S1 Table 2. First hits retrieved from the blastn according with ITS1, ITS2, D1-D2 and 18S rRNA sequence for each new fungal isolate.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **Mol. marker** | **Nucleotide blast (first hits)** | **e-value** | **id.** | **cov.** |
| **TS2** | ITS1 | *Cadaphora malorum* TS\_06\_017 | 1e-131 | 99% | 100% |
| ITS2 | *Cadaphora* sp. P1381 | 2e-139 | 100% | 100% |
| D1-D2 | Fungal endophyte voucher\* | 0.0 | 99% | 100% |
| 18S rRNA | Helotiales sp. MF580**** | 0.0 | 100% | 100% |
| **TS11** | ITS1 | *Emericellopsis pallida* DM12 | 3e-102 | 100% | 100% |
| ITS2 | *Acremonium zonatum* JCKQF3**✪** | 1e-146 | 100% | 100% |
| 18S rRNA | *Acremonium* sp. Y39-2**✪** | 0.0 | 100% | 100% |
| **TS12** | ITS1 | Fungal sp. MKOTU119**⌃** | 9e-113 | 100% | 100% |
| ITS2 | *Geomyces* sp. S7-Z-2-7 | 1e-137 | 99% | 100% |
| D1-D2 | *Geomyces pannorum* 38249-10 | 0.0 | 100% | 99% |
| 18S rRNA | Fungal sp. ZJ59**★** | 0.0 | 100% | 100% |

Mol. Marker, molecular markers; id., identity; cov., coverage.

\*The first ten hits retrieved from the blastn describe *Phialocephala* sp. and *Cadophora* sp. strains. In all cases, hits show: 99-100% of query cover, 0.0 of E value and 99% of identity.

****Helotiales is not a fungal genus. The second and third hits retrieved from the blastn belong to Cadophora fastigiata and Cadophora luteo-olivacea. The three hits show: 100% of query cover, 0.0 of E value and 100% of identity.

****D1-D2 ribosomal region did not amplify from genomic DNA isolated from TS11 strain.

**✪**The first ten hits retrieved from the blastn describe *Acremonium* sp. and *Emericellopsis* sp. strains. In all cases, hit show: 99-100% of query cover, e-145 or 0.0 of E value and 99-100% of identity.

**⌃**The first ten hits retrieved from the blastn describe *Pseudogymnoascus* sp. strains. In all cases, hit show: 100% of query cover, 9e-113 of E value and 100% of identity.

**★**The first ten hits retrieved from the blastn describe *Geomyces* sp. and *Pseudogymnoascus* sp. strains. In all cases, hit show: 100% of query cover, 0.0 of E value and 100% of identity.