**Stephen J. Mondo**

Fungal & Algal Genomics Program Phone: 607-342-8087

Fungal Multi-omics Work Lead E-mail: sjmondo@lbl.gov

DOE Joint Genome Institute

1 Cyclotron Road

Berkeley, CA, 94720

**CURRENT POSITION**

**DOE Joint Genome Institute** Walnut Creek, CA

Staff Data Scientist Jan 2020 – Present

Data Scientist 2014 – Jan 2020

**EDUCATION**

**Cornell University** Ithaca, NY

PhD, Department of Plant Pathology and Plant-Microbe Biology 2008 – 2013

Dissertation: Evolutionary Stability of Fungal-Bacterial Endosymbioses

**SUNY Binghamton**

BS: Ecology, Evolution and Behavioral Biology, *magna cum laude,* Binghamton, NY

distinguished honors in Biology 2003-2007

**PROFESSIONAL EXPERIENCE**

**DOE Joint Genome Institute, Walnut Creek, CA** Nov2014 – Present

Staff Data Scientist, Fungal and Algal Genomic Program Jan 2020 – Present

- Lead multi-omics research and development on the fungal and algal team

Data scientist, Fungal and Algal Genomic Program Nov 2014 – Jan 2020

Comparative genomics, epigenomics and evolution of kingdom Fungi.

- Discovered a new DNA modification, N6-methyldeoxyadenine (6mA), a major regulator of gene expression across Fungi (**Mondo** et al., 2017, ***Nature Genetics***).

- Annotated over 300 diverse fungal genomes, spanning the fungal tree of life.

- Collaborate with a large, international scientific community.

- Software development for comparative genomics and improved genome annotation.

**Cornell University, Ithaca, NY** Summer, 2008-Nov, 2014

Postdoctoral Associate, Bogdanove laboratory May, 2014 – Nov, 2014

- Characterization of bacterial tools (primarily Transcription Activator-Like [TAL] effectors) for manipulation of host gene expression in the *Rhizopus microsporus*-*Burkholderia rhizoxinica* endosymbiosis

Postdoctoral Associate, Pawlowska laboratory August, 2013 - May 2014

- Studying endosymbiont genome evolution and host-microbe interactions

Graduate Student, Pawlowska laboratory June 2009 - August 2013

- Studying endosymbiont evolution in Glomeromycota and Mucorales

Rotation Student, Pawlowska and Turgeon laboratories Summer, 2008-Spring, 2009

**Marine Biological Laboratories, Woods Hole, MA** Summer, 2010

- Participant in the Woods Hole Microbial Diversity program

**GRANTS & AWARDS**

**DOE Joint Genome Institute** September, 2013

Project Title: "Comparative genomics of early diverging terrestrial fungi and their bacterial endosymbionts"

Co-PIs: Gregory Bonito, Rytas Vilgalys (Duke University), Paola Bonfante, Stefano Ghignone, Alessandro Desirò, Alessandra Salvioli (Turin University, Italy), Andrii Gryganskyi, Jessie Uehling, Christopher Schadt, Jesse Labbé, Dale Pelletier, Gerald Tuskan, Tim Tschaplinski, Steven Brown, David Weston (Oak Ridge National Laboratory), Amy Schaefer (University of Washington), Teresa Pawlowska, Olga Lastovetsky, **Stephen Mondo**, Mizue Naito (Cornell University), Francis Martin (INRA-France)

**Cornell University, Ithaca, NY** Summer, 2008-Spring, 2009

Cornell Graduate School Fellowship, $24,000

**SUNY Binghamton, Binghamton, NY** Spring, 2007

Distinguished honors and Evolutionary Studies Certificate, Biology Department

**PROFESSIONAL SOCIETIES**

**Mycological Society of America** 2009-2010, 2014-Present

Mentor-Student Travel Awards Committee member Aug, 2016 – Aug, 2019

Committee chair Aug, 2019 – Aug., 2020

**PUBLICATIONS**

Franco, M.E.E., Wisecaver, J.H., Arnold, E.A., Ju, Y.M., Slot, J.C., Ahrendt, S., Moore, L.P., Eastman, K.E., Scott, K., Konkel, Z., **Mondo, S.J.**, Kuo, A., Hayes, R.D., Haridas, S., Andreopoulos, W., Riley, R., LaButti, K., Pangilinan, J., Lipzen, A., Amirebrahimi, M., Yan, J., Adam, C., Keymanesh, K., Ng, V., Louie, K., Northen, T., Drula, E., Henrissat, B., Hsieh, H., Youens‐Clark, K., Lutzoni, F., Miadlikowska, J., Eastwood, D.C., Hamelin, R.C., Grigoriev, I.V., U’Ren, J.M., 2022. Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. **New Phytologist** 233(3).

Brown, J.L., Swift, C.L., **Mondo, S.J.**, Seppälä, S., Salamov, A., Singan, V., Henrissat, B., Drula, E., Henske, J.K., Lee, S., LaButti, K., He, G., Yan, M., Barry, K., Grigoriev, I.V., O’Malley, M.A., 2021. Co‑cultivation of the anaerobic fungus *Caecomyces churrovis* with *Methanobacterium bryantii* enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. **Biotechnology for biofuels** 14(1).

Crowell, C.R., Wilkerson, D.G., Beckauri, M., Cala, A.R., McMullen, P.W., **Mondo, S.J.**, Andreopoulos, W., Lipzen, A., Lail, K., Yan, M., Ng, V., Grigoriev, I.V., Smart, L.B., Smart, C.D., 2021. The Melampsora americana population on Salix purpurea in the Great Lakes region is highly diverse with a contributory influence of clonality. **Phytopathology.**

Skerker, J.M., Pianalto, K.M., **Mondo, S.J.**, Yang, K., Arkin, A.P., Keller, N.P., Grigoriev, I.V., Glass, N.L., 2021. Chromosome assembled and annotated genome sequence of Aspergillus flavus NRRL 3357. **G3**, 11(8).

Nelson, A.R., Narrowe, A.B., Rhoades, C.C., Fegel, T.S., Daly, R.A., Roth, H.K., Chu, R.K., Amundson, K.K., Geonczy, S.E., Emerson, J.B., Young, R.B., Steindorff, A.S., **Mondo, S.J.**, Grigoriev, I.V., Salamov, A., Borch, T., Wilkins, M.J., 2021. Playing with FiRE: A genome resolved view of the soil microbiome responses to high severity forest wildfire. **bioRxiv.**

Swift, C.L., Louie, K.B., Bowen, B.P., Olson, H.M., Purvine, S.O., Salamov, A., **Mondo, S.J.**, Solomon, K.V., Wright, A.T., Northen, T.R., Grigoriev, I.V., Keller, N.P., O’Malley, M.A., 2021. Anaerobic gut fungi are an untapped reservoir of natural products. **Proceedings of the National Academy of Sciences** 118(18).

Wyka, S.A., **Mondo, S.J.**, Liu, M., Dettman, J., Nalam, V., Broders, K.D., 2021. Whole-Genome Comparisons of Ergot Fungi Reveals the Divergence and Evolution of Species within the Genus Claviceps Are the Result of Varying Mechanisms Driving Genome Evolution and Host Range Expansion. **Genome biology and evolution** 13(2)

Wilken, St. E., Monk, J.M., Leggieri, P.A., Lawson, C.E., Lankiewicz T.S., Seppälä S., Daum, C.G., Jenkins, J., Lipzen, A.M., **Mondo, S.J.**, Barry, K.W., Grigoriev, I.V., Henske, J.K., Theodorou, M.K., Palsson, B.O., Petzold, L.R., O’Malley, M.A., 2021. Experimentally validated reconstruction and analysis of a genome-scale metabolic model of an anaerobic Neocallimastigomycota fungus. **mSystems** 6(1).

Swift, C.L., Malinov, N.G., **Mondo, S.J.**, Salamov, A., Grigoriev, I.V., O'Malley, M.A., 2021. A Genomic Catalog of Stress Response Genes in Anaerobic Fungi for Applications in Bioproduction. **Frontiers in Fungal Biology**, 29.

Grigoriev, I.V., Hayes, R.D., Calhoun, S., Kamel, B., Wang, A., Ahrendt, S., Dusheyko, S., Nikitin, R., **Mondo, S.J.**, Salamov, A., Shabalov, I., Kuo, A., 2020. PhycoCosm, a comparative algal genomics resource. ***Nucleic Acids Research***.

Carter, M.E., Carpenter, S.C.D., Dubrow, Z.E., Sabol, M.R., Rinaldi, F.C., Lastovetsky, O.A., **Mondo, S.J.**, Pawlowska, T.E., Bogdanove, A.J., 2020. A TAL effector-like protein of an endofungal bacterium increases the stress tolerance and alters the transcriptome of the host. ***Proceedings of the National Academy of Sciences***, doi: [10.1073/pnas.2003857117](https://doi.org/10.1073/pnas.2003857117)

Tabima, J.F, Trautman, I.A, Chang, Y., Wang, Y., Mondo, S.J., Kuo, A., Salamov, A., Grigoriev, I.V., Stajich, J.E., Spatafora, J.W., 2020. Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont, *Basidiobolus*. ***G3 Genes|Genomes|Genetics***, doi: [10.1534/g3.120.401516](https://doi.org/10.1534/g3.120.401516)

Espino-Vázquez, A.N., Bermúdez-Barrientos, J.R., Cabrera-Rangel, J.F., Córdova-López, G., Cardoso-Martínez, F., Martínez-Vázquez, A., Camarena-Pozos, D.A., **Mondo, S.J.**, Pawlowska, T.E., Abreu-Goodger, C. and Partida-Martínez, L.P., 2020. Narnaviruses: novel players in fungal–bacterial symbioses. ***ISMEj***, pp.1-12.

Kjærbølling, Inge; Vesth, Tammi; Frisvad, Jens C; Nybo, Jane L; Theobald, Sebastian; Kildgaard, Sara; Petersen, Thomas Isbrandt; Kuo, Alan; Sato, Atsushi; Lyhne, Ellen K; Kogle, Martin E; Wiebenga, Ad; Kun, Roland S; Lubbers, Ronnie JM; Mäkelä, Miia R; Barry, Kerrie; Chovatia, Mansi; Clum, Alicia; Daum, Chris; Haridas, Sajeet; He, Guifen; LaButti, Kurt; Lipzen, Anna; **Mondo, Stephen**; Pangilinan, Jasmyn; Riley, Robert; Salamov, Asaf; Simmons, Blake A; Magnuson, Jon K; Henrissat, Bernard; Mortensen, Uffe H; Larsen, Thomas O; de Vries, Ronald P; Grigoriev, Igor V; Machida, Masayuki; Baker, Scott E; Andersen, Mikael R, 2020. A comparative genomics study of 23 Aspergillus species from section Flavi. ***Nature communications***, 11(1), 1-12.

Haridas, S; Albert, R; Binder, M; Bloem, J; LaButti, K; Salamov, A; Andreopoulos, B; Baker, SE; Barry, K; Bills, G; Bluhm, BH; Cannon, C; Castanera, R; Culley, DE; Daum, C; Ezra, D; González, JB; Henrissat, B; Kuo, A; Liang, C; Lipzen, A; Lutzoni, F; Magnuson, J; **Mondo, SJ**; Nolan, M; Ohm, RA; Pangilinan, J; Park, H-J; Ramírez, L; Alfaro, M; Sun, H; Tritt, A; Yoshinaga, Y; Zwiers, L-H; Turgeon, BG; Goodwin, SB; Spatafora, JW; Crous, PW; Grigoriev, IV, 2020. 101 Dothideomycetes genomes: a test case for predicting lifestyles and emergence of pathogens. ***Studies in Mycology***.

Jiménez, D.J., Wang, Y., Chaib de Mares, M., Cortes-Tolalpa, L., Mertens, J.A., Hector, R.E., Lin, J., Johnson, J., Lipzen, A., Barry, K., **Mondo,** **S.J.**, Grigoriev, I.V., Nichols, N.N., van Elsas, J.D., 2019. Defining the eco-enzymological role of the fungal strain *Coniochaeta* sp. 2T2. 1 in a tripartite lignocellulolytic microbial consortium. ***FEMS microbiology ecology***.

**Mondo, S.J.**, Jiménez, D.J., Hector, R.E., Lipzen, A., Yan, M., LaButti, K., Barry, K., van Elsas, J.D., Grigoriev, I.V., Nichols, N.N., 2019. Genome expansion by allopolyploidization in the fungal strain Coniochaeta 2T2.1 and its vast lignocellulolytic machinery. ***Biotechnology for Biofuels***, 12 (1), 229.

Navarro-Mendoza, M.I., Perez-Arques, C., Panchal, S., Nicolás, F.E., **Mondo, S.J.**, Ganguly, P., Pangilinan, J., Grigoriev, I.V., Heitman, J., Sanyal, K., Garre, V., 2019. Early Diverging Fungus Mucor circinelloides Lacks Centromeric Histone CENP-A and Displays a Mosaic of Point and Regional Centromeres. ***Current Biology***, 29 (22), 3791-3802.

Calhoun, S., **Mondo, S.J.**, Grigoriev, I.V., 2019. Yeasts and how they came to be. ***Nature Reviews Microbiology***, 17 (11), 649-649.

Krizsán, K., Almási, É., Merényi, Z., Sahu, N., Virágh, M., Kószó, T., **Mondo, S.J.**, Kiss, B., Bálint, B., Kües, U., Barry, K., Cseklye, J., Hegedüs, B., Henrissat, B., Johnson, J., Lipzen, A., Ohm, R.A., Nagy, I., Pangilinan, J., Yan, J., Xiong, Y., Grigoriev, I.V., Hibbett, D.S., Nagy L.G., 2019. Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. ***Proceedings of the National Academy of Sciences***, doi: 10.1073/pnas.1817822116.

Bewick, Adam J, Hofmeister, Brigitte T, Powers, Rob A, **Mondo, Stephen J**, Grigoriev, Igor V, James, Timothy Y, Stajich, Jason E, Schmitz, Robert J, 2019. Diversity of cytosine methylation across the fungal tree of life. ***Nature ecology & evolution***, (3) 479–490.

Aguilar-Pontes M.V., Brandl, J., McDonnell, E., Strasser, K., Nguyen, T.T.M., Riley, R., **Mondo, S.J.**, Salamov, A., Nybo, J.L., Vesth, T.C., Grigoriev, I.V., Andersen, M.R., Tsang, A., de Vries R.P., 2018. The gold-standard genome of *Aspergillus niger* NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. ***Studies in mycology***, (91) 61-78.

Pawlowska, T.E., Gaspar, M.L., Lastovetsky, O.A., **Mondo, S.J.**, Real-Ramirez, I., Shakya, E., Bonfante, P., 2018. Biology of Fungi and Their Bacterial Endosymbionts. ***Annual Review of Phytopathology,*** (56) 289-309.

Lastovetsky, O.A., Ahn, E., **Mondo, S.J.**, Toomer, K.H., Zhang, A., Johnson, L.M., Pawlowska, T.E., 2018. Distribution and population structure of endobacteria in arbuscular mycorrhizal fungi at North Atlantic dunes. ***ISMEj***, doi: 10.1038/s41396-018-0246-2.

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

Coradetti, S., Pinel, D., Geiselman, G., Ito, M., **Mondo, S.J.**, Reilly, M., Cheng, Y., Bauer, S., Grigoriev, I.V., Gladden, J., Simmons, B., Brem, R., Arkin, A., Skerker, J. Functional genomics of lipid metabolism in the oleaginous yeast *Rhodosporidum toruloides*. ***eLife***, doi: [10.7554/eLife.32110](https://doi.org/10.7554/eLife.32110).

Kijpornyongpan T., **Mondo, S.J.**, Barry, K., Sandor, L., Lee, J., Lipzen, A., Pangilinan, J., LaButti, K., Hainaut, M., Henrissat, B., Grigoriev, I.V., Spatafora, J.W., Aime, M.C., 2018. Broad genomic sampling reveals a smut pathogenic ancestry of the fungal clade Ustilaginomycotina. ***Molecular Biology and Evolution***, 24(13) 3485-3500.

Inge Kjærbølling, Tammi C Vesth, Jens C Frisvad, Jane L Nybo, Sebastian Theobald, Alan Kuo, Paul Bowyer, Yudai Matsuda, **Stephen Mondo**, Ellen K Lyhne, Martin E Kogle, Alicia Clum, Anna Lipzen, Asaf Salamov, Chew Yee Ngan, Chris Daum, Jennifer Chiniquy, Kerrie Barry, Kurt LaButti, Sajeet Haridas, Blake A Simmons, Jon K Magnuson, Uffe H Mortensen, Thomas O Larsen, Igor V Grigoriev, Scott E Baker, Mikael R Andersen, 2018. Linking secondary metabolites to gene clusters through genome sequencing of six diverse Aspergillus species. ***Proceedings of the National Academy of Sciences***, 201715954.

**Mondo, S.J.**, Lastovetsky, O.L., Gaspar, M.L., Schwardt, N.H., Barber, C.C., Riley, R.W., Sun, H., Grigoriev, I.V., Pawlowska, T.E., 2017. Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. ***Nature Communications***, 8(1), 1843.

**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, W.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., Grigoriev, I.V., 2017. Widespread adenine N6-methylation of active genes in fungi. ***Nature Genetics***, 49(6) 964-968.

Haitjema C.H., Gilmore S.P., Henske J.K., Solomon K.V., de Groot R., Kuo A.**, Mondo S.J.**, Salamov A.A., LaButti K., Zhao Z., Chiniquy J., Barry K., Brewer H.M., Purvine S.O., Wright A.T., Hainaut M., Boxma B., van Alen T., Hackstein J.H.P., Henrissat B., Baker S.E., Grigoriev I.V., O'Malley M.A., 2017. A parts list for fungal cellulosomes revealed by comparative genomics. ***Nature Microbiology***,2(8), 17087.

Daniel B Raudabaugh, Teresa Iturriaga, Akiko Carver, **Stephen Mondo**, Jasmyn Pangilinan, Anna Lipzen, Guifen He, Mojgan Amirebrahimi, Igor V Grigoriev, Andrew N Miller, 2017. *Coniella lustricola*, a new species from submerged detritus. ***Mycological Progress*,** 1-13.

Lastovetsky, O.A., Gaspar, M.L., **Mondo, S.J.**, LaButti, K.M., Sandor, L., Grigoriev, I.V., Henry, S.A., Pawlowska, T.E., 2017. Lipid metabolic changes in an early divergent fungus govern the establishment of a mutualistic symbiosis with endobacteria. ***Proceedings of the National Academy of Sciences*** (PNAS), **113**(52), 15102-15107.

**Mondo, S.J.**,Salvioli, A., Bonfante, P., Morton, J.B., Pawlowska, T.E., 2016. Nondegenerative evolution in ancient heritable bacterial endosymbionts of fungi. ***Molecular Biology and Evolution***, **33**(9), 2216–2231.

Walker, A., Frasz, S., Seifert, K., Miller, J.D., **Mondo, S.J.**, LaButti, K., Lipzen, A., Dockter, R., Kennedy, M., Grigoriev, I.V., Spatafora, J.W., 2016. Full genome of *Phialocephala scopiformis* DAOMC 229536, a fungal endophyte of spruce producing the potent anti-insectan compound rugulosin. ***Genome announcements*** **4.1**: e01768-15.

Toomer, K.H., Chen, X., Naito, M., **Mondo, S.J.**, Bakker, H.C., VanKuren, N.W., Lekberg, Y., Morton, J.B., Pawlowska, T.E., 2015. Molecular evolution patterns reveal life history features of mycoplasma-related endobacteria associated with arbuscular mycorrhizal fungi. ***Molecular ecology***, 24(13) 3485-3500.

Desirò, A., Salvioli, A., Ngonkeu, E.L., **Mondo, S.J.**, Epis, S., Faccio, A., Kaech, A., Pawlowska, T.E., Bonfante, P. 2014. Detection of a novel intracellular microbiome hosted in arbuscular mycorrhizal fungi. ***ISMEj***, **8**(2):257-70.

**Mondo, S.J.**, Toomer, K.H., Morton, J.B., Lekberg, Y., Pawlowska, T.E., 2012. Evolutionary stability in a 400-million-year-old heritable facultative mutualism. ***Evolution***, **66**(8):2564-76.

Pumplin, N., **Mondo, S.J.**, Topp, S., Starker, C.G., Gantt, J.S., and Harrison, M.J., 2009. *Medicago truncatula* Vapyrin is a novel protein required for arbuscular mycorrhizal symbiosis. ***The Plant Journal****.* **61**(3)**:**482-494.

Andam, C. P., **Mondo S. J.**, and Parker, M. A., 2007. Monophyly of *nodA* and *nifH* genes across Texan and Costa Rican populations of *Cupriavidus* nodule symbionts. ***Appl. Environ. Microbiol***. **73:**4686-4690.

**BOOK CHAPTERS**

**Mondo, S.J.**, Kuo, R.C., Singan, V., 2018. Fungal epigenomics: detection and analysis. ***Fungal Genomics: Methods and Protocols***. (Humana Press, 2018).

Aime, M.C., McTaggart, A.R., **Mondo, S.J.**, Duplessis, S., 2017. Phylogenetics and phylogenomics of rust fungi. ***Advances in Genetics***.

**TEACHING**

Spring, 2013 Graduate Teaching Assistant for Plant Pathology 3290: Medical and Veterinary Mycology

Fall, 2009 Graduate Teaching Assistant for Plant Pathology 3010: Biology and Management of Plant Diseases

**MENTORING AND TRAINING**

3 Graduate students/Postdocs, 7 undergraduates (3 honors theses), 3 research assistants

**SELECTED TALKS**

**Mondo, S.J.** Invited speaker: Periodic DNA patterns associated with chromatin regulation in Fungi. 31st Fungal Genetics Conference, Asilomar, CA. March, 2022

**Mondo, S.J.**, et al. Widespread adenine N6-methylation of active genes in fungi.

Invited speaker: ASM Microbe 2019, San Francisco, CA. June 2019

**Plenary presentation:** The 14th European Conference on Fungal Genetics, Haifa, Israel

Mycological Society of America (Session chair, Evolution I), Athens, GA. July, 2017

JGI User Meeting, Walnut Creek, CA. March, 2017

- YouTube: https://www.youtube.com/watch?v=AXzqAO-RY2Q

Fungal Genetics Conference, Asilomar, CA. March, 2017

PacBio West Coast User Meeting, Stanford, CA. Sept, 2016

**Mondo, S.J.,** et al. Endosymbiont regulated sexual reproduction in *Rhizopus microsporus*. The 11th International Mycological Congress, Puerto Rico, 2018. Bacterial-Fungal Interactions workshop.

**Mondo, S.J.**, et al. Ustilaginomycotina Comparative Genomics.

Fungal Genetics Conference, Asilomar, CA. March, 2017

**Mondo, S.J.** Fungal Genomics at JGI: Research and Tools

Microbial Genomics & Metagenomics Workshop, Walnut Creek, CA. Oct, 2016

Mycological Society of America, Edmonton, Canada. July, 2015

JGI User Meeting, Walnut Creek, CA. March, 2015

**Mondo, S.J.**, Pawlowska, T.E. Uncovering the evolutionary pressures shaping the Glomeromycota-*Glomeribacter* endosymbiosis.

Fungal Genetics Conference, Asilomar, CA, March 12th-17th, 2013.

**Mondo, S.J.**, et al. Evolutionary stability in a 400-million-year-old heritable facultative mutualism.

Fungal Genetics Conference, Asilomar, CA, March 15th-20th, 2011

**SPECIAL SKILLS AND INTERESTS**

Comparative genomics, epigenomics, phylogenetics, bioinformatics, chromatin dynamics, deep learning, molecular biology, evolutionary & co-evolutionary theory, host-endosymbiont interactions, population genetics, Python, SQL, bash, emacs, R, RNAseq, ChIP-seq, transcriptome assembly (both de novo and reference based), and differential expression analysis, ChIP-seq data analysis, DNA sequencing (Illumina, Sanger, and PacBio).