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.
33. **Stajich**, J. E., Wilke, S. K., Ahrèn, D., Au, C. H., Birren, B. W., Borodovsky, M., Burns, C., Canbäck, B., Casselton, L. A., Cheng, C. K., Deng, J., Dietrich, F. S., Fargo, D. C., Farman, M. L., Gathman, A. C., Goldberg, J., Guigó, R., Hoegger, P. J., Hooker, J. B., Huggins, A., James, T. Y., Kamada, T., Kilaru, S., Kodira, C., Kües, U., Kupfer, D., Kwan, H. S., Lomsadze, A., Li, W., Lilly, W. W., Ma, L.-J., Mackey, A. J., Manning, G., Martin, F., Muraguchi, H., Natvig, D. O., Palmerini, H., Ramesh, M. A., Rehmeyer, C. J., Roe, B. A., Shenoy, N., Stanke, M., Ter-Hovhannisyan, V., Tunlid, A., Velagapudi, R., Vision, T. J., Zeng, Q., Zolan, M. E., and Pukkila, P. J. 2010. Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*). *Proc Natl Acad Sci U S A* 107(26):11889–11894. doi:10.1073/pnas.1003391107.
34. Ohm, R. A., de Jong, J. F., Lugones, L. G., Aerts, A., Kothe, E., **Stajich**, J. E., de Vries, R. P., Record, E., Levasseur, A., Baker, S. E., Bartholomew, K. A., Coutinho, P. M., Fowler, T. J., Gathman, A. C., Lombard, V., Henrissat, B., Knabe, N., Kües, U., Lilly, W. W., Lindquist, E., Lucas, S., Magnuson, J. K., Piumi, F., Raudaskoski, M., Salamov, A., Schmutz, J., Schwarze, F. W., vanKuyk, P. A., Horton, J. S., Grigoriev, I. V., and Wösten, H. A. 2010. Genomic sequence of the wood-rotting *Schizophyllum commune* strain H4-8: a model mushroom system. *Nature Biotech* 28:957–963. doi:10.1038/nbt.1643.
35. Strandberg, R., Nygren, K., Menkis, A., James, T. Y., Wik, L., **Stajich**, J. E., and Johannesson, H. 2010. Conflict between reproductive gene trees and species phylogeny among outcrossing members of the filamentous ascomycete genus *Neurospora*. *Fungal Genetics & Biology* 11(7):869–878. doi:10.1016/j.fgb.2010.06.008.

36. Lévesque, C. A., Brouwer, H., Cano, L., Hamilton, J. P., Holt, C., Huitema, E., Raffaele, S., Robideau, G. P., Thines, M., Win, J., Zerillo, M. M., Beakes, G. W., Boore, J. L., Busam, D., Dumas, B., Ferriera, S., Fuerstenberg, S. I., Gachon, C. M., Gaulin, E., Govers, F., Grenville-Briggs, L., Horner, N., Hostetler, J., Jiang, R. H., Johnson, J., Krajaejun, T., Lin, H., Meijer, H. J., Moore, B., Morris, P., Phuntmart, V., Puiu, D., Shetty, J., **Stajich**, J. E., Tripathy, S., Wawra, S., van West, P., Whitty, B. R., Coutinho, P. M., Henrissat, B., Martin, F., Thomas, P. D., Tyler, B. M., De Vries, R. P., Kamoun, S., Yandell, M., Tisserat, N., and Buell, C. R. 2010. Genome sequence of the necrotrophic plant pathogen, *Pythium ultimum*, reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol* 11(7):R173. doi:10.1186/gb-2010-11-7-r73.

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

38. Burns, C., **Stajich**, J. E., Rechtsteiner, A., Hanlon, S. E., Wilke, S. K., Palmerini, H. J., Savytskyy, O. P., Gathman, A. C., Lilly, W. W., Lieb, J. D., Zolan, M. E., and Pukkila, P. J. 2010. Analysis of the basidiomycete *Coprinopsis cinerea* reveals conservation of the core meiotic expression program over half a billion years of evolution. *PLoS Genetics* 6(9):e1001135. doi:10.1371/journal.pgen.1001135.

39. D'Souza, C. A., Kronstad, J. W., Taylor, G., Warren, R., Yuen, M., Hu, G., Jung, W. H., Sham, A., Kidd, S. E., Tangen, K., Lee, N., Zeilmaker, T., Sawkins, J., McVicker, G., Shah, S., Gnerre, S., Griggs, A., Zeng, Q., Bartlett, K., Li, W., Wang, X., Heitman, J., **Stajich**, J. E., Fraser, J. A., Meyer, W., Carter, D., Schein, J., Krzywinski, M., Kwon-Chung, K. J., Varma, A., Wang, J., Brunham, R., Fyfe, M., Ouellette, B. F. F., Siddiqui, A., Marra, M., Jones, S., Holt, R., Birren, B. W., Galagan, J. E., and Cuomo, C. A. 2011. Genome variation in *Cryptococcus gattii*, an emerging pathogen of immunocompetent hosts. *MBio* 2(1):e00342–10. doi:10.1128/mBio.00342-10.

40. Ellison, C. E., **Stajich**, J. E., Jacobson, D. J., Natvig, D. O., Lapidus, A., Foster, B., Aerts, A., Riley, R., Lindquist, E. A., Grigoriev, I. V., and Taylor, J. W. 2011. Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus *Neurospora tetrasperma*. *Genetics* 189(1):55–69. doi:10.1534/genetics.111.130690.

41. Joneson, S., **Stajich**, J. E., Shiu, S.-H., and Rosenblum, E. B. 2011. Genomic transition to pathogenicity in chytrid fungi. *PLoS Pathogens* 7(11):e1002338. doi:10.1371/journal.ppat.1002338.

42. **Stajich**, J. E., Harris, T., Brunk, B. P., Brestelli, J., Fischer, S., Harb, O. S., Kissinger, J. C., Li, W., Nayak, V., Pinney, D. F., Stoeckert, C. J., Jr, and Roos, D. S. 2012. FungiDB: an integrated functional genomics database for fungi. *Nucleic Acids Res* 40(D1):D675–D681. doi:10.1093/nar/gkr918.

43. Gioti, A., Mushegian, A. A., Strandberg, R., **Stajich**, J. E., and Johannesson, H. 2012. Unidirectional evolutionary transitions in fungal mating systems and the role of transposable elements. *Mol Biol Evol* 29(10):3215–3226. doi:10.1093/molbev/mss132.

44. Abramyan, J. and **Stajich**, J. E. 2012. Species-specific chitin-binding module 18 expansion in the amphibian pathogen *Batrachochytrium dendrobatidis*. *MBio* 3(3):e00150–e00112. doi:10.1128/mBio.00150-12.

45. Nygren, K., Wallberg, A., Samils, N., **Stajich**, J. E., Townsend, J. P., Karlsson, M., and Johannesson, H. 2012. Analyses of expressed sequence tags in *Neurospora* reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. *BMC Evol Biol* 12:229. doi:10.1186/1471-2148-12-229.

46. Gioti, A., Nystedt, B., Li, W., Xu, J., Andersson, A., Averette, A. F., Münch, K., Wang, X., Kappauf, C., Kingsbury, J. M., Kraak, B., Walker, L. A., Johansson, H. J., Holm, T., Lehtiö, J., **Stajich**, J. E., Mieczkowski, P., Kahmann, R., Kennell, J. C., Cardenas, M. E., Lundeberg, J., Saunders,

C. W., Boekhout, T., Dawson, T. L., Munro, C. A., de Groot, P. W. J., Butler, G., Heitman, J., and Scheynius, A. 2013. Genomic insights into the atopic eczema-associated skin commensal yeast *Malassezia sympodialis*. *MBio* 4(1):e00572–e00512. doi:10.1128/mBio.00572-12.

47. Cheng, C. K., Au, C. H., Wilke, S. K., **Stajich**, J. E., Zolan, M. E., Pukkila, P. J., and Kwan, H. S. 2013. 5'-serial analysis of gene expression studies reveal a transcriptomic switch during fruiting body development in *Coprinopsis cinerea*. *BMC Genomics* 14(1):195. doi:10.1186/1471-2164-14-195.
48. Jamieson, K., Rountree, M. R., Lewis, Z. A., **Stajich**, J. E., and Selker, E. U. 2013. Regional control of histone H3 lysine 27 methylation in *Neurospora*. *Proc Natl Acad Sci U S A* 110(15):6027–6032. doi:10.1073/pnas.1303750110.
49. Robb, S. M. C., Lu, L., Valencia, E., Burnette, J. M., 3rd, Okumoto, Y., Wessler, S. R., and **Stajich**, J. E. 2013. The use of RelocaTE and unassembled short reads to produce high-resolution snapshots of transposable element generated diversity in rice. *G3: Genes | Genomes | Genetics* 3(6):949–57. doi:10.1534/g3.112.005348.
50. Rosenblum, E. B., James, T. Y., Zamudio, K. R., Poorten, T. J., Ilut, D., Rodriguez, D., Eastman, J. M., Richards-Hrdlicka, K., Joneson, S., Jenkinson, T. S., Longcore, J. E., Parra Olea, G., Toledo, L. F., Arellano, M. L., Medina, E. M., Restrepo, S., Flechas, S. V., Berger, L., Briggs, C. J., and **Stajich**, J. E. 2013. Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. *Proc Natl Acad Sci U S A* 110(23):9385–9390. doi:10.1073/pnas.1300130110.
51. James, T. Y., Pelin, A., Bonen, L., Ahrendt, S., Sain, D., Corradi, N., and **Stajich**, J. E. 2013. Shared signatures of parasitism and phylogenomics unite Cryptomycota and Microsporidia. *Curr Biol* 23(16):1548–1553. doi:10.1016/j.cub.2013.06.057.
52. Gioti, A., **Stajich**, J. E., and Johannesson, H. 2013. *N*eurospora and the dead-end hypothesis: genomic consequences of selfing in the model genus. *Evolution* 67(12):3600–3616. doi:10.1111/evo.12206.
53. Gryganskyi, A. P., Humber, R. A., **Stajich**, J. E., Mullens, B., Anishchenko, I. M., and Vilgalys, R. 2013. Sequential utilization of hosts from different fly families by genetically distinct, sympatric populations within the *Entomophthora muscae* species complex. *PLoS One* 8(8):e71168. doi:10.1371/journal.pone.0071168.
54. Traeger, S., Altegoer, F., Freitag, M., Gabaldon, T., Kempken, F., Kumar, A., Marcet-Houben, M., Pöggeler, S., **Stajich**, J. E., and Nowrousian, M. 2013. The genome and development-dependent transcriptome of *Pyronema confluens*: a window into fungal evolution. *PLoS Genetics* 9(9):e1003820. doi:10.1371/journal.pgen.1003820.
55. Sachs, J. L., Skophammer, R. G., Bansal, N., and **Stajich**, J. E. 2014. Evolutionary origins and diversification of proteobacterial mutualists. *Proc Biol Sci* 281(1775):20132146. doi:10.1098/rspb.2013.2146.
56. Janbon, G., Ormerod, K. L., Paulet, D., Byrnes, E. J., 3rd, Yadav, V., Chatterjee, G., Mullapudi, N., Hon, C.-C., Billmyre, R. B., Brunel, F., Bahn, Y.-S., Chen, W., Chen, Y., Chow, E. W. L., Coppée, J.-Y., Floyd-Averette, A., Gaillardin, C., Gerik, K. J., Goldberg, J., Gonzalez-Hilarion, S., Gujja, S., Hamlin, J. L., Hsueh, Y.-P., Ianiri, G., Jones, S., Kodira, C. D., Kozubowski, L., Lam, W., Marra, M., Mesner, L. D., Mieczkowski, P. A., Moyrand, F., Nielsen, K., Proux, C., Rossignol, T., Schein, J. E., Sun, S., Wollschlaeger, C., Wood, I. A., Zeng, Q., Neuvéglise, C., Newlon, C. S., Perfect, J. R., Lodge, J. K., Idnurm, A., **Stajich**, J. E., Kronstad, J. W., Sanyal, K., Heitman, J., Fraser, J. A., Cuomo, C. A., and Dietrich, F. S. 2014. Analysis of the genome and transcriptome of *Cryptococcus neoformans* var. *grubii* reveals complex RNA expression and microevolution leading to virulence attenuation. *PLoS Genetics* 10(4):e1004261. doi:10.1371/journal.pgen.1004261.
57. Treseder, K. K., Maltz, M. R., Hawkins, B. A., Fierer, N., **Stajich**, J. E., and McGuire, K. L. 2014. Evolutionary histories of soil fungi are reflected in their large-scale biogeography. *Ecol Lett* 17(9):1086–1093. doi:10.1111/ele.12311.

58. Inglis, D. O., Skrzypek, M. S., Liaw, E., Moktali, V., Sherlock, G., and **Stajich**, J. E. 2014. Literature-based gene curation and proposed genetic nomenclature for *Cryptococcus*. *Eukaryot Cell* 13(7):878–883. doi:10.1128/EC.00083-14.

59. Ouyang, S., Park, G., Atamian, H. S., Han, C. S., **Stajich**, J. E., Kaloshian, I., and Borkovich, K. A. 2014. MicroRNAs suppress NB domain genes in tomato that confer resistance to *Fusarium oxysporum*. *PLoS pathogens* 10:e1004464. doi:10.1371/journal.ppat.1004464.

60. Teixeira, M. M., de Almeida, L. G., Kubitschek-Barreira, P., Alves, F. L., Kioshima, E. S., Abadio, A. K., Fernandes, L., Derengowski, L. S., Ferreira, K. S., Souza, R. C., Ruiz, J. C., de Andrade, N. C., Paes, H. C., Nicola, A. M., Albuquerque, P., Gerber, A. L., Martins, V. P., Peconick, L. D., Neto, A. V., Chaucanez, C. B., Silva, P. A., Cunha, O. L., de Oliveira, F. F., Dos Santos, T. C., Barros, A. L., Soares, M. A., de Oliveira, L. M., Marini, M. M., Villalobos-Duno, H., Cunha, M. M., de Hoog, S., da Silveira, J. F., Henrissat, B., Niño-Vega, G. A., Cisalpino, P. S., Mora-Montes, H. M., Almeida, S. R., **Stajich**, J. E., Lopes-Bezerra, L. M., Vasconcelos, A. T., and Felipe, M. S. 2014. Comparative genomics of the major fungal agents of human and animal Sporotrichosis: *Sporothrix schenckii* and *Sporothrix brasiliensis*. *BMC Genomics* 15:943. doi:10.1186/1471-2164-15-943.

61. Mélida, H., Sain, D., **Stajich**, J. E., and Bulone, V. 2015. Deciphering the uniqueness of mucoromycotina cell walls by combining biochemical and phylogenomic approaches. *Environmental Microbiology* 17(5):1649–62. doi:10.1111/1462-2920.12601.

62. Collins, R. A., **Stajich**, J. E., Field, D. J., Olive, J. E., and DeAbreu, D. M. 2015. The low information content of *Neurospora* splicing signals: implications for RNA splicing and intron origin. *RNA* 21(5):997–1004. doi:10.1261/rna.047985.114.

63. Willger, S. D., Liu, Z., Olarte, R. A., Adamo, M. E., **Stajich**, J. E., Myers, L. C., Kettenbach, A. N., and Hogan, D. A. 2015. Analysis of the *Candida albicans* phosphoproteome. *Eukaryot Cell* 14(5):474–485. doi:10.1128/EC.00011-15.

64. Liu, P. and **Stajich**, J. E. 2015. Characterization of the Carbohydrate Binding Module 18 gene family in the amphibian pathogen *Batrachochytrium dendrobatidis*. *Fungal Genet Biol* 77:31–39. doi:10.1016/j.fgb.2015.03.003.

65. Wang, Y., Smith, K. M., Freitag, M., and **Stajich**, J. E. 2015. Endogenous small RNA mediates meiotic silencing of a novel DNA transposon. *G3: Genes|Genomes|Genetics* 5(10):g3.115.017921. doi:10.1534/g3.115.017921.

66. Pieuchot, L., Lai, J., Loh, R. A., Leong, F. Y., Chiam, K.-H., **Stajich**, J. E., and Jedd, G. 2015. Cellular subcompartments through cytoplasmic streaming. *Dev Cell* 34(4):410–420. doi:10.1016/j.devcel.2015.07.017.

67. U'Ren, J. M., Miadlikowska, J., Zimmerman, N. B., Lutzoni, F., **Stajich**, J. E., and Arnold, A. E. 2016. Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). *Mol Phylogenet Evol* 98:210–232. doi:10.1016/j.ympev.2016.02.010.

68. de Man, T. J. B., **Stajich**, J. E., Kubicek, C. P., Teiling, C., Chenthamara, K., Atanasova, L., Druzhinina, I. S., Levenkova, N., Birnbaum, S. S. L., Barribeau, S. M., Bozick, B. A., Suen, G., Currie, C. R., and Gerardo, N. M. 2016. Small genome of the fungus *Escovopsis weberi*, a specialized disease agent of ant agriculture. *Proc Natl Acad Sci U S A* 113(13):3567–3572. doi:10.1073/pnas.1518501113.

69. Lee, M. J., Geller, A. M., Bamford, N. C., Liu, H., Gravelat, F., Snarr, B. D., Le Mauff, F., Chabot, J., Ralph, B., Ostapska, H., Lehoux, M., Cerone, R. P., Baptisa, S. D., Vinogradov, E., **Stajich**, J. E., Filler, S. G., Howell, P. L., and Sheppard, D. C. 2016. Deacetylation of fungal exopolysaccharide mediates adhesion and biofilm formation. *mBio* 7(2):e00252–16. doi:10.1128/mBio.00252-16.

70. Castanera, R., López-Varas, L., Borgognone, A., LaButti, K., Lapidus, A., Schmutz, J., Grimwood, J., Pérez, G., Pisabarro, A. G., Grigoriev, I. V., **Stajich**, J. E., and Ramírez, L. 2016. Transposable

elements versus the fungal genome: Impact on whole-genome architecture and transcriptional profiles. *PLoS Genetics* 12(6):e1006108. doi:10.1371/journal.pgen.1006108.

71. Short, D. P., O'Donnell, K., **Stajich**, J. E., Hulcr, J., Kijimoto, T., Berger, M. C., Macias, A. M., Spahr, E. J., Bateman, C. C., Eskalen, A., et al. 2017. PCR multiplexes discriminate *Fusarium* symbionts of invasive *Euwallacea* ambrosia beetles that inflict damage on numerous tree species throughout the United States. *Plant Disease* 101(1):233–240. doi:10.1094/PDIS-07-16-1046-RE.

72. Spatafora, J. W., Chang, Y., Benny, G. L., Lazarus, K., Smith, M. E., Berbee, M. L., Bonito, G., Corradi, N., Grigoriev, I., Gryganskyi, A., James, T. Y., O'Donnell, K., Roberson, R. W., Taylor, T. N., Uehling, J., Vilgalys, R., White, M. M., and **Stajich**, J. E. 2016. A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. *Mycologia* 108:1028–1046. doi: 10.3852/16-042.

73. Chen, J., Wrightsman, T., Wessler, S. R., and **Stajich**, J. E. 2017. RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. *PeerJ* 5:e2942. doi:10.7717/peerj.2942.

74. Nguyen, T. A., Cissé, O. H., Yun Wong, J., Zheng, P., Hewitt, D., Nowrousian, M., **Stajich**, J. E., and Jedd, G. 2017. Innovation and constraint leading to complex multicellularity in the Ascomycota. *Nature Communications* 8:14444. doi:10.1038/ncomms14444.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

116. Coleine, C., **Stajich**, J. E., Zucconi, L., Onofri, S., and Selbmann, L. 2020. Sun exposure drives Antarctic cryptoendolithic community structure and composition. *Polar Biology* doi:10.1007/s00300-020-02650-1.

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

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

119. Coleine, C., Masonjones, S., Sterflinger, K., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus *Friedmanniomyces endolithicus*. *Fungal Biology* 124(5):458–467. doi:10.1016/j.funbio.2020.01.005.

120. Macias, A. M., Geiser, D. M., **Stajich**, J. E., Lukasik, P., Veloso, C., Bublitz, D. C., Berger, M. C., Boyce, G. R., Hodge, K., and Kasson, M. T. 2020. Evolutionary relationships among *Massospora spp.* (Entomophthorales), obligate pathogens of cicadas. *Mycologia* 112(6):1060–1074. doi:10.1080/00275514.2020.1742033.

121. Yang, C.-T., Vidal-Diez de Ulzurrun, G., Gonçalves, A. P., Lin, H.-C., Chang, C.-W., Huang, T.-Y., Chen, S.-A., Lai, C.-K., Tsai, I. J., Schroeder, F. C., **Stajich**, J. E., and Hsueh, Y.-P. 2020. Natural diversity in the predatory behavior facilitates the establishment of a robust model strain for nematode-trapping fungi. *Proceedings of the National Academy of Sciences of the United States of America* 117(12):6762–6770. doi:10.1073/pnas.1919726117.

122. Coleine, C., Pombubpa, N., Zucconi, L., Onofri, S., Turchetti, B., Buzzini, P., **Stajich**, J. E., and Selbmann, L. 2020. Uncovered microbial diversity in Antarctic cryptoendolithic communities sampling three representative locations of the Victoria Land. *Microorganisms* 8(6):942. doi:10.3390/microorganisms8060942.

123. Tabima, J. F., Trautman, I. A., Chang, Y., Wang, Y., Mondo, S. J., Salamov, A., Grigoriev, I. V., **Stajich**, J. E., and Spatafora, J. W. 2020. Phylogenomic analyses of non-dikarya fungi supports horizontal gene transfer driving diversification of secondary metabolism in the amphibian gastrointestinal symbiont, *Basidiobolus*. *G3: Genes|Genomes|Genetics* 10(9):3417–3433. doi:10.1534/g3.120.401516.

124. Pombubpa, N., Pietrasiak, N., De Ley, P., and **Stajich**, J. E. 2020. Insights into drylands biocrust microbiome: geography, soil depth, and crust type affect biocrust microbial communities and networks in Mojave Desert, USA. *FEMS Microbiology Ecology* 96(9). doi:10.1093/femsec/fiaa125.

125. Myers, J. M., Bonds, A. E., Clemons, R. A., Thapa, N. A., Simmons, D. R., Carter-House, D., Ortanez, J., Liu, P., Miralles-Durán, A., Desirò, A., Longcore, J. E., Bonito, G., **Stajich**, J. E., Spatafora, J. W., Chang, Y., Corrochano, L. M., Gryganskyi, A., Grigoriev, I. V., and James, T. Y. 2020. Survey of early-diverging lineages of fungi reveals abundant and diverse mycoviruses. *mBio* 11(5):e02027–20. doi:10.1128/mBio.02027-20.

126. Collins, C. G., Spasojevic, M. J., Alados, C. L., Aronson, E. L., Benavides, J. C., Cannone, N., Caviezel, C., Grau, O., Guo, H., Kudo, G., Kuhn, N. J., Müllerová, J., Phillips, M. L., Pombubpa, N., Reverchon, F., Shulman, H. B., **Stajich**, J. E., Stokes, A., Weber, S. E., and Diez, J. M. 2020. Belowground impacts of alpine woody encroachment are determined by plant traits, local climate and soil conditions. *Global Change Biology* 26(12):7112–7127. doi:10.1111/gcb.15340.

127. Vandepol, N., Liber, J., Desirò, A., Na, H., Kennedy, M., Barry, K., Grigoriev, I. V., Miller, A. N., O'Donnell, K., **Stajich**, J. E., and Bonito, G. 2020. Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. *Fungal Diversity* 104(1):267–289. doi:10.1007/s13225-020-00455-5.

128. Carrillo, A. J., Cabrera, I. E., Spasojevic, M., Schacht, P., **Stajich**, J. E., and Borkovich, K. A. 2020. Clustering analysis of large-scale phenotypic data in the model filamentous fungus *Neurospora crassa*. *BMC Genomics* 21(1):755. doi:10.1186/s12864-020-07131-7.

129. Chen, J., Lu, L., Robb, S. M. C., Collin, M., Okumoto, Y., **Stajich**, J. E., and Wessler, S. R. 2020. Genomic diversity generated by a transposable element burst in a rice recombinant inbred population. *Proc Natl Acad Sci U S A* 117:26288–26297. doi:10.1073/pnas.2015736117.

130. Eudes Filho, J., dos Santos, I. B., Reis, C. M. S., Patané, J. S., Paredes, V., Romualdo, J. P. A. B., Poggianni, S. S. C., Castro, T. B., Gomez, O. M., Pereira, S. A., Schubach, E. Y. P., Gomes, K. P., Mavengere, H., Alves, L. G. d. B., Lucas, J., Paes, H. C., Albuquerque, P., Cruz, L. M., McEwen, J. G., **Stajich**, J. E., Almeida-Paes, R., Zancopé-Oliveira, R. M., Matute, D. R., Barker, B. M., Felipe, M. S. S., Teixeira, M. d., and Nicola, A. M. 2020. A novel *Sporothrix brasiliensis* genomic variant in midwestern Brazil: evidence for an older and wider sporotrichosis outbreak. *Emerging Microbes & Infections* 9(1):2515–2525. doi:10.1080/22221751.2020.1847001.

131. Lee, Y.-Y., Vidal-Diez de Ulzurrun, G., Schwarz, E. M., **Stajich**, J. E., and Hsueh, Y.-P. 2021. Genome sequence of the oyster mushroom *Pleurotus ostreatus* strain PC9. *G3: Genes|Genomes|Genetics* 11(2):jkaa008. doi:10.1093/g3journal/jkaa008.

132. Vidal-Diez de Ulzurrun, G., Lee, Y.-Y., **Stajich**, J. E., Schwarz, E. M., and Hsueh, Y.-P. 2021. Genomic analyses of two italian oyster mushroom *Pleurotus pulmonarius* strains. *G3: Genes|Genomes|Genetics* 11(2):jkaa007. doi:10.1093/g3journal/jkaa007.

133. O'Donnell, K., Al-Hatmi, A. M. S., Aoki, T., Brankovics, B., Cano-Lira, J. F., Coleman, J. J., de Hoog, G. S., Pietro, A. D., Frandsen, R. J. N., Geiser, D. M., Gibas, C. F. C., Guarro, J., Kim, H.-S., Kistler, H. C., Laraba, I., Leslie, J. F., López-Berges, M. S., Lysøe, E., Meis, J. F., Monod, M., Proctor, R. H., Rep, M., Ruiz-Roldán, C., Sisic, A., **Stajich**, J. E., Steenkamp, E. T., Summerell, B. A., van der Lee, T. A. J., van Diepeningen, A. D., E.Verweij, P., Waalwijk, C., Ward, T. J., Wickes, B. L., Wiederhold, N. P., Wingfield, M. J., Zhang, N., and Zhang, S. X. 2020. No to *Neocosmospora*: Phylogenomic and practical reasons for continued inclusion of the *Fusarium solani* species complex in the genus *Fusarium*. *mSphere* 5(5):e00810–20. doi:10.1128/mSphere.00810-20.

134. Geiser, D. M., Al-Hatmi, A., Aoki, T., Arie, T., Balmas, V., Barnes, I., Bergstrom, G. C., Bhattacharyya, M. K. K., Blomquist, C. L., Bowden, R., Brankovics, B., Brown, D. W., Burgess, L. W., Bushley, K., Busman, M., Cano-Lira, J. F., Carrillo, J. D., Chang, H.-X., Chen, C.-Y., Chen, W., Chilvers, M. I., Chulze, S. N., Coleman, J. J., Cuomo, C. A., de Beer, Z. W., de Hoog, G. S., Del Castillo-Múnera, J., Del Ponte, E., Diéguez-Uribeondo, J., Di Pietro, A., Edel-Hermann, V., Elmer, W. H., Epstein, L., Eskalen, A., Esposto, M. C., Everts, K. L., Fernández-Pavía, S. P., da Silva, G. F., Foroud, N. A., Fourie, G., Frandsen, R. J. N., Freeman, S., Freitag, M., Frenkel, O., Fuller, K. K., Gagkaeva, T., Gardiner, D. M., Glenn, A. E., Gold, S., Gordon, T., Gregory, N. F., Gryzenhout, M., Guarro, J., Gugino, B., Gutiérrez, S., Hammond-Kosack, K., Harris, L. J., Homa, M., Hong, C.-F., Hornok, L., Huang, J.-W., Ilkit, M., Jacobs, A., Jacobs, K., Jiang, C., Jimenez-Gasco, M. D. M., Kang, S., Kasson, M. T., Kazan, K., Kennell, J. C., Kim, H., Kistler, H. C., Kuldau, G. A., Kulik, T., Kurzai, O., Laraba, I., Laurence, M. H., Lee, T. Y., Lee, Y.-W., Lee, Y.-H., Leslie, J. F., Liew, E. C. Y., Lofton, L. W., Logrieco, A., Sánchez López-Berges, M., Luque, A. G., Lysøe, E., Ma, L.-J., Marra, R. E., Martin, F. N., May, S. R., McCormick, S., McGee, C. T., Meis, J. F., Migheli, Q., Mohamed Nor, N. M. I., Monod, M., Moretti, A., Mostert, D., Mulé, G., Munaut, F., Munkvold, G. P., Nicholson, P., Nucci, M., O'Donnell, K., Pasquali, M., Pfenning, L. H., Prigitano, A., Proctor, R., Ranque, S., Rehner, S., Rep, M., Rodríguez-Alvarado, G., Rose, L. J., Roth, M. G., Ruiz-Roldán, C., Saleh, A. A., Salleh, B., Sang, H., Scandiani, M., Scauflaire, J., Schmale, D., Short, D. P., Šišić, A., Smith, J., Smyth, C. W., Son, H., Spahr, E., **Stajich**, J. E., Steenkamp, E., Steinberg, C., Subramaniam, R., Suga, H., Summerell, B. A., Susca, A., Swett, C. L., Toomajian, C., Torres-Cruz, T. J., Tortorano, A. M., Urban, M., Vaillancourt, L. J., Vallad, G. E., van der Lee, T., Vanderpool, D., van Diepeningen, A. D., Vaughan, M., Venter, E., Vermeulen, M., Verweij, P. E., Viljoen, A., Waalwijk, C., Wallace, E. C., Walther, G., Wang, J., Ward, T., Wickes, B., Wiederhold, N. P., Wingfield, M. J., Wood, A. K. M., Xu, J.-R., Yang, X. B., Yli-Matilla, T., Yun, S.-H., Zakaria, L., Zhang, H., Zhang, N., Zhang, S., and Zhang, X. 2020. Phylogenomic analysis of a 55.1 kb 19-gene dataset resolves a monophyletic Fusarium that includes the *Fusarium solani* Species Complex. *Phytopathology* doi: 10.1094/PHYTO-08-20-0330-LE.

135. Albanese, D., Coleine, C., Rota-Stabelli, O., Onofri, S., Tringe, S. G., **Stajich**, J. E., Selbmann, L., and Donati, C. 2021. Pre-cambrian roots of novel Antarctic cryptoendolithic bacterial lineages. *Microbiome* 9:63. doi:10.1186/s40168-021-01021-0.

136. Hollin, T., Jaroszewski, L., **Stajich**, J. E., Godzik, A., and Le Roch, K. G. 2021. Identification and phylogenetic analysis of RNA binding domain abundant in apicomplexans or RAP proteins. *Microbial Genomics* 7(3):mgen000541. doi:10.1099/mgen.0.000541.

137. Kowalski, C. H., Morelli, K. A., **Stajich**, J. E., Nadell, C. D., and Cramer, R. A. 2021. A heterogeneously expressed gene family modulates the biofilm architecture and hypoxic growth of *Aspergillus fumigatus*. *mBio* 12(1):e03579–20. doi:10.1128/mBio.03579-20.

138. Cissé, O. H., Ma, L., Dekker, J. P., Khil, P. P., Youn, J.-H., Brenchley, J. M., Blair, R., Pahar, B., Chabé, M., Van Rompay, K. K. A., Keesler, R., Sukura, A., Hirsch, V., Kutty, G., Liu, Y., Peng, L., Chen, J., Song, J., Weissenbacher-Lang, C., Xu, J., Upham, N. S., **Stajich**, J. E., Cuomo, C. A.,

Cushion, M. T., and Kovacs, J. A. 2021. Genomic insights into the host specific adaptation of the Pneumocystis genus. *Communications Biology* 4:305. doi:10.1038/s42003-021-01799-7.

139. Malar C, M., Krüger, M., Krüger, C., Wang, Y., **Stajich**, J. E., Keller, J., Chen, E. C. H., Yildirir, G., Villeneuve-Laroche, M., Roux, C., Delaux, P.-M., and Corradi, N. 2021. The genome of *Geosiphon pyriformis* reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. *Current Biology* 31(7):1578–1580. doi:10.1016/j.cub.2021.01.058.

140. Chang, Y., Rochon, D., Sekimoto, S., Wang, Y., Chovatia, M., Sandor, L., Salamov, A., Grigoriev, I. V., **Stajich**, J. E., and Spatafora, J. W. 2021. Genome-scale phylogenetic analyses confirm Olpidium as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. *Scientific reports* 11:3217. doi:10.1038/s41598-021-82607-4.

141. Demers, E. G., **Stajich**, J. E., Ashare, A., Occhipinti, P., and Hogan, D. A. 2021. Balancing positive and negative selection: *In Vivo* evolution of *Candida lusitaniae MRR1*. *mBio* 12(2):e03328–20. doi:10.1128/mBio.03328-20.

142. Tesei, D., Chiang, A. J., Kalkum, M., **Stajich**, J. E., Mohan, G. B. M., Sterflinger, K., and Venkateswaran, K. 2021. Effects of simulated microgravity on the proteome and secretome of the polyextremotolerant black fungus *Knufia chersonesos*. *Frontiers in Genetics* 12:638708. doi:10.3389/fgene.2021.638708.

143. Li, Y., Steenwyk, J. L., Chang, Y., Wang, Y., James, T. Y., **Stajich**, J. E., Spatafora, J. W., Groenewald, M., Dunn, C. W., Hittinger, C. T., Shen, X.-X., and Rokas, A. 2021. A genome-scale phylogeny of the kingdom Fungi. *Current Biology* 31(8):1653–1665.e5. doi:10.1016/j.cub.2021.01.074.

144. Selbmann, L., Stoppiello, G. A., Onofri, S., **Stajich**, J. E., and Coleine, C. 2021. Culture-dependent and amplicon sequencing approaches reveal diversity and distribution of black fungi in Antarctic cryptoendolithic communities. *Journal of Fungi* 7(3):213. doi:10.3390/jof7030213.

145. Rajewski, A., Carter-House, D., **Stajich**, J., and Litt, A. 2021. Datura genome reveals duplications of psychoactive alkaloid biosynthetic genes and high mutation rate following tissue culture. *BMC Genomics* 22:201. doi:10.1186/s12864-021-07489-2.

146. de Melo Teixeira, M., Lang, B. F., Matute, D. R., **Stajich**, J. E., and Barker, B. 2021. The mitochondrial genomes of the human pathogens *Coccidioides immitis* and *C. posadasii*. *G3: Genes|Genomes|Genetics* 11(7):jkab132. doi:10.1093/g3journal/jkab132.

147. Carlin, A. F., Beyhan, S., Peña, J. F., **Stajich**, J. E., Viriyakosol, S., Fierer, J., and Kirkland, T. N. 2021. Transcriptional analysis of *Coccidioides immitis* mycelia and spherules by RNA sequencing. *Journal of Fungi* 7(5):366. doi:10.3390/jof7050366.

148. Nielsen, K. N., Salgado, J. F. M., Natsopoulou, M. E., Kristensen, T., **Stajich**, J. E., and De Fine Licht, H. H. 2021. Diploidy within a haploid genus of entomopathogenic fungi. *Genome Biology and Evolution* 13(7):evab158. doi:10.1093/gbe/evab158.

149. Ettinger, C. L., Byrne, F. J., Collin, M. A., Carter-House, D., Walling, L. L., Atkinson, P. W., Redak, R. A., and **Stajich**, J. E. 2021. Improved draft reference genome for the Glassy-winged Sharpshooter (*Homalodisca vitripennis*), a vector for Pierce's disease. *G3: Genes|Genomes|Genetics* 11(10):jkab255. doi:10.1093/g3journal/jkab255.

150. Jones, J. T., Liu, K.-W., Wang, X., Kowalski, C. H., Ross, B. S., Mills, K. A. M., Kerkaert, J. D., Hohl, T. M., Lofgren, L. A., **Stajich**, J. E., Obar, J. J., and Cramer, R. A. 2021. *Aspergillus fumigatus* strain-specific conidia lung persistence causes an allergic broncho-pulmonary aspergillosis-like disease phenotype. *mSphere* 6(1):e01250–20. doi:10.1128/mSphere.01250-20.

151. Ross, B. S., Lofgren, L. A., Ashare, A., **Stajich**, J. E., and Cramer, R. A. 2021. *Aspergillus fumigatus* in-host HOG pathway mutation for cystic fibrosis lung microenvironment persistence. *mBio* 12:e0215321. doi:10.1128/mBio.02153-21.

152. Hopke, A., Mela, A., Ellett, F., Carter-House, D., Peña, J. F., **Stajich**, J. E., Altamirano, S., Lovett, B., Egan, M., Kale, S., Kronholm, I., Guerette, P., Szewczyk, E., McCluskey, K., Breslauer, D., Shah, H., Coad, B. R., Momany, M., and Irimia, D. 2021. Crowdsourced analysis of fungal growth and branching on microfluidic platforms. *PloS one* 16(9):e0257823. doi:10.1371/journal.pone.0257823.
153. Gostinčar, C., **Stajich**, J. E., Kejžar, A., Sinha, S., Nislow, C., Lenassi, M., and Gunde-Cimerman, N. 2021. Seven years at high salinity-experimental evolution of the extremely halotolerant black yeast *Hortaea werneckii*. *Journal of Fungi* 7(9):723. doi:10.3390/jof7090723.
154. Reynolds, N. K., Jusino, M. A., **Stajich**, J. E., and Smith, M. E. 2021. Understudied, underrepresented, and unknown: methodological biases that limit detection of early diverging fungi from environmental samples. *Molecular Ecology Resources* 22(3):1065–1085. doi:10.1111/1755-0998.13540.
155. Kirkland, M. E., Stannard, M., Kowalski, C. H., Mould, D., Caffrey-Carr, A., Temple, R. M., Ross, B. S., Lofgren, L. A., **Stajich**, J. E., Cramer, R. A., and Obar, J. J. 2021. Host lung environment limits *Aspergillus fumigatus* germination through an SskA-dependent signaling response. *mSphere* 6:e0092221. doi:10.1128/msphere.00922-21.
156. Parker, C. W., Teixeira, M. d., Singh, N. K., Raja, H. A., Cank, K. B., Spigolon, G., Oberlies, N. H., Barker, B. M., **Stajich**, J. E., Mason, C. E., and Venkateswaran, K. 2022. Genomic characterization of *Parengyodontium torokii* sp. nov., a biofilm-forming fungus isolated from Mars 2020 assembly facility. *Journal of Fungi* 8(1):66. doi:10.3390/jof8010066.
157. Duttke, S. H., Beyhan, S., Singh, R., Neal, S., Viriyakosol, S., Fierer, J., Kirkland, T. N., **Stajich**, J. E., Benner, C., and Carlin, A. F. 2022. Decoding transcription regulatory mechanisms associated with *Coccidioides immitis* phase transition using total RNA. *mSystems* 7(1):e0140421. doi:10.1128/msystems.01404-21.
158. de Melo Teixeira, M., **Stajich**, J. E., Sahl, J. W., Thompson, G. R., Brem, R. B., Dubin, C. A., Blackmon, A. V., Mead, H. L., Keim, P., and Barker, B. M. 2022. A chromosomal-level reference genome of the widely utilized *Coccidioides posadasii* laboratory strain "Silveira". *G3: Genes|Genomes|Genetics* 12(4):jkac031. doi:10.1093/g3journal/jkac031.
159. Coleine, C., Delgado-Baquerizo, M., Albanese, D., Singh, B. K., **Stajich**, J. E., Selbmann, L., and Egidi, E. 2022. Rocks support a distinctive and consistent mycobiome across contrasting dry regions of earth. *FEMS Microbiology Ecology* 98:fiac030. doi:10.1093/femsec/fiac030.
160. Lofgren, L. A., Lorch, J. M., Cramer, R. A., Blehert, D. S., Berlowski-Zier, B. M., Winzeler, M. E., Gutierrez-Perez, C., Kordana, N. E., and **Stajich**, J. E. 2022. Avian-associated *Aspergillus fumigatus* displays broad phylogenetic distribution, no evidence for host specificity, and multiple genotypes within epizootic events. *G3: Genes|Genomes|Genetics* 12(5):jkac075. doi:10.1093/g3journal/jkac075.
161. de Souza Pacheco, I., Doss, A.-L. A., Vindiola, B. G., Brown, D. J., Ettinger, C. L., **Stajich**, J. E., Redak, R. A., Walling, L. L., and Atkinson, P. W. 2022. Efficient CRISPR/Cas9-mediated genome modification of the glassy-winged sharpshooter *Homalodisca vitripennis* (Germar). *Scientific Reports* 12:6428. doi:10.1038/s41598-022-09990-4.
162. Malar C, M., Wang, Y., **Stajich**, J. E., Kokkoris, V., Villeneuve-Laroche, M., Yildirir, G., and Corradi, N. 2022. Early branching arbuscular mycorrhizal fungus *Paraglomus occultum*, carries a small and repeat-poor genome compared to relatives in the Glomeromycotina. *Microbial genomics* 8(4):000810. doi:10.1099/mgen.0.000810.
163. Maltz, M. R., Carey, C. J., Freund, H. L., Botthoff, J. K., Hart, S. C., **Stajich**, J. E., Aarons, S. M., Aciego, S. M., Blakowski, M., Dove, N. C., Barnes, M. E., Pombubpa, N., and Aronson, E. L. 2022. Landscape topography and regional drought alters dust microbiomes in the Sierra Nevada of California. *Frontiers in Microbiology* 13:856454. doi:10.3389/fmicb.2022.856454.

164. Blachowicz, A., Romsdahl, J., Chiang, A. J., Masonjones, S., Kalkum, M., **Stajich**, J. E., Torok, T., Wang, C. C. C., and Venkateswaran, K. 2022. The International Space Station environment triggers molecular responses in *Aspergillus niger*. *Frontiers in Microbiology* 13:893071. doi:10.3389/fmicb.2022.893071.

165. Maccaro, J. J., Moreira Salgado, J. F., Klinger, E., Argueta Guzmán, M. P., Ngor, L., **Stajich**, J. E., and McFrederick, Q. S. 2022. Comparative genomics reveals that metabolism underlies evolution of entomopathogenicity in bee-loving *Ascosphaera* spp. fungi. *Journal of Invertebrate Pathology* 194:107804. doi:10.1016/j.jip.2022.107804.

166. Chang, Y., Wang, Y., Mondo, S., Ahrendt, S., Andreopoulos, W., Barry, K., Beard, J., Benny, G. L., Blankenship, S., Bonito, G., Cuomo, C., Desiro, A., Gervers, K. A., Hundley, H., Kuo, A., LaButti, K., Lang, B. F., Lipzen, A., O'Donnell, K., Pangilinan, J., Reynolds, N., Sandor, L., Smith, M. E., Tsang, A., Grigoriev, I. V., **Stajich**, J. E., and Spatafora, J. W. 2022. Evolution of zygomycete secretomes and the origins of terrestrial fungal ecologies. *iScience* 25(8):104840. doi:10.1016/j.isci.2022.104840.

167. Gryganskyi, A. P., Nie, Y., Hajek, A. E., Hodge, K. T., Liu, X.-Y., Aadland, K., Voigt, K., Anishchenko, I. M., Kutovenko, V. B., Kava, L., Vuek, A., Vilgalys, R., Huang, B., and **Stajich**, J. E. 2022. The early terrestrial fungal lineage of *Conidiobolus* -transition from saprotroph to parasitic lifestyle. *Journal of Fungi* 8(8):789. doi:10.3390/jof8080789.

168. Amses, K. R., Simmons, D. R., Longcore, J. E., Mondo, S. J., Seto, K., Jerônimo, G. H., Bonds, A. E., Quandt, C. A., Davis, W. J., Chang, Y., Federici, B. A., Kuo, A., LaButti, K., Pangilinan, J., Andreopoulos, W., Tritt, A., Riley, R., Hundley, H., Johnson, J., Lipzen, A., Barry, K., Lang, B. F., Cuomo, C. A., Buchler, N. E., Grigoriev, I. V., Spatafora, J. W., **Stajich**, J. E., and James, T. Y. 2022. Diploid-dominant life cycles characterize the early evolution of fungi. *Proceedings of the National Academy of Sciences of the United States of America* 119:e2116841119. doi:10.1073/pnas.2116841119.

169. de Melo Teixeira, M., Almeida-Paes, R., Reis Bernardes-Engemann, A., Moraes Nicola, A., Marques de Macedo, P., Carlos Francesconi do Valle, A., Clara Gutierrez-Galhardo, M., Francis Saraiva Freitas, D., Barker, B. M., Matute, D. R., **Stajich**, J. E., and Maria Zancopé-Oliveira, R. 2022. Single nucleotide polymorphisms and chromosomal copy number variation may impact the *Sporothrix brasiliensis* antifungal susceptibility and sporotrichosis clinical outcomes. *Fungal Genetics and Biology* page 103743. doi:10.1016/j.fgb.2022.103743.

170. Narunsky-Haziza, L., Sepich-Poore, G., Livyatan, I., Asraf, O., Martino, C., Nejman, D., Gavert, N., **Stajich**, J. E., Amit, G., González, A., Wandro, S., Perry, G., Meltser, A., Shaffer, A., Zhu, J., Balint-Lahat, Q., Barshack, N., Dadiani, I., Gal-Yam, M., Patel, E., Bashan, S., Swafford, A., Pilpel, A., Knight, Y., Straussman, R., and R. 2022. Pan-cancer analyses reveal cancer type-specific fungal ecologies and bacteriome interactions. *Cell* 185(20):P3789–3806.E17. doi:10.1016/j.cell.2022.09.005.

171. Yuan, B., Keller, N. P., Oakley, B. R., **Stajich**, J. E., and Wang, C. C. C. 2022. Manipulation of the global regulator *mcrA* upregulates secondary metabolite production in *Aspergillus wentii* using CRISPR-Cas9 with *in vitro* assembled ribonucleoproteins. *ACS Chemical Biology* doi:10.1021/acschembio.2c00456.

172. Ettinger, C. L., Byrne, F. J., de Souza Pacheco, I., Brown, D. J., Walling, L. L., Atkinson, P. W., Redak, R. A., and **Stajich**, J. E. 2022. Transcriptome and population structure of glassy-winged sharpshooters (*Homalodisca vitripennis*) with varying insecticide resistance in southern California. *BMC Genomics* 23:721. doi:10.1186/s12864-022-08939-1.

173. Winter, D. J., Weir, B. S., Glare, T., Rhodes, J., Perrott, J., Fisher, M. C., **Stajich**, J. E., Consortium, K. A. R., Digby, A., Dearden, P. K., and Cox, M. P. 2022. A single fungal strain was the unexpected cause of a mass aspergillosis outbreak in the world's largest and only flightless parrot. *iScience* 25:105470. doi:10.1016/j.isci.2022.105470.

174. Lofgren, L. A., Ross, B. S., Cramer, R. A., and **Stajich**, J. E. 2022. Combined pan-, population-, and phylo-genomic analysis of *Aspergillus fumigatus* reveals population structure and lineage-specific diversity. *PLoS Biology* 20(11):e3001890. doi:10.1371/journal.pbio.3001890.

175. Reynolds, N. K., **Stajich**, J. E., Benny, G. L., Barry, K., Mondo, S., LaButti, K., Lipzen, A., Daum, C., Grigoriev, I. V., Ho, H.-M., Crous, P. W., Spatafora, J. W., and Smith, M. E. 2023. Mycoparasites, gut dwellers, and saprotrophs: Phylogenomic reconstructions and comparative analyses of kickxellomycotina fungi. *Genome biology and Evolution* 15. doi:10.1093/gbe/evac185.

176. Liu, X., Lyu, L., Li, J., Sen, B., Bai, M., **Stajich**, J. E., Collier, J. L., and Wang, G. 2023. Comparative genomic analyses of cellulolytic machinery reveal two nutritional strategies of marine Labyrinthulomycetes protists. *Microbiology Spectrum* page e0424722. doi:10.1128/spectrum.04247-22.

177. Chander, A. M., Teixeira, M. d., Singh, N. K., Williams, M. P., Simpson, A. C., Damle, N., Parker, C. W., **Stajich**, J. E., Mason, C. E., Torok, T., and Venkateswaran, K. 2023. Description and genome characterization of three novel fungal strains isolated from Mars 2020 mission-associated spacecraft assembly facility surfaces – recommendations for two new genera and one species. *Journal of Fungi* 9(1):31. doi:10.3390/jof9010031.

178. Xi, M., Deyett, E., **Stajich**, J. E., El-Kereamy, A., Roper, M. C., and Rolshausen, P. E. 2023. Microbiome diversity, composition and assembly in a California citrus orchard. *Frontiers in microbiology* 14:1100590. doi:10.3389/fmicb.2023.1100590.

179. Wang, Y., Chang, Y., Ortañez, J., Peña, J. F., Carter-House, D., Reynolds, N. K., Smith, M. E., Benny, G., Mondo, S. J., Salamov, A., Lipzen, A., Pangilinan, J., Guo, J., LaButti, K., Andreopolous, W., Tritt, A., Keymanesh, K., Yan, M., Barry, K., Grigoriev, I. V., Spatafora, J. W., and **Stajich**, J. E. 2023. Divergent evolution of early terrestrial fungi reveals the evolution of Mucormycosis pathogenicity factors. *Genome Biology and Evolution* doi:10.1093/gbe/evad046.

180. Ettinger, C. L., Ostovar, T., Yacoub, M., Ahrendt, S., Hice, R. H., Federici, B. A., and **Stajich**, J. E. 2023. Genomes and transcriptomes help unravel the complex life cycle of the blastoclad fungus, *Coelomomyces lativittatus*, an obligate parasite of mosquitoes and microcrustaceans. *Mycologia* 115:630–647. doi:10.1080/00275514.2023.2228182.

181. Yuan, B., Grau, M. F., Murata, R. M., Torok, T., Venkateswaran, K., **Stajich**, J. E., and Wang, C. C. C. 2023. Identification of the Neoaspergillic Acid biosynthesis gene cluster by establishing an *In Vitro* crispr-ribonucleoprotein genetic system in *Aspergillus melleus*. *ACS Omega* 8(19):16713–16721. doi:10.1021/acsomega.2c08104.

182. Hanafy, R. A., Wang, Y., **Stajich**, J. E., Pratt, C. J., Youssef, N. H., and Elshahed, M. S. 2023. Phylogenomic analysis of the *Neocallimastigomycota*: proposal of *Caecomycetaceae* fam. nov., *Piromycetaceae* fam. nov., and emended description of the families *Neocallimastigaceae*, and *Anaeromycetaceae*. *Int J Syst Evol Microbiol* 73(2). doi:10.1099/ijsem.0.005735.

183. Hansen, F. A., James, D. K., Anderson, J., Meredith, C., Dominguez, A. J., Pombubpa, N., **Stajich**, J. E., Romero-Olivares, A. L., Salley, S. W., and Pietrasiak, N. 2023. Landscape characteristics shape surface soil microbiomes in the Chihuahuan Desert. *Frontiers in Microbiology* 14:1581. doi:10.3389/fmicb.2023.1135800.

184. Kurbessoian, T., Murante, D., Crocker, A., Hogan, D. A., and **Stajich**, J. E. 2023. In host evolution of *Exophiala dermatitidis* in Cystic Fibrosis lung micro-environment. *G3: Genes|Genomes|Genetics* page jkad126. doi:10.1093/g3journal/jkad126.

185. Merényi, Z., Krizsán, K., Sahu, N., Liu, X.-B., Bálint, B., **Stajich**, J. E., Spatafora, J. W., and Nagy, L. G. 2023. Genomes of fungi and relatives reveal delayed loss of ancestral gene families and evolution of key fungal traits. *Nature Ecology and Evolution* doi:10.1038/s41559-023-02095-9.

186. Meili, C. H., Jones, A. L., Arreola, A. X., Habel, J., Pratt, C. J., Hanafy, R. A., Wang, Y., Yassin, A. S., TagElDein, M. A., Moon, C. D., Janssen, P. H., Shrestha, M., Rajbhandari, P., Nagler, M., Vinzelj, J. M., Podmirseg, S. M., **Stajich**, J. E., Goetsch, A. L., Hayes, J., Young, D., Fliegerova, K.,

Grilli, D. J., Vodička, R., Moniello, G., Mattiello, S., Kashef, M. T., Nagy, Y. I., Edwards, J. A., Dagar, S. S., Foote, A. P., Youssef, N. H., and Elshahed, M. S. 2023. Patterns and determinants of the global herbivorous mycobiome. *Nature Communications* 14(1):3798. doi:10.1038/s41467-023-39508-z.

187. Murante, D., Demers, E. G., Kurbessoian, T., Ruzic, M., Ashare, A., **Stajich**, J. E., and Hogan, D. A. 2023. Mrs4 loss of function in fungi during adaptation to the cystic fibrosis lung. *mBio* 14:e0117123. doi:10.1128/mbio.01171-23.
188. Gryganskyi, A. P., Golan, J., Muszewska, A., Idnurm, A., Dolatabadi, S., Mondo, S. J., Kutovenko, V. B., Kutovenko, V. O., Gajdeczka, M. T., Anishchenko, I. M., Pawlowska, J., Tran, N. V., Ebersberger, I., Voigt, K., Wang, Y., Chang, Y., Pawlowska, T. E., Heitman, J., Vilgalys, R., Bonito, G., Benny, G. L., Smith, M. E., Reynolds, N., James, T. Y., Grigoriev, I. V., Spatafora, J. W., and **Stajich**, J. E. 2023. Sequencing the genomes of the first terrestrial fungal lineages: What have we learned? *Microorganisms* 11(7):1830. doi:10.3390/microorganisms11071830.
189. Ettinger, C. L., Saunders, M., Selbmann, L., Delgado-Baquerizo, M., Donati, C., Albanese, D., Roux, S., Tringe, S., Pennacchio, C., Del Rio, T. G., **Stajich**, J. E., and Coleine, C. 2023. Highly diverse and unknown viruses may enhance antarctic endoliths' adaptability. *Microbiome* 11:103. doi:10.1186/s40168-023-01554-6.
190. Leo, P., de Melo Texeira, M., Chander, A. M., Singh, N. K., Simpson, A. C., Yurkov, A., Karouia, F., **Stajich**, J. E., Mason, C. E., and Venkateswaran, K. 2023. Genomic characterization and radiation tolerance of *Naganishia kalamii* sp. nov. and *Cystobasidium onofrii* sp. nov. from Mars 2020 mission assembly facilities. *IMA fungus* 14:15. doi:10.1186/s43008-023-00119-4.
191. Adams, J. N., Escalona, M., Marimuthu, M. P. A., Fairbairn, C. W., Beraut, E., Seligmann, W., Nguyen, O., Chumchim, N., and **Stajich**, J. E. 2023. The reference genome assembly of the bright cobblestone lichen, acarospora socialis. *The Journal of heredity* doi:10.1093/jhered/esad052.
192. Ettinger, C. L., Wu-Woods, J., Kurbessoian, T., Brown, D. J., Souza Pacheco, I. d., Vindiola, B. G., Walling, L. L., Atkinson, P. W., Byrne, F. J., Redak, R., and **Stajich**, J. E. 2023. Geographical survey of the mycobiome and microbiome of southern california glassy-winged sharpshooters. *mSphere* page e0026723. ISSN 2379-5042. doi:10.1128/msphere.00267-23.

Microbial Resource Announcements

1. Coleine, C., Masonjones, S., Selbmann, L., Zucconi, L., Onofri, S., Pacelli, C., and **Stajich**, J. E. 2017. Draft genome sequences of the Antarctic endolithic fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018. *Genome Announcements* 5(27):e00397–17. doi:10.1128/genomeA.00397-17.
2. Kasson, M. T., Kasson, L. R., Wickert, K. L., Davis, D. D., and **Stajich**, J. E. 2019. Genome sequence of a lethal vascular wilt fungus, *Verticillium nonalfalfae*, a biological control used against the invasive *Ailanthus altissima*. *Microbiology Resource Announcements* 8(4):e01619–18. doi: 10.1128/MRA.01619-18.
3. Coleine, C., Selbmann, L., Masonjones, S., Onofri, S., Zucconi, L., and **Stajich**, J. E. 2019. Draft genome sequence of an Antarctic isolate of the black yeast fungus *Exophiala mesophila*. *Microbiology Resource Announcements* 8(19):e00142–19. doi:10.1128/MRA.00142-19.
4. de MeloTeixeira, M., Barker, B. M., and **Stajich**, J. E. 2019. Improved reference genome sequence of *Coccidioides immitis* strain WA 211, isolated in Washington State. *Microbial Resource Announcements* 8(33):e00149–19. doi:10.1128/MRA.00149-19.
5. Coleine, C., Albanese, D., Onofri, S., Zucconi, L., Tringe, S. G., Pennacchio, C., Donati, C., **Stajich**, J. E., and Selbmann, L. 2020. Metagenomes in the borderline ecosystems of the Antarctic cryptoendolithic communities. *Microbial Resource Announcements* 9(10):e01599–19. doi: 10.1128/MRA.01599-19.

6. Coleine, C., Masonjones, S., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Draft genome sequence of yeast *Rhodotorula* sp. CCFEE 5036, isolated from McMurdo Dry Valleys, Antarctica. *Microbiology Resource Announcements* 9(14):e00020–20. doi:10.1128/MRA.00020-20.
7. **Stajich**, J. E., Vu, A. L., Judelson, H. S., Vogel, G. M., Gore, M. A., Carlson, M. O., Devitt, N., Jacobi, J., Mudge, J., Lamour, K. H., and Smart, C. D. 2021. High-quality reference genome sequence for the oomycete vegetable pathogen *Phytophthora capsici* strain LT1534. *Microbial Resource Announcements* pages e00295–21. doi:10.1128/MRA.00295-21.
8. Ward, R. D., **Stajich**, J. E., Johansen, J. R., Huntemann, M., Clum, A., Foster, B., Foster, B., Roux, S., Palaniappan, K., Varghese, N., Mukherjee, S., Reddy, T. B. K., Daum, C., Copeland, A., Chen, I.-M. A., Ivanova, N. N., Kyrpides, N. C., Shapiro, N., Eloe-Fadrosh, E. A., and Pietrasiak, N. 2021. Metagenome sequencing to explore phylogenomics of terrestrial cyanobacteria. *Microbiology Resource Announcements* 10:e0025821. doi:10.1128/MRA.00258-21.
9. Coleine, C., Selbmann, L., Pombubpa, N., and **Stajich**, J. E. 2021. Amplicon sequencing of rock-inhabiting microbial communities from Joshua Tree National Park, USA. *Microbiology Resource Announcements* 10:e0049421. doi:10.1128/MRA.00494-21.
10. Ettinger, C. L., Byrne, F. J., Redak, R. A., and **Stajich**, J. E. 2022. Metagenome-assembled genomes of bacterial symbionts associated with insecticide-resistant and -susceptible individuals of the glassy-winged sharpshooter (*Homalodisca vitripennis*). *Microbiology Resource Announcements* 11:e0050622. doi:10.1128/mra.00506-22.
11. Ettinger, C. L., Lovett, B., Kasson, M. T., and **Stajich**, J. E. 2022. Metagenome-assembled genomes of bacteria associated with *Massospora cicadina* fungal plugs from infected brood viii periodical cicadas. *Microbiology Resource Announcements* page e0041322. doi:10.1128/mra.00413-22.
12. **Stajich**, J. E., Lovett, B., Ettinger, C. L., Carter-House, D. A., Kurbessoian, T., and Kasson, M. T. 2022. An improved 1.5-gigabase draft assembly of *Massospora cicadina* (Zoopagomycota), an obligate fungal parasite of 13- and 17-year cicadas. *Microbiology Resource Announcements* 11(10):e0036722. doi:10.1128/mra.00367-22.
13. Kurbessoian, T., Heimlich-Villalta, G., Ginnan, N., Vieira, F. C., Rolshausen, P. E., Roper, M. C., and **Stajich**, J. E. 2023. Genome sequence and assembly of 18 Fusarium isolates from Florida citrus under high Huanglongbing disease pressure and California citrus under low Huanglongbing disease pressure. *Microbiology Resource Announcements* 12:e0010123. doi:10.1128/mra.00101-23.
14. Shea, T., Mohabir, J. T., Kurbessoian, T., Berdy, B., Fontaine, J., Gnirke, A., Livny, J., **Stajich**, J. E., and Cuomo, C. A. 2023. Genome sequence of *Lichtheimia ornata*, an emerging opportunistic mucorales pathogen. *Microbiology resource announcements* page e0033823. doi:10.1128/mra.00338-23.

Submitted Manuscripts and Preprints

1. Unruh, S. A., Pires, C. A., Zettler, L. W., Erba, L., Grigoriev, I. V., Barry, K. W., Daum, C., Lipzen, A. V., and **Stajich**, J. E. 2019. Shallow genome sequencing for phylogenomics of mycorrhizal fungi from endangered orchids. *Biorxiv* doi:10.1101/862763.
2. Alvarado, P., de Melo Teixeir, M., Pérez-Rojas, Y., Barker, B., **Stajich**, J. E., Zambrano, E. A., and Gonzatti, M. I. 2020. Genomic characterization and biochemical identification of secreted antigens and peptidases in a Venezuelan clinical isolate of *Histoplasma suramericanum*. *Submitted* .
3. Carter-House, D., Chung, J., McDonald, S., Mauck, K., and **Stajich**, J. E. 2020. Volatiles from *Serratia marcescens*, *S. proteamaculans*, and *Bacillus subtilis* inhibit growth of *Rhizopus stolonifer* and other fungi. *bioRxiv* doi:10.1101/2020.09.07.286443.
4. Clemons, R., Yacoub, M., Faust, E., Toledo, L. F., Jenkinson, T. S., Kalinka, E., Fritz-Laylin, L. K., James, T. Y., and **Stajich**, J. E. 2023. DNA virus BdDV-1 of the amphibian pathogen *Batrachochytrium dendrobatidis* is associated with hypervirulence. *bioRxiv* doi:10.1101/2023.03.16.532857.

5. He, B., Cai, Q., Weiberg, A., Li, W., Cheng, A.-P., Ouyang, S., Borkovich, K., **Stajich**, J., Abreu-Goodger, C., and Jin, H. 2023. *Botrytis cinerea* small RNAs are associated with tomato AGO1 and silence tomato defense-related target genes supporting cross-kingdom RNAi. *bioRxiv* doi: 10.1101/2022.12.30.522274.
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. Lovett, B., Barrett, H., Macias, A. M., **Stajich**, J. E., Kasson, L. R., and Kasson, M. T. 2023. Morphological and phylogenetic resolution of *Conoideocrella luteorostrata* (hypocreales: Claviciptaceae), a potential biocontrol fungus for *Fiorinia externa* in united states christmas tree production areas. *bioRxiv* doi:10.1101/2022.10.18.512709.

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)
2020-2023	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.
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.

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

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–	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.

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 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)
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
ongoing	Julia Adams, Plant Biology ⋆
	Danielle Stevenson, Environmental Sciences
	Talieh Ostovar, Program in Evolutionary Biology SDSU-UCR ⋆
	Fabiola Pulido-Chavez, Plant Pathology
	Dylan Enright, Microbiology
	Yagna Oza, Genetics, Genomics, Bioinformatics
	Jericho Ortañez, Microbiology
	Linton 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
	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 ⋆

⋆ 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

October 8, 2023