Jason E. Stajich

Contact Department of Microbiology & Plant Pathology and 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., 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 of 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., Lehväslaiho, 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 fungalysin 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., Ahrèn, 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., Rehmeyer, 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., Ferriera, 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.

37. Smith, K. M., Sancar, G., Dekhang, R., Sullivan, C. M., Li, S., Tag, A. G., Sancar, C., Bredeweg, E. L., Priest, H. D., McCormick, R. F., Thomas, T. L., Carrington, J. C., **Stajich**, J. E., Bell-Pedersen, D., Brunner, M., and Freitag, M. 2010. Transcription factors in light and circadian clock signaling networks revealed by genomewide mapping of direct targets for Neurospora White Collar Complex. *Eukaryot Cell* 9(10):1549–1556. doi:10.1128/EC.00154-10.

38. 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.

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.

46. 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.

47. 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.

48. 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.

49. 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.

50. 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.

51. 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.

52. Gioti, A., **Stajich**, J. E., and Johannesson, H. 2013. *N*eurospora and the dead-end hypothesis: genomic consequences of selfing in the model genus. *Evolution* 67(12):3600–3616. doi:10.1111/evo.12206.

53. 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.

54. 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.

55. 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.

56. 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.

57. 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.

58. Inglis, D. O., Skrzypek, M. S., Liaw, E., Moktali, V., Sherlock, G., and **Stajich**, J. E. 2014. Literature-based gene curation and proposed genetic nomenclature for *Cryptococcus*. *Eukaryot Cell* 13(7):878–883. doi:10.1128/EC.00083-14.
59. 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.
60. 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.
61. Mélida, H., Sain, D., **Stajich**, J. E., and Bulone, V. 2015. Deciphering the uniqueness of mucoromycotina cell walls by combining biochemical and phylogenomic approaches. *Environmental Microbiology* 17(5):1649–62. doi:10.1111/1462-2920.12601.
62. 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.
63. 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.
64. 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.
65. 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.
66. 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.
67. 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.
68. 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.
69. Lee, M. J., Geller, A. M., Bamford, N. C., Liu, H., Gravelat, F., Snarr, B. D., Le Mauff, F., Chabot, J., Ralph, B., Ostapska, H., Lehoux, M., Cerone, R. P., Baptisa, S. D., Vinogradov, E., **Stajich**, J. E., Filler, S. G., Howell, P. L., and Sheppard, D. C. 2016. Deacetylation of fungal exopolysaccharide mediates adhesion and biofilm formation. *mBio* 7(2):e00252–16. doi:10.1128/mBio.00252-16.
70. 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.

71. 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.

72. 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.

73. 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.

74. 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.

75. Ahrendt, S. R., Medina, E. M., Chia-en, A. C., and **Stajich**, J. E. 2017. Exploring the binding properties and structural stability of an opsin in the chytrid *Spizellomyces punctatus* using comparative and molecular modeling. *PeerJ* 5:e3206. doi:10.7717/peerj.3206.

76. Mondo, S. J., Dannebaum, R. O., Kuo, R. C., Louie, K. B., Bewick, A. J., LaButti, K., Haridas, S., Kuo, A., Salamov, A., Ahrendt, S. R., Lau, R., Bowen, B. P., Lipzen, A., Sullivan, W., Andreopoulos, B. B., Clum, A., Lindquist, E., Daum, C., Northen, T. R., Kunde-Ramamoorthy, G., Schmitz, R. J., Gryganskyi, A., Culley, D., Magnuson, J., James, T. Y., O'Malley, M. A., **Stajich**, J. E., Spatafora, J. W., Visel, A., and Grigoriev, I. V. 2017. Widespread adenine N6-methylation of active genes in fungi. *Nature Genetics* 49:964–968. doi:10.1038/ng.3859.

77. Sinha, S., Flibotte, S., Neira, M., Formby, S., Plemenitaš, A., Cimerman, N. G., Lenassi, M., Gostinčar, C., **Stajich**, J. E., and Nislow, C. 2017. Insight into the recent genome duplication of the halophilic yeast *Hortaea werneckii*: combining an improved genome with gene expression and chromatin structure. *G3: Genes|Genomes|Genetics* 7(7):2015–2022. doi:10.1534/g3.117.040691.

78. Torres-Cruz, T. J., Billingsley Tobias, T. L., Almatruk, M., Hesse, C. N., Kuske, C. R., Desirò, A., Benucci, G. M. N., Bonito, G., **Stajich**, J. E., Dunlap, C., Arnold, A. E., and Porras-Alfaro, A. 2017. *Bifiguratus adelaidae*, gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. *Mycologia* 109:363–378. doi:10.1080/00275514.2017.1364958.

79. Park, S.-Y., Scranton, M. A., **Stajich**, J. E., Yee, A., and Walling, L. L. 2017. Chlorophyte aspartyl aminopeptidases: Ancient origins, expanded families, new locations, and secondary functions. *PloS One* 12:e0185492. doi:10.1371/journal.pone.0185492.

80. Aryal, S. K., Carter-House, D., **Stajich**, J. E., and Dillman, A. R. 2017. Microbial associates of the southern mole cricket (*Scapteriscus borellii*) are highly pathogenic. *Journal of invertebrate pathology* 150:54–62. doi:10.1016/j.jip.2017.09.008.

81. Lu, L., Chen, J., Robb, S. M. C., Okumoto, Y., **Stajich**, J. E., and Wessler, S. R. 2017. Tracking the genome-wide outcomes of a transposable element burst over decades of amplification. *Proc Natl Acad Sci U S A* 114:E10550–E10559. doi:10.1073/pnas.1716459114.

82. Beaudet, D., Chen, E. C. H., Mathieu, S., Yildirir, G., Ndikumana, S., Yolande, D., Séuin, S., Farinelli, L., **Stajich**, J. E., and Corradi, N. 2017. Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. *DNA Research* 25(2):217–227. doi:10.1093/dnares/dsx051.

83. Na, F., Carrillo, J. D., Mayorquin, J. S., Ndinga-Muniania, C., **Stajich**, J. E., Stouthamer, R., Huang, Y.-T., Lin, Y.-T., Chen, C.-Y., and Eskalen, A. 2018. Two novel fungal symbionts *Fusarium kuroshium* sp. nov. and *Graphium kuroshium* sp. nov. of Kuroshio shot hole borer (*Euwallacea* sp. nr. *fornicatus*) cause Fusarium Dieback on woody host species in California. *Plant Disease* 102(6). doi:10.1094/PDIS-07-17-1042-RE.

84. Leonard, G., Labarre, A., Milner, D. S., Monier, A., Soanes, D., Wideman, J. G., Maguire, F., Stevens, S., Sain, D., Grau-Bové, X., Sebé-Pedrós, A., **Stajich**, J. E., Paszkiewicz, K., Brown, M. W., Hall, N., Wickstead, B., and Richards, T. A. 2018. Comparative genomic analysis of the 'pseudofungus' *Hyphochytrium catenoides*. *Open biology* 8:170184. doi:10.1098/rsob.170184.

85. Kirkland, T. N., Muszewska, A., and **Stajich**, J. E. 2018. Analysis of transposable elements in *Coccidioides* species. *Journal of fungi (Basel, Switzerland)* 4(1):13. doi:10.3390/jof4010013.

86. Gryganskyi, A. P., Golan, J., Dolatabadi, S., Mondo, S., Robb, S., Idnurm, A., Muszewska, A., Steczkiewicz, K., Masonjones, S., Liao, H.-L., Gajdeczka, M. T., Anike, F., Vuek, A., Anishchenko, I. M., Voigt, K., de Hoog, G. S., Smith, M. E., Heitman, J., Vilgalys, R., and **Stajich**, J. E. 2018. Phylogenetic and phylogenomic definition of *Rhizopus* species. *G3: Genes|Genomes|Genetics* doi:10.1534/g3.118.200235.

87. Collins, C., **Stajich**, J. E., Weber, S., Pombubpa, N., and Diez, J. 2018. Shrub range expansion alters diversity and distribution of soil fungal communities in a high elevation alpine ecosystem. *Molecular Ecology* 27:2461–2476. doi:10.1111/mec.14694.

88. Wang, Y., Stata, M., Wang, W., **Stajich**, J. E., White, M. M., and Moncalvo, J.-M. 2018. Comparative genomics reveals the core gene toolbox for the fungus-insect symbiosis. *mBio* 9(3):e00636–18. doi:10.1128/mBio.00636-18.

89. Cissé, O. H., Ma, L., Wei Huang, D., Khil, P. P., Dekker, J. P., Kutty, G., Bishop, L., Liu, Y., Deng, X., Hauser, P. M., Pagni, M., Hirsch, V., Lempicki, R. A., **Stajich**, J. E., Cuomo, C. A., and Kovacs, J. A. 2018. Comparative population genomics analysis of the mammalian fungal pathogen *Pneumocystis*. *mBio* 9(3):e00381–18. doi:10.1128/mBio.00381-18.

90. Gostinčar, C., **Stajich**, J. E., Zupančič, J., Zalar, P., and Gunde-Cimerman, N. 2018. Genomic evidence for intraspecific hybridization in a clonal and extremely halotolerant yeast. *BMC Genomics* 19:364. doi:10.1186/s12864-018-4751-5.

91. Coleine, C., **Stajich**, J. E., Zucconi, L., Onofri, S., Pombubpa, N., Egidi, E., Franks, A., Buzzini, P., and Selbmann, L. 2018. Antarctic cryptoendolithic fungal communities are highly adapted and dominated by Lecanoromycetes and Dothideomycetes. *Frontiers in Microbiology* 9:1392. doi:10.3389/fmicb.2018.01392.

92. Coleine, C., Zucconi, L., Onofri, S., Pombubpa, N., **Stajich**, J., and Selbmann, L. 2018. Sun exposure shapes functional grouping of fungi in cryptoendolithic Antarctic communities. *Life* 8(2):19. doi:10.3390/life8020019.

93. Song, Z., **Stajich**, J. E., Xie, Y., Liu, X., He, Y., Chen, J., Hicks, G. R., and Wang, G. 2018. Comparative analysis reveals unexpected genome features of newly isolated Thraustochytrids strains: on ecological function and PUFAs biosynthesis. *BMC Genomics* 19(1):541. doi:10.1186/s12864-018-4904-6.

94. Romsdahl, J., Blachowicz, A., Chiang, A., **Stajich**, J. E., Kalkum, M., Venkateswaran, K., and Wang, C. C. 2018. Genomic and proteomic characterization of *Aspergillus niger* isolated from the international space station. *mSystems* 3(5):e00112–18. doi:10.1128/mSystems.00112-18.

95. Arnesen, J. A., Malagocka, J., Gryganskyi, A. P., Grigoriev, I. V., Voigt, K., **Stajich**, J. E., and De Fine Licht, H. H. 2018. Early diverging insect-pathogenic fungi of the order entomophthorales possess diverse and unique subtilisin-like serine proteases. *G3: Genes|Genomes|Genetics* 8(10):3311–3319. doi:10.1534/g3.118.200656.

96. Arvidson, R., Kaiser, M., Lee, S. S., Urenda, J. P., Dail, C. J., Mohammed, H., Nolan, C., Pan, S.-Q., **Stajich**, J. E., Libersat, F., and Adams, M. E. 2018. Parasitoid Jewel Wasp Mounts Multi-Pronged Neurochemical Attack to Hijack a Host Brain. *Molecular & Cellular Proteomics* 18(1):99–114. doi: 10.1074/mcp.RA118.000908.

97. Demers, E., Biermann, A. R., Masonjones, S., Crocker, A. W., Ashare, A., **Stajich**, J. E., and Hogan, D. A. 2018. Evolution of drug resistance in an antifungal-naive chronic *Candida lusitaniae* infection. *Proc Natl Acad Sci U S A* 115(47):12040–12045. doi:10.1073/pnas.1807698115.

98. Chang, Y., Desiró, A., Na, H., Sandor, L., Lipzen, A., Clum, A., Barry, K., Grigoriev, I., Martin, F., **Stajich**, J. E., Smith, M., Bonito, G., and Spatafora, J. W. 2018. Phylogenomics of Endogonaceae and evolution of mycorrhizae within Mucoromycota. *New Phytologist* 222:511–525. doi:10.1111/nph.15613.

99. Romsdahl, J., Blachowicz, A., Chiang, A. J., Chiang, Y.-M., Masonjones, S., Yaegashi, J., Countryman, S., Karouia, F., Kalkum, M., **Stajich**, J. E., Venkateswaran, K., and Wang, C. C. C. 2019. International space station conditions alter genomics, proteomics, and metabolomics in *Aspergillus nidulans*. *Applied microbiology and biotechnology* 103:1363–1377. doi:10.1007/s00253-018-9525-0.

100. Davis, W. J., Amses, K. R., Benny, G. L., Carter-House, D., Chang, Y., Grigoriev, I., Smith, M. E., Spatafora, J. W., **Stajich**, J. E., and James, T. Y. 2019. Genome-scale phylogenetics reveals a monophyletic Zoopagales (Zoopagomycota, Fungi). *Molecular Phylogenetics and Evolution* 133:152–163. doi:10.1016/j.ympev.2019.01.006.

101. Chen, J., Lu, L., Benjamin, J., Diaz, S., Hancock, C. N., **Stajich**, J. E., and Wessler, S. R. 2019. Tracking the origin of two genetic components associated with transposable element bursts in domesticated rice. *Nature Communications* 10:641. doi:10.1038/s41467-019-08451-3.

102. Bewick, A. J., Hofmeister, B. T., Powers, R. A., Mondo, S. J., Grigoriev, I. V., James, T. Y., **Stajich**, J. E., and Schmitz, R. J. 2019. Diversity of cytosine methylation across the fungal tree of life. *Nature Ecology & Evolution* 3:479–490. doi:10.1038/s41559-019-0810-9.

103. Cissé, O. H. and **Stajich**, J. E. 2019. FGMP: assessing fungal genome completeness and gene content. *BMC Bioinformatics* 20:184. doi:10.1186/s12859-019-2782-9.

104. Blachowicz, A., Chiang, A. J., Elsaesser, A., Kalkum, M., Ehrenfreund, P., **Stajich**, J. E., Torok, T., Wang, C. C. C., and Venkateswaran, K. 2019. Proteomic and metabolomic characteristics of extremophilic fungi under simulated mars conditions. *Frontiers in Microbiology* 10:1013. doi: 10.3389/fmicb.2019.01013.

105. Boyce, G. R., Gluck-Thaler, E., Slot, J. C., **Stajich**, J. E., Davis, W. J., James, T. Y., Cooley, J. R., Panaccione, D. G., Eilenberg, J., Licht, H. H. D. F., Macias, A. M., Berger, M. C., Wickert, K. L., Stauder, C. M., Spahr, E. J., Maust, M. D., Metheny, A. M., Simon, C., Kritsky, G., Hodge, K. T., Humber, R. A., Gullion, T., Short, D. P., Kijimoto, T., Mozgai, D., Arguedas, N., and Kasson, M. T. 2019. Psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens. *Fungal Ecology* 41:147–164. doi:10.1016/j.funeco.2019.06.002.

106. Murphy, C. L., Youssef, N. H., Hanafy, R. A., Couger, M. B., Stajich, J. E., Wang, Y., Baker, K., Dagar, S. S., Griffith, G. W., Farag, I. F., Callaghan, T. M., and Elshahed, M. S. 2019. Horizontal gene transfer as an indispensable driver for evolution of Neocallimastigomycota into a distinct gut-dwelling fungal lineage. *Applied and Environmental Microbiology* 85(15):e00988–19. doi: 10.1128/AEM.00988-19.

107. Macias, A. M., Marek, P. E., Morrissey, E. M., Brewer, M. S., Short, D. P. G., Stauder, C. M., Wickert, K. L., Berger, M. C., Metheny, A. M., Stajich, J. E., Boyce, G., Rio, R. V. M., Panaccione, D. G., Wong, V., Jones, T. H., and Kasson, M. T. 2019. Diversity and function of fungi associated with the fungivorous millipede, *Brachycybe lecontii*. *Fungal Ecology* 41:187–197. doi:10.1016/j.funeco.2019.06.006.

108. Coleine, C., **Stajich**, J. E., Pombubpa, N., Zucconi, L., Onofri, S., Canini, F., and Selbmann, L. 2019. Altitude and fungal diversity influence the structure of Antarctic cryptoendolithic Bacteria communities. *Environmental Microbiology Reports* 11(5):718–726. doi:10.1111/1758-2229.12788.

109. Wang, Y., Youssef, N., Couger, M., Hanafy, R., Elshahed, M., and **Stajich**, J. E. 2019. Molecular dating of the emergence of anaerobic rumen fungi and the impact of laterally acquired genes. *mSystems* 4(4):e00247–19. doi:10.1128/mSystems.00247-19.

110. Kowalski, C. H., Kerkaert1, J. D., Liu, K.-W., Nadell, C. D., **Stajich**, J. E., and Cramer, R. A. 2019. *Aspergillus fumigatus* Colony Biofilm Morphology Impacts Hypoxia Fitness, Inflammation, and Disease Progression. *Nature Microbiology* 4(12):2430–2441. doi:10.1038/s41564-019-0558-7.

111. Carrillo, J. D., Rugman-Jones, P. F., Husein, D., **Stajich**, J. E., Kasson, M. T., Carrillo, D., Stouthamer, R., and Eskalen, A. 2019. Members of the *Euwallacea fornicatus* species complex exhibit promiscuous mutualism with ambrosia fungi in taiwan. *Fungal Genetics and Biology* 133:103269. doi:10.1016/j.fgb.2019.103269.

112. Uehling, J., Entler, M., Meredith, H., Millet, L., Timm, C., Aufrecht, J., G Bonito, J. L., N Engle, Doktycz, M., Retterer, S., Spatafora, J. W., **Stajich**, J. E., Tschaplinski, T., and Vilgalys, R. 2019. Microfluidics and metabolomics reveal symbiotic bacterial-fungal interactions between *Mortierella elongata* and *Burkholderia* include metabolite exchange. *Front Microbiol* 10:2163. doi:10.3389/fmicb.2019.02163.

113. Odebode, A., Adekunle, A., **Stajich**, J., and Adeonipekun, P. 2020. Airborne fungi spores distribution in various locations in Lagos, Nigeria. *Environmental monitoring and assessment* 192:87. doi:10.1007/s10661-019-8038-3.

114. Carrillo, J. D., Mayorquin, J. S., **Stajich**, J. E., and Eskalen, A. 2020. Probe-based multiplex Real-Time PCR as a diagnostic tool to distinguish distinct fungal symbionts associated with *Euwallacea kuroshio* and *Euwallacea whitfordiodendrus* in California. *Plant Disease* 104(1):227–238. doi:10.1094/PDIS-01-19-0201-RE.

115. Knudsen, K., Adams, J. N., Kocourková, J., Wang, Y., Ortañez, J., and **Stajich**, J. E. 2020. The monophyletic *Sarcogyne canadensis*–wheeleri clade, a newly recognized group sister to the European *Acarospora glaucocarpa* group. *The Bryologist* 123(1):11–30. doi:10.1639/0007-2745-123.1.011.

116. Coleine, C., **Stajich**, J. E., Zucconi, L., Onofri, S., and Selbmann, L. 2020. Sun exposure drives Antarctic cryptoendolithic community structure and composition. *Polar Biology* In press. doi:10.1101/676692.

117. Coleine, C., Pombubpa, N., Zucconi, L., Onofri, S., **Stajich**, J. E., and Selbmann, L. 2020. Endolithic fungal species markers for harshest conditions in the McMurdo Dry Valleys, Antarctica. *Life* 10(2):E13. doi:10.3390/life10020013.

118. Coleine, C., **Stajich**, J. E., Pombubpa, N., Zucconi, L., Onofri, S., and Selbmann, L. 2020. Sampling strategies to assess microbial diversity of Antarctic cryptoendolithic communities. *Polar Biology* 43:225–235. doi:10.1007/s00300-020-02625-2.

119. Coleine, C., Masonjones, S., Sterflinger, K., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus *Friedmanniomyces endolithicus*. *Fungal Biology* In press. doi:10.1016/j.funbio.2020.01.005.

120. Macias, A. M., Geiser, D. M., **Stajich**, J. E., Lukasik, P., Veloso, C., Bublitz, D. C., Berger, M. C., Boyce, G. R., Hodge, K., and Kasson, M. T. 2020. Evolutionary relationships among *Massospora spp.* (Entomophthorales), obligate pathogens of cicadas. *Mycologia In Press*. doi:10.1101/811836.

121. Yang, C.-T., Vidal-Diez de Ulzurrun, G., Goncalves, P., Lin, H.-C., Chang, C.-W., Huang, T.-Y., Chen, S.-A., Lai, C.-K., Tsai, I. J., Schroeder, F. C., **Stajich**, J. E., and Hsueh, Y.-P. 2020. Natural variation in the predatory behavior of nematode-trapping fungi facilitates the establishment of a new robust model strain. *Proc National Acad Sciences In press*. doi:10.1073/pnas.1919726117.

Genome Announcements

1. Coleine, C., Masonjones, S., Selbmann, L., Zucconi, L., Onofri, S., Pacelli, C., and **Stajich**, J. E. 2017. Draft genome sequences of the Antarctic endolithic fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018. *Genome Announcements* 5. doi:10.1128/genomeA.00397-17.
2. Kasson, M. T., Kasson, L. R., Wickert, K. L., Davis, D. D., and **Stajich**, J. E. 2019. Genome sequence of a lethal vascular wilt fungus, *Verticillium nonalfalfae*, a biological control used against the invasive *Ailanthus altissima*. *Microbiology Resource Announcements* 8. doi:10.1128/MRA.01619-18.
3. Coleine, C., Selbmann, L., Masonjones, S., Onofri, S., Zucconi, L., and **Stajich**, J. E. 2019. Draft genome sequence of an Antarctic isolate of the black yeast fungus *Exophiala mesophila*. *Microbiology Resource Announcements* 8(19):e00142–19. doi:10.1128/MRA.00142-19.
4. de Melo Teixeira, M., Barker, B. M., and **Stajich**, J. E. 2019. Improved reference genome sequence of *Coccidioides immitis* strain WA 211, isolated in Washington State. *Microbial Resource Announcements* 8(33):e00149–19. doi:10.1128/MRA.00149-19.
5. Coleine, C., Albanese, D., Onofri, S., Zucconi, L., Tringe, S. G., Pennacchio, C., Donati, C., **Stajich**, J. E., and Selbmann, L. 2020. Metagenomes in the borderline ecosystems of the Antarctic cryptoendolithic communities. *Microbial Resource Announcements* 9(10):e01599–19. doi:10.1128/MRA.01599-19.

Submitted Manuscripts and Preprints

1. Coeline, C., Masonjones, S., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Draft genome sequence of yeast *Rhodotorula* sp. CCFEE 5306, isolated from McMurdo Dry Valleys, Antarctica. *Submitted* .
2. Pombubpa, N., Pietrasiak, N., De Ley, P., and **Stajich**, J. E. 2019. Insights into the desert living skin microbiome: geography, soil depth, and crust type affect biocrust microbial communities and networks in Mojave Desert, USA. *bioRxiv* page 810002. doi:10.1101/810002.
3. Unruh, S. A., Pires, C. A., Zettler, L. W., Erba, L., Grigoriev, I. V., Barry, K. W., Daum, C., Lipzen, A. V., and **Stajich**, J. E. 2019. Shallow genome sequencing for phylogenomics of mycorrhizal fungi from endangered orchids. *Biorxiv* doi:10.1101/862763.
4. Albanese, D., Coleine, C., Rota-Stabelli, O., Onofri, S., Tringe, S., **Stajich**, J. E., Selbmann, L., and Donati, C. 2020. Antarctic cryptoendolithic bacterial lineages of pre-Cambrian origin as proxy for Mars colonization. *Submitted* doi:10.1101/2020.02.27.967604.
5. James, T. Y., **Stajich**, J. E., Hittinger, C. T., and Rokas, A. 2020. Towards a fully resolved fungal tree of life. *Annual Reviews of Microbiology Submitted*.
6. Carrillo, A. J., Cabrera, I. E., Spasojevic, M., Schacht, P., **Stajich**, J. E., and Borkovich, K. A. 2020. Clustering analysis of large-scale phenotypic data in the model filamentous fungus *Neurospora crassa*. *Submitted* .
7. Collins, C. G., Spasojevic, M. J., Alados, C. L., Aronson, E. L., Benavides, J. C., Cannone, N., Caviezel, C., Grau, O., Guo, H., Kudo, G., Kuhn, N. J., Müllerová, J., Phillips, M. L., Pombubpa, N., Reverchon, F., Shulman, H. B., **Stajich**, J. E., Stokes, A., Weber, S. E., and Diez, J. M. 2020. Global impacts of alpine woody encroachment on soil microbial communities. *Submitted* .
8. Myers, J. M., Bonds, A. E., Clemons, R. A., Thapa, N. A., Simmons, D. R., Carter-House, D., Ortanez, J., Liu, P., Miralles-Durán, A., Longcore, J. E., Bonito, G., **Stajich**, J. E., Spatafora, J. W., Chang, Y., Corrochano, L. M., Gryganskyi, A., Grigoriev, I. V., and James, T. Y. 2020. Survey of early-diverging lineages of fungi reveals abundant and diverse mycoviruses. *Submitted* .
9. Vandepol, N., Liber, J., Desirò, A., Na, H., Kennedy, M., Barry, K., Grigoriev, I. V., Miller, A. N., O'Donnell, K., **Stajich**, J. E., and Bonito, G. 2020. Resolving the Mortierellaceae phylogeny through synthesis of Multi-Locus Sequence Typing (MLST) and phylogenomics. *Submitted* .

Reviews (Refereeed)

1. **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.
2. **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.
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. 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.
5. 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.
6. Amend, A., Burgaud, G., Cunliffe, M., Edgcomb, V. P., Ettinger, C. L., GutiÃľrrez, M. H., Heitman, J., Hom, E. F. Y., Ianiri, G., Jones, A. C., Kagami, M., Picard, K. T., Quandt, C. A., Raghukumar, S., Riquelme, M., **Stajich**, J., Vargas-MuÃśiz, J., Walker, A. K., Yarden, O., and Gladfelter, A. S. 2019. Fungi in the marine environment: Open questions and unsolved problems. *mBio* 10. ISSN 2150-7511. doi:10.1128/mBio.01189-18.
7. Warren, S. D., Clair, L. L. S., Stark, L. R., Lewis, L. A., Pombubpa, N., Kurbessoian, T., **Stajich**, J. E., and Aanderud, Z. T. 2019. Reproduction and dispersal of biological soil crust organisms. *Frontiers In Ecology & Evolution* 7:344. doi:10.3389/fevo.2019.00344.

Books and Book Chapters

1. 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.
2. **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.
3. **Stajich**, J. E. 2007. An introduction to BioPerl. *Methods Mol Biol* 406:535–548.
4. Edwards, D., **Stajich**, J. E., and Hansen, D., editors. 2009. *Bioinformatics*. Springer, NY.
5. 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.
6. 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.
7. **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.
8. **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.
9. Spatafora, J. W., Aime, M. C., Grigoriev, I. V., Martin, F., **Stajich**, J. E., and Blackwell, M. 2017. The fungal tree of life: from molecular systematics to genome-scale phylogenies. *Microbiology spectrum* 5(5). doi:10.1128/microbiolspec.FUNK-0053-2016.

10. **Stajich**, J. E. 2017. Fungal genomes and insights into the evolution of the kingdom. *Microbiology spectrum* 5(4). doi:10.1128/microbiolspec.FUNK-0055-2016.

Meeting and Technical Reports

1. 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.
2. 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.
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. MIxS-BE: a MIxS 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. 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.
5. 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.
6. Gaya, E., Kooija, P., Dentinger, B. T. M., Grigoriev, I. V., Nagy, L., **Stajich**, J. E., Coker, T., and Leitcha, I. J. 2018. *State of the World's Fungi. Report*, chapter Fungal tree of life., pages 12–17. Royal Botanic Gardens, Kew.
7. Pombubpa, N., Kurbessoian, T., **Stajich**, J. E., and Pietrasiak, N. 2019. Exploring the microbial diversity in biological soil crusts at Joshua Tree National Park. *Joshua Tree Science Updates In Press*.
8. Baltrus, D. A., Cuomo, C. A., Dennehy, J. J., Dunning Hotopp, J. C., Maresca, J. A., Newton, I. L. G., Rasko, D. A., Rokas, A., Roux, S., and **Stajich**, J. E. 2019. Future-proofing your *Microbiology Resource Announcements* genome assembly for reproducibility and clarity. *Microbiology resource announcements* 8(36):e00954–19. ISSN 2576-098X. doi:10.1128/MRA.00954-19.

Commentaries and Book Reviews

1. **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.
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. 2016. Fungal Evolution: *Mucor* and *Phycomyces* see double. *Curr Biol* 26(16):R775–R777. doi:10.1016/j.cub.2016.06.049.
4. Valent, B., Farman, M., Tosa, Y., Begerow, D., Fournier, E., Gladieux, P., Islam, M. T., Kamoun, S., Kemler, M., Kohn, L. M., Lebrun, M.-H., **Stajich**, J. E., Talbot, N. J., Terauchi, R., Tharreau, D., and Zhang, N. 2019. *Pyricularia graminis-tritici* is not the correct species name for the wheat blast fungus: response to Ceresini *et al.* (mpp 20:2). *Molecular Plant Pathology* 20:173–179. doi:10.1111/mpp.12778.

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

2011-2017	National Science Foundation. IOS-1027542. (No Cost Ext thru 02/2021) "CPGS: Genome-wide impact of *mPing* transposition on rice phenotypic diversity." Role: Co-I. PI: SR Wessler (UC Riverside). `http://dynamiterice.org`
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) `http://zygolife.org`
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)
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
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
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 *Aspergillus fumigatus* 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)
2019-2024	Canadian Institute For Advanced Research “Fungal Kingdom: Threats and Opportunities” Role: CIFAR Fellow. PI/Directors: L Cowen and J Heitman

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.

Service:

University and Departmental

2017–2020	UC Riverside Graduate Council. Chair & member of Senate Executive Council (2018-2020).
2015–	Director, Microbiology Graduate Program (except Sabbatical 2016-17)
2018–2019	Graduate Advisor, & Admissions Advisor, Microbiology Graduate Program
2015–2018	Admissions Advisor, Microbiology Graduate Program (except Sabbatical 2016-17)
2014–2015	Graduate Advisor, Microbiology Graduate Program

Editorial Boards

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

2018–2020	Co-Chair (2020) of Cellular and Molecular Fungal Biology, Gordon Research Conference; Co-Vice Chair (2018).
2017–2020	Karling Lecture Committee, Mycologia 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 Welcome 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:

2007–	Mycological Society of America
2007–	American Society for Microbiology
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

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-Scarbourgh.
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, SWEDEN
2010	Suzanne Joneson, PhD, Department of Biology, University of Idaho
2011	Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, Bogota, COLOMBIA
2012	Andrii Gryganski, PhD, Visiting Researcher, Duke University
2013–2014	Venkatesh Moktali, PhD, FungiDB Project, Visiting Research Fellow, Oregon State University
2014	Raúl Castanera Andrés, Visiting Graduate Student, Universidad Pública de Navarra, Pamplona, SPAIN
2015	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 Assocation Fellowship, University of Lagos, NIGERIA.
2015	Marco Marconi, Visiting Graduate Student, Universidad Politécnica de Madrid, Madrid, SPAIN
2015–2016	Claudia Coleine, Visiting Graduate Student, Universitá 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–	Felipe Salgado, Federal University of Rio de Janeiro, BRAZIL.
2020–	Omar Valencia, Volunteer.

Staff:

2011–2012	Daniel Borcherding, Programmer (FungiDB). Current: Senior Software Build Engineer, Apple, Inc.
2011–2013	Raghuraman Ramamurthy, Programmer (FungiDB). Current: Senior Bioinformatics Associate, Gilead Sciences.
2013–2014	Venkatesh Moktali, 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://biodataprog.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–	Renata Haro, UCR.
2018–	Skylar McDonald, UCR.
2019	Saisuki Putumbaka, The College of New Jersey, Summer REU student.
2019–	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 ⋆
2020	Andrea Vu, Plant Pathology
ongoing	Nuttapon Pombubpa, Plant Pathology ⋆
	Sawyer Masonjones, GGB ⋆
	Jesús Peña, Microbiology ⋆
	Julia Adams, Plant Biology ⋆
	Tania Kurbessoian, Microbiology ⋆
	Nicole Ginnan, Plant Pathology
	Beth Peacock, Plant Pathology
	Caleb Hubbard, Medical and Veterinary Entomology
	Alex Rajewski, Plant Biology
	Glen Morrison, Plant Biology
	Nathan Robinett, Joint Doctoral Prog. Evolutionary Biology, SDSU-UCR
	Mari West, Entomology
	Yi Huang, Plant Biology
	Christopher Ficus, GGB

Shannon Lynch, Environmental Studies (Univ of California-Santa Cruz)
Glen Morrison, Plant Biology
Hannah Schulman, Microbiology

⋆ Stajich is Dissertation advisor or △ co-advisor / substitute

Invited Seminars and conference presentations (2015–Present)

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 NATIONAL 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.