

**Supplemental Figure S1.** The number of DEGs in drought-tolerant and drought-sensitive mycorrhizal seedlings under drought (field capacity 30%-35%) and well-watered (field capacity 85%-90%) treatments. S, shoot; R, root.

**Supplemental Table S1.** Geographic information of different ecotypes of *Cenococcum geophilum*.

|  |  |
| --- | --- |
| Isolate | Isolate location |
| Jacg16 | Miyasaki, Japan |
| Jacg21 | Miyasaki, Japan |
| Jacg37 | Numazu Senbonhama, Japan |
| Jacg81 | Nagano, Japan |
| Jacg121 | Tokyo, Japan |
| Jacg189 | Tokyo, Japan |
| Jacg243 | The Ryukyus University, Japan |
| Chcg57 | Qinghai Province, China |

**Supplemental Table S2.** Correlation coefficient matrix of single index of different ecotypes mycorrhizal seedlings after 7 days of drought stress (field capacity 30%-35%).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Index | SWR | RWC | Pn | Gs | Ci | Tr | CAT(S) | CAT(R) | POD(S) | POD(R) | SOD(S) | SOD(R) | MDA(S) | MDA(R) | PRO(S) | PRO(R) | SP(S) | SP(R) |
| SWR | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| RWC | 0.963\*\* | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Pn | 0.672\* | 0.611 | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gs | 0.801\*\* | 0.787\* | 0.717\* | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ci | 0.670\* | 0.672\* | 0.121 | 0.697\* | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Tr | 0.582 | 0.576 | 0.670\* | 0.929\*\* | 0.500 | 1.000 |  |  |  |  |  |  |  |  |  |  |  |  |
| CAT(S) | -0.666 | -0.567 | -0.757\* | -0.457 | 0.008 | -0.353 | 1.000 |  |  |  |  |  |  |  |  |  |  |  |
| CAT(R) | -0.693\* | -0.585 | -0.735\* | -0.360 | 0.038 | -0.236 | 0.919\*\* | 1.000 |  |  |  |  |  |  |  |  |  |  |
| POD(S) | 0.624 | 0.618 | 0.307 | 0.724\* | 0.586 | 0.711\* | -0.396 | -0.307 | 1.000 |  |  |  |  |  |  |  |  |  |
| POD(R) | 0.572 | 0.559 | 0.443 | 0.740\* | 0.468 | 0.800\*\* | -0.395 | -0.333 | 0.943\*\* | 1.000 |  |  |  |  |  |  |  |  |
| SOD(S) | 0.666 | 0.636 | 0.650 | 0.873\*\* | 0.451 | 0.903\*\* | -0.479 | -0.446 | 0.836\*\* | 0.865\*\* | 1.000 |  |  |  |  |  |  |  |
| SOD(R) | 0.869\*\* | 0.822\*\* | 0.902\*\* | 0.842\*\* | 0.361 | 0.741\* | -0.823\*\* | -0.77\* | 0.563 | 0.584 | 0.785\* | 1.000 |  |  |  |  |  |  |
| MDA(S) | -0.761\* | -0.707\* | -0.415 | -0.544 | -0.490 | -0.478 | 0.471 | 0.540 | -0.520 | -0.56 | -0.481 | -0.607 | 1.000 |  |  |  |  |  |
| MDA(R) | -0.892\*\* | -0.837\*\* | -0.743\* | -0.819\*\* | -0.486 | -0.729\* | 0.725\* | 0.685\* | -0.596 | -0.596 | -0.741\* | -0.93\*\* | 0.819\*\* | 1.000 |  |  |  |  |
| Pro(S) | 0.779\* | 0.780\* | 0.747\* | 0.953\*\* | 0.557 | 0.894\*\* | -0.503 | -0.438 | 0.661 | 0.655 | 0.902\*\* | 0.888\*\* | -0.480 | -0.84\*\* | 1.000 |  |  |  |
| Pro(R) | 0.702\* | 0.726\* | 0.661 | 0.927\*\* | 0.555 | 0.882\*\* | -0.411 | -0.343 | 0.710\* | 0.687\* | 0.921\*\* | 0.809\*\* | -0.355 | -0.73\* | 0.979\*\* | 1.000 |  |  |
| SP(S) | 0.611 | 0.600 | 0.648 | 0.864\*\* | 0.450 | 0.865\*\* | -0.367 | -0.345 | 0.660 | 0.661 | 0.940\*\* | 0.760\* | -0.306 | -0.678\* | 0.945\*\* | 0.970\*\* | 1.000 |  |
| SP(R) | 0.812\*\* | 0.842\*\* | 0.476 | 0.709\* | 0.500 | 0.601 | -0.545 | -0.578 | 0.809\*\* | 0.713\* | 0.819\*\* | 0.755\* | -0.580 | -0.754\* | 0.789\*\* | 0.803\*\* | 0.755\* | 1.000 |

Note: SWC and RWC, shoot and root water contents; Pn, net photosynthetic rate; Gs, stomatal conductance; Ci, intercellular CO2 concentration; Tr, transpiration rate; CAT, POD, and SOD, catalase, peroxidase, and superoxide dismutase activities; Pro, proline content; SP and SP, soluble protein contents; MDA, malondialdehyde (MDA) contents, S, shoot; R, root. \* and \*\* mean significant differences at the levels of *P* < 0.05 and *P* < 0.01, respectively.

**Supplemental Table S3.** The index coefficient and proportion of comprehensive coefficient *CI* (comprehensive index).

|  |  |  |  |
| --- | --- | --- | --- |
| Principle factors | *CI1* | *CI2* | *CI3* |
| Eigen values | 12.317 | 2.225 | 1.39 |
| Contributive ratio | 68.426 | 12.359 | 7.722 |
| Cumulative contributive ratio | 68.426 | 80.785 | 88.508 |
| Eigenevector |  |  |  |
| SWR | 0.073 | -0.092 | -0.239 |
| RWC | 0.071 | -0.051 | -0.247 |
| Pn | 0.062 | -0.179 | 0.272 |
| Gs | 0.076 | 0.102 | 0.041 |
| Ci | 0.047 | 0.213 | -0.384 |
| Tr | 0.069 | 0.148 | 0.18 |
| CAT(S) | -0.053 | 0.302 | -0.075 |
| CAT(R) | -0.05 | 0.334 | -0.013 |
| POD(S) | 0.064 | 0.151 | -0.119 |
| POD(R) | 0.064 | 0.131 | -0.027 |
| SOD(S) | 0.074 | 0.104 | 0.163 |
| SOD(R) | 0.076 | -0.135 | 0.095 |
| MDA(S) | -0.055 | 0.096 | 0.391 |
| MDA(R) | -0.074 | 0.106 | 0.092 |
| PRO(S) | 0.077 | 0.065 | 0.139 |
| PRO(R) | 0.073 | 0.125 | 0.175 |
| SP(S) | 0.069 | 0.127 | 0.257 |
| SP(R) | 0.071 | 0.013 | -0.107 |

Note: *CI*, comprehensive index; SWC and RWC, shoot and root water contents; Pn, net photosynthetic rate; Gs, stomatal conductance; Ci, intercellular CO2 concentration; Tr, transpiration rate; CAT, POD, and SOD, catalase, peroxidase, and superoxide dismutase activities; Pro, proline content; SP and SP, soluble protein contents; MDA, malondialdehyde (MDA) contents, S, shoot; R, root.

**Supplemental Table S4.** List of transcriptome data quality.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| SampleID | Clean Reads | Mapped Reads | Mapped Ratio | Base Number |
| S121-DS1 | 22,950,191 | 6,871,129,962 | 45.74% | 95.98% |
| S121-DS2 | 21,220,386 | 6,353,254,570 | 46.13% | 95.88% |
| S121-DS3 | 22,095,266 | 6,616,185,438 | 46.06% | 95.75% |
| S121-WW1 | 23,767,903 | 7,116,748,812 | 46.49% | 95.79% |
| S121-WW2 | 19,695,861 | 5,893,797,682 | 46.61% | 95.60% |
| S121-WW3 | 23,547,580 | 7,050,286,352 | 46.31% | 95.51% |
| S57-DS1 | 21,223,106 | 6,356,316,998 | 45.55% | 95.41% |
| S57-DS2 | 21,984,327 | 6,581,915,034 | 45.46% | 95.51% |
| S57-DS3 | 21,435,830 | 6,417,880,884 | 45.95% | 95.85% |
| S57-WW1 | 20,837,390 | 6,237,924,178 | 47.03% | 95.66% |
| S57-WW2 | 20,113,617 | 6,022,856,442 | 46.58% | 95.03% |
| S57-WW3 | 21,745,303 | 6,509,574,290 | 46.90% | 95.92% |
| R121-DS1 | 21,972,497 | 6,575,392,614 | 46.40% | 95.60% |
| R121-DS2 | 20,899,011 | 6,255,863,804 | 46.14% | 95.35% |
| R121-DS3 | 20,166,029 | 6,036,205,202 | 45.46% | 95.20% |
| R121-WW1 | 20,995,108 | 6,284,374,384 | 47.01% | 95.42% |
| R121-WW2 | 20,880,607 | 6,251,771,070 | 47.28% | 95.88% |
| R121-WW3 | 19,220,048 | 5,750,275,160 | 46.80% | 95.82% |
| R57-DS1 | 21,598,880 | 6,462,707,120 | 46.63% | 94.58% |
| R57-DS2 | 21,395,481 | 6,403,622,146 | 45.87% | 94.98% |
| R57-DS3 | 20,113,218 | 6,013,574,536 | 46.56% | 95.68% |
| R57-WW1 | 20,463,370 | 6,122,283,592 | 46.30% | 95.82% |
| R57-WW2 | 21,059,284 | 6,303,590,750 | 46.46% | 95.75% |
| R57-WW3 | 20,178,868 | 6,037,348,128 | 46.20% | 95.42% |

Note: S, Shoot; R, root; DS, drought stress; WW, well-watered;

**Supplemental Table S5.** Unigene length distribution statistics.

|  |  |  |
| --- | --- | --- |
| Length Range | Transcript | Unigene |
| 300-500 | 14,575(21.12%) | 10,201(31.85%) |
| 500-1000 | 7,271(10.53%) | 3,772(11.78%) |
| 1000-2000 | 10,186(14.76%) | 5,057(15.79%) |
| >2000 | 36,989(53.59%) | 13,002(40.59%) |
| Total Number | 69,021 | 32,032 |
| Total Length | 144,203,542 | 55,051,729 |
| N50 Length | 2,846 | 2,673 |
| Mean Length | 2089.27 | 1718.65 |

**Supplemental Table S6.** Sequences of primers used for RT-qPCR analysis.

|  |  |  |
| --- | --- | --- |
| Gene-ID | Primer orientation | Primer sequence |
| TRINITY\_DN14578\_c0\_g1 | Forward | TCTATCCCACGCCTCTTCCA |
| Reverse | AGCCCTCAACGACATCAAGG |
| TRINITY\_DN3930\_c0\_g1 | Forward | CACGGTCACGCATTGACATC |
| Reverse | GCCTTCGACCCAGCTCTATC |
| TRINITY\_DN6096\_c0\_g1 | Forward | ACGACTGGACAATACGCTCG |
| Reverse | CCGCAGCCAGGATACATAGG |
| TRINITY\_DN11509\_c1\_g1 | Forward | ACGGTGGCATGCACAGAATA |
| Reverse | TTCCAGTTGCCTCACTCGTC |
| TRINITY\_DN12846\_c0\_g3 | Forward | AGCTGATCCCGTTCCTTTGG |
| Reverse | GGAATGCCTCCACCAGACTC |
| TRINITY\_DN18667\_c0\_g1 | Forward | AACAACGTCAACCTGCCTGA |
| Reverse | GGTCGTTCAGTCTCTGGTGG |
| TRINITY\_DN20940\_c0\_g2 | Forward | AGGGACTCATGCAGACAATCT |
| Reverse | GCATAAGGTGCCTCTCCGAC |
| TRINITY\_DN40689\_c0\_g2 | Forward | GCGCGCTCACATTTCTTCTG |
| Reverse | TATTCACCAGCCCTCTGTGC |
| Aquaporin protein gene | Forward | CACCTTGCCACAATTCCTATCA |
| Reverse | TCCAATGGTCATCCCAAACAC |