

# Jason E. Stajich

**Contact** Department of Plant Pathology & Microbiology, Institute for Integrative Genome Biology,  
University of California, Riverside, CA 92521  
**Telephone:** +1 951-827-2363 **Email:** jason.stajich@ucr.edu  
**Web:** <http://lab.stajich.org/> @stajichlab @hyphaltip

## 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:

2014– Associate Professor (with tenure)  
Dept of Plant Pathology & Microbiology. University of California Riverside  
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:

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. Nguyen, T. A., Cissé, O. H., Wong, J. Y., Zheng, P., Hewitt, D., Nowrousian, M., **Stajich, J. E.**, and Jedd, G. 2016. Innovation and constraint leading to complex multicellularity in the Ascomycota. Submitted.
2. Torres-Cruz, T. J., Billingsley Tobias, T. L., Almatruk, M., Hesse, C., Kuske, C. R., Desiro, A., Benucci, G. N., Bonito, G., **Stajich, J. E.**, Dunlap, C., Arnold, A. E., and Porras-Alfaro, A. 2016. *Bifiguratus adelaidae* gen. et sp. nov., a new lineage of Mucoromycotina with endophytic and soil-dwelling strains. Submitted.
3. Ahrendt, S. R., Medina, E. M., Chia-en, A. C., and **Stajich, J. E.** 2016. Exploring the binding properties and structural stability of an opsin in the chytrid *Spizellomyces punctatus* using comparative and molecular modeling. *PeerJ Preprints* 4:e2397v1. doi:10.7287/peerj.preprints.2397v1. Submitted.
4. Chen, J., Wrightsman, T., Wessler, S. R., and **Stajich, J. E.** 2016. RelocaTE2: a high resolution transposable element polymorphism mapping tool for population resequencing. *PeerJ Preprints* 4:e2447v1. doi:10.7287/peerj.preprints.2447v1. Submitted.
5. Cissé, O. H. and **Stajich, J. E.** 2016. FGMP: assessing fungal genome completeness and gene content. *bioRxiv* doi:10.1101/049619. Submitted.
6. 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. 2016. PCR multiplexes discriminate *Fusarium* symbionts

of invasive *Euwallacea* ambrosia beetles that inflict damage on numerous tree species throughout the United States. *Plant Disease* In press. doi:10.1094/PDIS-07-16-1046-RE.

7. 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.
8. 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.
9. 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). doi:10.1128/mBio.00252-16.
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. Mérida, 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.
18. 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.
19. 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.
  20. Inglis, D. O., Skrzypek, M. S., Liaw, E., Muktali, 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.
  21. 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.
  22. 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., Neuvéglise, 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.
  23. 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.
  24. 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.
  25. 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.
  26. 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.
  27. 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.
  28. 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.
  29. 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.

30. 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.
31. 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.
32. Gioti, A., Nystedt, B., Li, W., Xu, J., Andersson, A., Averette, A. F., MÅijnch, K., Wang, X., Kappauf, C., Kingsbury, J. M., Kraak, B., Walker, L. A., Johansson, H. J., Holm, T., LehtiÄ, 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.
33. 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.
34. Abramyan, J. and **Stajich, J. E.** 2012. Species-specific chitin-binding module 18 expansion in the amphibian pathogen *Batrachochytrium dendrobatidis*. *MBio* 3(3):e00150–e00112. doi:10.1128/mBio.00150-12.
35. 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.
36. **Stajich, J. E.**, Harris, T., Brunk, B. P., Brestelli, J., Fischer, S., Harb, O. S., Kissinger, J. C., Li, W., Nayak, V., Pinney, D. F., Stoeckert, C. J., Jr, and Roos, D. S. 2012. FungiDB: an integrated functional genomics database for fungi. *Nucleic Acids Res* 40(D1):D675–D681. doi:10.1093/nar/gkr918.
37. 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.
38. 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.
39. D'Souza, C. A., Kronstad, J. W., Taylor, G., Warren, R., Yuen, M., Hu, G., Jung, W. H., Sham, A., Kidd, S. E., Tangen, K., Lee, N., Zeilmaker, T., Sawkins, J., McVicker, G., Shah, S., Gnerre, S., Griggs, A., Zeng, Q., Bartlett, K., Li, W., Wang, X., Heitman, J., **Stajich, J. E.**, Fraser, J. A., Meyer, W., Carter, D., Schein, J., Krzywinski, M., Kwon-Chung, K. J., Varma, A., Wang, J., Brunham, R., Fyfe, M., Ouellette, B. F. F., Siddiqui, A., Marra, M., Jones, S., Holt, R., Birren, B. W., Galagan, J. E., and Cuomo, C. A. 2011. Genome variation in *Cryptococcus gattii*, an emerging pathogen of immunocompetent hosts. *MBio* 2(1):e00342–10. doi:10.1128/mBio.00342-10.
40. 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.
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43. 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.
44. 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., Horton, J. S., Grigoriev, I. V., and Wösten, H. A. 2010. Genomic sequence of the wood-rotting *Schizophyllum commune* strain H4-8: a model mushroom system. *Nature Biotech* 28:957–963. doi:10.1038/nbt.1643.
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- Pfister, D. H., Hewitt, D., Hansen, K., Hambleton, S., Shoemaker, R. A., Kohlmeyer, J., Volkmann-Kohlmeyer, B., Spotts, R. A., Serdani, M., Crous, P. W., Hughes, K. W., Matsuura, K., Langer, E., Langer, G., Untereiner, W. A., Lücking, R., Büdel, B., Geiser, D. M., Aptroot, A., Diederich, P., Schmitt, I., Schultz, M., Yahr, R., Hibbett, D. S., Lutzoni, F., McLaughlin, D. J., Spatafora, J. W., and Vilgalys, R. 2006. Reconstructing the early evolution of Fungi using a six-gene phylogeny. *Nature* 443(7113):818–822. doi:10.1038/nature05110.
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#### Reviews (Refereed)

1. Hibbett, D. S., **Stajich**, J. E., and Spatafora, J. W. 2013. Toward genome-enabled mycology. *Mycologia* 105(6):1339–1349. doi:10.3852/13-196.
2. Rosenblum, E. B., Fisher, M. C., James, T. Y., **Stajich**, J. E., Longcore, J. E., Gentry, L. R., and Porten, T. J. 2010. A molecular perspective on the biology of the emerging pathogen *Batrachochytrium dendrobatidis*. *Diseases of Aquatic Organisms* 92(2-3):131–147. doi:10.3354/dao02179.
3. Rosenblum, E. B., Voyles, J., Porten, T. J., and **Stajich**, J. E. 2010. The deadly chytrid fungus: a story of an emerging pathogen. *PLoS Pathogens* 6(1):e1000550. doi:10.1371/journal.ppat.1000550.
4. **Stajich**, J. E., Berbee, M. L., Blackwell, M., Hibbet, D. S., James, T. Y., Spatafora, J. W., and Taylor, J. W. 2009. The Fungi. *Current Biol* 19(18):R840–R845. doi:10.1016/j.cub.2009.07.004.
5. **Stajich**, J. E. and Lapp, H. 2006. Open source tools and toolkits for bioinformatics: significance, and where are we? *Brief Bioinform* 7(3):287–296. doi:10.1093/bib/bbl026.

#### Books and Book Chapters

1. **Stajich**, J. E. 2015. Phylogenomics enabling genome based mycology. In D. J. McLaughlin, M. Blackwell, and J. W. Spatafora, editors, *The Mycota VII*, Systematics and Evolution. Springer.
2. **Stajich**, J. E. 2013. Comparative genomics. In J. Losos, D. Baum, D. J. Futuyma, H. Hoekstra, R. Lenski, A. Moore, D. Schluter, and M. Whitlock, editors, *The Princeton Guide to Evolution*. Princeton University Press.
3. Fisher, M. C., **Stajich**, J. E., and Farrer, R. A. 2012. Emergence of the chytrid fungus *Batrachochytrium dendrobatidis* and global amphibian declines. In D. Sibley, B. Howlett, and J. Heitman, editors, *Evolution of Virulence in Eukaryotic Microbes*. Wiley Blackwell.



4. McKay, S. J., Vergara, I. A., and **Stajich**, J. E. 2010. Using the Generic Synteny Browser (GBrowse\_syn). *Curr Protoc Bioinformatics* Chapter 9:Unit9.12. doi:10.1002/0471250953.bi0912s31.
5. Edwards, D., **Stajich**, J. E., and Hansen, D., editors. 2009. *Bioinformatics*. Springer, NY.
6. **Stajich**, J. E. 2007. An introduction to BioPerl. *Methods Mol Biol* 406:535–548.
7. **Stajich**, J. E. and Dietrich, F. S. 2006. Genomic perspectives on the fungal kingdom. In J. Heitman, S. G. Filler, J. E. Edwards Jr, and A. P. Mitchell, editors, *Molecular principles of fungal pathogenesis*, pages 657–666. ASM press.
8. Coghlan, A., **Stajich**, J. E., and Harris, T. W. 2006. Comparative genomics in *C. elegans*, *C. briggsae*, and other *Caenorhabditis* species. *Methods Mol Biol* 351:13–29. doi:10.1385/1-59745-151-7:13.

### Meeting and Technical Reports

1. Momany, M., Di Pietro, A., Alexander, W. G., Barker, B. M., Harb, O. S., Kamoun, S., Martin, F., Pires, J. C., **Stajich**, J. E., Thomma, B. P. H. J., and Unruh, S. 2015. Meeting report: Fungal genomics meets social media: Highlights of the 28th fungal genetics conference at asilomar. *G3: Genes|Genomes|Genetics* 5(12):2523–2525. doi:10.1534/g3.115.024158.
2. Kennedy, P. and **Stajich**, J. E. 2015. Twenty-first century mycology: a diverse, collaborative, and highly relevant science. *New Phytol* 205(1):23–26. doi:10.1111/nph.13165.
3. Glass, E. M., Dribinsky, Y., Yilmaz, P., Levin, H., Van Pelt, R., Wendel, D., Wilke, A., Eisen, J. A., Huse, S., Shipanova, A., Sogin, M., **Stajich**, J., Knight, R., Meyer, F., and Schriml, L. M. 2014. MlXs-BE: a MlXs extension defining a minimum information standard for sequence data from the built environment. *ISME J* 8(1):1–3. doi:10.1038/ismej.2013.176.
4. Bates, S. T., Ahrendt, S., Bik, H., Bruns, T. D., Caparaso, J., Cole, J., Dwan, M., Fierer, N., Gu, D., Houston, S., Knight, R., Leff, J., Lewis, C., McDonald, D., Nilsson, H., Porras-Alfaro, A., Robert, V., Schoch, C., Scott, J., Taylor, D. L., Wegener-Parfrey, L., and **Stajich**, J. E. 2013. Meeting Report: Fungal ITS Workshop (October 2012). *SIGS* 8:118–23.
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., Vielella, 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/hyphaltip> - 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  
”New Active Transposable Elements for Mosquito Genetics.”  
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  
”CPGS: Genome-wide impact of *mPing* transposition on rice phenotypic diversity.”  
Role: Co-I. PI: SR Wessler (UC Riverside). Co-I: T Brutnell (Danforth Center), Q Sun (Cornell).  
<http://dynamiterice.org>  
2014-2017 National Institutes of Health - 1-R01-GM108492-01. \$1.5M  
”Dynamics of bacterial-fungal interactions in chronic lung infections”  
Role: Co-I. PI: D Hogan (Dartmouth)  
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 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 award with PI: Noha Youssef and Mostafa Elshahed (Oklahoma State)

### 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. Coordinated 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)

## **Service**

### **University and Departmental**

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

### **Editorial Boards**

- 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– 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 for NSF funded Computer Science Education Revitalization project to PI Owen Astrachan, Duke University.  
 2005–2008 Scientific advisory committee for Information Technology and Computing infrastructure for the National Center for Evolutionary Synthesis (NESCent).  
 2005–2011 President and Board Member [2005–Present], Open Bioinformatics Foundation <http://www.open-bio.org/>  
 2001– Co-Project leader, BioPerl. <http://www.bioperl.org/>

### **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 Bioinformatician 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

### **Postdoctoral Fellows:**

2010–2011 John Abramyan, PhD. Currently: Postdoc at Univ of West Virginia  
 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.

### **Visitors:**

2010–13 (4, 2-3 month visits) 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  
 2013–14 Venkatesh Muktali, 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  
 2015–16 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://hyphaltip.github.io/GEN220\\_2015](http://hyphaltip.github.io/GEN220_2015)  
 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
ongoing	Kelsey Gano, Microbiology
	Kun Liu, Plant Biology
	Raissa Green, GGB
	Amelia Lindsey, Entomology
	Patrick Schriener, GGB
	Cynthia Dick, EEOB
	Eric Gordon, Entomology
	Eric Smith, GGB
	Dereck O'Meara, EEOB
	Yi Zhai, CMDB
	Andrea Vu, Plant Pathology
	Steven Bolaris, GGB
	Dinusha Maheepala Mudalige, Plant Biology
	Nuttapon Pombubpa, Plant Pathology ★
	Derreck Carter-House, Plant Pathology ★
	Sawyer Masonjones, GGB ★
	Jesús Peña, Microbiology ★
	Nathan Robinett, Joint Doctoral Program in Evolutionary Biology, SDSU-UCR
	Katherine Picard, UPGG - Duke University
	Edgar Medina, UPGG - Duke University
	Lluvia Vargas, Microbiología - CICESE, MEXICO
	Dan Vanderpool, Biology, University of Montana

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

- 2016 · *Fungal population genomics of emerging diseases in plants, frogs, and people*  
Mycological Society of America 2016 Meeting. Berkeley, CA.
- *Genomes of early diverging fungi enable new insights into the evolution of complexity in fungi*  
CIFAR Integrated Microbial Biodiversity Program/Review, Toronto, ON, CANADA.
- *Genome evolution in early diverging fungi from the 1000 fungal genomes perspective*  
Plenary Speaker. 13th European Fungal Genetics Conference. Paris, France.
- *A Novel DNA transposon is recognized and silenced by Meiotic Silencing by small RNAs*  
Neurospora Conference. Asilomar Conference Center, Pacific Grove, CA.
- *Insights from the 1000 Fungal Genomes project: Comparative biology and phylogeny*  
University Program in Genetics & Genomics. Duke University, Durham, NC.
- *Genomics of early diverging fungi for phylogeny and comparative biology*  
Dept of Plant Pathology. University of California, Davis, CA.
- *Insights from the 1000 Fungal Genomes project: Comparative biology and phylogeny*  
University of Exeter. United Kingdom.
- 2015 · *Evolutionary Genomics of Early Branches of the Fungal Tree of Life*  
Exploring the genomic complexity and diversity of eukaryotes. EMBO Conference, San Feliu de Guixols, SPAIN.

- *Comparing molecular and morphological fungal evolution through studies of fungal genomes*  
XI CONGRESO NACIONAL DE MICOLOGIA, Sociedad Mexicana de Micologia. Merida, Yucatan, MEXICO.
- *Evolution of complexity in fungi from evolutionary genomics of early diverging lineage*  
School of Plant Sciences, University of Arizona, Tucson, AZ.
- *Evolutionary genomics of early branches of the fungal tree & the ZyGoLife project*  
Eighth International Conference on Mycorrhiza. Flagstaff, AZ.
- *Evolutionary genomics of early branches of the fungal tree: A view from the 1000 Fungal Genomes Project and ZyGoLife Project*  
Mycological Society of America 2015 Meeting. Edmonton, AB, CANADA.
- *Evolutionary genomics of early branches of the fungal tree: The 1000 Fungal Genomes Project*  
Society for Molecular Biology & Evolution 2015. Vienna, Austria.
- *Evolutionary and functional genomics in early diverging fungi*  
Bioinformatics Seminar series. University of California, Los Angeles.
- *Evolutionary and functional genomics in early diverging fungi*  
University of California, Merced, CA.
- *Phylogenomics of the Zygomycete lineages: Exploring phylogeny and genome evolution*  
28th Fungal Genetics Conference. Asilomar Conference Center, Pacific Grove, CA.
- *Evolutionary and functional genomics in early diverging fungi*  
Center for Genome Research and Biocomputing Seminar. Oregon State University, Corvallis, OR.
- *Clues to multicellular evolution of fungi from comparative genomics & studies of early diverging fungi*  
Microbiology and Molecular Genetics. Oklahoma State University, Stillwater, OK.

October 30, 2016