**Figure 3 – source data 1.** Overview of host range features for the 45 fungal species analyzed in this work

| **Species** | **Code name** | **NCBI ID** | **Source for host range information** | **host type** | **Number of host genera** |
| --- | --- | --- | --- | --- | --- |
| *Rozella allomycis* | Rozal | 281847 | http://genome.jgi.doe.gov/Rozal1\_1/Rozal1\_1.home.html | Fungi | 1 |
| *Rhizopus oryzae* | Rhior | 64495 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm Plants | | 28 |
| *Nosema ceranae* | Nocse\_v2 | 40302 | Maside X, Gómez-Moracho T, Jara L, Martín-Hernández R, De la Rúa P, Higes M, Bartolomé C. Population Genetics of Nosema apis and Nosema ceranae: One Host (Apis mellifera) and Two Different Histories. PLoS One. 2015 Dec 31;10(12):e0145609. | Insects | 1 |
| *Encephalitozoon intestinalis* | Encin | 58839 | Bornay-Llinares FJ, da Silva AJ, Moura H, Schwartz DA, Visvesvara GS, Pieniazek NJ, Cruz-López A, Hernández-Jaúregui P, Guerrero J, Enriquez FJ. Immunologic, microscopic, and molecular evidence of Encephalitozoon intestinalis (Septata intestinalis) infection in mammals other than humans. J Infect Dis. 1998 Sep;178(3):820-6.; Mathis A, Weber R, Deplazes P. Zoonotic potential of the microsporidia. Clin Microbiol Rev. 2005 Jul;18(3):423-45. | Mammals | 7 |
| *Batrachochytrium dendrobatidis* | Batde | 109871 | Olson DH, Aanensen DM, Ronnenberg KL, Powell CI, Walker SF, Bielby J, Garner TW, Weaver G; Bd Mapping Group, Fisher MC. Mapping the global emergence of Batrachochytrium dendrobatidis, the amphibian chytrid fungus. PLoS One. 2013;8(2):e56802. | Animals | 153 |
| *Gonapodya prolifera* | Gonpr | 1E+06 | non pathogenic | None | 0 |
| *Sporisorium reilianum* | Spore | 72558 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 5 |
| *Rhodotorula toruloides* | Rhoto | 5286 | non pathogenic | None | 0 |
| *Melampsora larici-populina* | Mellp | 203908 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 7 |
| *Puccinia triticina* | Puctr | 208348 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Puccinia graminis* | Pucgr | 5297 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 2 |
| *Cryptococcus neoformans* | Cryne | 5207 | The hosts include birds, mammals, amoeba, insects (diptera and lepidoptera), and nematodes based on Lin X, Heitman J. The biology of the Cryptococcus neoformans species complex. Annu Rev Microbiol. 2006;60:69-105. The corresponding number of genera was 2154 for birds (https://en.wikipedia.org/wiki/List\_of\_bird\_genera); 1258 for mammals (https://en.wikipedia.org/wiki/List\_of\_mammal\_genera), 1346 for Diptera (http://bugguide.net/node/view/52/tree/all), 2268 for Lepidoptera (http://bugguide.net/node/view/52/tree/all), 30 for amoeaba (https://en.wikipedia.org/wiki/Amoebozoa), 456 for nematodes (http://plpnemweb.ucdavis.edu/nemaplex/Uppermnus/Classifmnu.htm), giving a total of 7512. We considered that host range covers 8% of these genera (601) as a conservative estimate. | Animals, Insects,… | 800 |
| *Wolfiporia cocos* | Wolco | 81056 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm Plants | | 2 |
| *Rhizoctonia solani* | Rhiso\_v2 | 456999 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm Plants | | 690 |
| *Serpula lacrymans* | Serla | 85982 | non pathogenic | None | 0 |
| *Moniliophthora roreri* | Monro | 221103 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 2 |
| *Laccaria bicolor* | Lacbi | 29883 | non pathogenic | None | 0 |
| *Agaricus bisporus* | Agabi | 5341 | non pathogenic | None | 0 |
| *Taphrina deformans* | Tapde | 5011 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 4 |
| *Tuber melanosporum* | Tubme | 39416 | non pathogenic | None | 0 |
| *Penicillium digitatum* | Pendi | 36651 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm Plants | | 17 |
| *Aspergillus fumigatus* | Aspfu | 746128 | The host includes "Humans, cows, dolphins, birds, and horses" as per http://www.phac-aspc.gc.ca/lab-bio/res/psds-ftss/aspergillus-spp-eng.php:. The corresponding number of genera was 2154 for birds (https://en.wikipedia.org/wiki/List\_of\_bird\_genera); 22 for dolphins (https://en.wikipedia.org/wiki/Dolphin); 10 for cows (https://en.wikipedia.org/wiki/Bovinae) and 1 for horses and human, giving a total of 2188 genera. We considered that host range covers 8% of these genera (175) as a conservative estimate. | Animals | 175 |
| *Stagonospora nodorum* | Stano | 13684 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 7 |
| *Alternaria brassicicola* | Altbr | 29001 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 16 |
| *Pyrenophora tritici-repentis* | Pyrtr | 45151 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 11 |
| *Dothistroma septosporum* | Dotse | 64363 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Pseudocercospora fijiensis (Mycosphaerella fijiensis)* | Mycfi | 83344 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Zymoseptoria tritici (Mycosphaerella graminicola)* | Mycgr | 1E+06 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Passalora fulva* | Clafu | 5499 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 2 |
| *Blumeria graminis* | Blugr | 34373 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Erysiphe necator* | Eryne | 52586 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 1 |
| *Botrytis cinerea* | Botci\_v2 | 40559 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 556 |
| *Sclerotinia sclerotiorum* | Sclsc\_v2 | 5180 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 332 |
| *Oidiodendron maius* | Oidma | 78148 | non pathogenic | None | 0 |
| *Pseudogymnoascus destructans (Geomyces destructans)* | Geode | 655981 | https://en.wikipedia.org/wiki/Pseudogymnoascus\_destructans | Animals | 8 |
| *Magnaporthe oryzae* | Maggr | 318829 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 4 |
| *Myceliophthora thermophila* | Mycth | 78579 | non pathogenic | None | 0 |
| *Chaetomium globosum* | Chagl | 38033 | non pathogenic | None | 0 |
| *Verticilium dahliae* | Verda | 27337 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 78 |
| *Colletotrichum higginsianum* | Colhi | 80884 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 6 |
| *Colletotrichum graminicola* | Colgr | 31870 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 59 |
| *Ophiocordyceps unilateralis* | Ophun | 268505 | de Bekker C, Quevillon LE, Smith PB, Fleming KR, Ghosh D, Patterson AD, Hughes DP. Species-specific ant brain manipulation by a specialized fungal parasite. BMC Evol Biol. 2014 Aug 29;14:166. | insects | 1 |
| *Beauveria bassiana* | Beaba | 176275 | The list of host families was obtained from Marcos R. de Faria, Stephen P. Wraight, Mycoinsecticides and Mycoacaricides: A comprehensive list with worldwide coverage and international classification of formulation types, Biological Control 2007 Dec;43(3):237-56.; the list of genus in these families (a total of 3366) was obtained from http://bugguide.net/node/view/52/tree/all. We considered that host range covers 8% of these genera (269) so that the number of infected genera does not exceeds that of infected species (700) reported in Xiao G, Ying SH, Zheng P, Wang ZL, Zhang S, Xie XQ, Shang Y, St Leger RJ, Zhao GP, Wang C, Feng MG Genomic perspectives on the evolution of fungal entomopathogenicity in Beauveria bassiana. Sci Rep. 2012;2:483. | Insects | 269 |
| *Fusarium graminearum* | Fusgr | 5518 | http://nt.ars-grin.gov/fungaldatabases/fungushost/FungusHost.cfm | Plants | 72 |
| *Metarhizium acridum* | Metac | 92637 | Insects from order orthoptera as per Hu X, Xiao G, Zheng P, Shang Y, Su Y, Zhang X, Liu X, Zhan S, St Leger RJ, Wang C. Trajectory and genomic determinants of fungal-pathogen speciation and host adaptation. Proc Natl Acad Sci U S A. 2014 Nov 25;111(47):16796-801. The list of genus from this order was obtained from http://bugguide.net/node/view/52/tree/all. | Insects | 228 |

Overview of genome features for the 45 fungal species analyzed in this work

| **Species** | **Genome sequence reference** | **Sequence files source** | **No. contigs** | **CDS** | **Full CDS** |
| --- | --- | --- | --- | --- | --- |
| *Rozella allomycis* | James TY, Pelin A, Bonen L, Ahrendt S, Sain D, Corradi N, Stajich JE Shared signatures of parasitism and phylogenomics unite Cryptomycota and microsporidia. Curr Biol. 2013 Aug 19;23(16):1548-53. | http://genome.jgi.doe.gov/Rozal1\_1/Rozal1\_1.download.html | 1059 | 6350 | 5932 |
| *Rhizopus oryzae* | Ma LJ, Ibrahim AS, Skory C, Grabherr MG, Burger G, Butler M, Elias M, Idnurm A, Lang BF, Sone T, Abe A, Calvo SE, Corrochano LM, Engels R, Fu J, Hansberg W, Kim JM, Kodira CD, Koehrsen MJ, Liu B, Miranda-Saavedra D, O'Leary S, Ortiz-Castellanos L, Poulter R, Rodriguez-Romero J, Ruiz-Herrera J, Shen YQ, Zeng Q, Galagan J, Birren BW, Cuomo CA, Wickes BL Genomic analysis of the basal lineage fungus Rhizopus oryzae reveals a whole-genome duplication. PLoS Genet. 2009 Jul;5(7):e1000549. | http://genome.jgi.doe.gov/Rhior3/Rhior3.home.html | 81 | 17467 | 17412 |
| *Nosema ceranae* | Cornman RS, Chen YP, Schatz MC, Street C, Zhao Y, Desany B, Egholm M, Hutchison S, Pettis JS, Lipkin WI, Evans JD Genomic analyses of the microsporidian Nosema ceranae, an emergent pathogen of honey bees. PLoS Pathog. 2009 Jun;5(6):e1000466. | http://www.ebi.ac.uk/ena/data/view/GCA\_000988165.1 | 536 | 3208 | 2932 |
| *Encephalitozoon intestinalis* | Corradi N, Pombert JF, Farinelli L, Didier ES, Keeling PJ The complete sequence of the smallest known nuclear genome from the microsporidian Encephalitozoon intestinalis. Nat Commun. 2010 Sep 21;1:77. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Encin1 | 11 | 1833 | 1830 |
| *Batrachochytrium dendrobatidis* | Batrachochytrium dendrobatidis Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/) | https://www.broadinstitute.org/annotation/genome/batrachochytrium\_dendrobatidis/MultiDownloads.html | 69 | 8819 | 8805 |
| *Gonapodya prolifera* | Chang Y, Wang S, Sekimoto S, Aerts AL, Choi C, Clum A, LaButti KM, Lindquist EA, Yee Ngan C, Ohm RA, Salamov AA, Grigoriev IV, Spatafora JW, Berbee ML Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. Genome Biol Evol. 2015 May 14;7(6):1590-601. | http://genome.jgi.doe.gov/Ganpr1/Ganpr1.download.html | 352 | 13902 | 13140 |
| *Sporisorium reilianum* | Schirawski J, Mannhaupt G, Münch K, Brefort T, Schipper K, Doehlemann G, Di Stasio M, Rössel N, Mendoza-Mendoza A, Pester D, Müller O, Winterberg B, Meyer E, Ghareeb H, Wollenberg T, Münsterkötter M, Wong P, Walter M, Stukenbrock E, Güldener U, Kahmann R. Pathogenicity determinants in smut fungi revealed by genome comparison. Science. 2010 Dec 10;330(6010):1546-8. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Spore1 | 44 | 6648 | 6614 |
| *Rhodotorula toruloides* | Zhu Z, Zhang S, Liu H, Shen H, Lin X, Yang F, Zhou YJ, Jin G, Ye M, Zou H, Zhao ZK A multi-omic map of the lipid-producing yeast Rhodosporidium toruloides. Nat Commun. 2012;3:1112. | http://genome.jgi.doe.gov/Rhoto1/Rhoto1.home.html | 94 | 8140 | 8117 |
| *Melampsora larici-populina* | Duplessis S, Cuomo CA, Lin YC, Aerts A, Tisserant E, Veneault-Fourrey C, Joly DL, Hacquard S, Amselem J, Cantarel BL, Chiu R, Coutinho PM, Feau N, Field M, Frey P, Gelhaye E, Goldberg J, Grabherr MG, Kodira CD, Kohler A, Kües U, Lindquist EA, Lucas SM, Mago R, Mauceli E, Morin E, Murat C, Pangilinan JL, Park R, Pearson M, Quesneville H, Rouhier N, Sakthikumar S, Salamov AA, Schmutz J, Selles B, Shapiro H, Tanguay P, Tuskan GA, Henrissat B, Van de Peer Y, Rouzé P, Ellis JG, Dodds PN, Schein JE, Zhong S, Hamelin RC, Grigoriev IV, Szabo LJ, Martin F. Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proc Natl Acad Sci U S A. 2011 May 31;108(22):9166-71. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Mellp2\_3 | 462 | 16399 | 15525 |
| *Puccinia triticina* | “Puccinia Group Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/)” | https://www.broadinstitute.org/annotation/genome/puccinia\_group/MultiDownloads.html | 14820 | 15585 | 13576 |
| *Puccinia graminis* | Duplessis S, Cuomo CA, Lin YC, Aerts A, Tisserant E, Veneault-Fourrey C, Joly DL, Hacquard S, Amselem J, Cantarel BL, Chiu R, Coutinho PM, Feau N, Field M, Frey P, Gelhaye E, Goldberg J, Grabherr MG, Kodira CD, Kohler A, Kües U, Lindquist EA, Lucas SM, Mago R, Mauceli E, Morin E, Murat C, Pangilinan JL, Park R, Pearson M, Quesneville H, Rouhier N, Sakthikumar S, Salamov AA, Schmutz J, Selles B, Shapiro H, Tanguay P, Tuskan GA, Henrissat B, Van de Peer Y, Rouzé P, Ellis JG, Dodds PN, Schein JE, Zhong S, Hamelin RC, Grigoriev IV, Szabo LJ, Martin F. Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proc Natl Acad Sci U S A. 2011 May 31;108(22):9166-71. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Pucgr2 | 394 | 22534 | 15820 - 20534 ATG STOP unknown |
| *Cryptococcus neoformans* | Loftus BJ, Fung E, Roncaglia P, Rowley D, Amedeo P, Bruno D, Vamathevan J, Miranda M, Anderson IJ, Fraser JA, Allen JE, Bosdet IE, Brent MR, Chiu R, Doering TL, Donlin MJ, D'Souza CA, Fox DS, Grinberg V, Fu J, Fukushima M, Haas BJ, Huang JC, Janbon G, Jones SJ, Koo HL, Krzywinski MI, Kwon-Chung JK, Lengeler KB, Maiti R, Marra MA, Marra RE, Mathewson CA, Mitchell TG, Pertea M, Riggs FR, Salzberg SL, Schein JE, Shvartsbeyn A, Shin H, Shumway M, Specht CA, Suh BB, Tenney A, Utterback TR, Wickes BL, Wortman JR, Wye NH, Kronstad JW, Lodge JK, Heitman J, Davis RW, Fraser CM, Hyman RW The genome of the basidiomycetous yeast and human pathogen Cryptococcus neoformans. Science. 2005 Feb 25;307(5713):1321-4. | http://genome.jgi.doe.gov/Cryne\_JEC21\_1/Cryne\_JEC21\_1.download.html | 14 | 6475 | 6475 |
| *Wolfiporia cocos* | Floudas D, Binder M, Riley R, Barry K, Blanchette RA, Henrissat B, Martinez AT, Otillar R, Spatafora JW, Yadav JS, Aerts A, Benoit I, Boyd A, Carlson A, Copeland A, Coutinho PM, de Vries RP, Ferreira P, Findley K, Foster B, Gaskell J, Glotzer D, Gorecki P, Heitman J, Hesse C, Hori C, Igarashi K, Jurgens JA, Kallen N, Kersten P, Kohler A, Kues U, Kumar TK, Kuo A, LaButti K, Larrondo LF, Lindquist E, Ling A, Lombard V, Lucas S, Lundell T, Martin R, McLaughlin DJ, Morgenstern I, Morin E, Murat C, Nagy LG, Nolan M, Ohm RA, Patyshakuliyeva A, Rokas A, Ruiz-Duenas FJ, Sabat G, Salamov A, Samejima M, Schmutz J, Slot JC, St John F, Stenlid J, Sun H, Sun S, Syed K, Tsang A, Wiebenga A, Young D, Pisabarro A, Eastwood DC, Martin F, Cullen D, Grigoriev IV, Hibbett DS. The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. Science. 2012 Jun 29;336(6089):1715-9. | http://genome.jgi-psf.org/Wolco1/Wolco1.home.html | 348 | 12746 | 11568 |
| *Rhizoctonia solani* | Cubeta MA, Thomas E, Dean RA, Jabaji S, Neate SM, Tavantzis S, Toda T, Vilgalys R, Bharathan N, Fedorova-Abrams N, Pakala SB, Pakala SM, Zafar N, Joardar V, Losada L, Nierman WC. Draft Genome Sequence of the Plant-Pathogenic Soil Fungus Rhizoctonia solani Anastomosis Group 3 Strain Rhs1AP. Genome Announc. 2014 Oct 30;2(5). pii: e01072-14. | http://www.ebi.ac.uk/ena/data/view/GCA\_000524645.1 | 326 | 12737 | 9470 |
| *Serpula lacrymans* | Eastwood DC, Floudas D, Binder M, Majcherczyk A, Schneider P, Aerts A, Asiegbu FO, Baker SE, Barry K, Bendiksby M, Blumentritt M, Coutinho PM, Cullen D, de Vries RP, Gathman A, Goodell B, Henrissat B, Ihrmark K, Kauserud H, Kohler A, LaButti K, Lapidus A, Lavin JL, Lee YH, Lindquist E, Lilly W, Lucas S, Morin E, Murat C, Oguiza JA, Park J, Pisabarro AG, Riley R, Rosling A, Salamov A, Schmidt O, Schmutz J, Skrede I, Stenlid J, Wiebenga A, Xie X, Kues U, Hibbett DS, Hoffmeister D, Hogberg N, Martin F, Grigoriev IV, Watkinson SC. The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. Science. 2011 Aug 5;333(6043):762-5. | http://genome.jgi-psf.org/SerlaS7\_9\_2/SerlaS7\_9\_2.home.html | 36 | 12789 | 10740 - 11618 ATG no STOP |
| *Moniliophthora roreri* | Meinhardt LW, Costa GG, Thomazella DP, Teixeira PJ, Carazzolle MF, Schuster SC, Carlson JE, Guiltinan MJ, Mieczkowski P, Farmer A, Ramaraj T, Crozier J, Davis RE, Shao J, Melnick RL, Pereira GA, Bailey BA. Genome and secretome analysis of the hemibiotrophic fungal pathogen, Moniliophthora roreri, which causes frosty pod rot disease of cacao: mechanisms of the biotrophic and necrotrophic phases. BMC Genomics. 2014 Feb 27;15:164. | http://0-www.ncbi.nlm.nih.gov.elis.tmu.edu.tw/Traces/wgs/?val=AWSO01 | 3280 | 17910 | 16792 |
| *Laccaria bicolor* | Martin F, Aerts A, Ahrén D, Brun A, Danchin EG, Duchaussoy F, Gibon J, Kohler A, Lindquist E, Pereda V, Salamov A, Shapiro HJ, Wuyts J, Blaudez D, Buée M, Brokstein P, Canbäck B, Cohen D, Courty PE, Coutinho PM, Delaruelle C, Detter JC, Deveau A, DiFazio S, Duplessis S, Fraissinet-Tachet L, Lucic E, Frey-Klett P, Fourrey C, Feussner I, Gay G, Grimwood J, Hoegger PJ, Jain P, Kilaru S, Labbé J, Lin YC, Legué V, Le Tacon F, Marmeisse R, Melayah D, Montanini B, Muratet M, Nehls U, Niculita-Hirzel H, Oudot-Le Secq MP, Peter M, Quesneville H, Rajashekar B, Reich M, Rouhier N, Schmutz J, Yin T, Chalot M, Henrissat B, Kües U, Lucas S, Van de Peer Y, Podila GK, Polle A, Pukkila PJ, Richardson PM, Rouzé P, Sanders IR, Stajich JE, Tunlid A, Tuskan G, Grigoriev IV. The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature. 2008 Mar 6;452(7183):88-92. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Lacbi2 | 55 | 23130 | 20235 |
| *Agaricus bisporus* | Morin E, Kohler A, Baker AR, Foulongne-Oriol M, Lombard V, Nagy LG, Ohm RA, Patyshakuliyeva A, Brun A, Aerts AL, Bailey AM, Billette C, Coutinho PM, Deakin G, Doddapaneni H, Floudas D, Grimwood J, Hilden K, Kues U, Labutti KM, Lapidus A, Lindquist EA, Lucas SM, Murat C, Riley RW, Salamov AA, Schmutz J, Subramanian V, Wosten HA, Xu J, Eastwood DC, Foster GD, Sonnenberg AS, Cullen D, de Vries RP, Lundell T, Hibbett DS, Henrissat B, Burton KS, Kerrigan RW, Challen MP, Grigoriev IV, Martin F Genome sequence of the button mushroom Agaricus bisporus reveals mechanisms governing adaptation to a humic-rich ecological niche. Proc Natl Acad Sci U S A. 2012 Oct 23;109(43):17501-6. | http://genome.jgi.doe.gov/Agabi\_varbisH97\_2/Agabi\_varbisH97\_2.download.html | 29 | 10438 | 9411 |
| *Taphrina deformans* | Cissé OH, Almeida JM, Fonseca A, Kumar AA, Salojärvi J, Overmyer K, Hauser PM, Pagni M. Genome sequencing of the plant pathogen Taphrina deformans, the causal agent of peach leaf curl. MBio. 2013 Apr 30;4(3):e00055-13. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Tapde1\_1 | 394 | 4609 | 4528 |
| *Tuber melanosporum* | Martin F, Aerts A, Ahrén D, Brun A, Danchin EG, Duchaussoy F, Gibon J, Kohler A, Lindquist E, Pereda V, Salamov A, Shapiro HJ, Wuyts J, Blaudez D, Buée M, Brokstein P, Canbäck B, Cohen D, Courty PE, Coutinho PM, Delaruelle C, Detter JC, Deveau A, DiFazio S, Duplessis S, Fraissinet-Tachet L, Lucic E, Frey-Klett P, Fourrey C, Feussner I, Gay G, Grimwood J, Hoegger PJ, Jain P, Kilaru S, Labbé J, Lin YC, Legué V, Le Tacon F, Marmeisse R, Melayah D, Montanini B, Muratet M, Nehls U, Niculita-Hirzel H, Oudot-Le Secq MP, Peter M, Quesneville H, Rajashekar B, Reich M, Rouhier N, Schmutz J, Yin T, Chalot M, Henrissat B, Kües U, Lucas S, Van de Peer Y, Podila GK, Polle A, Pukkila PJ, Richardson PM, Rouzé P, Sanders IR, Stajich JE, Tunlid A, Tuskan G, Grigoriev IV. The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature. 2008 Mar 6;452(7183):88-92. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Tubme1 | 7 | 7496 | 7468 |
| *Penicillium digitatum* | Marcet-Houben M, Ballester AR, de la Fuente B, Harries E, Marcos JF, González-Candelas L, Gabaldón T. Genome sequence of the necrotrophic fungus Penicillium digitatum, the main postharvest pathogen of citrus. BMC Genomics. 2012 Nov 21;13:646. | http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Pendi1 | 100 | 9118 | 9118 |
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| *Colletotrichum graminicola* | Colletotrichum Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/) | http://www.broadinstitute.org/annotation/genome/colletotrichum\_group/MultiHome.html | 654 | 12006 | 11849 |
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