

Jason E. Stajich

Contact Department of Microbiology & Plant Pathology and Institute for Integrative Genome Biology,
University of California, Riverside, CA 92521
Telephone: +1 951-827-2363 **Email:** jason.stajich@ucr.edu
Web: <http://lab.stajich.org/> @stajichlab @hyphaltip

Education

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

Academic appointments:

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

Honors and Awards:

2020 Fellow of American Academy of Microbiology, American Society of Microbiology
2019–2024 CIFAR Fellow (Fungal Kingdom: Threats & Opportunities)
2017 Whetzel-Westcott-Dimock Special Lecturer, Cornell University
2015 Kavli Fellow, Kavli Frontiers of Science
2014 C. J. Alexopoulos Prize, Mycological Society for America
2006–2009 Miller Institute for Basic Research in Science, Postdoctoral Research Fellowship
2003–2006 National Science Foundation, Graduate Research Fellowship

Publications:

Peer Reviewed Publications

1. Baxter, R. V., Othmane, K. B., Rochelle, J. M., **Stajich**, J. E., Hulette, C., Dew-Knight, S., Hentati, F., Hamida, M. B., Bel, S., Stenger, J. E., Gilbert, J. R., Pericak-Vance, M. A., and Vance, J. M. 2002. Ganglioside-induced differentiation-associated protein-1 is mutant in Charcot-Marie-Tooth disease type 4A/8q21. *Nat Genet* 30(1):21–22. doi:10.1038/ng796.
2. **Stajich**, J. E., Block, D., Boulez, K., Brenner, S. E., Chervitz, S. A., Dagdigian, C., Fuellen, G., Gilbert, J. G. R., Korf, I., Lapp, H., Lehväslaiho, H., Matsalla, C., Mungall, C. J., Osborne, B. I., Pocock, M. R., Schattner, P., Senger, M., Stein, L. D., Stupka, E., Wilkinson, M. D., and Birney, E. 2002. The Bioperl toolkit: Perl modules for the life sciences. *Genome Res* 12(10):1611–1618. doi:10.1101/gr.361602.
3. Stein, L. D., Mungall, C., Shu, S., Caudy, M., Mangone, M., Day, A., Nickerson, E., **Stajich**, J. E., Harris, T. W., Arva, A., and Lewis, S. 2002. The generic genome browser: a building block for a model organism system database. *Genome Res* 12(10):1599–1610. doi:10.1101/gr.403602.
4. Hahn, M. W., **Stajich**, J. E., and Wray, G. A. 2003. The effects of selection against spurious transcription factor binding sites. *Mol Biol Evol* 20(6):901–906. doi:10.1093/molbev/msg096.
5. Stein, L. D., Bao, Z., Blasiar, D., Blumenthal, T., Brent, M. R., Chen, N., Chinwalla, A., Clarke, L., Clee, C., Coghlan, A., Coulson, A., D'Eustachio, P., Fitch, D. H. A., Fulton, L. A., Fulton, R. E.,

- Griffiths-Jones, S., Harris, T. W., Hillier, L. W., Kamath, R., Kuwabara, P. E., Mardis, E. R., Marra, M. A., Miner, T. L., Minx, P., Mullikin, J. C., Plumb, R. W., Rogers, J., Schein, J. E., Sohrmann, M., Spieth, J., **Stajich**, J. E., Wei, C., Willey, D., Wilson, R. K., Durbin, R., and Waterston, R. H. 2003. The genome sequence of *Caenorhabditis briggsae*: a platform for comparative genomics. *PLoS Biol* 1(2):E45. doi:10.1371/journal.pbio.0000045.
6. Kraus, P. R., Boily, M.-J., Giles, S. S., **Stajich**, J. E., Allen, A., Cox, G. M., Dietrich, F. S., Perfect, J. R., and Heitman, J. 2004. Identification of *Cryptococcus neoformans* temperature-regulated genes with a genomic-DNA microarray. *Eukaryot Cell* 3(5):1249–1260. doi:10.1128/EC.3.5.1249-1260.2004.
 7. Fraser, J. A., Giles, S. S., Wenink, E. C., Geunes-Boyer, S. G., Wright, J. R., Diezmann, S., Allen, A., **Stajich**, J. E., Dietrich, F. S., Perfect, J. R., and Heitman, J. 2005. Same-sex mating and the origin of the Vancouver Island *Cryptococcus gattii* outbreak. *Nature* 437(7063):1360–1364. doi:10.1038/nature04220.
 8. Hahn, M. W., Bie, T. D., **Stajich**, J. E., Nguyen, C., and Cristianini, N. 2005. Estimating the tempo and mode of gene family evolution from comparative genomic data. *Genome Res* 15(8):1153–1160. doi:10.1101/gr.3567505.
 9. Leman, S. C., Chen, Y., **Stajich**, J. E., Noor, M. A. F., and Uyenoyama, M. K. 2005. Likelihoods from summary statistics: recent divergence between species. *Genetics* 171(3):1419–1436. doi:10.1534/genetics.104.040402.
 10. Mitreva, M., McCarter, J. P., Arasu, P., Hawdon, J., Martin, J., Dante, M., Wylie, T., Xu, J., **Stajich**, J. E., Kapulkin, W., Clifton, S. W., Waterston, R. H., and Wilson, R. K. 2005. Investigating hookworm genomes by comparative analysis of two *Ancylostoma* species. *BMC Genomics* 6(1):58. doi:10.1186/1471-2164-6-58.
 11. **Stajich**, J. E. and Hahn, M. W. 2005. Disentangling the effects of demography and selection in human history. *Mol Biol Evol* 22(1):63–73. doi:10.1093/molbev/msh252.
 12. Hesselberth, J. R., Miller, J. P., Golob, A., **Stajich**, J. E., Michaud, G. A., and Fields, S. 2006. Comparative analysis of *Saccharomyces cerevisiae* WW domains and their interacting proteins. *Genome Biol* 7(4):R30. doi:10.1186/gb-2006-7-4-r30.
 13. Cramer, R. A., **Stajich**, J. E., Yamanaka, Y., Dietrich, F. S., Steinbach, W. J., and Perfect, J. R. 2006. Phylogenomic analysis of non-ribosomal peptide synthetases in the genus *Aspergillus*. *Gene* 383:24–32. doi:10.1016/j.gene.2006.07.008.
 14. Giles, S. S., **Stajich**, J. E., Nichols, C., Gerrald, Q. D., Alspaugh, J. A., Dietrich, F., and Perfect, J. R. 2006. The *Cryptococcus neoformans* catalase gene family and its role in antioxidant defense. *Eukaryot Cell* 5(9):1447–1459. doi:10.1128/EC.00098-06.
 15. **Stajich**, J. E. and Dietrich, F. S. 2006. Evidence of mRNA-mediated intron loss in the human-pathogenic fungus *Cryptococcus neoformans*. *Euk Cell* 5(5):789–793. doi:10.1128/EC.5.5.789-793.2006.
 16. Kämper, J., Kahmann, R., Bölker, M., Ma, L.-J., Brefort, T., Saville, B. J., Banuett, F., Kronstad, J. W., Gold, S. E., Müller, O., Perlin, M. H., Wösten, H. A. B., de Vries, R., Ruiz-Herrera, J., na, C. G. R.-P., Snetselaar, K., McCann, M., Pérez-Martín, J., Feldbrügge, M., Basse, C. W., Steinberg, G., Ibeas, J. I., Holloman, W., Guzman, P., Farman, M., **Stajich**, J. E., Sentandreu, R., González-Prieto, J. M., Kennell, J. C., Molina, L., Schirawski, J., Mendoza-Mendoza, A., Greilinger, D., Münch, K., Rössel, N., Scherer, M., Vranes, M., Ladendorf, O., Vincon, V., Fuchs, U., Sandrock, B., Meng, S., Ho, E. C. H., Cahill, M. J., Boyce, K. J., Klose, J., Klosterman, S. J., Deelstra, H. J., Ortiz-Castellanos, L., Li, W., Sanchez-Alonso, P., Schreier, P. H., Häuser-Hahn, I., Vaupel, M., Koopmann, E., Friedrich, G., Voss, H., Schlüter, T., Margolis, J., Platt, D., Swimmer, C., Gnirke, A., Chen, F., Vysotskaia, V., Mannhaupt, G., Güldener, U., Münsterkötter, M., Haase, D., Oesterheld, M., Mewes, H.-W., Mauceli, E. W., DeCaprio, D., Wade, C. M., Butler, J., Young, S., Jaffe, D. B., Calvo, S.,

- Nusbaum, C., Galagan, J., and Birren, B. W. 2006. Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. *Nature* 444(7115):97–101. doi:10.1038/nature05248.
17. James, T. Y., Kauff, F., Schoch, C. L., Matheny, P. B., Hofstetter, V., Cox, C. J., Celio, G., Gueidan, C., Fraker, E., Miadlikowska, J., Lumbsch, H. T., Rauhut, A., Reeb, V., Arnold, A. E., Amtoft, A., **Stajich, J. E.**, Hosaka, K., Sung, G.-H., Johnson, D., O'Rourke, B., Crockett, M., Binder, M., Curtis, J. M., Slot, J. C., Wang, Z., Wilson, A. W., Schüßler, A., Longcore, J. E., O'Donnell, K., Mozley-Standridge, S., Porter, D., Letcher, P. M., Powell, M. J., Taylor, J. W., White, M. M., Griffith, G. W., Davies, D. R., Humber, R. A., Morton, J. B., Sugiyama, J., Rossman, A. Y., Rogers, J. D., Pfister, D. H., Hewitt, D., Hansen, K., Hambleton, S., Shoemaker, R. A., Kohlmeyer, J., Volkmann-Kohlmeyer, B., Spotts, R. A., Serdani, M., Crous, P. W., Hughes, K. W., Matsuura, K., Langer, E., Langer, G., Untereiner, W. A., Lücking, R., Büdel, B., Geiser, D. M., Aptroot, A., Diederich, P., Schmitt, I., Schultz, M., Yahr, R., Hibbett, D. S., Lutzoni, F., McLaughlin, D. J., Spatafora, J. W., and Vilgalys, R. 2006. Reconstructing the early evolution of Fungi using a six-gene phylogeny. *Nature* 443(7113):818–822. doi:10.1038/nature05110.
 18. Demuth, J. P., Bie, T. D., **Stajich, J. E.**, Cristianini, N., and Hahn, M. W. 2006. The evolution of mammalian gene families. *PLoS One* 1:e85. doi:10.1371/journal.pone.0000085.
 19. Fitzpatrick, D. A., Logue, M. E., **Stajich, J. E.**, and Butler, G. 2006. A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. *BMC Evol Biol* 6:99. doi:10.1186/1471-2148-6-99.
 20. Erwin, T. A., Jewell, E. G., Love, C. G., Lim, G. A. C., Li, X., Chapman, R., Batley, J., **Stajich, J. E.**, Mongin, E., Stupka, E., Ross, B., Spangenberg, G., and Edwards, D. 2007. BASC: an integrated bioinformatics system for *Brassica* research. *Nucleic Acids Res* 35(Database issue):D870–D873. doi:10.1093/nar/gkl998.
 21. Harrison, L. B., Yu, Z., **Stajich, J. E.**, Dietrich, F. S., and Harrison, P. M. 2007. Evolution of budding yeast prion-determinant sequences across diverse fungi. *J Mol Biol* 368(1):273–282. doi:10.1016/j.jmb.2007.01.070.
 22. Fraser, J. A., **Stajich, J. E.**, Tarcha, E. J., Cole, G. T., Inglis, D. O., Sil, A., and Heitman, J. 2007. Evolution of the mating type locus: insights gained from the dimorphic primary fungal pathogens *Histoplasma capsulatum*, *Coccidioides immitis*, and *Coccidioides posadasii*. *Eukaryot Cell* 6(4):622–629. doi:10.1128/EC.00018-07.
 23. **Stajich, J. E.**, Dietrich, F. S., and Roy, S. W. 2007. Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. *Genome Biol* 8(10):R223. doi:10.1186/gb-2007-8-10-r223.
 24. Hu, G., Liu, I., Sham, A., **Stajich, J. E.**, Dietrich, F. S., and Kronstad, J. W. 2008. Comparative hybridization reveals extensive genome variation in the aids-associated pathogen *Cryptococcus neoformans*. *Genome Biol* 9(2):R41. doi:10.1186/gb-2008-9-2-r41.
 25. Lilly, W. W., **Stajich, J. E.**, Pukkila, P. J., Wilke, S. K., Inoguchi, N., and Gathman, A. C. 2008. An expanded family of fungalsin extracellular metallopeptidases of *Coprinopsis cinerea*. *Mycol Res* 112(Pt 3):389–398. doi:10.1016/j.mycres.2007.11.013.
 26. Martin, F., Aerts, A., Ahrén, D., Brun, A., Danchin, E. G. J., Duchaussoy, F., Gibon, J., Kohler, A., Lindquist, E., Pereda, V., Salamov, A., Shapiro, H. J., Wuyts, J., Blaudez, D., Buée, M., Brokstein, P., Canbäck, B., Cohen, D., Courty, P. E., Coutinho, P. M., Delaruelle, C., Detter, J. C., Deveau, A., DiFazio, S., Duplessis, S., Fraissinet-Tachet, L., Lucic, E., Frey-Klett, P., Fourrey, C., Feussner, I., Gay, G., Grimwood, J., Hoegger, P. J., Jain, P., Kilaru, S., Labbé, J., Lin, Y. C., Legué, V., Tacon, F. L., Marmeisse, R., Melayah, D., Montanini, B., Muratet, M., Nehls, U., Niculita-Hirzel, H., Secq, M. P. O.-L., Peter, M., Quesneville, H., Rajashekar, B., Reich, M., Rouhier, N., Schmutz, J., Yin, T., Chalot, M., Henrissat, B., Kües, U., Lucas, S., de Peer, Y. V., Podila, G. K., Polle, A., Pukkila, P. J., Richardson, P. M., Rouzé, P., Sanders, I. R., **Stajich, J. E.**, Tunlid, A., Tuskan, G., and Grigoriev, I. V. 2008. The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature* 452(7183):88–92. doi:10.1038/nature06556.

27. Regier, J. C., Shultz, J. W., Ganley, A. R. D., Hussey, A., Shi, D., Ball, B., Zwick, A., **Stajich, J. E.**, Cummings, M. P., Martin, J. W., and Cunningham, C. W. 2008. Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. *Syst Biol* 57(6):920–938. doi:10.1080/10635150802570791.
28. Rosenblum, E. B., **Stajich, J. E.**, Maddox, N., and Eisen, M. B. 2008. Global gene expression profiles for life stages of the deadly amphibian pathogen *Batrachochytrium dendrobatidis*. *Proc Natl Acad Sci U S A* 105(44):17034–17039. doi:10.1073/pnas.0804173105.
29. Fisher, M. C., Bosch, J., Yin, Z., Stead, D. A., Walker, J., Selway, L., Brown, A. J. P., Walker, L. A., Gow, N. A. R., **Stajich, J. E.**, and Garner, T. W. J. 2009. Proteomic and phenotypic profiling of the amphibian pathogen *Batrachochytrium dendrobatidis* shows that genotype is linked to virulence. *Mol Ecol* 18(3):415–429. doi:10.1111/j.1365-294X.2008.04041.x.
30. Sharpton, T. J., **Stajich, J. E.**, Rounsley, S. D., Gardner, M. J., Wortman, J. R., Jordar, V. S., Maiti, R., Kodira, C. D., Neafsey, D. E., Zeng, Q., Hung, C.-Y., McMahan, C., Muszewska, A., Grynberg, M., Mandel, M. A., Kellner, E. M., Barker, B. M., Galgiani, J. N., Orbach, M. J., Kirkland, T. N., Cole, G. T., Henn, M. R., Birren, B. W., and Taylor, J. W. 2009. Comparative genomic analyses of the human fungal pathogens *Coccidioides* and their relatives. *Genome Res* 19(10):1722–1731. doi:10.1101/gr.087551.108.
31. Nowrousian, M., **Stajich, J. E.**, Engh, I., Espagne, E., Kamerewerd, J., Kempken, F., Kunstmann, B., Kuo, H.-C., Osiewacz, H. D., Pöggeler, S., Read, N., Seiler, S., Smith, K., Zickler, D., Kück, U., and Freitag, M. 2010. Next-generation sequencing of the 40 Mb genome of the filamentous fungus *Sordaria macrospora*. *PLoS Genetics* 6(4):e1000891. doi:10.1371/journal.pgen.1000891.
32. Neafsey, D. E., Barker, B. M., Sharpton, T. J., **Stajich, J. E.**, Park, D. J., Whiston, E., Hung, C.-Y., McMahan, C., White, J., Sykes, S., Heiman, D., Young, S., Zeng, Q., Abouelleil, A., Aftuck, L., Bessette, D., Brown, A., Fitzgerald, M., Lui, A., Macdonald, J. P., Priest, M., Orbach, M. J., Galgiani, J. N., Kirkland, T. N., Cole, G. T., Birren, B. W., Henn, M. R., Taylor, J. W., and Rounsley, S. D. 2010. Population genomic sequencing of *Coccidioides* fungi reveals recent hybridization and transposon control. *Genome Res* 20(7):938–946. doi:10.1101/gr.103911.109.
33. **Stajich, J. E.**, Wilke, S. K., Ahrén, D., Au, C. H., Birren, B. W., Borodovsky, M., Burns, C., Canbäck, B., Casselton, L. A., Cheng, C. K., Deng, J., Dietrich, F. S., Fargo, D. C., Farman, M. L., Gathman, A. C., Goldberg, J., Guigó, R., Hoegger, P. J., Hooker, J. B., Huggins, A., James, T. Y., Kamada, T., Kilaru, S., Kodira, C., Kües, U., Kupfer, D., Kwan, H. S., Lomsadze, A., Li, W., Lilly, W. W., Ma, L.-J., Mackey, A. J., Manning, G., Martin, F., Muraguchi, H., Natvig, D. O., Palmerini, H., Ramesh, M. A., Rehmeier, C. J., Roe, B. A., Shenoy, N., Stanke, M., Ter-Hovhannisyan, V., Tunlid, A., Velagapudi, R., Vision, T. J., Zeng, Q., Zolan, M. E., and Pukkila, P. J. 2010. Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom *Coprinopsis cinerea* (*Coprinus cinereus*). *Proc Natl Acad Sci U S A* 107(26):11889–11894. doi:10.1073/pnas.1003391107.
34. Ohm, R. A., de Jong, J. F., Lugones, L. G., Aerts, A., Kothe, E., **Stajich, J. E.**, de Vries, R. P., Record, E., Levasseur, A., Baker, S. E., Bartholomew, K. A., Coutinho, P. M., Fowler, T. J., Gathman, A. C., Lombard, V., Henrissat, B., Knabe, N., Kües, U., Lilly, W. W., Lindquist, E., Lucas, S., Magnuson, J. K., Piumi, F., Raudaskoski, M., Salamov, A., Schmutz, J., Schwarze, F. W., vanKuyk, P. A., Horton, J. S., Grigoriev, I. V., and Wösten, H. A. 2010. Genomic sequence of the wood-rotting *Schizophyllum commune* strain H4-8: a model mushroom system. *Nature Biotech* 28:957–963. doi:10.1038/nbt.1643.
35. Strandberg, R., Nygren, K., Menkis, A., James, T. Y., Wik, L., **Stajich, J. E.**, and Johannesson, H. 2010. Conflict between reproductive gene trees and species phylogeny among outcrossing members of the filamentous ascomycete genus *Neurospora*. *Fungal Genetics & Biology* 11(7):869–878. doi:10.1016/j.fgb.2010.06.008.

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38. Burns, C., **Stajich**, J. E., Rechtsteiner, A., Hanlon, S. E., Wilke, S. K., Palmerini, H. J., Savitsky, O. P., Gathman, A. C., Lilly, W. W., Lieb, J. D., Zolan, M. E., and Pukkila, P. J. 2010. Analysis of the basidiomycete *Coprinopsis cinerea* reveals conservation of the core meiotic expression program over half a billion years of evolution. *PLoS Genetics* 6(9):e1001135. doi:10.1371/journal.pgen.1001135.
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41. Joneson, S., **Stajich**, J. E., Shiu, S.-H., and Rosenblum, E. B. 2011. Genomic transition to pathogenicity in chytrid fungi. *PLoS Pathog* 7(11):e1002338. doi:10.1371/journal.ppat.1002338.
42. **Stajich**, J. E., Harris, T., Brunk, B. P., Brestelli, J., Fischer, S., Harb, O. S., Kissinger, J. C., Li, W., Nayak, V., Pinney, D. F., Stoeckert, C. J., Jr, and Roos, D. S. 2012. FungiDB: an integrated functional genomics database for fungi. *Nucleic Acids Res* 40(D1):D675–D681. doi:10.1093/nar/gkr918.
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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., Kerkaert, 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 whitfordiendrus* 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., Ortáñez, J., and **Stajich**, J. E. 2020. The monophyletic *Sarcogyne canadensis*–*wheeleri* clade, a newly recognized group sister to the European *Acarospora glaucocarpa* group. *The Bryologist* 123(1):11–30. doi:10.1639/0007-2745-123.1.011.
116. Coleine, C., **Stajich**, J. E., Zucconi, L., Onofri, S., and Selbmann, L. 2020. Sun exposure drives Antarctic cryptoendolithic community structure and composition. *Polar Biology* In press. doi:10.1101/676692.
117. Coleine, C., Pombubpa, N., Zucconi, L., Onofri, S., **Stajich**, J. E., and Selbmann, L. 2020. Endolithic fungal species markers for harshest conditions in the McMurdo Dry Valleys, Antarctica. *Life* In Press. 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* In Press. doi:10.1101/676775.
119. Coleine, C., Masonjones, S., Sterflinger, K., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus *Friedmanniomyces endolithicus*. *Fungal Biology* In press. doi:10.1016/j.funbio.2020.01.005.
120. Yang, C.-T., Vidal-Diez de Ulzurrun, G., Goncalves, P., Lin, H.-C., Chang, C.-W., Huang, T.-Y., Chen, S.-A., Lai, C.-K., Tsai, I. J., Schroeder, F. C., **Stajich**, J. E., and Hsueh, Y.-P. 2020. Natural variation in the predatory behavior of nematode-trapping fungi facilitates the establishment of a new robust model strain. *Proc National Acad Sciences* In press.

Genome Announcements

1. Coleine, C., Masonjones, S., Selbmann, L., Zucconi, L., Onofri, S., Pacelli, C., and **Stajich**, J. E. 2017. Draft genome sequences of the Antarctic endolithic fungi *Rachicladosporium antarcticum* CCFEE 5527 and *Rachicladosporium* sp. CCFEE 5018. *Genome Announcements* 5. doi:10.1128/genomeA.00397-17.
2. Kasson, M. T., Kasson, L. R., Wickert, K. L., Davis, D. D., and **Stajich**, J. E. 2019. Genome sequence of a lethal vascular wilt fungus, *Verticillium nonalfalfae*, a biological control used against the invasive *Ailanthus altissima*. *Microbiology Resource Announcements* 8. doi:10.1128/MRA.01619-18.
3. Coleine, C., Selbmann, L., Masonjones, S., Onofri, S., Zucconi, L., and **Stajich**, J. E. 2019. Draft genome sequence of an Antarctic isolate of the black yeast fungus *Exophiala mesophila*. *Microbiology Resource Announcements* 8(19):e00142–19. doi:10.1128/MRA.00142-19.
4. de Melo Teixeira, M., Barker, B. M., and **Stajich**, J. E. 2019. Improved reference genome sequence of *Coccidioides immitis* strain WA 211, isolated in Washington State. *Microbial Resource Announcements* 8(33):e00149–19. doi:10.1128/MRA.00149-19.
5. Coleine, C., Albanese, D., Onofri, S., Zucconi, L., Tringe, S. G., Pennacchio, C., Donati, C., **Stajich**, J. E., and Selbmann, L. 2020. Metagenomes in the borderline ecosystems of the Antarctic cryptoendolithic communities. *Microbial Resource Announcements* In Press. doi:10.1101/725200.

Submitted Manuscripts and Preprints

1. Coeline, C., Masonjones, S., Onofri, S., Selbmann, L., and **Stajich**, J. E. 2020. Draft genome sequence of yeast *Rhodotorula* sp. CCFEE 5306, isolated from McMurdo Dry Valleys, Antarctica. *Submitted*.
2. Pombubpa, N., Pietrasiak, N., De Ley, P., and **Stajich**, J. E. 2019. Insights into the desert living skin microbiome: geography, soil depth, and crust type affect biocrust microbial communities and networks in Mojave Desert, USA. *bioRxiv* page 810002. doi:10.1101/810002.
3. 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. 2019. Evolutionary relationships among *Massospora* spp. (Entomophthorales), obligate pathogens of cicadas. *bioRxiv (In Revision, Mycologia)* page 811836. doi:10.1101/811836.
4. 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.

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-Muñoz, J., Walker, A. K., Yarden, O., and Gladfelter, A. S. 2019. Fungi in the marine environment: Open questions and unsolved problems. *mBio* 10. ISSN 2150-7511. doi:10.1128/mBio.01189-18.
7. Warren, S. D., Clair, L. L. S., Stark, L. R., Lewis, L. A., Pombubpa, N., Kurbessoian, T., **Stajich, J. E.**, and Aanderud, Z. T. 2019. Reproduction and dispersal of biological soil crust organisms. *Frontiers In Ecology & Evolution* 7:344. doi:10.3389/fevo.2019.00344.

Books and Book Chapters

1. Coghlan, A., **Stajich, J. E.**, and Harris, T. W. 2006. Comparative genomics in *C. elegans*, *C. briggsae*, and other *Caenorhabditis* species. *Methods Mol Biol* 351:13–29. doi:10.1385/1-59745-151-7:13.
2. **Stajich, J. E.** and Dietrich, F. S. 2006. Genomic perspectives on the fungal kingdom. In J. Heitman, S. G. Filler, J. E. Edwards Jr, and A. P. Mitchell, editors, *Molecular principles of fungal pathogenesis*, pages 657–666. ASM press.
3. **Stajich, J. E.** 2007. An introduction to BioPerl. *Methods Mol Biol* 406:535–548.
4. Edwards, D., **Stajich, J. E.**, and Hansen, D., editors. 2009. *Bioinformatics*. Springer, NY.
5. McKay, S. J., Vergara, I. A., and **Stajich, J. E.** 2010. Using the Generic Synteny Browser (GBrowse_syn). *Curr Protoc Bioinformatics* Chapter 9:Unit9.12. doi:10.1002/0471250953.bi0912s31.
6. Fisher, M. C., **Stajich, J. E.**, and Farrer, R. A. 2012. Emergence of the chytrid fungus *Batrachochytrium dendrobatidis* and global amphibian declines. In D. Sibley, B. Howlett, and J. Heitman, editors, *Evolution of Virulence in Eukaryotic Microbes*. Wiley Blackwell.
7. **Stajich, J. E.** 2013. Comparative genomics. In J. Losos, D. Baum, D. J. Futuyma, H. Hoekstra, R. Lenski, A. Moore, D. Schluter, and M. Whitlock, editors, *The Princeton Guide to Evolution*. Princeton University Press.
8. **Stajich, J. E.** 2015. Phylogenomics enabling genome based mycology. In D. J. McLaughlin, M. Blackwell, and J. W. Spatafora, editors, *The Mycota VII, Systematics and Evolution*. Springer.
9. Spatafora, J. W., Aime, M. C., Grigoriev, I. V., Martin, F., **Stajich, J. E.**, and Blackwell, M. 2017. The fungal tree of life: from molecular systematics to genome-scale phylogenies. *Microbiology spectrum* 5(5). doi:10.1128/microbiolspec.FUNK-0053-2016.
10. **Stajich, J. E.** 2017. Fungal genomes and insights into the evolution of the kingdom. *Microbiology spectrum* 5(4). doi:10.1128/microbiolspec.FUNK-0055-2016.

Meeting and Technical Reports

1. Lapp, H., Bala, S., Balhoff, J., Bouck, A., Goto, N., Holder, M., Holland, R., Holloway, A., Katayama, T., Lewis, P. O., Mackey, A. J., Osborne, B. I., Piel, W. H., Kosakovsky Pond, S. L., Poon, A., Qiu, W., **Stajich, J. E.**, Stoltzfus, A., Thierer, T., Vilella, 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. MlXs-BE: a MlXs 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., Kooijia, P., Dentinger, B. T. M., Grigoriev, I. V., Nagy, L., **Stajich**, J. E., Coker, T., and Leitcha, I. J. 2018. *State of the World's Fungi. Report*, chapter Fungal tree of life., pages 12–17. Royal Botanic Gardens, Kew.
7. Pombubpa, N., Kurbessoian, T., **Stajich**, J. E., and Pietrasiak, N. 2019. Exploring the microbial diversity in biological soil crusts at Joshua Tree National Park. *Joshua Tree Science Updates In Press*.
8. Baltrus, D. A., Cuomo, C. A., Dennehy, J. J., Dunning Hotopp, J. C., Maresca, J. A., Newton, I. L. G., Rasko, D. A., Rokas, A., Roux, S., and **Stajich**, J. E. 2019. Future-proofing your *Microbiology Resource Announcements* genome assembly for reproducibility and clarity. *Microbiology resource announcements* 8(36):e00954–19. ISSN 2576-098X. doi:10.1128/MRA.00954-19.

Commentaries and Book Reviews

1. **Stajich**, J. E. 2009. Review of Bioinformatics, Volume I: Data, Sequence Analysis and Evolution; Volume II: Structure, Function and Applications. *The Quarterly Review of Biology* 84(3):284–285. doi:10.1086/644662. Book Review.
2. **Stajich**, J. E. 2011. Review of cellular and molecular biology of filamentous fungi. *The Quarterly Review of Biology* 86(1):59–59. doi:10.1086/658451. Book Review.
3. **Stajich**, J. E. 2016. Fungal Evolution: *Mucor* and *Phycomyces* see double. *Curr Biol* 26(16):R775–R777. doi:10.1016/j.cub.2016.06.049.
4. Valent, B., Farman, M., Tosa, Y., Begerow, D., Fournier, E., Gladieux, P., Islam, M. T., Kamoun, S., Kemler, M., Kohn, L. M., Lebrun, M.-H., **Stajich**, J. E., Talbot, N. J., Terauchi, R., Tharreau, D., and Zhang, N. 2019. *Pyricularia graminis-tritici* is not the correct species name for the wheat blast fungus: response to Ceresini *et al.* (mpp 20:2). *Molecular Plant Pathology* 20:173–179. doi: 10.1111/mpp.12778.

Essays

1. **Stajich**, J. E. 2014. Top 5 real wolves of wall street. <http://nautil.us/issue/10/mergers--acquisitions/top-5-real-wolves-of-wall-street>. "Moldy Monopolies" and "Creepy Crawly Conglomerate" in the "Mergers & Acquisitions" issue.

Software and other Products

BioPerl - <http://bioperl.org> - Core developer
 Github <http://github.com/hyphal-tip> - individual projects
 Github <http://github.com/stajichlab> - lab projects
 Github <http://github.com/1KFG> - 1000 Fungal genomes project
 Github <http://github.com/zygolife> - ZyGoLife NSF project and associated phylogenomics
 Website: <http://1000.fungalgenomes.org> - 1KFG project
 Website: <http://zygolife.org> - NSF ZygoLife
 Website: <http://dynamiterice.org> - NSF Rice Transposable Element project
 Website: <http://fungalgenomes.org/blog> - "The Hyphal Tip" A Blog I write about Fungal Genomics
 Website & Database (Collaboration): <http://fungidb.org>

Grant Support:

Ongoing support

- 2011-2017 National Science Foundation. IOS-1027542. (No Cost Ext thru 02/2021)
“CPGS: Genome-wide impact of *mPing* transposition on rice phenotypic diversity.”
Role: Co-I. PI: SR Wessler (UC Riverside).
<http://dynamiterice.org>
- 2015-2018 National Science Foundation. GO Life DEB-1441715. (No Cost Ext thru 08/2020)
“Collaborative Research: The Zygomycetes Genealogy of Life (ZyGoLife)- the conundrum of Kingdom Fungi”
Role: PI. Collaborative linked award with 3 other PIs and 12 collaborating labs: J Spatafora (Oregon State), TY James (U Michigan), R Robertson (Arizona State)
<http://zygolife.org>
- 2016-2019 National Science Foundation. DEB-1557110. (No Cost Ext thru 04/2020)
“Collaborative Research: Phylogenomics and evolutionary history of the anaerobic fungal group, Neocallimastigomycota”
Role: PI. Collaborative linked award PI: N Youssef (Oklahoma State)
- 2017-2020 Univ of California-Office of the President, MRPI.
“UC Valley Fever Research Initiative”
Role: Co-PI. PI: Anita Sil (UCSF) and Co-PIs at UC Berkeley, UC Merced, UC San Diego
- 2019-2022 Univ of California-Office of the President
“Investigating fundamental gaps in Valley Fever research”
Role: Co-PI. PI: Anita Sil (UCSF) and Co-PIs at UC Berkeley, UC Davis, UC Merced, UC San Diego
- 2019-2020 City of Hope / Univ of California-Riverside
“Antifungal drug resistance in Southern California: Discovery of novel mechanisms by genomics and proteomics.”
Role: PI with Co-PIs M Kalkum and S Dadwal at City of Hope Hospital
- 2017-2021 National Institutes of Health. R01-AI127548-01A1
“Evolved Heterogeneity contributes to chronic fungal lung infections”
Role: Senior Personnel. PI: D Hogan (Dartmouth)
- 2017-2022 National Institutes of Health. R01-AI130128-01A1
“Evolution of *Aspergillus fumigatus* virulence”
Role: Senior Personnel. PI: RA Cramer, Jr (Dartmouth)
- 2019-2021 National Institutes of Health. R15-GM132869
“Understanding The Mechanisms Of Spatial Protein Quality Control In A Model Filamentous Fungus”
Role: Senior Personnel. PI: Egans, M (U Arkansas)
- 2019-2024 Canadian Institute For Advanced Research
“Fungal Kingdom: Threats and Opportunities”
Role: CIFAR Fellow. PI/Directors: L Cowen and J Heitman

Completed support

- 2010-2013 Burroughs Wellcome Fund.
“FungiDB: A Pan Fungal Genome Database”.
Role: Co-I. PI: DS Roos (U Pennsylvania)
- 2011-2012 UC Riverside, Chancellor’s Strategic Investment Funds.
“Coelomomyces Genomics for Mosquito Vector Control”
Role: Co-I. PI: B Federici. Co-I: A Ray (UC Riverside)
- 2013-2014 UC Riverside, Office of Research Strategic Investment Funds.
“High-throughput synthetic biology for natural products discovery”
Role: Co-I. PI: K Borkovich. Co-I: C Larive (UC Riverside)
- 2013-2014 National Institutes of Health - 1-R03-AI105636-01.

	“Annotation of <i>Cryptococcus</i> genomes by comprehensive curation of published literature” Role: PI. Co-I G Sherlock (Stanford)
2011-2014	Alfred P. Sloan Foundation. “MoBe DAC: A data coordinating center for the Sloan Indoor Environment Metagenomic Project - Fungal resources”. Role: PI. Linked grants with F Meyer (U Chicago/ANL), R Knight (U Colorado), M Sogin (Marine Biological Lab).
2014-2015	National Science Foundation. DBI-1429826. “MRI: Acquisition of a Big Data Compute Cluster for Interdisciplinary Research” Role: Co PI. PI T Girke. Co-Is J Bailey-Serres, M Allen, and S Lonardi (UCR)
2014-2017	National Institutes of Health - 1-R01-GM108492-01. “Dynamics of bacterial-fungal interactions in chronic lung infections” Role: Co-I. PI: D Hogan (Dartmouth)
2011-2016	W.M. Keck Foundation. (No Cost Extension thru 2018) “New Active Transposable Elements for Mosquito Genetics.” Role: Co-I. PI: SR Wessler (UC Riverside). Co-I: P Atkinson (UC Riverside).
2017	Burroughs Wellcome Fund. “Meeting grant to support Fungal Cell Wall (FCW2017) Conference in Ensenada, Mexico” Role: PI.

Service:

University and Departmental

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

Editorial Boards

2019–	Associate Editor, Genome Biology & Evolution
2019–	Associate Editor, Mycologia
2018–	Senior Editor, Microbial Resource Announcements
2018–	Associate Editor, Genetics
2016–	Editorial Board, Current Opinion in Microbiology
2015–2019	Associate Editor, Microbial Genomics
2014–	Associate Editor, Fungal Genetics & Biology
2013,2015	Guest Associate Editor, PLoS Genetics
2013	Guest Associate Editor, Mycologia
2011–2016	Faculty Member in Microbial Genetics & Genomics, Faculty of 1000
2010–2015	Editorial Board, Eukaryotic Cell.
2009–2016	Section Editor, PLoS One.
2007–2016	Academic Editor, PLoS One.

Professional Service

2018–2020	Co-Chair (2020) of Cellular and Molecular Fungal Biology, Gordon Research Conference; Co-Vice Chair (2018).
2017–2020	Karling Lecture Committee, Mycologia Society of America (Chair 2019-2020)
2018-2021	Councilor for Cell Biology & Physiology. Mycological Society of America.
2014–2018	Neurospora Policy Committee, Co-Organized 2016 Neurospora conference
2013–2019	Fungal Genetics Policy Committee
2012–	Scientific advisory board, Plant Microbe Interactions - DOE Science Focus Area, Oak Ridge

National Laboratory
 2012–2018 Scientific advisory board, WormBase
 2012–2015 Scientific advisory board, Ensembl Genomes
 2010–2012 Councilor for Genetics & Molecular Biology, Mycological Society of America
 2009–2010 Advisory Board for Genomic Encyclopedia of Fungi, Joint Genome Institute, US Department of Energy.
 2009–2010 Pan-Fungal Database Steering Committee for Burroughs Wellcome Fund.
 2007–2009 Scientific advisory board NSF Computer Science Education Revitalization (PI Owen Astrachan, Duke University)
 2005–2008 Scientific advisory committee Information Technology and Computing infrastructure, National Center for Evolutionary Synthesis (NESCent).
 2005–2011 President and Board Member [2005–2014], Open Bioinformatics Foundation <http://www.open-bio.org/>
 2001–2015 Co-Project leader, BioPerl. <http://www.bioperl.org/>

Membership in Professional Societies:

2007– Mycological Society of America
 2007– American Society for Microbiology
 2004– Genetics Society of America
 2004– Society for Molecular Biology and Evolution
 2002– Open Bioinformatics Foundation
 2002– International Society for Computational Biology

Graduate Students:

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

Postdoctoral Fellows:

2010–2011 John Abramyan, Ph.D.
 Current: Assistant Professor, Univ of Michigan-Dearborn
 2011–2014 Sofia Robb, Ph.D.
 Current: Genomics Scientist at Stowers Institute.
 2012–2014 Brad Cavinder, Ph.D.
 Current: Research Associate at Michigan State University
 2012–2015 Peng Liu, Ph.D.
 Current: Research Associate, Yangzhou University, CHINA

2013–2019 Jinfeng Chen, Ph.D.
Current: Staff Scientist, City of Hope, CA

2013–2015 Ousmane Cissé, Ph.D. - Swiss National Science Foundation Fellow.
Current: Staff Scientist at Critical Care Department, NIH Clinical Center.

2014–2015 Rodrigo Olarte, Ph.D.
Current: NSF Postdoctoral Fellow at Univ of Minnesota.

2017–19 Yan Wang, Ph.D.
Current: Assistant Professor, University of Toronto-Scarborough.

2019– Lotus Lofgren, Ph.D.

2020– Ying Sun, Ph.D.

Visitors:

2010–2013 (4, 2-3 month vists) Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWE-DEN

2010 Suzanne Joneson, PhD, Department of Biology, University of Idaho

2011 Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, 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 Association Fellowship, University of Lagos, NIGERIA.

2015 Marco Marconi, Visiting Graduate Student, Universidad Politécnica de Madrid, Madrid, SPAIN

2015–2016 Claudia Coleine, Visiting Graduate Student, Università degli Studi della Tuscia, Viterbo, ITALY

2017 Jane Lind Nybo, Visiting Graduate Student, Technical University of Denmark, Copenhagen, DENMARK

2019 Guillermo Vidal-Diez de Ulzurrun, Visiting Postdoc scientist, IMB, Academia Sinica, Taipei, Taiwan

2019– Felipe Salgado, Federal University of Rio de Janeiro, BRAZIL.

2020– Omar Valencia, Volunteer.

Staff:

2011–2012 Daniel Borcharding, Programmer (FungiDB).
Current: Senior Software Build Engineer, Apple, Inc.

2011–2013 Raghuraman Ramamurthy, Programmer (FungiDB).
Current: Senior Bioinformatics Associate, Gilead Sciences.

2013–2014 Venkatesh Moktali, Bioinformatics Scientist (FungiDB).
Current: Product Manager, Thermo Fisher Scientific.

2017–2018 Jericho Ortanez, Junior Specialist. Current: Graduate Student, UC Riverside

Teaching:

2010,2012 BIO5C - Introductory Ecology & Evolution

2011 BIO20 - The Dynamic Genome - Research module for *Neurospora* research

2011,2013 GEN240B - Tools for Bioinformatics and Genome Analysis

2015 MCBL124 - Microbial Pathogenesis

2011–2016 MCBL211 - Microbial Ecology

2012-2015 MCBL202 - Microbial Pathogenesis & Physiology

- 2012– GEN220 - Computational Analysis of High Throughput Biological Data <http://biodataprogram.github.io/>
- 2016– BIO119 - Introduction to Genomics and Bioinformatics

Undergraduate Researchers:

- 2010– Sponsor for summer research students in MARCU, STEM, and CAMP programs at UCR.
- 2010–2012 Jessica De Anda, UCR. STEM grant participant (2010); MARC USTAR student 2010-12. Current: Career Development Coordinator at Unitek College
- 2010–2011 Annie Nguyen, UCR.
- 2011–2012 Carlos Rojas Torres, UCR. CAMP (2011); lab researcher. Current: Gilead Pharmaceuticals.
- 2011 Ramy Wissa, UCR. Pre-MARC USTAR Summer student.
- 2011–2012 Lorena Rivera, UCR. Pre-MARC USTAR student (2011); lab researcher, CNAS Dean's Fellow Summer Undergraduate Research (Summer 2012)
- 2012–2014 Erum Khan, UCR.
- 2012–2014 Sapphire Ear, UCR. Current: MD student at UCSF
- 2012–2014 Megna Tiwari, UCR. Current: PhD student at Univ of Georgia
- 2013–2014 Dylan McVay, UCR.
- 2013–2016 Na Jeong, UCR, Summer RISE Scholar (2013) and lab researcher
- 2014 Spencer Swansen, Summer NSF REU student (Seattle Pacific University)
- 2015–2017 Justin Shen, UCR.
- 2015–2016 Serena Choi, UCR.
- 2015–2017 Dillon McDonald, UCR Summer HSI-STEM (2015) and lab researcher
- 2015 Christina Uriarte, UCR. Pre-MARC USTAR student.
- 2015–2017 Jericho Ortanez, UCR. Current: PhD student UCR Microbiology
- 2015–2016 Leandra Ibrahim, UCR.
- 2015–2017 Deane Kim, UCR.
- 2016–2017 Georgiy Smirnov, UCR.
- 2016–2018 Meng (Josh) Chung, UCR.
- 2017–2019 Estefania Caldera, UCR.
- 2018 Lily Bautista, UCR.
- 2018– Renata Haro, UCR.
- 2018– Skylar McDonald, UCR.
- 2019 Saisuki Putumbaka, The College of New Jersey, Summer REU student.
- 2019– Nicole Leung, UCR.

Dissertation committees:

- 2011 Sourav Roy, PhD, GGB
Yi Zhou, MS, GGB *
- 2012 Andrew Defries, PhD, Plant Sciences
- 2013 Gilbert Uribe, MS, Plant Pathology
Divya Sain, PhD, GGB *
- 2014 Yizhou Wang, PhD, Plant Sciences *
- Zhigang Wu, PhD, GGB
- 2015 Presha Shah, PhD, Biochemistry
Ming Wang, PhD, Plant Pathology
Steven Ahrendt, PhD, GGB *
- Ilva Cabrera, PhD, GGB
Jinfeng Lu, PhD, GGB
James Ricci, MS, Entomology
- 2016 Ryan Arvidson, PhD, Biochemistry
Francis Na, MS, Microbiology

	Jishu Ha, PhD, GGB
	Arit Gosh, PhD, GGB
	Kelsey Gano, PhD, Microbiology
	Kun Liu, PhD, Plant Biology
2017	Raissa Green, PhD, GGB
	Amelia Lindsey, PhD, Entomology
	Patrick Schriener, PhD, GGB
	Eric Smith, PhD, GGB
	Katherine Picard, Univ Prog in Genetics & Genomics (Duke University)
	Eric Gordon, Entomology
2018	Cynthia Dick, EEOB
	Dan Vanderpool, Biology (University of Montana)
	Steven Bolaris, GGB △
2019	Joseph Carrillo, Plant Pathology △
	Dinusha Maheepala Mudalige, Plant Biology
	Aaron Robinson, Biology (University of New Mexico)
	Courtney Collins, Plant Biology
	Edgar Medina, Genetics & Genomics (Duke University)
	Lluvia Vargas, Microbiología (CICESE, MEXICO)
	Derreck Carter-House, Plant Pathology ★
2020	Andrea Vu, Plant Pathology
ongoing	Nuttapon Pombubpa, Plant Pathology ★
	Sawyer Masonjones, GGB ★
	Jesús Peña, Microbiology ★
	Julia Adams, Plant Biology ★
	Tania Kurbessoian, Microbiology ★
	Nicole Ginnan, Plant Pathology
	Caleb Hubbard, Medical and Veterinary Entomology
	Alex Rajewski, Plant Biology
	Glen Morrison, Plant Biology
	Nathan Robinett, Joint Doctoral Prog. Evolutionary Biology, SDSU-UCR
	Mari West, Entomology
	Yi Huang, Plant Biology
	Christopher Ficus, GGB
	Shannon Lynch, Environmental Studies (Univ of California-Santa Cruz)
	Glen Morrison, Plant Biology
	Hannah Schulman, Microbiology

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

Invited Seminars and conference presentations (2015–Present)

- 2019 · Phylogenomics Workshop, Cesky Krumlov, Czech Republic
- Middle Tennessee State University, Murfreesboro, TN
- Rosie Perez Memorial Seminar, North Carolina State University, Raleigh, NC
- University of North Carolina, Chapel Hill, NC
- California State University, Northridge, CA
- 2018 · UC Riverside Data Science Series. Riverside, CA
- University of Nebraska-Lincoln, Lincoln, NE
- Creighton University, Omaha, NE
- Marine Fungi Workshop. Marine Biological Lab, Woods Hole, MA.
- 11th International Mycological Congress. San Juan, Puerto Rico

- CIFAR workshop "Microbial Pathogens in the Fungal Kingdom". Toronto, Ontario, CANADA
- 2017 · Oregon State University. Corvallis, OR
- 29th Fungal Genetics Conference. *Plenary Speaker*. Pacific Grove, CA.
- Oomycete Molecular Genetics Network. *Plenary Speaker*. Pacific Grove, CA
- Population Genomics of Oomycete and Fungal Pathogens. Ascona, Switzerland
- American Society of Microbiology Microbe Meeting. New Orleans, LA
- FASEB Microbial Pathogenesis. Aspen, CO.
- Mycological Society of America 2017 Meeting. Athens, GA
- American Academy of Microbiology Colloquium on Fungal Pathogenesis. Washington, DC
- Fungal Cell Wall Conference. Ensenada, Mexico
- Whetzel-Westcott-Dimock Special Lecturer, Cornell University, Ithaca, NY
- 2016 · Mycological Society of America 2016 Meeting. Berkeley, CA.
- CIFAR Integrated Microbial Biodiversity Program. Toronto, ON, CANADA.
- 13th European Fungal Genetics Conference. Paris, France. *Plenary Speaker*
- Neurospora Conference. Asilomar Conference Center, Pacific Grove, CA.
- Duke University, Durham, NC.
- University of California, Davis, CA.
- University of Exeter. United Kingdom.
- 2015 · EMBO Conference: Genomic complexity and diversity of eukaryotes. Sant Feliu de Guixols, SPAIN.
- XI CONGRESO NACIONAL DE MICOLOGIA, Sociedad Mexicana de Micologia. Merida, Yucatan, MEXICO. *Plenary Speaker*
- University of Arizona, Tucson, AZ.
- Eighth International Conference on Mycorrhiza. Flagstaff, AZ.
- Mycological Society of America 2015 Meeting. Edmonton, AB, CANADA.
- Society for Molecular Biology & Evolution 2015. Vienna, Austria.
- University of California, Los Angeles, CA.
- University of California, Merced, CA.
- 28th Fungal Genetics Conference. Asilomar Conference Center, Pacific Grove, CA.
- Oregon State University, Corvallis, OR.
- Oklahoma State University, Stillwater, OK.

February 28, 2020