Jason E. Stajich

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Education

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

Academic appointments:

2014–	Associate Professor with tenure
2009–2014	Assistant Professor
	Department of Plant Pathology & Microbiology.
	Institute of Integrative Genome Biology.
	University of California, Riverside, CA.

Honors and Awards:

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: (Listed in reverse chronological order.)

Peer Reviewed Publications

1. Nguyen, T. A., Cissé, O. H., Wong, J. Y., Zheng, P., Hewitt, D., Nowrousian, M., **Stajich**, J. E., and Jedd, G. 2016. Innovation and constraint leading to complex multicellularity in the Ascomycota. *Submitted* .
2. Ahrendt, S. R., Medina, E. M., Chia-en, A. C., and **Stajich**, J. E. 2016. Exploring the binding properties and structural stability of an opsin in the chytrid *Spizellomyces punctatus* using comparative and molecular modeling. *Peerj Preprints* 4:e2397v1. doi:10.7287/peerj.preprints.2397v1. Submitted.
3. Chen, J., Wrightsman, T., Wessler, S. R., and **Stajich**, J. E. 2016. RelocaTE2: a high resolution transposable element polymorphism mapping tool for population resequencing. *Peerj Preprints* 4:e2447v1. doi:10.7287/peerj.preprints.2447v1. Submitted.
4. Cissé, O. H. and **Stajich**, J. E. 2016. FGMP: assessing fungal genome completeness and gene content. *bioRxiv* doi:10.1101/049619. Submitted.
5. 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. 2016. PCR multiplexes discriminate *Fusarium* symbionts of invasive *Euwallacea* ambrosia beetles that inflict damage on numerous tree species throughout the United States. *Plant Disease* In press. doi:10.1094/PDIS-07-16-1046-RE.
6. Spatafora, J. W., Chang, Y., Benny, G., Lazarus, K., Smith, M., Berbee, M., Bonito, G., Corradi, N., Grigoriev, I., Gryganskyi, A., James, T., O'Donnell, K., Roberson, R., Taylor, T., Uehling, J., Vilgalys, R., White, M., and **Stajich**, J. E. 2016. Zygomycete Genealogy of Life (ZyGoLife): a phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. *Mycologia* In press.

7. 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 Genet* 12(6):e1006108. doi:10.1371/journal.pgen.1006108.
8. 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). doi:10.1128/mBio.00252-16.
9. 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.
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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.
18. Ouyang, S., Park, G., Atamian, H. S., Han, C. S., **Stajich**, J. E., Kaloshian, I., and Borkovich, K. A. 2014. Regulation of innate immunity to the fungal pathogen *Fusarium oxysporum* by microRNAs in tomato. *PLoS Path* 10(10):e1004464. doi:10.1371/journal.ppat.1004464.

19. 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.
20. 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.
21. 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 Genet* 10(4):e1004261. doi:10.1371/journal.pgen.1004261.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.

31. Gioti, A., Nystedt, B., Li, W., Xu, J., Andersson, A., Averette, A. F., MÃijnch, K., Wang, X., Kappauf, C., Kingsbury, J. M., Kraak, B., Walker, L. A., Johansson, H. J., Holm, T., LehtiÃű, 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.
32. 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.
33. 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.
34. 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.
35. **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.
36. 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.
37. 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.
38. 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.
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pathogen, *Pythium ultimum*, reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol* 11(7):R173. doi:10.1186/gb-2010-11-7-r73.

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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.

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Reviews (Refereeed)

1. 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.
2. 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.
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. **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.
5. **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.

Books and Book Chapters

1. **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.
2. **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.
3. 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.
4. 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.
5. Edwards, D., **Stajich**, J. E., and Hansen, D., editors. 2009. *Bioinformatics*. Springer, NY.
6. **Stajich**, J. E. 2007. An introduction to BioPerl. *Methods Mol Biol* 406:535–548.

7. **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.
8. 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.

Meeting and Technical Reports

1. 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.
2. 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.
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. 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.
5. 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.

Commentaries and Book Reviews

1. 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.
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. 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.

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.

Grant Support:

Ongoing support

2011-2016	W.M. Keck Foundation. ”New Active Transposable Elements for Mosquito Genetics.” Co-PI with PI SR Wessler and P Atkinson (UC Riverside).

2011-2017	National Science Foundation. Plant Genome - IOS-1027542 “CPGS: Genome-wide impact of *mPing* transposition on rice phenotypic diversity.” Co-PI with PI SR Wessler (UC Riverside); T Brutnell (Danforth), Q Sun (Cornell). `http://dynamiterice.org`
2014-2017	National Institutes of Health - 1-R01-GM108492-01 “Dynamics of bacterial-fungal interactions in chronic lung infections” Co-PI with PI D Hogan (Dartmouth)
2015-2018	National Science Foundation. GO Life DEB-1441715 “Collaborative Research: The Zygomycetes Genealogy of Life (ZyGoLife)- the conundrum of Kingdom Fungi” PI with Co-PIs J Spatafora (Oregon State), TY James (U Michigan), R Robertson (Arizona State) `http://zygolife.org`
2016-2019	National Science Foundation. DEB-1557110 “Collaborative Research: Phylogenomics and evolutionary history of the anaerobic fungal group, Neocallimastigomycota” Co-PI with Noha Youssef and Mostafa Elshahed (Oklahoma State)

Completed support

2010-2013	Burroughs Wellcome Fund. “FungiDB: A Pan Fungal Genome Database”. Co-PI with PI DS Roos (U Pennsylvania)
2011-2012	UC Riverside, Chancellor’s Strategic Investment Funds. “Coelomomyces Genomics for Mosquito Vector Control” Co-PI with B Federici, A Ray (UC Riverside)
2013-2014	UC Riverside, Office of Research Strategic Investment Funds. “High-throughput synthetic biology for natural products discovery” Co-PI with PI K Borkovich, C. Larive (UC Riverside)
2013-2014	National Institutes of Health - 1-R03-AI105636-01 “Annotation of *Cryptococcus* genomes by comprehensive curation of published literature” PI with Co-PI G Sherlock (Stanford)
2011-2014	Alfred P. Sloan Foundation. “MoBe DAC: A data coordinating center for the Sloan Indoor Environment Metagenomic Project - Fungal resources”. PI. Coordinated 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” Co-PI with PI T Girke, Co-PIs J Bailey-Serres, M Allen, and S Lonardi (UCR)

Service

University and Departmental

2015–2016	Director & Admissions Advisor, Microbiology Graduate Program
2014–2015	Gradute Advisor, Microbiology Graduate Program

Editorial Boards

2015–	Associate Editor, Microbial Genomics
2014–	Associate Editor, Fungal Genetics & Biology
2013,2015	Guest Associate Editor, PLoS Genetics
2013	Guest Associate Editor, Mycologia
2011–	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-Vice Chair (2018) and Co-Chair (2020) of Cellular and Molecular Fungal Biology, Gordon Research Conference
2014–2018	Neurospora Policy Committee
2013–2019	Fungal Genetics Policy Committee
2012–2017	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 for NSF funded Computer Science Education Revitalization project to PI Owen Astrachan, Duke University.
2005–2008	Scientific advisory committee for Information Technology and Computing infrastructure for the National Center for Evolutionary Synthesis (NESCent).
2005–2011	President and Board Member [2005–Present], Open Bioinformatics Foundation `http://www.open-bio.org/`
2001–	Co-Project leader, BioPerl. `http://www.bioperl.org/`

Membership in Professional Societies:

2002–	International Society for Computational Biology
2004–	Society for Molecular Biology and Evolution
2007–	American Society for Microbiology
2004–	Genetics Society of America
2007–	Mycological Society of America
2001–	BioPerl developed. Co-Project leader (2001-2012).
2002–	Open Bioinformatics Foundation

Graduate Students:

2009–13	PhD student, Divya Sain. Genetics, Genomics, & Bioinformatics. Currently: Bioinformatics Scientist at Ambry Genetics.
2010–12	MS student, Yi (Zoe) Zhu. Genetics, Genomics, & Bioinformatics. Currently: Biostatistician at Biostatistical Consulting Inc.
2014	MS student, Elizabeth Holmes, Plant Pathology & Microbiology
2010–14	PhD student, Yizhou Wang. Plant Biology. Currently: Research Bioinformatician at Cedars Sinai.
2011–15	PhD student, Steven Ahrendt. Genetics, Genomics, & Bioinformatics. Currently: Postdoc at UC Berkeley/LBNL & DOE Joint Genome Institute.
2015–	PhD Student, Sawyer Masonjones. Genetics, Genomics, & Bioinformatics
2015–	PhD Student, Nuttapom Pombubpa. Plant Pathology.
2016–	PhD Student, Derreck Carter-House. Plant Pathology
2016–	PhD Student, Jesús Peña, Microbiology

Postdoctoral Fellows:

2010–2011	John Abramyan, PhD. Currently: Postdoc at Univ of West Virgina

2011–2014	Sofia Robb, PhD. Currently: Genomics Scientist at Stowers Institute.
2012–2014	Brad Cavinder, PhD. Currently: Research Associate at Michigan State University
2012–2015	Peng Liu, PhD.
2013–	Jinfeng Chen, PhD
2013–2015	Ousmane Cissé, PhD - Swiss National Science Foundation Fellow. Currently: Postdoctoral Fellow at NIH Clinical Center.
2014–2015	Rodrigo Olarte. Currently: NSF Postdoctoral Fellow at Univ of Minnesota.

Visitors:

2010–13 (4, 2-3 month vists)	Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWEDEN
2010 (Spring)	Suzanne Joneson, PhD, Department of Biology, University of Idaho
2011 (Spring)	Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, Bogota, COLOMBIA
2012 (Summer)	Andrii Gryganski, PhD, Visiting Researcher, Duke University
2013–14	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 (Spring)	Natalie Vande Pol, Visiting Graduate Student (Bonito Lab), Michigan State University
2015–16	Zhinquan Song, Visiting Graduate Student (Guangyi Wang Lab), Tianjin University, CHINA
2015 (Fall)	John Yinka Odebode, Visiting Graduate Student on a West African Research Assocation Fellowship, University of Lagos, NIGERIA.
2015 (Fall)	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

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–	MCBL211 - Microbial Ecology
2012-2015	MCBL202 - Microbial Pathogenesis & Physiology
2012-	GEN220 - Computational Analysis of High Throughput Biological Data `http://hyphaltip.github.io/GEN220_2015`
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 MS Student, Claremont 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.
2012–2014	Megna Tiwari, UCR. Current: MS student at CSU-LB
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)
2015–2016	Justin Shen, UCR.

2015–2016	Serena Choi, UCR.
2015–	Dillon McDonald, UCR Summer HSI-STEM (2015) and lab researcher
2015	Christina Uriarte, UCR. Pre-MARC USTAR student.
2015–	Jericho Ortanez, UCR.
2015–2016	Leandra Ibrahim, UCR.
2015–	Deane Kim, UCR.
2016–	Georgiy Smirnov, UCR.
2016–	Meng (Josh) Chung, UCR.

Dissertation and thesis 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, GGB
	James Ricci, MS, Entomology
2016	Ryan Arvidson, PhD, Biochemistry
	Francis Na, MS, Microbiology
	Jishu Ha, PhD, GGB
	Arit Gosh, PhD, GGB
ongoing	Kelsey Gano, Microbiology
	Kun Liu, Plant Biology
	Raissa Green, GGB
	Amelia Lindsey, Entomology
	Patrick Schriener, GGB
	Cynthia Dick, EEOB
	Eric Gordon, Entomology
	Eric Smith, GGB
	Dereck O'Meara, EEOB
	Nathan Robinett, Joint Doctoral Program in Evolutionary Biology, SDSU-UCR
	Dinusha Maheepala Mudalige, Plant Biology
	Katherine Picard, UPGG - Duke University
	Edgar Medina, UPGG - Duke University
	Lluvia Vargas, Microbiología - CICESE, MEXICO

September 25, 2016