubpa. Plant Pathology  
 2016– PhD Student, Derreck Carter-House. Plant Pathology  
 2016– PhD Student, Jesús Peña, Microbiology  
 2017– PhD Student, Julia Adams, Plant Biology  
 2017– PhD Student, Tania Kurbessoian, Microbiology

### **Postdoctoral Fellows:**

2010–2011 John Abramyan, PhD. Currently: Assistant Professor, Univ of Michigan-Dearborn  
 2011–2014 Sofia Robb, PhD. Currently: Genomics Scientist at Stowers Institute.  
 2012–2014 Brad Cavinder, PhD. Currently: Research Associate at Michigan State University  
 2012–2015 Peng Liu, PhD.  
 2013– Jinfeng Chen, PhD  
 2013–2015 Ousmane Cissé, PhD - Swiss National Science Foundation Fellow. Currently: Postdoctoral Fellow at NIH Clinical Center.  
 2014–2015 Rodrigo Olarte. Currently: NSF Postdoctoral Fellow at Univ of Minnesota.  
 2017– Yan Wang, PhD.

### **Visitors:**

2010–2013 (4, 2-3 month vists) Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWEDEN  
 2010 (Spring) Suzanne Joneson, PhD, Department of Biology, University of Idaho  
 2011 (Spring) Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, Bogota, COLOMBIA  
 2012 (Summer) Andrii Gryganski, PhD, Visiting Researcher, Duke University  
 2013–2014 Venkatesh Moktali, PhD, FungiDB Project, Visiting Research Fellow, Oregon State University  
 2014 Raúl Castanera Andrés, Visiting Graduate Student, Universidad Pública de Navarra, Pamplona, SPAIN  
 2015 (Spring) Natalie Vande Pol, Visiting Graduate Student (Bonito Lab), Michigan State University  
 2015–2016 Zhinquan Song, Visiting Graduate Student (Guangyi Wang Lab), Tianjin University, CHINA  
 2015 (Fall) John Yinka Odebode, Visiting Graduate Student on a West African Research Association Fellowship, University of Lagos, NIGERIA.  
 2015 (Fall) Marco Marconi, Visiting Graduate Student, Universidad Politécnica de Madrid, Madrid, SPAIN  
 2015–2016 Claudia Coleine, Visiting Graduate Student, Università degli Studi della Tuscia, Viterbo, ITALY

### **Teaching:**

2010,2012 BIO5C - Introductory Ecology & Evolution  
 2011 BIO20 - The Dynamic Genome - Research module for *Neurospora* research  
 2011,2013 GEN240B - Tools for Bioinformatics and Genome Analysis  
 2015 MCBL124 - Microbial Pathogenesis  
 2011– MCBL211 - Microbial Ecology

2012-2015 MCBL202 - Microbial Pathogenesis & Physiology  
 2012- GEN220 - Computational Analysis of High Throughput Biological Data <http://biodataprogram.github.io/>  
 2016- BIO119 - Introduction to Genomics and Bioinformatics

### **Undergraduate Researchers:**

2010- Sponsor for summer research students in MARCU, STEM, and CAMP programs at UCR.  
 2010-2012 Jessica De Anda, UCR. STEM grant participant (2010); MARC USTAR student 2010-12. Current MS Student, Claremont College  
 2010-2011 Annie Nguyen, UCR.  
 2011-2012 Carlos Rojas Torres, UCR. CAMP (2011); lab researcher. Current: Gilead Pharmaceuticals.  
 2011 Ramy Wissa, UCR. Pre-MARC USTAR Summer student.  
 2011-2012 Lorena Rivera, UCR. Pre-MARC USTAR student (2011); lab researcher, CNAS Dean's Fellow Summer Undergraduate Research (Summer 2012)  
 2012-2014 Erum Khan, UCR.  
 2012-2014 Sapphire Ear, UCR. Current: CityYear and matriculating MD student (TBD).  
 2012-2014 Megna Tiwari, UCR. Current: MS student at Cal State-Long Beach  
 2013-2014 Dylan McVay, UCR.  
 2013-2016 Na Jeong, UCR, Summer RISE Scholar (2013) and lab researcher  
 2014 Spencer Swansen, Summer NSF REU student (Seattle Pacific University)  
 2015-2016 Justin Shen, UCR.  
 2015-2016 Serena Choi, UCR.  
 2015- Dillon McDonald, UCR Summer HSI-STEM (2015) and lab researcher  
 2015 Christina Uriarte, UCR. Pre-MARC USTAR student.  
 2015- Jericho Ortanez, UCR.  
 2015-2016 Leandra Ibrahim, UCR.  
 2015- Deane Kim, UCR.  
 2016- Georgiy Smirnov, UCR.  
 2016- Meng (Josh) Chung, UCR.

### **Dissertation and thesis committees:**

2011 Sourav Roy, PhD, GGB  
 Yi Zhou, MS, GGB ★  
 2012 Andrew Defries, PhD, Plant Sciences  
 2013 Gilbert Uribe, MS, Plant Pathology  
 Divya Sain, PhD, GGB ★  
 2014 Yizhou Wang, PhD, Plant Sciences ★  
 Zhigang Wu, PhD, GGB  
 2015 Presha Shah, PhD, Biochemistry  
 Ming Wang, PhD, Plant Pathology  
 Steven Ahrendt, PhD, GGB ★  
 Ilva Cabrera, PhD, GGB  
 Jinfeng Lu, PhD, GGB  
 James Ricci, MS, Entomology  
 2016 Ryan Arvidson, PhD, Biochemistry  
 Francis Na, MS, Microbiology  
 Jishu Ha, PhD, GGB  
 Arit Gosh, PhD, GGB  
 Kelsey Gano, PhD, Microbiology

2017	Kun Liu, PhD, Plant Biology Raissa Green, PhD, GGB Amelia Lindsey, PhD, Entomology Patrick Schriener, PhD, GGB Eric Smith, PhD, GGB Katherine Picard, Univ Prog in Genetics & Genomics (Duke University) Eric Gordon, Entomology
ongoing	Cynthia Dick, EEOB Dereck O'Meara, EEOB Yi Zhai, CMDB Andrea Vu, Plant Pathology Steven Bolaris, GGB Dinusha Maheepala Mudalige, Plant Biology Joseph Carrillo, Plant Pathology Nuttapon Pombubpa, Plant Pathology ★ Derreck Carter-House, Plant Pathology ★ Sawyer Masonjones, GGB ★ Jesús Peña, Microbiology ★ Julia Adams, Plant Biology ★ Tania Kurbessoian, Microbiology ★ Caleb Hubbard, Medical and Veterinary Entomology Nathan Robinett, Joint Doctoral Program in Evolutionary Biology, SDSU-UCR Alex Rajewski, Plant Biology Edgar Medina, Univ Prog in Genetics & Genomics (Duke University) Lluvia Vargas, Microbiología (CICESE, MEXICO) Dan Vanderpool, Biology (University of Montana) Shannon Lynch, Environmental Studies (Univ of California-Santa Cruz)

### Invited Seminars and conference presentations (2015–Present)

- 2018 · UC Riverside Data Science Center. Riverside, CA
- 2017 · Dept Seminar. Botany & Plant Pathology. Oregon State University. Corvallis, OR
- 29th Fungal Genetics Conference. *Plenary Speaker*. Pacific Grove, CA.
- Oomycete Molecular Genetics Network. *Plenary Speaker*. Pacific Grove, CA
- Population Genomics of Oomycete and Fungal Pathogens. Ascona, Switzerland
- American Society of Microbiology Microbe Meeting. New Orleans, LA
- FASEB Microbial Pathogenesis. Aspen, CO.
- Mycological Society of America 2017 Meeting. Athens, GA
- Fungal Cell Wall Conference. Ensenada, Mexico
- Whetzel-Westcott-Dimock Special Lecturer, Cornell University, Ithaca, NY
- 2016 · Mycological Society of America 2016 Meeting. Berkeley, CA.
- CIFAR Integrated Microbial Biodiversity Program. Toronto, ON, CANADA.
- 13th European Fungal Genetics Conference. Paris, France. *Plenary Speaker*
- Neurospora Conference. Asilomar Conference Center, Pacific Grove, CA.
- University Program in Genetics & Genomics. Duke University, Durham, NC.
- Dept of Plant Pathology. University of California, Davis, CA.
- University of Exeter. United Kingdom.
- 2015 · Exploring the genomic complexity and diversity of eukaryotes. EMBO Conference, San Feliu de Guixols, SPAIN.
- XI CONGRESO NACIONAL DE MICOLOGIA, Sociedad Mexicana de Micología. Merida, Yucatan, MEXICO. *Plenary Speaker*



- School of Plant Sciences, University of Arizona, Tucson, AZ.
- Eighth International Conference on Mycorrhiza. Flagstaff, AZ.
- Mycological Society of America 2015 Meeting. Edmonton, AB, CANADA.
- Society for Molecular Biology & Evolution 2015. Vienna, Austria.
- Bioinformatics Seminar series. University of California, Los Angeles, CA.
- University of California, Merced, CA.
- 28th Fungal Genetics Conference. Asilomar Conference Center, Pacific Grove, CA.
- Center for Genome Research and Biocomputing Seminar. Oregon State University, Corvallis, OR.
- Dept of Microbiology and Molecular Genetics. Oklahoma State University, Stillwater, OK.

February 20, 2018