

# 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., Genetics and Genomics, Duke University, Durham, NC. Advisor: Dr. Fred S Dietrich  
1995–1999 B.S., 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:

2020 Fellow, Mycological Society of America  
2020 Fellow, American Academy of Microbiology, American Society of Microbiology  
2019–2024 CIFAR Fellow (Fungal Kingdom: Threats & Opportunities)  
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:

### Peer Reviewed Publications

1. Baxter, R. V., Othmane, K. B., Rochelle, J. M., **Stajich**, J. E., Hulette, C., Dew-Knight, S., Hentati, F., Hamida, M. B., Bel, S., Stenger, J. E., Gilbert, J. R., Pericak-Vance, M. A., and Vance, J. M. 2002. Ganglioside-induced differentiation-associated protein-1 is mutant in Charcot-Marie-Tooth disease type 4A/8q21. *Nat Genet* 30(1):21–22. doi:10.1038/ng796.
2. **Stajich**, J. E., Block, D., Boulez, K., Brenner, S. E., Chervitz, S. A., Dagdigian, C., Fuellen, G., Gilbert, J. G. R., Korf, I., Lapp, H., Lehtväslaiho, H., Matsalla, C., Mungall, C. J., Osborne, B. I., Pocock, M. R., Schattner, P., Senger, M., Stein, L. D., Stupka, E., Wilkinson, M. D., and Birney, E. 2002. The Bioperl toolkit: Perl modules for the life sciences. *Genome Res* 12(10):1611–1618. doi:10.1101/gr.361602.
3. Stein, L. D., Mungall, C., Shu, S., Caudy, M., Mangone, M., Day, A., Nickerson, E., **Stajich**, J. E., Harris, T. W., Arva, A., and Lewis, S. 2002. The generic genome browser: a building block for a model organism system database. *Genome Res* 12(10):1599–1610. doi:10.1101/gr.403602.
4. Hahn, M. W., **Stajich**, J. E., and Wray, G. A. 2003. The effects of selection against spurious transcription factor binding sites. *Mol Biol Evol* 20(6):901–906. doi:10.1093/molbev/msg096.

5. Stein, L. D., Bao, Z., Blasiar, D., Blumenthal, T., Brent, M. R., Chen, N., Chinwalla, A., Clarke, L., Clee, C., Coghlan, A., Coulson, A., D'Eustachio, P., Fitch, D. H. A., Fulton, L. A., Fulton, R. E., Griffiths-Jones, S., Harris, T. W., Hillier, L. W., Kamath, R., Kuwabara, P. E., Mardis, E. R., Marra, M. A., Miner, T. L., Minx, P., Mullikin, J. C., Plumb, R. W., Rogers, J., Schein, J. E., Sohrmann, M., Spieth, J., **Stajich**, J. E., Wei, C., Willey, D., Wilson, R. K., Durbin, R., and Waterston, R. H. 2003. The genome sequence of *Caenorhabditis briggsae*: a platform for comparative genomics. *PLoS Biol* 1(2):E45. doi:10.1371/journal.pbio.0000045.
6. Kraus, P. R., Boily, M.-J., Giles, S. S., **Stajich**, J. E., Allen, A., Cox, G. M., Dietrich, F. S., Perfect, J. R., and Heitman, J. 2004. Identification of *Cryptococcus neoformans* temperature-regulated genes with a genomic-DNA microarray. *Eukaryot Cell* 3(5):1249–1260. doi:10.1128/EC.3.5.1249-1260.2004.
7. Fraser, J. A., Giles, S. S., Wenink, E. C., Geunes-Boyer, S. G., Wright, J. R., Diezmann, S., Allen, A., **Stajich**, J. E., Dietrich, F. S., Perfect, J. R., and Heitman, J. 2005. Same-sex mating and the origin of the Vancouver Island *Cryptococcus gattii* outbreak. *Nature* 437(7063):1360–1364. doi:10.1038/nature04220.
8. Hahn, M. W., Bie, T. D., **Stajich**, J. E., Nguyen, C., and Cristianini, N. 2005. Estimating the tempo and mode of gene family evolution from comparative genomic data. *Genome Res* 15(8):1153–1160. doi:10.1101/gr.3567505.
9. Leman, S. C., Chen, Y., **Stajich**, J. E., Noor, M. A. F., and Uyenoyama, M. K. 2005. Likelihoods from summary statistics: recent divergence between species. *Genetics* 171(3):1419–1436. doi:10.1534/genetics.104.040402.
10. Mitreva, M., McCarter, J. P., Arasu, P., Hawdon, J., Martin, J., Dante, M., Wylie, T., Xu, J., **Stajich**, J. E., Kapulkin, W., Clifton, S. W., Waterston, R. H., and Wilson, R. K. 2005. Investigating hookworm genomes by comparative analysis of two *Ancylostoma* species. *BMC Genomics* 6(1):58. doi:10.1186/1471-2164-6-58.
11. **Stajich**, J. E. and Hahn, M. W. 2005. Disentangling the effects of demography and selection in human history. *Mol Biol Evol* 22(1):63–73. doi:10.1093/molbev/msh252.
12. Hesselberth, J. R., Miller, J. P., Golob, A., **Stajich**, J. E., Michaud, G. A., and Fields, S. 2006. Comparative analysis of *Saccharomyces cerevisiae* WW domains and their interacting proteins. *Genome Biol* 7(4):R30. doi:10.1186/gb-2006-7-4-r30.
13. Cramer, R. A., **Stajich**, J. E., Yamanaka, Y., Dietrich, F. S., Steinbach, W. J., and Perfect, J. R. 2006. Phylogenomic analysis of non-ribosomal peptide synthetases in the genus *Aspergillus*. *Gene* 383:24–32. doi:10.1016/j.gene.2006.07.008.
14. Giles, S. S., **Stajich**, J. E., Nichols, C., Gerrald, Q. D., Alspaugh, J. A., Dietrich, F., and Perfect, J. R. 2006. The *Cryptococcus neoformans* catalase gene family and its role in antioxidant defense. *Eukaryot Cell* 5(9):1447–1459. doi:10.1128/EC.00098-06.
15. **Stajich**, J. E. and Dietrich, F. S. 2006. Evidence of mRNA-mediated intron loss in the human-pathogenic fungus *Cryptococcus neoformans*. *Euk Cell* 5(5):789–793. doi:10.1128/EC.5.5.789-793.2006.
16. Kämper, J., Kahmann, R., Bölker, M., Ma, L.-J., Brefort, T., Saville, B. J., Banuett, F., Kronstad, J. W., Gold, S. E., Müller, O., Perlin, M. H., Wösten, H. A. B., de Vries, R., Ruiz-Herrera, J., na, C. G. R.-P., Snetselaar, K., McCann, M., Pérez-Martín, J., Feldbrügge, M., Basse, C. W., Steinberg, G., Ibeas, J. I., Holloman, W., Guzman, P., Farman, M., **Stajich**, J. E., Sentandreu, R., González-Prieto, J. M., Kennell, J. C., Molina, L., Schirawski, J., Mendoza-Mendoza, A., Greilinger, D., Münch, K., Rössel, N., Scherer, M., Vranes, M., Ladendorf, O., Vincon, V., Fuchs, U., Sandrock, B., Meng, S., Ho, E. C. H., Cahill, M. J., Boyce, K. J., Klose, J., Klosterman, S. J., Deelstra, H. J., Ortiz-Castellanos, L., Li, W., Sanchez-Alonso, P., Schreier, P. H., Häuser-Hahn, I., Vaupel, M., Koopmann, E., Friedrich, G., Voss, H., Schlüter, T., Margolis, J., Platt, D., Swimmer, C., Gnirke, A., Chen, F.,

- Vysotskaia, V., Mannhaupt, G., Güldener, U., Münsterkötter, M., Haase, D., Oesterheld, M., Mewes, H.-W., Mauceli, E. W., DeCaprio, D., Wade, C. M., Butler, J., Young, S., Jaffe, D. B., Calvo, S., Nusbaum, C., Galagan, J., and Birren, B. W. 2006. Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. *Nature* 444(7115):97–101. doi:10.1038/nature05248.
17. James, T. Y., Kauff, F., Schoch, C. L., Matheny, P. B., Hofstetter, V., Cox, C. J., Celio, G., Gueidan, C., Fraker, E., Miadlikowska, J., Lumbsch, H. T., Rauhut, A., Reeb, V., Arnold, A. E., Amtoft, A., **Stajich**, J. E., Hosaka, K., Sung, G.-H., Johnson, D., O'Rourke, B., Crockett, M., Binder, M., Curtis, J. M., Slot, J. C., Wang, Z., Wilson, A. W., Schüßler, A., Longcore, J. E., O'Donnell, K., Mozley-Standridge, S., Porter, D., Letcher, P. M., Powell, M. J., Taylor, J. W., White, M. M., Griffith, G. W., Davies, D. R., Humber, R. A., Morton, J. B., Sugiyama, J., Rossman, A. Y., Rogers, J. D., 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.
  18. Demuth, J. P., Bie, T. D., **Stajich**, J. E., Cristianini, N., and Hahn, M. W. 2006. The evolution of mammalian gene families. *PLoS One* 1:e85. doi:10.1371/journal.pone.0000085.
  19. Fitzpatrick, D. A., Logue, M. E., **Stajich**, J. E., and Butler, G. 2006. A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. *BMC Evol Biol* 6:99. doi:10.1186/1471-2148-6-99.
  20. Erwin, T. A., Jewell, E. G., Love, C. G., Lim, G. A. C., Li, X., Chapman, R., Batley, J., **Stajich**, J. E., Mongin, E., Stupka, E., Ross, B., Spangenberg, G., and Edwards, D. 2007. BASC: an integrated bioinformatics system for *Brassica* research. *Nucleic Acids Res* 35(Database issue):D870–D873. doi:10.1093/nar/gkl998.
  21. Harrison, L. B., Yu, Z., **Stajich**, J. E., Dietrich, F. S., and Harrison, P. M. 2007. Evolution of budding yeast prion-determinant sequences across diverse fungi. *J Mol Biol* 368(1):273–282. doi:10.1016/j.jmb.2007.01.070.
  22. Fraser, J. A., **Stajich**, J. E., Tarcha, E. J., Cole, G. T., Inglis, D. O., Sil, A., and Heitman, J. 2007. Evolution of the mating type locus: insights gained from the dimorphic primary fungal pathogens *Histoplasma capsulatum*, *Coccidioides immitis*, and *Coccidioides posadasii*. *Eukaryot Cell* 6(4):622–629. doi:10.1128/EC.00018-07.
  23. **Stajich**, J. E., Dietrich, F. S., and Roy, S. W. 2007. Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. *Genome Biol* 8(10):R223. doi:10.1186/gb-2007-8-10-r223.
  24. Hu, G., Liu, I., Sham, A., **Stajich**, J. E., Dietrich, F. S., and Kronstad, J. W. 2008. Comparative hybridization reveals extensive genome variation in the aids-associated pathogen *Cryptococcus neoformans*. *Genome Biol* 9(2):R41. doi:10.1186/gb-2008-9-2-r41.
  25. Lilly, W. W., **Stajich**, J. E., Pukkila, P. J., Wilke, S. K., Inoguchi, N., and Gathman, A. C. 2008. An expanded family of fungalsin extracellular metallopeptidases of *Coprinopsis cinerea*. *Mycol Res* 112(Pt 3):389–398. doi:10.1016/j.mycres.2007.11.013.
  26. Martin, F., Aerts, A., Ahrén, D., Brun, A., Danchin, E. G. J., Duchaussoy, F., Gibon, J., Kohler, A., Lindquist, E., Pereda, V., Salamov, A., Shapiro, H. J., Wuyts, J., Blaudez, D., Buée, M., Brokstein, P., Canbäck, B., Cohen, D., Courty, P. E., Coutinho, P. M., Delaruelle, C., Detter, J. C., Deveau, A., DiFazio, S., Duplessis, S., Fraissinet-Tachet, L., Lucic, E., Frey-Klett, P., Fourrey, C., Feussner, I., Gay, G., Grimwood, J., Hoegger, P. J., Jain, P., Kilaru, S., Labbé, J., Lin, Y. C., Legué, V., Tacon, F. L., Marmeisse, R., Melayah, D., Montanini, B., Muratet, M., Nehls, U., Niculita-Hirzel, H., Secq, M. P. O.-L., Peter, M., Quesneville, H., Rajashekar, B., Reich, M., Rouhier, N., Schmutz, J., Yin, T., Chalot, M., Henrissat, B., Kües, U., Lucas, S., de Peer, Y. V., Podila, G. K., Polle, A., Pukkila, P. J., Richardson, P. M., Rouzé, P., Sanders, I. R., **Stajich**, J. E., Tunlid, A., Tuskan, G., and Grigoriev,

- I. V. 2008. The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature* 452(7183):88–92. doi:10.1038/nature06556.
27. Regier, J. C., Shultz, J. W., Ganley, A. R. D., Hussey, A., Shi, D., Ball, B., Zwick, A., **Stajich, J. E.**, Cummings, M. P., Martin, J. W., and Cunningham, C. W. 2008. Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. *Syst Biol* 57(6):920–938. doi:10.1080/10635150802570791.
  28. Rosenblum, E. B., **Stajich, J. E.**, Maddox, N., and Eisen, M. B. 2008. Global gene expression profiles for life stages of the deadly amphibian pathogen *Batrachochytrium dendrobatidis*. *Proc Natl Acad Sci U S A* 105(44):17034–17039. doi:10.1073/pnas.0804173105.
  29. Fisher, M. C., Bosch, J., Yin, Z., Stead, D. A., Walker, J., Selway, L., Brown, A. J. P., Walker, L. A., Gow, N. A. R., **Stajich, J. E.**, and Garner, T. W. J. 2009. Proteomic and phenotypic profiling of the amphibian pathogen *Batrachochytrium dendrobatidis* shows that genotype is linked to virulence. *Mol Ecol* 18(3):415–429. doi:10.1111/j.1365-294X.2008.04041.x.
  30. 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.
  31. Nowrousian, M., **Stajich, J. E.**, Engh, I., Espagne, E., Kamerewerd, J., Kempken, F., Kunstmann, B., Kuo, H.-C., Osiewacz, H. D., Pöggeler, S., Read, N., Seiler, S., Smith, K., Zickler, D., Kück, U., and Freitag, M. 2010. Next-generation sequencing of the 40 Mb genome of the filamentous fungus *Sordaria macrospora*. *PLoS Genetics* 6(4):e1000891. doi:10.1371/journal.pgen.1000891.
  32. Neafsey, D. E., Barker, B. M., Sharpton, T. J., **Stajich, J. E.**, Park, D. J., Whiston, E., Hung, C.-Y., McMahan, C., White, J., Sykes, S., Heiman, D., Young, S., Zeng, Q., Abouelleil, A., Aftuck, L., Bessette, D., Brown, A., Fitzgerald, M., Lui, A., Macdonald, J. P., Priest, M., Orbach, M. J., Galgiani, J. N., Kirkland, T. N., Cole, G. T., Birren, B. W., Henn, M. R., Taylor, J. W., and Rounsley, S. D. 2010. Population genomic sequencing of *Coccidioides* fungi reveals recent hybridization and transposon control. *Genome Res* 20(7):938–946. doi:10.1101/gr.103911.109.
  33. **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.
  34. 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.
  35. 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.

36. Lévesque, C. A., Brouwer, H., Cano, L., Hamilton, J. P., Holt, C., Huitema, E., Raffaele, S., Robideau, G. P., Thines, M., Win, J., Zerillo, M. M., Beakes, G. W., Boore, J. L., Busam, D., Dumas, B., Ferreira, S., Fuerstenberg, S. I., Gachon, C. M., Gaulin, E., Govers, F., Grenville-Briggs, L., Horner, N., Hostetler, J., Jiang, R. H., Johnson, J., Krajaejun, 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.
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38. Burns, C., **Stajich, J. E.**, Rechtsteiner, A., Hanlon, S. E., Wilke, S. K., Palmerini, H. J., Savitsky, 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.
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. 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.
41. 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.
42. **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.
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.
44. 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.
45. 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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## Books and Book Chapters

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## Commentaries and Book Reviews

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## Essays

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## 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

2011-2017	National Science Foundation. IOS-1027542. (No Cost Ext thru 02/2021) “CPGS: Genome-wide impact of <i>mPing</i> transposition on rice phenotypic diversity.” Role: Co-I. PI: SR Wessler (UC Riverside). <a href="http://dynamiterice.org">http://dynamiterice.org</a>
2015-2018	National Science Foundation. GO Life DEB-1441715. (No Cost Ext thru 08/2020) “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) <a href="http://zygolife.org">http://zygolife.org</a>
2017-2020	Univ of California-Office of the President, MRPI. “UC Valley Fever Research Initiative” Role: Co-PI. PI: Anita Sil (UCSF) and Co-PIs at UC Berkeley, UC Merced, UC San Diego
2017-2021	National Institutes of Health. R01-AI127548-01A1 “Evolved Heterogeneity contributes to chronic fungal lung infections” Role: Senior Personnel. PI: D Hogan (Dartmouth)
2017-2022	National Institutes of Health. R01-AI130128-01A1 “Evolution of <i>Aspergillus fumigatus</i> virulence” Role: Senior Personnel. PI: RA Cramer, Jr (Dartmouth)
2019-2021	National Institutes of Health. R15-GM132869 “Understanding The Mechanisms Of Spatial Protein Quality Control In A Model Filamentous Fungus” Role: Senior Personnel. PI: Egans, M (U Arkansas)
2019-2022	Univ of California-Office of the President “Investigating fundamental gaps in Valley Fever research” Role: Co-PI. PI: Anita Sil (UCSF) and Co-PIs at UC Berkeley, UC Davis, UC Merced, UC San Diego
2019-2020	City of Hope / Univ of California-Riverside “Antifungal drug resistance in Southern California: Discovery of novel mechanisms by genomics and proteomics.” Role: PI with Co-PIs M Kalkum and S Dadwal at City of Hope Hospital
2019-2024	Canadian Institute For Advanced Research “Fungal Kingdom: Threats and Opportunities” Role: CIFAR Fellow. PI/Directors: L Cowen and J Heitman
2020-2021	Canadian Institute For Advanced Research “Pilot investigation of avian-origin <i>Aspergillus fumigatus</i> infections in the United States” Role: PI. Co-PI: David Blehert, National Wildlife Health Center, USGS
2020-2023	Gordon and Betty Moore Foundation



2020-2022 “New Tools for Advancing Model Systems in Aquatic Symbiosis”  
Role: Co-PI. PI: Lillian Fritz-Laylin. With Co-PI Tim James  
California Conservation Genomics Project  
“Landscape and Population Genomics of the lichen *Acarospora socialis* in California”  
Role: PI.

2020-2023 California Department of Agriculture / Glassywinged Sharptshooter Board  
“CRISPR-mediated genome modification of *Homalodisca vitripennis* for the genetic control of Pierce’s disease”  
Role: Co-PI. PI Peter Atkinson, UCR

2020-2021 USDA-ANIMAL AND PLANT HEALTH INSPECTION SERVICE  
“Tracking seasonal changes of endophytic communities in *Fusarium* dieback – invasive shot hole borers host trees in California.”  
Role: Co-I. PI Akif Eskalen, UC Davis

2020 Burroughs Wellcome Fund.  
“Meeting grant to support 2020 Fungal Cellular and Molecular Biology Gordon Research Conference”  
Role: PI.

**Completed support**

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

2011-2012 UC Riverside, Chancellor’s Strategic Investment Funds.  
“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.  
“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.  
“Annotation of *Cryptococcus* genomes by comprehensive curation of published literature”  
Role: PI. Co-I G Sherlock (Stanford)

2011-2014 Alfred P. Sloan Foundation.  
“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.  
“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)

2011-2016 W.M. Keck Foundation. (No Cost Extension thru 2018)  
“New Active Transposable Elements for Mosquito Genetics.”  
Role: Co-I. PI: SR Wessler (UC Riverside). Co-I: P Atkinson (UC Riverside).

2017 Burroughs Wellcome Fund.  
“Meeting grant to support Fungal Cell Wall (FCW2017) Conference in Ensenada, Mexico”  
Role: PI.

2016-2019 National Science Foundation. DEB-1557110. (No Cost Ext thru 04/2020)  
“Collaborative Research: Phylogenomics and evolutionary history of the anaerobic fungal group, Neocallimastigomycota”  
Role: PI. Collaborative linked award PI: N Youssef (Oklahoma State)

## **Service:**

### **University and Departmental**

2020-2022 Chair, UC Riverside Academic Senate (01-Sep-2020)  
2017-2020 UC Riverside Graduate Council. Chair & member of Senate Executive Council (2018-2020).  
2015-2020 Director, Microbiology Graduate Program (except Sabbatical 2016-17)  
2014-2015, 2018-2020 Graduate Advisor, Microbiology Graduate Program  
2015-16, 17-2018 Admissions Advisor, Microbiology Graduate Program

### **Editorial Boards**

2020- Editorial Board, Annual Reviews of Microbiology  
2019- Associate Editor, Genome Biology & Evolution  
2019- Associate Editor, Mycologia  
2018- Senior Editor, Microbial Resource Announcements  
2018- Associate Editor, Genetics  
2016- Editorial Board, Current Opinion in Microbiology  
2015-2019 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**

2018-2022 Co-Chair (2020, moved to 2022) of Cellular and Molecular Fungal Biology, Gordon Research Conference; Co-Vice Chair (2018).  
2017-2020 Karling Lecture Committee, Mycological Society of America (Chair 2019-2020)  
2018-2021 Councilor for Cell Biology & Physiology. Mycological Society of America.  
2014-2018 Neurospora Policy Committee, Co-Organized 2016 Neurospora conference  
2013-2019 Fungal Genetics Policy Committee  
2012- 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 <http://www.open-bio.org/>  
2001-2015 Co-Project leader, BioPerl. <http://www.bioperl.org/>

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

2015- American Academy of Arts and Sciences  
2007- Mycological Society of America  
2007- American Society for Microbiology, Fellow (2020)

2004– Genetics Society of America  
 2004– Society for Molecular Biology and Evolution  
 2002– Open Bioinformatics Foundation  
 2002– International Society for Computational Biology

### **Graduate Students:**

2009–13 PhD student, Divya Sain. Genetics, Genomics, & Bioinformatics.  
 Current: Bioinformatics Scientist at Ambry Genetics.  
 2010–12 MS student, Yi (Zoe) Zhou. Genetics, Genomics, & Bioinformatics.  
 Current: Biostatistician at dMed Biopharmaceutical Co.  
 2010–14 PhD student, Yizhou Wang. Plant Biology.  
 Current: Research Bioinformatician and Associate Director at Applied Genomics, Computation & Translational Core, Cedars-Sinai.  
 2011–15 PhD student, Steven Ahrendt. Genetics, Genomics, & Bioinformatics.  
 Current: Data Scientist at DOE Joint Genome Institute.  
 2016–19 PhD Student, Derreck Carter-House. Plant Pathology.  
 Current: Postdoc, UC Riverside  
 2015– PhD Student, Sawyer Masonjones. Genetics, Genomics, & Bioinformatics  
 2015– PhD Student, Nuttapom Pombubpa. Plant Pathology  
 2016– PhD Student, Jesús Peña, Microbiology  
 2017– PhD Student, Julia Adams, Plant Biology  
 2017– PhD Student, Tania Kurbessoian, Microbiology  
 2020– PhD Student, Talieh Ostovar, Evolutionary Biology, San Diego State - UCR Joint Doctoral Program

### **Postdoctoral Fellows:**

2010–2011 John Abramyan, Ph.D.  
 Current: Assistant Professor, Univ of Michigan-Dearborn  
 2011–2014 Sofia Robb, Ph.D.  
 Current: Genomics Scientist at Stowers Institute.  
 2012–2014 Brad Cavinder, Ph.D.  
 Current: Research Associate at Michigan State University  
 2012–2015 Peng Liu, Ph.D.  
 Current: Research Associate, Yangzhou University, CHINA  
 2013–2019 Jinfeng Chen, Ph.D.  
 Current: Staff Scientist, City of Hope, CA  
 2013–2015 Ousmane Cissé, Ph.D. - Swiss National Science Foundation Fellow.  
 Current: Staff Scientist at Critical Care Department, NIH Clinical Center.  
 2014–2015 Rodrigo Olarte, Ph.D.  
 Current: NSF Postdoctoral Fellow at Univ of Minnesota.  
 2017–19 Yan Wang, Ph.D.  
 Current: Assistant Professor, University of Toronto-Scarborough.  
 2019– Lotus Lofgren, Ph.D.  
 2020– Ying Sun, Ph.D.

### **Visitors:**

2010–2013 (4, 2-3 month vists) Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWE-DEN  
 2010 Suzanne Joneson, PhD, Department of Biology, University of Idaho  
 2011 Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, Bo-

gotia, COLOMBIA  
 2012 Andrii Gryganski, PhD, Visiting Researcher, Duke University  
 2013–2014 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 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 John Yinka Odebode, Visiting Graduate Student on a West African Research Association Fellowship, University of Lagos, NIGERIA.  
 2015 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  
 2017 Jane Lind Nybo, Visiting Graduate Student, Technical University of Denmark, Copenhagen, DENMARK  
 2019 Guillermo Vidal-Diez de Ulzurrun, Visiting Postdoc scientist, IMB, Academia Sinica, Taipei, Taiwan  
 2019–2020 Felipe Salgado, Federal University of Rio de Janeiro, BRAZIL.  
 2020– Omar Valencia, Volunteer.

### Staff:

2011–2012 Daniel Borcharding, Programmer (FungiDB).  
 Current: Senior Software Build Engineer, Apple, Inc.  
 2011–2013 Raghuraman Ramamurthy, Programmer (FungiDB).  
 Current: Senior Bioinformatics Associate, Gilead Sciences.  
 2013–2014 Venkatesh Muktali, Bioinformatics Scientist (FungiDB).  
 Current: Product Manager, Thermo Fisher Scientific.  
 2017–2018 Jericho Ortanez, Junior Specialist. Current: Graduate Student, UC Riverside

### 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  
 2011–2016 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: Career Development Coordinator at Unitek 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: MD student at UCSF  
 2012–2014 Megna Tiwari, UCR. Current: PhD student at Univ of Georgia  
 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)  
 2015–2017 Justin Shen, UCR.  
 2015–2016 Serena Choi, UCR.  
 2015–2017 Dillon McDonald, UCR Summer HSI-STEM (2015) and lab researcher  
 2015 Christina Uriarte, UCR. Pre-MARC USTAR student.  
 2015–2017 Jericho Ortanez, UCR. Current: PhD student UCR Microbiology  
 2015–2016 Leandra Ibrahim, UCR.  
 2015–2017 Deane Kim, UCR.  
 2016–2017 Georgiy Smirnov, UCR.  
 2016–2018 Meng (Josh) Chung, UCR.  
 2017–2019 Estefania Caldera, UCR.  
 2018 Lily Bautista, UCR.  
 2018–2020 Renata Haro, UCR.  
 2018– Skylar McDonald, UCR.  
 2019 Saisuki Putumbaka, The College of New Jersey, Summer REU student.  
 2019–2020 Nicole Leung, UCR.

### **Dissertation 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  
 Kun Liu, PhD, Plant Biology  
 2017 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  
 2018 Cynthia Dick, EEOB  
 Dan Vanderpool, Biology (University of Montana)  
 Steven Bolaris, GGB △  
 2019 Joseph Carrillo, Plant Pathology △  
 Dinusha Maheepala Mudalige, Plant Biology  
 Aaron Robinson, Biology (University of New Mexico)  
 Courtney Collins, Plant Biology

	Edgar Medina, Genetics & Genomics (Duke University)
	Lluvia Vargas, Microbiología (CICESE, MEXICO)
	Derreck Carter-House, Plant Pathology *
	Nathan Robinett, Evolutionary Biology, Joint Doctoral Prog. SDSU-UCR
2020	Andrea Vu, Plant Pathology
	Nichole Ginnan, Plant Pathology
ongoing	Nuttapon Pombubpa, Plant Pathology *
	Sawyer Masonjones, GGB *
	Jesús Peña, Microbiology *
	Julia Adams, Plant Biology *
	Tania Kurbessoian, Microbiology *
	Beth Peacock, Plant Pathology
	Caleb Hubbard, Medical and Veterinary Entomology
	Alex Rajewski, Plant Biology
	Glen Morrison, Plant Biology
	Mari West, Entomology
	Yi Huang, Plant Biology
	Christopher Ficus, GGB
	Glen Morrison, Plant Biology
	Hannah Schulman, Microbiology
	Sarah Thorwall, Chemical and Environmental Engineering
	Samantha Smith, Entomology

\* Stajich is Dissertation advisor or  $\triangle$  co-advisor / substitute

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

- 2020 · Microbiology and Infectious Disease Grad Student retreat speaker, Univ Texas Health Sciences, Houston, TX (postponed)
- 2019 · Phylogenomics Workshop, Cesky Krumlov, Czech Republic
- Middle Tennessee State University, Murfreesboro, TN
- Rosie Perez Memorial Seminar, North Carolina State University, Raleigh, NC
- University of North Carolina, Chapel Hill, NC
- California State University, Northridge, CA
- 2018 · UC Riverside Data Science Series. Riverside, CA
- University of Nebraska-Lincoln, Lincoln, NE
- Creighton University, Omaha, NE
- Marine Fungi Workshop. Marine Biological Lab, Woods Hole, MA.
- 11th International Mycological Congress. San Juan, Puerto Rico
- CIFAR workshop "Microbial Pathogens in the Fungal Kingdom". Toronto, Ontario, CANADA
- 2017 · 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
- American Academy of Microbiology Colloquium on Fungal Pathogenesis. Washington, DC
- 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.
- Duke University, Durham, NC.
- University of California, Davis, CA.
- University of Exeter. United Kingdom.
- 2015 · EMBO Conference: Genomic complexity and diversity of eukaryotes. Sant Feliu de Guixols, SPAIN.
- XI CONGRESO NACIONAL DE MICOLOGIA, Sociedad Mexicana de Micologia. Merida, Yucatan, MEXICO. *Plenary Speaker*
- 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.
- University of California, Los Angeles, CA.
- University of California, Merced, CA.
- 28th Fungal Genetics Conference. Asilomar Conference Center, Pacific Grove, CA.
- Oregon State University, Corvallis, OR.
- Oklahoma State University, Stillwater, OK.

August 12, 2020