

21st Century Guidebook to Fungi

Genomic systems analysis of fungi

MycoCosm is a fungal genomics portal (<http://jgi.doe.gov/fungi>), developed by the US Department of Energy Joint Genome Institute to support integration, analysis and dissemination of fungal genome sequences and other ‘omics’ data by providing interactive web-based tools. MycoCosm also promotes and facilitates user community participation through the nomination of new species of fungi for sequencing, and the annotation and analysis of resulting data. View the current list on the following page, and links to publications about the sequences: <https://genome.jgi.doe.gov/fungi/fungi.info.html>.

Grigoriev, I.V., Nikitin, R., Haridas, S., Kuo, A., Ohm, R., Otilar, R., Riley, R., Salamov, A., Zhao, X., Korzeniewski, F., Smirnova, T., Nordberg, H., Dubchak, I. & Shabalov, I. (2014). MycoCosm portal: gearing up for 1000 fungal genomes. *Nucleic Acids Research*, **42**: D699-D704. DOI: <https://doi.org/10.1093/nar/gkt1183>.

The following is a list of published papers (additional to those cited in the text) that will ease you into the world of fungal genomics. The list has been put together favouring these criteria: (a) open access publishing; and (b) illustrating different approaches. The list is in alphabetical order of the first author’s name.

- Banks, A.M., Barker, G.L.A., Bailey, A.M. & Foster, G.D. (2017). Draft genome sequence of the coprinoid mushroom *Coprinopsis strossmayeri*. *Genome Announcements*, **5**: e00044-17. DOI: <https://doi.org/10.1128/genomeA.00044-17>.
- Bao, D., Gong, M., Zheng, H., Chen, M., Zhang, L. and eleven others. (2013). Sequencing and comparative analysis of the Straw Mushroom (*Volvariella volvacea*) genome. *PLoS ONE*, **8**: article e58294. DOI: <https://doi.org/10.1371/journal.pone.0058294>.
- Carter, G.W., Galas, D.J. & Galitski, T. (2009). Maximal extraction of biological information from genetic interaction data. *PLoS Computational Biology*, **5**: article e1000347. DOI: <https://doi.org/10.1371/journal.pcbi.1000347>.
- de Freitas Pereira, ., Narvaes da Rocha Campos, A., Anastacio, T.C., Morin, E., Brommonschenkel, S.H., Martin, F., Kohler, A. & Costa, M.D. (2017). The transcriptional landscape of basidiosporogenesis in mature *Pisolithus microcarpus* basidiocarp. *BMC Genomics*, **18**: 157. DOI: <https://doi.org/10.1186/s12864-0173545-5>.
- Jin, L., Li, G., Yu, D., Huang, W., Cheng, C., Liao, S., Wu, Q. & Zhang, Y. (2017). Transcriptome analysis reveals the complexity of alternative splicing regulation in the fungus *Verticillium dahlia*. *BMC Genomics*, **18**: 130. DOI: <https://doi.org/10.1186/s12864-017-3507-y>.
- Li, H., Wu, S., Ma, X., Chen, W., Zhang, J. and 17 others (2018). The genome sequences of 90 mushrooms. *Scientific Reports*, **8**: article 9982. DOI: <https://doi.org/10.1038/s41598-018-28303-2>.
- Liu, J.-Y., Chang, M.-C., Meng, J.-L., Feng, C.P., Zhao, H. & Zhang, M.L. (2017). Comparative proteome reveals metabolic changes during the fruiting process in *Flammulina velutipes*. *Journal of Agricultural and Food Chemistry*, **65**: 5091-5100. DOI: <https://doi.org/10.1021/acs.jafc.7b01120>.

- Martin, F., Aerts, A., Ahrén, D., Brun, A., Danchin, E.G., and 63 others. (2008). The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature*, **452**: 88-92. DOI: <https://doi.org/10.1038/nature06556>.
- Martinez, D., Challacombe, J., Morgenstern, I., Hibbett, D., Schmoll, M., and 48 others. (2009). Genome, transcriptome, and secretome analysis of wood decay fungus *Postia placenta* supports unique mechanisms of lignocellulose conversion. *Proceedings of the National Academy of Sciences of the United States of America*, **106**: 1954-1959. DOI: <https://doi.org/10.1073/pnas.0809575106>.
- McCluskey, K. & Baker, S.E. (2017). Diverse data supports the transition of filamentous fungal model organisms into the post-genomics era. *Mycology*, **8**: 67-83. DOI: <https://doi.org/10.1080/21501203.2017.1281849>.
- Morin, E., Kohler, A., Baker, A.R., Foulongne-Oriol, M., Lombard, V. and 38 others. (2012). Genome sequence of the button mushroom *Agaricus bisporus* reveals mechanisms governing adaptation to a humic-rich ecological niche. *Proceedings of the National Academy of Sciences of the United States of America*, **109**: 17501-17506. DOI: <https://doi.org/10.1073/pnas.1206847109>.
- Murat, C., Payen, T., Noel, B., Kuo, A., Morin, E. and 50 others (2018). Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. *Nature Ecology & Evolution*, **2**: 1956-1965. DOI: <https://doi.org/10.1038/s41559-018-0710-4>.
- Nowrousian, M. (2018). Genomics and transcriptomics to study fruiting body development: an update. *Fungal Biology Reviews*, **32**: 231-235. DOI: <https://doi.org/10.1016/j.fbr.2018.02.004>.
- Ohm, R.A., de Jong, J.F., Lugones, L.G., Aerts, A., Kothe, E., and 27 others. (2010). Genome sequence of the model mushroom *Schizophyllum commune*. *Nature Biotechnology*, **28**: 957-963. DOI: <https://doi.org/10.1038/nbt.1643>.
- Toyotome, T., Hamada, S., Yamaguchi, S., Takahashi, H., Kondoh, D., Takino, M., Kanesaki, Y. & Kamei, K. (2018). Comparative genome analysis of *Aspergillus flavus* clinically isolated in Japan. *DNA Research*, article dsy041. DOI: <https://doi.org/10.1093/dnares/dsy041>.
- Wang, L., Wu, X., Gao, W., Zhao, M., Zhang, J. & Huang, C. (2017). Differential expression patterns of *Pleurotus ostreatus* catalase genes during developmental stages and under heat stress. *Genes*, **8**: 335. DOI: <https://doi.org/10.3390/genes8110335>.
- Wang, M., Gu, B., Huang, J., Jiang, S., Chen, Y., Yin, Y., Pan, Y., Yu, G., Li, Y., Wong, B.H., Liang, Y. & Sun, H. (2013). Transcriptome and proteome exploration to provide a resource for the study of *Agrocybe aegerita*. *PLoS ONE*, **8**: article e56686. DOI: <https://doi.org/10.1371/journal.pone.0056686>.
- Wang, Z., Gudibanda, A., Ugwuowo, U., Trail, F. & Townsend, J.P. (2018). Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. *Fungal Biology Reviews*, **32**: 249-264. DOI: <https://doi.org/10.1016/j.fbr.2018.02.001>.
- Wu, B., Xu, Z., Knudson, A., Carlson, A., Chen, N. and 12 others (2018). Genomics and development of *Lentinus tigrinus*: a white-rot wood-decaying mushroom with dimorphic fruiting bodies. *Genome Biology and Evolution*, **10**: 3250-3261. DOI: <https://doi.org/10.1093/gbe/evy246>.

- Zhang, J., Ren, A., Chen, H., Zhao, M., Shi, L., Chen, M., Wang, H. & Feng, Z. (2015). Transcriptome analysis and its application in identifying genes associated with fruiting body development in basidiomycete *Hypsizygus marmoreus*. *PLoS ONE*, **10**: article e0123025. DOI: <https://doi.org/10.1371/journal.pone.0123025>.
- Zheng, Y.-M., Lin, F.-L., Gao, H., Zou, G., Zhang, J.-W., and five others. (2017). Development of a versatile and conventional technique for gene disruption in filamentous fungi based on CRISPR-Cas9 technology. *Scientific Reports* **7**: article 9250. DOI: <https://doi.org/10.1038/s41598-017-10052-3>.

And check out this special issue of the journal *Fungal Genetics and Biology* (Volume **89**, pages 1-156, April 2016) entitled *The Era of Synthetic Biology in Yeast and Filamentous Fungi* at <https://www.sciencedirect.com/journal/fungal-genetics-and-biology/vol/89/suppl/C>.

The **Earth BioGenome Project** aims to sequence, catalogue, and characterise *the genomes of all of Earth's eukaryotic biodiversity*, as described in the following:

- Lewin, H.A., Robinson, G.E., Kress, W.J., Baker, W.J., Coddington, J., Crandall, K.A., Durbin, R., Edwards, S.V., Forest, F., Gilbert, M.T.P., Goldstein, M.M., Grigoriev, I.V., Hackett, K.J., Haussler, D., Jarvis, E.D., Johnson, W.E., Patrinos, A., Richards, S., Castilla-Rubio, J.C., van Sluys, M.-A., Soltis, P.S., Xu, X., Yang, H. & Zhang, G. (2018). Earth BioGenome Project: Sequencing life for the future of life. *Proceedings of the National Academy of Sciences of the United States of America*, **115**: 4325-4333. DOI: <https://doi.org/10.1073/pnas.1720115115>.

See also the *Earth BioGenome Project* website at <https://www.earthbiogenome.org/> and the *Darwin Tree of Life Project* at <https://www.sanger.ac.uk/news/view/genetic-code-66000-uk-species-be-sequenced>.
