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

Honors and Awards:

2020 Fellow, American Association for the Advancement of Science
2020 Fellow, Mycological Society of America
2020 Fellow, American Academy of Microbiology, American Society for Microbiology
2019–2025 CIFAR Fellow in program 'Fungal Kingdom: Threats & Opportunities'
2019 Rosie Perez Memorial Seminar, North Carolina State University
2017 Whetzel-Westcott-Dimock Special Lecturer, Cornell University
2015 Kavli Fellow, Kavli Frontiers of Science
2014 C. J. Alexopoulos Prize, Mycological Society of 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.

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6. **Stajich**, J. E., Lovett, B., Lee, E., Macias, A. M., Hajek, A. E., de Bivort, B. L., Kasson, M. T., Licht, H. H. D. F., and Elya, C. 2023. Signatures of transposon-mediated genome inflation, host specialization, and photoentrainment in *Entomophthora muscae* and allied entomophthoralean fungi. *bioRxiv* doi:10.1101/2023.09.13.557621.

7. Carpenter, S. C. D., Bogdanove, A. J., **Stajich**, J. E., Uehling, J., Lovett, B., Kasson, M., and Carter, M. E. 2023. Prevalence and diversity of TAL effector-like proteins in fungal endosymbiotic *Mycetohabitans spp*. *bioRxiv* doi:10.1101/2023.10.16.562584.

8. Myers, J. M., Schulz, F., Rahimlou, S., Amses, K. R., Simmons, D. R., **Stajich**, J. E., and James, T. Y. 2024. Large dna viruses in early diverging fungal genomes are relics of past and present infections. *bioRxiv* page 2024.01.04.574182. doi:10.1101/2024.01.04.574182.

9. Yacoub, M. N. and **Stajich**, J. E. 2024. Comparative genomics reveals intra and inter species variation in the pathogenic fungus *Batrachochytrium dendrobatidis*. *bioRxiv* doi:10.1101/2024.01.24.576925.

Reviews (Refereed)

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., Gutiérrez, 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-Muñiz, J., Walker, A. K., Yarden, O., and Gladfelter, A. S. 2019. Fungi in the marine environment: Open questions and unsolved problems. *mBio* 10(2):e01189–18. 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.
8. Fisher, M. C., Gurr, S. J., Cuomo, C. A., Blehert, D. S., Jin, H., Stukenbrock, E. H., **Stajich**, J. E., Kahmann, R., Boone, C., Denning, D. W., Gow, N. A. R., Klein, B. S., Kronstad, J. W., Sheppard, D. C., Taylor, J. W., Wright, G. D., Heitman, J., Casadevall, A., and Cowen, L. E. 2020. Threats posed by the fungal kingdom to humans, wildlife, and agriculture. *mBio* 11(3):e00449–20. doi:10.1128/mBio.00449-20.
9. Lovett, B., Macias, A., **Stajich**, J. E., Cooley, J., Eilenberg, J., de Fine Licht, H. H., and Kasson, M. T. 2020. Behavioral betrayal: how select fungal parasites enlist living insects to do their bidding. *PLoS Pathogens* 16(6):e1008598. doi:10.1371/journal.ppat.1008598.
10. 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* 74:291–313. doi:10.1146/annurev-micro-022020-051835.
11. Coleine, C., **Stajich**, J. E., de Los Ríos, A., and Selbmann, L. 2020. Beyond the extremes: Rocks as ultimate refuge for fungi in drylands. *Mycologia* 113(1):108–133. doi:10.1080/00275514.2020.1816761.
12. Selbmann, L., Benkö, Z., Coleine, C., de Hoog, S., Donati, C., Druzhinina, I., Emri, T., Ettinger, C. L., Gladfelter, A. S., Gorbushina, A. A., Grigoriev, I. V., Grube, M., Gunde-Cimerman, N., Karányi, Z. A., Kocsis, B., Kubressoian, T., Miklós, I., Miskei, M., Muggia, L., Northen, T., Novak-Babic, M., Pennacchio, C., Pfliegler, W. P., Pócsi, I., Prigione, V., Riquelme, M., Segata, N., Schumacher, J., Shelest, E., Sterflinger, K., Tesei, D., U'Ren, J. M., Varese, G. C., Vázquez-Campos, X., Vicente, V. A., Souza, E. M., Zalar, P., Walker, A. K., and **Stajich**, J. E. 2020. Shed light in the DaRk LineagES of the fungal tree of life-STRES. *Life* 10(12):362. doi:10.3390/life10120362.
13. Lofgren, L. A. and **Stajich**, J. E. 2021. Fungal biodiversity and conservation mycology in light of new technology, big data, and changing attitudes. *Current Biology* 31:R1312–R1325. doi:10.1016/j.cub.2021.06.083.

14. Coleine, C., **Stajich**, J. E., and Selbmann, L. 2022. Fungi are key players in extreme ecosystems. *Trends in Ecology & Evolution* doi:10.1016/j.tree.2022.02.002.

15. Gostinčar, C., **Stajich**, J. E., and Gunde-Cimerman, N. 2023. Extremophilic and extremotolerant fungi. *Current Biology* 33:R752–R756. doi:10.1016/j.cub.2023.06.011.

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. In J. Heitman, B. J. Howlett, P. W. Crous, E. H. Stukenbrock, T. Y. James, and N. A. R. Gow, editors, *The Fungal Kingdom*, chapter 1, pages 1–34. John Wiley & Sons, Ltd. doi:10.1128/9781555819583.ch1.

10. **Stajich**, J. E. 2017. Fungal genomes and insights into the evolution of the kingdom. In J. Heitman, B. J. Howlett, P. W. Crous, E. H. Stukenbrock, T. Y. James, and N. A. R. Gow, editors, *The Fungal Kingdom*, chapter 29, pages 619–633. John Wiley & Sons, Ltd. doi:10.1128/microbiolspec.FUNK-0055-2016.

Consortia publications

1. Bidartondo, M. I. 2008. Preserving accuracy in GenBank. *Science* 319(5870):1616–1616. doi:10.1126/science.319.5870.1616a.

2. West, A. G., Digby, A., Lear, G., Digby, A., Armstrong, D., Armstrong-James, D., Bromley, M., Buckley, E., Chatterton, J., Cox, M. P., Cramer, R. A., Crane, J., Dearden, P. K., Eason, D., Fisher, M. C., Gago, S., Gartrell, B., Gemmell, N. J., Glare, T. R., Guhlin, J., Howard, J., Lacap-Bugler, D., Le Lec, M., Lin, X. X., Lofgren, L., Mackay, J., Meis, J., Morelli, K. A., Perrott, J., Petterson, M., Quinones-Mateu, M., Rhodes, J., Roberts, J., **Stajich**, J., Taylor, M. W., Tebbutt, S. J., Truter-Meyer, A., Uddstrom, L., Urban, L., van Rhijn, N., Vercoe, D., Vesely, E., Weir, B. S., West, A. G., Winter, D. J., Yeung, J., Taylor, M. W., Kākāpō Recovery Team, and Kākāpō Aspergillosis Research Consortium. 2022. Influence of management practice on the microbiota of a critically endangered species: a longitudinal study of kākāpō chick faeces and associated nest litter. *Animal Microbiome* 4(1):55. doi:10.1186/s42523-022-00204-w.

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. Fungal tree of life. In K. J. Willis, editor, *State of the World's Fungi. Report*, pages 12–17. Royal Botanic Gardens, Kew.
7. 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. doi:10.1128/MRA.00954-19.
8. Pombubpa, N., Kurbessoian, T., **Stajich**, J. E., and Pietrasiak, N. 2020. Exploring the microbial diversity in biological soil crusts at Joshua Tree National Park. `https://www.nps.gov/articles/exploring-the-microbial-diversity-in-biological-soil-crusts-at-joshua-tree-national-park.htm`.
9. Dunning Hotopp, J. C., Baltrus, D. A., Bruno, V. M., Dennehy, J. J., Gill, S. R., Maresca, J. A., Matthijnssens, J., Newton, I. L. G., Putonti, C., Rasko, D. A., Rokas, A., Roux, S., **Stajich**, J. E., Stedman, K. M., Stewart, F. J., and Thrash, J. C. 2020. Best practices for successfully writing and publishing a genome announcement in *Microbial Resource Announcements*. *Microbiology Resource Announcements* 9(36):e00763–20. doi:10.1128/MRA.00763-20.
10. Case, N. T., Berman, J., Blehert, D. S., Cramer, R. A., Cuomo, C., Currie, C. R., Ene, I. V., Fisher, M. C., Fritz-Laylin, L. K., Gerstein, A. C., Glass, N. L., Gow, N. A. R., Gurr, S. J., Hittinger, C. T., Hohl, T. M., Iliev, I. D., James, T. Y., Jin, H., Klein, B. S., Kronstad, J. W., Lorch, J. M., McGovern, V., Mitchell, A. P., Segre, J. A., Shapiro, R. S., Sheppard, D. C., Sil, A., **Stajich**, J. E., Stukenbrock, E. E., Taylor, J. W., Thompson, D., Wright, G. D., Heitman, J., and Cowen, L. E. 2022. The future of fungi: threats and opportunities. *G3* 12(11):jkac224. doi:10.1093/g3journal/jkac224.
11. Case, N. T., Song, M., Fulford, A. H., Graham, H. V., Orphan, V. J., **Stajich**, J. E., Casadevall, A., Mustard, J., Heitman, J., Lollar, B. S., and Cowen, L. E. 2022. Exploring space via astromycology: A report on the CIFAR programs *Earth 4D* and *Fungal Kingdom* inaugural joint meeting. *Astrobiology* doi:10.1089/ast.2021.0186.

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
Protocols.io Protocols `https://www.protocols.io/researchers/jason-stajich` - public protocols
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://herptilemicrobiomes.org` - NSF URoL Herptile Microbiomes
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

2017-2026	National Institutes of Health. R01-AI127548 "Evolved Heterogeneity contributes to chronic fungal lung infections" Role: Senior Personnel. PI: D Hogan (Dartmouth)
2017-2028	National Institutes of Health. R01-AI130128 "Evolution of *Aspergillus fumigatus* virulence" Role: Senior Personnel. PI: RA Cramer, Jr (Dartmouth)
2019-2025	Canadian Institute For Advanced Research. Fellowship "Fungal Kingdom: Threats and Opportunities" Role: CIFAR Fellow. PI/Directors: L Cowen and J Heitman
2020-2023	Gordon and Betty Moore Foundation "New Tools for Advancing Model Systems in Aquatic Symbiosis" Role: Co-PI. PI: Lillian Fritz-Laylin (U Mass-Amherst). With Co-PI Tim James (U Michigan)

2020-2025 USDA-NIFA, Emergency Citrus Disease Research and Extension
"CAP: Combining Cultural And Genetic Approaches For Grove Success To Unravel And Enhance Resistance/Tolerance To Huanglongbing."
Role: Co-PI. PI Caroline Roper, UCR

2022-2024 Canadian Institute For Advanced Research. Catalyst Award
"Discovering and describing fungi from deep biosphere environments"
Role: PI. Co-PI: Tim James, U Michigan

2022-2026 National Science Foundation. EF-2125066.
"Collaborative Research: MIM: Gut-inhabiting fungi influence structure and function of herptile microbiomes through horizontal gene transfer and novel metabolic function"
Role: PI. Collaborative linked award with 3 other PIs: J Spatafora & K McPhail (Oregon State), D Walker (Middle Tennessee State) `https://herptilemicrobiomes.org/`

2022-2026 National Science Foundation. IOS-2134912
"Research-PGR: Impact of transposable element bursts on the rice genome and epigenome."
Role: Co-I. PI: SR Wessler (UC Riverside). Co-I: R Schmitz (U Georgia), K Ostivek (UC Riverside), J Burnette (UC Riverside)

2022-2026 National Science Foundation. DBI-2215705
"Research Infrastructure: MRI: Acquisition of a Big Data HPC Cluster for Interdisciplinary Research and Training."
Role: Co-I. PI: Thomas Girke (UC Riverside). Co-I: Wenxiu Ma, Mark Alber, Adam Godzik (UC Riverside)

2022-2027 National Science Foundation. IOS-2141858
"CAREER: Dissecting the molecular regulation of septin-mediated plant invasion by the blast fungus *Magnaporthe oryzae*"
Role: Senior Personnel. PI: Martin Egan (U Arkansas)

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)

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`

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

2019-2020 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

2020-2021 Canadian Institute For Advanced Research
"Pilot investigation of avian-origin *Aspergillus fumigatus* infections in the United States"
Role: PI. Co-PI: David Blehert, National Wildlife Health Center, USGS

2020 Burroughs Wellcome Fund.
"Meeting grant to support 2022 Fungal Cellular and Molecular Biology Gordon Research Conference"
Role: PI.

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

2022 National Science Foundation. MCB-2227426
"Meeting grant to support Fungal Cellular and Molecular Biology Gordon Research Conference 2022"
Role: PI.

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

2019-2022 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)

2020-2022 California Conservation Genomics Project (subproject)
"Landscape and Population Genomics of the lichen *Acarospora socialis* in California"
Role: PI.

2021-2023 Canadian Institute For Advanced Research. Catalyst Award
"Exploring the extended phenotypes of BdDV-1, a DNA mycovirus associated with enzootic strains of amphibian chytridiomycosis"
Role: Co-PI. PI: Tim James, U Michigan; Co-PI: Lillian Fritz-Laylin, U Mass Amherst; Co-PI Mat Fisher, Imperial College (UK)

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

Service:

University and Departmental

2020-2022 Division Chair, Riverside Division of the University of California Academic Senate
2020-2022 Member UC Academic Senate Academic Council (as per role as UCR Senate Chair)
2021-2022 Member Senate/UCOP Leadership Budget Call (as per role as UCR Senate Chair)
2020-2021 Member UC Academic Planning Committee (as per role as UCR Senate Chair)
2020-2021 Member UCR Campus Safety Taskforce (as per role as UCR Senate Chair)
2021 Member UCR Provost Search Committee (as per role as UCR Senate Chair)
2018–2020 Chair, UC Riverside Graduate Council and member of Senate Executive Council
2017-2018 Member, UC Riverside Graduate Council
2015–2020 Director, Microbiology Graduate Program (except Sabbatical 2016-17)
2014–2015, 2018–2020 Graduate Advisor, Microbiology Graduate Program
2015–2016,2017–2018 Admissions Advisor, Microbiology Graduate Program

Editorial Boards

2021– Editorial Board, Annual Reviews of Microbiology
2019–2023 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
2014–2022 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, 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
2012–2020 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/`

Graduate Students:

2009–2013 PhD student, Divya Sain. Genetics, Genomics, & Bioinformatics.
Current: Bioinformatics Scientist at Ambry Genetics.
2010–2012 MS student, Yi (Zoe) Zhou. Genetics, Genomics, & Bioinformatics.
Current: Biostatistician at dMed Biopharmaceutical Co.
2010–2014 PhD student, Yizhou Wang. Plant Biology.
Current: Research Bioinformatician and Associate Director at Applied Genomics, Computation & Translational Core, Cedars-Sinai.
2011–2015 PhD student, Steven Ahrendt. Genetics, Genomics, & Bioinformatics.
Current: Data Scientist at DOE Joint Genome Institute.
2016–2019 PhD Student, Derreck Carter-House. Plant Pathology.
Current: Research Scientist, Clear Labs
2015–2021 MS Student, Sawyer Masonjones. Genetics, Genomics, & Bioinformatics
2015–2021 PhD Student, Nuttapon Pombubpa. Plant Pathology.
Current: Assistant Professor, Chulalongkorn, Bangkok, THAILAND
2016–2022 PhD Student, Jesús Peña, Microbiology.
Current: Visiting Assistant Professor, Harvey-Mudd College
2017–2022 PhD Student, Tania Kurbessoian, Microbiology
2017– PhD Student, Julia Adams, Plant Biology
2020– PhD Student, Talieh Ostovar, Evolutionary Biology, San Diego State - UCR Joint Doctoral Program
2021– PhD Student, Mark Yacoub, Microbiology
2021– PhD Student, Cheng-Hung Tsai, Genetics, Genomics, & Bioinformatics
2022– PhD Student, Jessica Wu-Woods, Microbiology
2022– PhD Student, Leila Shadmani, Microbiology
2022– PhD Student, Xueyan (Sharon) Xu, Cellular, Molecular, and Developmental Biology.
2023– PhD Student, Kian Kelly, Plant Pathology
2023– PhD Student, Nathan Matheiu, Genetics, Genomics, & Bioinformatics
2023– PhD Student, Nora Ismail, 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: Assistant Professor, Institute of Zoology of Chinese Academy of Science; 1st position: 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.
2019–2021 Lotus Lofgren, Ph.D.
Current: Postdoctoral Researcher, Duke University.
2020–2021 Ying Sun, Ph.D.
Current: Postdoctoral Researcher at Salk Institute
2020– Cassie Ettinger, Ph.D.
2020–2023 Kelsey Aadland, Ph.D.
2023– Claudia Coleine, Ph.D. - Marie Curie Fellow.

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
2019–2020 Felipe Salgado, Federal University of Rio de Janeiro, BRAZIL.
2020–2021 Omar Valencia, Volunteer.
2021–2022 Jaehyuk Choi, Incheon National University, SOUTH KOREA.
2022–2023 Xinzhan Liu, Institute of Microbiology, Chinese Academy of Sciences, CHINA.

Staff:

2011–2012 Daniel Borcherding, Programmer (FungiDB).
Current: Senior Software Build Engineer, Apple, Inc.
2011–2013 Raghuraman Ramamurthy, Programmer (FungiDB).
Current: Lead Bioinformatician - Natera.
2012–2014 Edward Liaw, Programmer (FungiDB).
Current: Bioinformatics Engineer - Twist Bioscience.
2012–2014 Greg Gu, Programm (FungiDB).
Current: Chief Engineer - PH Engineering Corp.

2013–2014 Venkatesh Moktali, Bioinformatics Scientist (FungiDB).
Current: Biotech and Healthcare Product Management - Twist Bioscience.
2017–2018 Jericho Ortanez, Junior Specialist. Current: Graduate Student, UC Riverside.
2021 Omar Valencia, Junior Specialist.
2022–2023 Sadikshya Sharma, Assistant Specialist.

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–Present GEN220 - Computational Analysis of High Throughput Biological Data `http://biodataprog.github.io/`
2016–2020 BIO119 - Introduction to Genomics and Bioinformatics
2022–Present MCBL221 - Microbial Genetics

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 UC Berkeley School of Buisiness
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. Current: DO Student, Western University of Health Sciences in Oregon
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. Current: Dentistry Student
2017–2019 Estefania Caldera, UCR.
2018 Lily Bautista, UCR.
2018–2020 Renata Haro, UCR.
2018–2020 Skylar McDonald, UCR. Current: MS student in UCR Engineering.
2019 Saisuki Putumbaka, The College of New Jersey, Summer REU student. Current: PhD student at Univ of Georgia
2019–2020 Nicole Leung, UCR.
2020–2021 Dionne Martin, UCR - won IIGB Undergraduate Research Award. Next: PhD student at Univ

	of Georgia
2021–2023	Amy Do, UCR. Current: MS student in UCR Engineering.
2023	Jared Coyle, CSUSB. - Summer REU student.
2023–	Varshini Balaji, UCR.
2023–	Mia Miyatake, UCR.

Thesis/Dissertation committees:

2011	Sourav Roy, PhD, Genetics, Genomics & Bioinformatics
	Yi Zhou, MS, Genetics, Genomics & Bioinformatics ⋆
2012	Andrew Defries, PhD, Plant Sciences
2013	Gilbert Uribe, MS, Plant Pathology
	Divya Sain, PhD, Genetics, Genomics & Bioinformatics ⋆
2014	Yizhou Wang, PhD, Plant Sciences ⋆
	Zhigang Wu, PhD, Genetics, Genomics & Bioinformatics
2015	Presha Shah, PhD, Biochemistry
	Ming Wang, PhD, Plant Pathology
	Steven Ahrendt, PhD, Genetics, Genomics & Bioinformatics ⋆
	Ilva Cabrera, PhD, Genetics, Genomics & Bioinformatics
	Jinfeng Lu, PhD, Genetics, Genomics & Bioinformatics
	James Ricci, MS, Entomology
2016	Ryan Arvidson, PhD, Biochemistry
	Francis Na, MS, Microbiology
	Jishu Ha, PhD, Genetics, Genomics & Bioinformatics
	Arit Gosh, PhD, Genetics, Genomics & Bioinformatics
	Kelsey Gano, PhD, Microbiology
	Kun Liu, PhD, Plant Biology
2017	Raissa Green, PhD, Genetics, Genomics & Bioinformatics
	Amelia Lindsey, PhD, Entomology
	Patrick Schriener, PhD, Genetics, Genomics & Bioinformatics
	Eric Smith, PhD, Genetics, Genomics & Bioinformatics
	Katherine Picard, PhD, Univ Prog in Genetics & Genomics (Duke University)
	Eric Gordon, PhD, Entomology
2018	Cynthia Dick, PhD, EEOB
	Dan Vanderpool, PhD, Biology (University of Montana)
	Steven Bolaris, PhD, Genetics, Genomics & Bioinformatics △
2019	Joseph Carrillo, PhD, Plant Pathology △
	Dinusha Maheepala Mudalige, PhD, Plant Biology
	Aaron Robinson, PhD, Biology (University of New Mexico)
	Courtney Collins, PhD, Plant Biology
	Edgar Medina, PhD, Univ Prog in Genetics & Genomics (Duke University)
	Lluvia Vargas, PhD, Microbiología (CICESE, MEXICO)
	Derreck Carter-House, PhD, Plant Pathology ⋆
2020	Andrea Vu, PhD, Plant Pathology
	Nichole Ginnan, PhD, Plant Pathology
	Alex Rajewski, PhD, Plant Biology
2021	Nuttapon Pombubpa, PhD, Plant Pathology ⋆
	Caleb Hubbard, PhD, Medical and Veterinary Entomology
	Sawyer Masonjones, MS, Genetics, Genomics & Bioinformatics ⋆
	Markus Hiltunen, PhD, Evolutionary Biology, Uppsala University (external opponent)
2022	Yi Huang, PhD, Plant Biology
	Jesús Peña, PhD, Microbiology ⋆

Hannah Shulman, PhD, Microbiology
Christopher Fiscus, PhD, Genetics, Genomics & Bioinformatics
Celia Xi, PhD, Plant Biology
Sarah Thorwall, Chemical and Environmental Engineering
Tania Kurbessoian, Microbiology ⋆
Moira Kelly, Ghent University (external PhD Exam committee)

2023 Robyn Anderson, University of Western Australia (external PhD Exam committee)
Samantha (Smith) Standring, Entomology
Zachary Konkel, The Ohio State University (external PhD Exam committee)
Glen Morrison, Plant Biology
Peggy Brady, EEOB
Danielle Stevenson, Environmental Sciences
Fabiola Pulido-Chavez, Plant Pathology
Aidan Shands, Plant Pathology

ongoing Julia Adams, Plant Biology ⋆
Talieh Ostovar, Program in Evolutionary Biology SDSU-UCR ⋆
Dylan Enright, Microbiology
Yagna Oza, Genetics, Genomics, Bioinformatics
Jericho Ortañez, Microbiology
Linton Freund, Genetics, Genomics, & Bioinformatics
Isaac Diaz, Genetics, Genomics, & Bioinformatics
Tamsen Dunn, Program in Evolutionary Biology SDSU-UCR
Angela Buehlman, Plant Biology
Colin Todd, Plant Biology
Ben Hoyt, Plant Pathology
Mark Yacoub, Microbiology ⋆
Jessica Maccaro, Entomology
Aida Tafrishi, Chemical and Environmental Engineering
Mark Yacoub, Microbiology ⋆
Jessica Wu-Woods, Microbiology ⋆
Leila Shadmani, Microbiology ⋆
Xueyan (Sharon) Xu, Cellular, Molecular and Developmental Biology ⋆
Nathan Mathieu, Genetics, Genomics, Bioinformatics ⋆ (co-advised with Sue Wessler)
Sadikshya Sharma, Genetics, Genomics, Bioinformatics ⋆
Kian Kelly, Plant Pathology ⋆
Nora Ismail, Microbiology ⋆

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

Invited Seminars and conference presentations (2015–Present)

2022 · CIFAR Fungal Kingdom: Threats & Opportunities, Presenter for Feb and March Meetings (Virtual)
· Keynote speaker, Bark Beetle Mycobiome Research community meeting (Virtual)
· Department Seminar, Scripps Institution of Oceanography, UCSD (Virtual)
· Mycological Society of Japan Annual Meeting (Virtual)

2021 · CIFAR Fungal Kingdom: Threats & Opportunities, Presenter for Feb and March Meetings
· University of Georgia, Guest lecture for undergraduate seminar course "Genome Biology Across the Tree of Life" (Virtual)
· Rochester Institute of Technology, Georgia Gosnell Seminar Series (Virtual)
· University of Deleware, Microbiology Graduate Program (Virtual)
· Canadian Fungal Network Conference, Plenary Speaker (Virtual)
· Botany / Mycological Society of America 2021 meeting (Virtual)

· Metaorganisms: Collaborative Research Center Seminar series, Germany (Virtual)

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 for 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

February 11, 2024