Jason E. Stajich

Academic appointments:

2017–	Professor, Dept of Plant Pathology & Microbiology. University of California-Riverside.
2014–2017	Associate Professor (with tenure), University of California-Riverside.
2009–2014	Assistant Professor, University of California-Riverside.

Education

2006–2009	Postdoctoral training, University of California-Berkeley
2001–2006	Ph.D. Genetics and Genomics, Duke University
1995–1999	B.S. Computer Science, Duke University, Durham, NC

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
2019–2026	CIFAR Fellow in program 'Fungal Kingdom: Threats & Opportunities'
2014	C. J. Alexopoulos Prize, Mycological Society of America
2006–2009	Miller Institute for Basic Research in Science, Postdoctoral Research Fellowship, UC Berkeley

Selected Publications

1. 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.
2. 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.
3. 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.
4. 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.
5. 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.
6. 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.

7. 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.

8. 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.

9. 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.

10. 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.

11. 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.

12. 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.

13. 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.

14. 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.

15. 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.

16. **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* page e0036722. doi:10.1128/mra.00367-22.

17. 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.