Table S1. Assembly statistics and gene content for the Dothideomycete genome sequences generated or downloaded in this study

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Source | Genome assembly accession | Genome coverage | Total size (Mpb) | # of scaffolds | N50 (Mb) | BUSCO coverage | # of predicted gene models |
| Capnodiales |  |  |  |  |  |  |  |  |
|  | *Dothistroma pini*  | TAIGA | GCA\_002116355.1 | 1264.0x | 30.0 | 642 | 0.13 | 1436 (99.9%) | 12,610 |
|  | *Lecanostica acicula* [=*M. dearnessii*] | TAIGA | GCA\_000504345.1 | 295.0x | 34.8 | 2052 | 0.18 | 1436 (99.9%) | 13,049 |
|  | *Pseudocercospora pini-densiflorae* [=*M. gibsonii*] | TAIGA | GCA\_000504365.1 | 304.0x | 45.2 | 5537 | 0.08 | 1434 (99.7%) | 16,709 |
|  | *Mycosphaerella laricina* | TAIGA | GCA\_000504385.1 | 527.0x | 26.6 | 642 | 0.14 | 1435 (99.8%) | 10,387 |
|  | *Ramularia endophylla* [=*M. punctiformis*] | TAIGA | GCA\_002116395.1 | 926.0x | 41.3 | 3592 | 0.06 | 1432 (99.6%) | 13,120 |
|  | *Mycosphaerella* sp. STON1 | TAIGA | GCA\_000504405.1 | 491.0x | 27.5 | 1929 | 0.07 | 1428 (99.3%) | 9709 |
|  | *Passalora fulva* [=*Cladosporium fulvum*] | DOE-JGI | GCA\_000301015.1  | 21.0x | 61.1 | 4864 | 0.06 | 1417 (98.5%) | 14,127 |
|  | *D. septosporum* [=*M. pini*] | DOE-JGI | GCA\_000340195.1 | 34.28x | 30.2 | 20 | 2.6 | 1435 (99.8%) | 12,580 |
|  | *Zymoseptoria tritici* [=*M. graminicola*] | DOE-JGI | GCA\_000219625.1  | 8.9x | 39.7 | 21 | 2.7 | 1434 (99.7%) | 10,952 |
|  | *Paracercospora fijiensis* [=*M. fijiensis*] | DOE-JGI | GCA\_000340215.1 | 7.11x | 74.1 | 56 | 5.9 | 1433 (99.7%) | 13,107 |
|  | *Sphaerulina populicola* [= *M. populicola*] | DOE-JGI | GCA\_000291705.1 | 18x | 33.2 | 502 | 0.25 | 1430 (99.4%) | 9739 |
|  | *Sphaerulina musiva* [=*M. populorum*] | DOE-JGI | GCA\_000320565.2  | 35x | 29.3 | 72 | 2.04 | 1429 (99.4%) | 10,233 |
|  | *Baudoinia compniacensis* | DOE-JGI | NA | 43.5x | 21.8 | 19 | 1.3 | 1434 (99.7%) | 10,513 |
|  | *Cercospora zeae-maydis* | DOE-JGI | NA | 39.3x | 46.6 | 917 | 0.72 | 1436 (99.9%) | 12,020 |
| Dothideales |  |  |  |  |  |  |
|  | *Phaeocryptopus gaeumannii* [*=Adelopus gaeumannii*] | TAIGA | GCA\_002116385.1 | 1016.0x | 34.0 | 737 | 0.14 | 1433 (99.7%) | 14,295 |
| Pleosporales |  |  |  |  |  |  |  |  |
|  | *Didymella zeae-maydis* | DOE-JGI | NA | 1x | 32.6 | 2072 | 0.07 | 1438 (100%) | 10,299 |

Table S2. Assembly statistics and gene content for the rust genome sequences generated or downloaded in this study

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Source | Genome assembly accession | Genome coverage | Total size (Mpb) | # of scaffolds | N50 | BUSCO coverage | # of predicted gene models |
| Uredinales |  |  |  |
|  | Melampsoraceae |  |  |  |
|  |  | *Melampsora alli-populina* | TAIGA |  |  |  |  |  |  | 11,682 |
|  |  | *M. larici-populina* | DOE-JGI | GCA\_000204055.1 | 8.4x | 101.1 | 462 | 1.1 | 682 (47.4%) | 16,399 |
|  |  | *M. medusae* f. sp *deltoides* | TAIGA |  |  | 92.3 |  | 0.006 | 569 (39.6%) | 25,813 |
|  |  | *M. occidentalis* | TAIGA |  |  | 109.8 |  | 0.004 | 628 (43.7%) | 21,406 |
|  |  | *M. abietis-canadensis* | TAIGA |  |  | 83.6 |  | 0.022 | 662 (46.0%) | 17,309 |
|  |  | *M. aecidioides* | TAIGA |  |  | 87.4 |  | 0.001 | 331 (23.0%) | 22,170 |
|  |  | *M. pinitorqua* | TAIGA | GCA\_000464645.1 | 959.0x | 34.0 | 12,325 | 0.005 | 287 (20.0%) | 4879 |
|  | Cronartiaceae |  |  |  |
|  |  | *Cronartium ribicola* | TAIGA | GCA\_000500245.1 | 629.0x | 94.3 | 41,096 | 0.004 | 941 (65.4%) | 12,010 |
|  |  | *C. quercum* f. sp. *fusiforme* | DOE-JGI | NA | 70.4x | 76.6 | 1,198 | 0.31 | 929 (64.6%) | 13,903 |
|  |  | *Endocronartium harknesii* | TAIGA | GCA\_000500795.1 | 671.0x | 56.9 | 25,178 | 0.003 |  | 4180 |
|  |  | *C. comandrae* | TAIGA | GCA\_000464975.1 | 549x | 68.6 | 35,717 | 0.002 | 289 (20.1%) | 3026 |
| Pucciniales |  |  |  |
|  | Pucciniaceae |  |  |  |
|  |  | *Puccinia graminis* f. sp. *tritici* | Broad | GCA\_000149925.1 | NA | 88.7 | 393 | 0.96 | 1060 (73.7%) | 20,534 |
|  |  | *P. triticina* | Broad | GCA\_000151525.2 | 31.0x | 135.3 | 14,818 | 0.54 | 1141 (79.3%) | 15,685 |
|  |  | *P. striiformis* | Broad | GCA\_001191645.1 | 81.0x | 117.4 | 9716 | 0.52 | 744 (51.7%) | 20,482 |
| Mixiales |  |  |  |
|  | Mixiaceae |  |  |  |
|  |  | *Mixia osmundae* | DOE-JGI | GCA\_000708205.1 | 150.9x | 13.6 | 156 | 1.2 | 1340 (93.2%) | 6903 |
| Sporidiobolales |  |  |  |
|  | Incertae sedis |  |  |  |
|  |  | *Sporobolomyces roseus* | DOE-JGI | NA |  |  |  |  | 1280 (89.0%) | 5536 |
| Sporidiales |  |  |  |
|  | Incertae sedis  |  |  |  |
|  |  | *Rhodotorula graminis* | DOE-JGI | GCA\_001329695.1 | 8.55x | 21.0 | 26 | 1.42 | 1336 (92.9%) | 7283 |

Table S3. Assembly statistics and gene content for the *Phytophthora* genome sequences generated or downloaded in this study

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Source | Genome assembly accession | Genome coverage | Total size (Mpb) | # of scaffolds | N50 | BUSCO coverage | # of predicted gene models |
| Clade 1 |  |  |  |  |  |  |  |  |
|  | *P. infestans* | Broad Institute | GCA\_000142945.1 | NA | 228.5 | 4921 | 1.5 | 348 (81.1%) | 18,140 |
| Clade 2 |  |  |  |  |  |  |  |  |
|  | *P. capsici* | DOE-JGI | GCA\_000325885.1 | 35.0x | 56.0 | 10,750 | 0.70 | 351 (81.8%) | 19,805 |
| Clade 7 |  |  |  |  |  |  |  |  |
|  | *P. sojae* | DOE-JGI | GCA\_000149755.2 | 8x | 82.6 | 82 | 7.6 | 353 (82.3%) | 26,584 |
|  | *P. cinnamomi* var*. cinnamomi* | DOE-JGI | NA | 69.6x | 78.0 | 1314 | 0.26 | 349 (81.4%) | 26,131 |
| Clade 8 |  |  |  |  |  |  |  |  |
|  | *P. ramorum* | DOE-JGI | GCA\_000149735.1  | NA | 66.7 | 2576 | 0.3 | 350 (81.6%) | 15,743 |
|  | *P. lateralis* | TAIGA | GCA\_000500205.2 | 470.0x | 52.4 | 9039 | 0.023 | 353 (82.3%) | 17,533 |
|  | *P. hibernalis* | Tyler’s lab | NA | NA | 71.2 | 6587 | 0.022 | 344 (80.2%) | 20,209 |
|  | *P. foliorum* | Tyler’s lab | NA | NA | 49.0 | 5320 | 0.016 | 339 (79.0%) | 15,849 |
|  | *P. syringae* | Tyler’s lab | NA | NA | 57.0 | 6572 | 0.016 | 352 (82.1%) | 18,201 |
|  | *P. brassicae* | Tyler’s lab | NA | NA | 72.8 | 12,447 | 0.012 | 350 (81.6%) | 22,241 |
|  | *P. cryptogea* | TAIGA | GCA\_000468175.1 | 345.0x | 103.0 | 20,849 | 0.012 | 347 (80.9%) | 30,812 |
| Clade 10 |  |  |  |  |  |  |  |  |
|  | *P. kernoviae* | TAIGA | GCA\_000448265.2 | 474.0X | 39.4 | 5,026 | 0.064 | 344 (80.2%) | 10,012 |