Jason E. Stajich

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Education

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

Academic appointments:

2014–	Associate Professor with tenure
2009–2014	Assistant Professor Dept. of Plant Pathology & Microbiology. Member of Institute of Integrative Genome Biology, Center for Plant Cell Biology Member of graduate programs in: Genetics, Genomics, & Bioinformatics; Microbiology; Botany & Plant Sciences; Plant Pathology; Ecology, Evolution, & Organismal Biology; UCR-SDSU Joint Doctoral program in Evolutionary Biology University of California, Riverside, CA.

Honors and Awards:

2003–2006	National Science Foundation, Graduate Research Fellowship
2006–2009	Miller Institute for Basic Research in Science, Postdoctoral Research Fellowship
2014	C. J. Alexopoulos Prize, Mycological Society for America

Publications: (Listed in reverse chronological order.)

Peer Reviewed Publications

1. 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.
2. Wang, Y., Smith, K. M., Freitag, M., and **Stajich**, J. E. 2015. Endogenous small RNA mediates meiotic silencing of a novel DNA transposon. *G3* 5(10):g3.115.017921. doi:10.1534/g3.115.017921.
3. 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.
4. 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.
5. 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.
6. Mélida, H., Sain, D., **Stajich**, J. E., and Bulone, V. 2015. Deciphering the uniqueness of mucormycotina cell walls by combining biochemical and phylogenomic approaches. *Environmental Microbiology* 17(5):1649–62. doi:10.1111/1462-2920.12601.

7. 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.
8. 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.
9. 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.
10. 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* doi: 10.1111/ele.12311.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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

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18. 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* 3(6):949–57. doi:10.1534/g3.112.005348.
19. 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.
20. 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.
21. Gioti, A., Nystedt, B., Li, W., Xu, J., Andersson, A., Averette, A. F., Mnch, K., Wang, X., Kappauf, C., Kingsbury, J. M., Kraak, B., Walker, L. A., Johansson, H. J., Holm, T., Lehti, 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.
22. 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.
23. 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.
24. 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.
25. **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.
26. 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.
27. 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.
28. 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.
29. 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.

30. 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.

31. 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.

32. 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.

33. 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.

34. **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.

35. Neafsey, D. E., Barker, B. M., Sharpton, T. J., **Stajich**, J. E., Park, D. J., Whiston, E., Hung, C.-Y., McMahan, C., White, J., Sykes, S., Heiman, D., Young, S., Zeng, Q., Abouelleil, A., Aftuck, L., Bessette, D., Brown, A., Fitzgerald, M., Lui, A., Macdonald, J. P., Priest, M., Orbach, M. J., Galgiani, J. N., Kirkland, T. N., Cole, G. T., Birren, B. W., Henn, M. R., Taylor, J. W., and Rounsley, S. D. 2010. Population genomic sequencing of *Coccidioides* fungi reveals recent hybridization and transposon control. *Genome Res* 20(7):938–946. doi:10.1101/gr.103911.109.

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37. 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.

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Refereed Reviews

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. Kennedy, P. and **Stajich**, J. 2015. Twenty-first century mycology: a diverse, collaborative, and highly relevant science. *New Phytol* 205(1):23–26. doi:10.1111/nph.13165.
2. 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.
3. 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.
4. 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.

Grant Support:

Ongoing support

2011-2015	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)
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)

2015-2019	National Science Foundation. GO Life - DEB-1441715 “Collaborative Research: The Zygomycetes Genealogy of Life (ZyGoLife)- the conundrum of Kingdom Fungi” PI with Co-PI J Spatafora (Oregon State), TY James (U Michigan), R Robertson (Arizona State) `http://zygolife.org`

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 the *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. In collaboration with F Meyer (U Chicago/ANL), R Knight (U Colorado), M Sogin (Marine Biological Lab).

Service

University and Departmental

2015–	Director, 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–	Review Editor, Frontiers in Evolutionary and Genomic Microbiology
2010–	Editorial Board, Eukaryotic Cell.
2009–	Section Editor, PLoS One.
2007–	Academic Editor, PLoS One.

Professional Service

2014-2020	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

Graduate Students:

2009–13	PhD student, Divya Sain. Genetics, Genomics, & Bioinformatics
2010–12	MS student, Yi (Zoe) Zhu. Genetics, Genomics, & Bioinformatics
2014	MS student, Elizabeth Holmes, Plant Pathology & Microbiology
2010–14	PhD student, Yizhou Wang. Plant Biology
2011–15	PhD student, Steven Ahrendt. Genetics, Genomics, & Bioinformatics
2015–	PhD Student, Sawyer Masonjones. Genetics, Genomics, & Bioinformatics
2015–	PhD Student, Nuttapom Pombubpa. Plant Pathology.

Postdoctoral Fellows:

2010–2011	John Abramyan, PhD
2011–2014	Sofia Robb, PhD
2012–2014	Brad Cavinder, PhD
2012–	Peng Liu, PhD
2013–	Jinfeng Chen, PhD
2013–2015	Ousmane Cissé, PhD - Swiss National Science Foundation Fellow
2014–2015	Rodrigo Olarte

Visitors:

2010 (Spring)	Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWEDEN
2010 (Spring)	Suzanne Joneson, PhD, Department of Biology, University of Idaho
2011(Spring)	Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWEDEN
2011 (Spring)	Edgar Medina Tovar, MSc Mycology and Phytopathology Lab, Universidad de Los Andes, Bogota, COLOMBIA
2012 (Summer)	Andrii Gryganski, PhD, Duke University
2012-13	Anastasia Gioti, PhD, Dept of Evolution Biology, Uppsala University, SWEDEN
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 (Spring)	Natalie Vande Pol, Visiting Graduate Student (Bonito Lab), Michigan State University
2015–	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

Teaching:

Bio5C - Introductory Ecology & Evolution (co-taught)
Bio20 - Dynamic Genomes - Research module for *Neurospora* research
Gen240B - Tools for Bioinformatics and Genome Analysis (co-taught)
MCBL124 - Microbial Pathogenesis (co-taught)
MCBL211 - Microbial Ecology (co-taught)
MCBL202 - Microbial Pathogenesis & Physiology (co-taught)
GEN220 - Computational Analysis of High Throughput Biological Data (co-taught 2012-3)

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 U STAR student 2010-12.
2010–2011	Annie Nguyen, UCR
2011–2012	Carlos Rojas Torres, UCR. CAMP (2011); Undergraduate researcher
2011	Ramy Wissa, UCR. Pre-MARC student
2011–2012	Lorena Rivera, UCR. Pre-MARC student (2011); Undergraduate 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.
2013–2014	Dylan McVay, UCR.
2013–	Na Jeong, UCR, Summer RISE Scholar (2013) and lab researcher and ongoing research.
2014	Spencer Swansen, Summer REU student (Seattle Pacific University)
2015–	Justin Shen, UCR.
2015–	Serena Choi, UCR.
2015–	Dillon McDonald, UCR Summer HSI-STEM (2015) and lab researcher
2015–	Jericho Ortanez, UCR
2015–	Leandra Ibrahim, UCR
2015–	Deane Kim, 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
2015	Zhigang Wu, PhD, GGB Presha Shah, PhD, Biochemistry Ming Wang, PhD, Plant Pathology Steven Ahrendt, PhD, GGB Ilva Cabrera, PhD, GGB James Ricci, MS, Entomology
ongoing	Kelsey Gano, Microbiology Jinfeng Lu, GGB Jishu Ha, GGB Kun Lu, Plant Biology Raissa Green, GGB

Amelia Lindsey, Entomology
Patrick Schriener, GGB
Arit Gosh, GGB
Cynthia Dick, EEOB
Eric Gordon, Entomology

October 2, 2015