Jason E. Stajich

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Education

2006–2009 Postdoctoral training, University of California, Berkeley, CA. Mentor: Dr. John W Taylor
2001–2006 Ph.D., Genetics and Genomics, Duke University, Durham, NC. Advisor: Dr. Fred S Dietrich
1995–1999 B.S., Computer Science, Duke University, Durham, NC

Academic appointments:

2017– Professor, 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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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. State of the world's fungi. report. chapter Fungal tree of life., 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)
2017-2022	National Institutes of Health. R01-AI130128 "Evolution of *Aspergillus fumigatus* virulence" Role: Senior Personnel. PI: RA Cramer, Jr (Dartmouth)
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)
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

2019-2025 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)

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

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

2020-2025 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

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)

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.

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 Leaderhip 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– 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

2021– Scientific Advisory Board, Sincarne.
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– 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:

2015– American Association for the Advancement of Science
2007– Mycological Society of America
2007– American Society for Microbiology, Fellow (2020)
2004– Genetics Society of America
2004– Society for Molecular Biology and Evolution
2002– Open Bioinformatics Foundation
2002– International Society for Computational Biology

Graduate Students:

2009–2013 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

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– 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–	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

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.
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

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 ⋆
Nathan Robinett, Evolutionary Biology, Joint Doctoral Prog. SDSU-UCR ○
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 Schulman, 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)
ongoing	Julia Adams, Plant Biology ⋆
	Beth Peacock, Plant Pathology
	Glen Morrison, Plant Biology
	Talieh Ostovar, Program in Evolutionary Biology SDSU-UCR ⋆
	Fabiola Pulido-Chavez, Plant Pathology
	Dylan Enright, Microbiology
	Samantha (Smith) Standring, Entomology
	Jericho Ortañez, Microbiology
	Peggy Brady, EEOB
	Hannah Freund, Genetics, Genomics, & Bioinformatics
	Isaac Diaz, Genetics, Genomics, & Bioinformatics
	Aidan Shands, Plant Pathology
	Tamsen Dunn, Program in Evolutionary Biology SDSU-UCR
	Angela Buehlman, Plant Biology
	Colin Todd, Plant Biology
	Mark Yacoub, Microbiology ⋆
	Jessica Maccaro, Entomology
	Aida Tafrishi, Chemical and Environmental Engineering

⋆ Stajich is Dissertation advisor or △ co-advisor / substitute ○ Withdrawn from program

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

December 30, 2022