

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:

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:

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. Mondo, S., Dannebaum, R., Kuo, R., LaButti, K., Haridas, S., Kuo, A., Salamov, A., Ahrendt, S., Lipzen, A., Lindquist, E., Sullivan, W., Andreopoulos, W., Clum, A., Daum, C., Ramamoorthy, G., Gryganskyi, A., Culley, D., Magnuson, J., James, T., O'Malley, M., **Stajich**, J. E., Spatafora, J., Visel, A., Louie, K., Lau, R., Bewick, A., Schmitz, B., Northen, T., Bowen, B., and Grigoriev, I. V. 2017. Pervasive adenine N6-methylation of active genes in fungi. *Nature Genetics* In Press.
2. 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* doi:10.7287/peerj.preprints.2397v1. In Press.
3. 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.
4. 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.
5. 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.

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. 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.
7. 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.
8. 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., Baptista, 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.
9. 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.
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. Mélida, H., Sain, D., **Stajich**, J. E., and Bulone, V. 2015. Deciphering the uniqueness of microcomycotina cell walls by combining biochemical and phylogenomic approaches. *Environmental Microbiology* 17(5):1649–62. doi:10.1111/1462-2920.12601.
17. 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.

18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.

30. 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.
31. 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., Lundeberg, 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.
32. 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.
33. 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.
34. 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.
35. **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.
36. 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.
37. 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.
38. 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.
39. 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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- Ferriera, S., Fuerstenberg, S. I., Gachon, C. M., Gaulin, E., Govers, F., Grenville-Briggs, L., Horner, N., Hostetler, J., Jiang, R. H., Johnson, J., Krajaeun, T., Lin, H., Meijer, H. J., Moore, B., Morris, P., Phuntmart, V., Puiu, D., Shetty, J., **Stajich**, J. E., Tripathy, S., Wawra, S., van West, P., Whitty, B. R., Coutinho, P. M., Henrissat, B., Martin, F., Thomas, P. D., Tyler, B. M., De Vries, R. P., Kamoun, S., Yandell, M., Tisserat, N., and Buell, C. R. 2010. Genome sequence of the necrotrophic plant pathogen, *Pythium ultimum*, reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol* 11(7):R173. doi:10.1186/gb-2010-11-7-r73.
42. 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.
 43. 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.
 44. **Stajich**, J. E., Wilke, S. K., Ahrén, D., Au, C. H., Birren, B. W., Borodovsky, M., Burns, C., Canbäck, B., Casselton, L. A., Cheng, C. K., Deng, J., Dietrich, F. S., Fargo, D. C., Farman, M. L., Gathman, A. C., Goldberg, J., Guigó, R., Hoegger, P. J., Hooker, J. B., Huggins, A., James, T. Y., Kamada, T., Kilaru, S., Kodira, C., Kües, U., Kupfer, D., Kwan, H. S., Lomsadze, A., Li, W., Lilly, W. W., Ma, L.-J., Mackey, A. J., Manning, G., Martin, F., Muraguchi, H., Natvig, D. O., Palmerini, H., Ramesh, M. A., Rehmeier, C. J., Roe, B. A., Shenoy, N., Stanke, M., Ter-Hovhannisyan, V., Tunlid, A., Velagapudi, R., Vision, T. J., Zeng, Q., Zolan, M. E., and Pukkila, P. J. 2010. Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*). *Proc Natl Acad Sci U S A* 107(26):11889–11894. doi:10.1073/pnas.1003391107.
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 47. Sharpton, T. J., **Stajich**, J. E., Rounsley, S. D., Gardner, M. J., Wortman, J. R., Jordar, V. S., Maiti, R., Kodira, C. D., Neafsey, D. E., Zeng, Q., Hung, C.-Y., McMahan, C., Muszewska, A., Grynberg, M., Mandel, M. A., Kellner, E. M., Barker, B. M., Galgiani, J. N., Orbach, M. J., Kirkland, T. N., Cole, G. T., Henn, M. R., Birren, B. W., and Taylor, J. W. 2009. Comparative genomic analyses of the human fungal pathogens *Coccidioides* and their relatives. *Genome Res* 19(10):1722–1731. doi:10.1101/gr.087551.108.
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Submitted Manuscripts and Preprints

1. Cissé, O. H. and **Stajich**, J. E. 2016. FGMP: assessing fungal genome completeness and gene content. *bioRxiv* doi:10.1101/049619. 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. 2017. *Bifiguratus adelaidae* gen. et sp. nov., a new lineage of Mucoromycotina with endophytic and soil-dwelling strains. Submitted.
3. Beaudet, D., Chen, E., Ndikumana, S., Dalpé, Y., Séguin, S., Farinelli, L., **Stajich**, J. E., and Corradi, N. 2017. Single-cell transcriptomics reveals hidden functional diversity and novel phylogenetic affiliations within arbuscular mycorrhizal fungi Submitted.
4. 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 Submitted.
5. Coleine, C., Masonjones, S., Selbmann, L., Zucconi, L., Onofri, S., Pacelli, C., and **Stajich**, J. E. 2017. Draft genomes of the Antarctic endolithic fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018. *Genome Announcements* Submitted.

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., 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 "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 <i>mPing</i> 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)
- 2017-2020 Univ of California-Office of the President, MRPI. \$105k (\$1.7M total award)
 “UC Valley Fever Research Initiative”
 Role: Co-PI. Collaborative award with PI: Anita Sil (UCSF)
- 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.
2017–	Yan Wang, PhD.

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 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
- 2015–16 Zhinquan Song, Visiting Graduate Student (Guangyi Wang Lab), Tianjin University, CHINA
- 2015 (Fall) John Yinka Odebo, 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
- 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, Microbiology Kun Liu, Plant Biology
ongoing	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
 - 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 Micologia. 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.

April 24, 2017