**Supporting tables S1 to S5**

**Table S1. Statistics of contig-level assembly length, accuracy, and heterozygosity of *Gastrodia elata* genome**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Canu** | | |  | **GCpp (3r)** | | |  | **Pilon (3r)** | | |
| **Size** | **Count** | **Base** |  | **Size** | **Count** | **Base** |  | **Size** | **Count** | **Base** |
| **Contig lengths** |  |  |  |  |  |  |  |  |  |  |  |
| N10 | 53669662 | 2 | 120781624 |  | 53671888 | 2 | 120786694 |  | 53671121 | 2 | 120782939 |
| N20 | 35886880 | 5 | 237615054 |  | 35888498 | 5 | 237625100 |  | 35887815 | 5 | 237618787 |
| N30 | 27898790 | 8 | 329530099 |  | 27900270 | 8 | 329544496 |  | 27899702 | 8 | 329533426 |
| N40 | 23805623 | 12 | 428632885 |  | 23806778 | 12 | 428651494 |  | 23806665 | 12 | 428639761 |
| N50 | 21331786 | 17 | 541232049 |  | 21332373 | 17 | 541255473 |  | 21332058 | 17 | 541242390 |
| N60 | 18688958 | 22 | 640229019 |  | 18689754 | 22 | 640256862 |  | 18689676 | 22 | 640242649 |
| N70 | 15381652 | 28 | 740403848 |  | 15382202 | 28 | 740435895 |  | 15382121 | 28 | 740419990 |
| N80 | 12606561 | 35 | 836068462 |  | 12607237 | 35 | 836105423 |  | 12606738 | 35 | 836086766 |
| N90 | 7891549 | 46 | 944861069 |  | 7891908 | 46 | 944903503 |  | 7891847 | 46 | 944881838 |
| N100 | 1008 | 457 | 1042817824 |  | 1010 | 457 | 1042883617 |  | 1010 | 457 | 1042834688 |
| **Contig accuracy and heterozygosity** |  |  |  |  |  |  |  |  |  |  |  |
| NGS reads mapping ratio | 95.69% | | |  | 97.75% | | |  | 97.89% | | |
| Heterozygosity | 29941 bp | | |  | 37119 bp | | |  | 40451 bp | | |
|  | 0.002871163 | | |  | 0.003559266 | | |  | 0.003878947 | | |
| Homozygosity (error) | 31718 bp | | |  | 10051 bp | | |  | 9845 bp | | |
|  | 0.003041567 | | |  | 0.00096377 | | |  | 0.000944061 | | |
| Total Length | 1042817824 bp | | |  | 1042883617 bp | | |  | 1042834688 bp | | |

**Table S2. Transcriptome data for assessment of genome assembly completeness and gene annotation**

|  |  |  |  |
| --- | --- | --- | --- |
| **SRA Accession\*** | **Total Reads** | **Total Bases** | **Mapping Ratio** |
| SRR5643663 | 30,480,297 | 9.1G | 93.70% |
| SRR5643664 | 26,069,882 | 7.8G | 93.30% |
| SRR5643662 | 22,587,832 | 6.8G | 93.80% |
| SRR5643661 | 22,120,928 | 6.6G | 92.90% |
| SRR5643660 | 22,013,452 | 6.6G | 93.10% |
| SRR5643659 | 24,535,796 | 7.4G | 93.10% |
| SRR5643658 | 28,495,316 | 8.5G | 94.80% |
| SRR5643528 | 23,068,008 | 6.9G | 94.70% |
| SRR5643525 | 22,574,459 | 6.8G | 94.60% |
| SRR5643524 | 25,124,081 | 7.5G | 90.00% |
| SRR5643515 | 22,263,732 | 6.7G | 92.60% |
| SRR5643514 | 25,368,440 | 7.6G | 92.80% |
| SRR5643513 | 20,368,701 | 6.1G | 91.70% |

\*: from Yuan et al. (2018)

**Table S3. Protein-coding genes, RNA genes, and repetitive elements in *Gastrodia elata* genome**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | | **Number of Feature** | | **Sum of Length (bp)** | | **Average of Length (bp)** | | **Percentage** | |
| Class I (retrotransposons) | | | |  | |  | |  | |  | |
|  | LTR |  | |  | |  | |  | |  | |
|  |  | Copia | | 19162 | | 9006933 | | 470.041384 | | 0.87% | |
|  |  | Gypsy | | 369668 | | 384752302 | | 1040.805 | | 37.11% | |
|  |  | unknown | | 200571 | | 124502306 | | 620.739319 | | 12.01% | |
|  |  |  | |  | |  | |  | |  | |
| Class II (DNA transposons) | | | |  | |  | |  | |  | |
|  | TIR | |  | |  | |  | |  | |  | |
|  |  | | CACTA | | 88491 | | 30689678 | | 346.811292 | | 2.96% | |
|  |  | | Mutator | | 104321 | | 41360041 | | 396.468985 | | 3.99% | |
|  |  | | PIF\_Harbinger | | 31505 | | 9396595 | | 298.257261 | | 0.91% | |
|  |  | | Tc1\_Mariner | | 13935 | | 3831192 | | 274.933046 | | 0.37% | |
|  |  | | hAT | | 17354 | | 5239894 | | 301.94157 | | 0.51% | |
|  | nonTIR | |  | |  | |  | |  | |  | |
|  |  | | helitron | | 101792 | | 36678925 | | 360.332099 | | 3.54% | |
|  |  | |  | |  | |  | |  | |  | |
| MITE |  | |  | | 44257 | | 14488728 | | 327.377093 | | 1.40% | |
| Centromere | | |  | | 154 | | 5594876 | | 36330.3636 | | 0.54% | |
| Simple repeat | | |  | | - | | 19089724 | | - | | 1.84% | |
|  |  | |  | |  | |  | |  | |  | |
| RNA |  | |  | |  | |  | |  | |  | |
|  | 5S rRNA | |  | | 1998 | | 231561 | | 115.896396 | | 0.02% | |
|  | 45S rRNA | |  | | 698 | | 392872 | | 562.853868 | | 0.04% | |
|  | snoRNA | |  | | 25329 | | 2697099 | | 106.482648 | | 0.26% | |
|  | tRNA | |  | | 757 | | 54491 | | 71.9828269 | | 0.01% | |
|  |  | |  | |  | |  | |  | |  | |
| Protein Gene | | |  | |  | |  | |  | |  | |
|  | Gene | |  | | 21115 | | 303543638 | | 14375.7347 | | 29.28% | |
|  | CDS of gene | | | 21115 | | 23355971 | | 1106.13171 | | 2.25% | |
|  | Pseudogene | | | 3664 | | 22937535 | | 6260.24427 | | 2.21% | |
|  | CDS of Pseudogene | | | 3664 | | 2772686 | | 756.737445 | | 0.27% | |

**Table S4. Results of BUSCO analysis for the genome and protein-coding gene set of *Gastrodia elata* from this work and Yuan et al.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Complete BUSCOs** | **Complete and single-copy BUSCOs** | **Complete and duplicated BUSCOs** | **Fragmented BUSCOs** | **Missing BUSCOs** | **Total BUSCO groups searched** |
| Genome assembly from this work (genome model) | 70.80% | 70.10% | 0.70% | 3.70% | 25.50% | 1614 |
| Protein-coding gene set from this work (protein model) | 76.40% | 75.00% | 1.40% | 2.00% | 21.60% | 1614 |
| Protein-coding gene set from Yuan et al. (protein model) | 74.00% | 72.50% | 1.50% | 3.40% | 22.60% | 1614 |

**Table S5. Plant genomes for comparative genomics analysis**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Species Name** | **Abbreviation** | **Taxon**  **ID** | **Order Name** | **Lifestyle** | **Number of Gene Models** | **Reference** |
| *Amborella trichopoda* | Atr | 13333 | Amborellales | autotrophic | 26846 | Ref. (2013) |
| *Nymphaea colorata* | Nco | 210225 | Nymphaeales | autotrophic | 31475 | Ref. (Zhang et al., 2020) |
| *Piper nigrum* | Pni | 13216 | Piperales | autotrophic | 62382 | (Hu et al., 2019) |
| *Liriodendron chinense* | Lch | 3414 | Magnoliales | autotrophic | 35269 | (Chen et al., 2019) |
| *Cinnamomum kanehirae* | Cka | 337451 | Laurales | autotrophic | 27899 | Ref. (Chaw et al., 2019) |
| *Dioscorea alata* | Dal | 55571 | Dioscoreales | autotrophic | 25189 | Ref. (Bredeson et al., 2021) |
| *Xerophyta viscosa* | Xvi | 90708 | Pandanales | autotrophic | 25425 | Ref. (Costa et al., 2017) |
| *Asparagus officinalis* | Aof | 4686 | Asparagales | autotrophic | 27395 | Ref. (Harkess et al., 2017) |
| *Apostasia shenzhenica* | Ash | 1088818 | Asparagales | mycoheterotrophic | 21743 | Ref. (Zhang et al., 2017) |
| *Vanilla planifolia* | Vpl | 51239 | Asparagales | mycoheterotrophic | 29044 | Ref. (Hasing et al., 2020) |
| *Dendrobium catenatum* | Dca | 906689 | Asparagales | mycoheterotrophic | 21196 | Ref. (Zhang et al., 2016) |
| *Phalaenopsis equestris* | Peq | 78828 | Asparagales | mycoheterotrophic | 18718 | Ref. (Cai et al., 2015) |
| *Gastrodia elata* | Gel | 91201 | Asparagales | mycoheterotrophic | 21115 | This Work |
| *Calamus simplicifolius* | Csi | 746888 | Arecales | autotrophic | 51235 | Ref. (Zhao et al., 2018) |
| *Cocos nucifera* | Cnu | 13894 | Arecales | autotrophic | 28039 | Ref. (Lantican et al., 2019) |
| *Ananas comosus* | Acom | 4615 | Poales | autotrophic | 27024 | Ref. (Ming et al., 2015) |
| *Brachypodium distachyon* | Bdi | 15368 | Poales | autotrophic | 32439 | Ref. (International Brachypodium, 2010) |
| *Oropetium thomaeum* | Oth | 1148796 | Poales | autotrophic | 28315 | Ref. (VanBuren et al., 2015) |
| *Oryza sativa* | Osa | 4530 | Poales | autotrophic | 42182 | Ref. (Goff et al., 2002) |
| *Zea mays* | Zma | 4577 | Poales | autotrophic | 39498 | Ref. (Jiao et al., 2017) |
| *Ensete ventricosum* | Eve | 4639 | Zingiberales | autotrophic | 58438 | Ref. (Harrison et al., 2014) |
| *Musa acuminata* | Mac | 4641 | Zingiberales | autotrophic | 36518 | Ref. (D'Hont et al., 2012) |
| *Aquilegia coerulea* | Aco | 218851 | Ranunculales | autotrophic | 30023 | Ref. (Filiault et al., 2018) |
| *Nelumbo nucifera* | Nnu | 4432 | Proteales | autotrophic | 22785 | Ref. (Ming et al., 2013) |
| *Kalanchoe fedtschenkoi* | Kfe | 63787 | Saxifragales | autotrophic | 30964 | Ref. (Yang et al., 2017) |
| *Vitis vinifera* | Vvi | 29760 | Vitales | autotrophic | 31845 | Ref. (Jaillon et al., 2007) |
| *Populus trichocarpa* | Ptr | 3694 | Malpighiales | autotrophic | 34699 | Ref. (Tuskan et al., 2006) |
| *Manihot esculenta* | Mes | 3983 | Malpighiales | autotrophic | 33849 | Ref. (Wang et al., 2014b) |
| *Sapria himalayana* | Shi | 289637 | Malpighiales | parasitic | 55162 | Ref. (Cai et al., 2021) |
| *Glycine max* | Gma | 3847 | Fabales | autotrophic | 56044 | Ref. (Schmutz et al., 2010) |
| *Fragaria vesca* | Fve | 57918 | Rosales | autotrophic | 33537 | Ref. (Shulaev et al., 2011) |
| *Cucumis sativus* | Csa | 3659 | Cucurbitales | autotrophic | 20563 | Ref. (Huang et al., 2009) |
| *Arabidopsis thaliana* | Ath | 3702 | Brassicales | autotrophic | 27620 | Ref. (Cheng et al., 2016) |
| *Gossypium raimondii* | Gra | 29730 | Malvales | autotrophic | 37505 | Ref. (Paterson et al., 2012) |
| *Coffea canephora* | Cca | 49390 | Gentianales | autotrophic | 25574 | Ref. (Denoeud et al., 2014) |
| *Mimulus guttatus* | Mgu | 4155 | Lamiales | autotrophic | 28140 | Ref. (Hellsten et al., 2013) |
| *Striga asiatica* | Sas | 4170 | Lamiales | parasitic | 33426 | Ref. (Yoshida et al., 2019) |
| *Olea europaea* | Oeu | 4146 | Lamiales | autotrophic | 50684 | Ref. (Unver et al., 2017) |
| *Sesamum indicum* | Sin | 4182 | Lamiales | autotrophic | 22704 | Ref. (Wang et al., 2014a) |
| *Capsicum annuum* | Can | 4072 | Solanales | autotrophic | 29103 | Ref. (Kim et al., 2014) |
| *Cuscuta australis* | Cau | 267555 | Solanales | parasitic | 19658 | Ref. (Sun et al., 2018) |
| *Ipomoea nil* | Ini | 35883 | Solanales | autotrophic | 41993 | Ref. (Hoshino et al., 2016) |
| *Solanum lycopersicum* | Sly | 4081 | Solanales | autotrophic | 33741 | Ref. (Tomato Genome, 2012) |
| *Solanum tuberosum* | Stu | 4113 | Solanales | autotrophic | 39028 | Ref. (Sharma et al., 2013) |

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