

A) No. differences incl. gaps in ITS1 region

| | EU414755 | EU414757 | EU414758 | EU414759 | EU414756 |
|----------|----------|----------|----------|----------|----------|
| EU414755 | | 14 | 15 | 15 | 27 |
| EU414757 | 14 | | 1 | 1 | 20 |
| EU414758 | 15 | 1 | | 0 | 19 |
| EU414759 | 15 | 1 | 0 | | 19 |
| EU414756 | 27 | 20 | 19 | 19 | |

B) Percentage identity in ITS1 region

| | EU414755 | EU414757 | EU414758 | EU414759 | EU414756 |
|----------|----------|----------|----------|----------|----------|
| EU414755 | | 93.2% | 92.8% | 92.8% | 87.1% |
| EU414757 | 93.2% | | 99.5% | 99.5% | 90.2% |
| EU414758 | 92.8% | 99.5% | | 100% | 90.6% |
| EU414759 | 92.8% | 99.5% | 100% | | 90.6% |
| EU414756 | 87.1% | 90.2% | 90.6% | 90.6% | |

C) Percentage identity over whole sequence 171bp 18S, 198-207bp ITS1, 159bp 5.8S and 51-52bp ITS2

| | EU414755 | EU414757 | EU414758 | EU414759 | EU414756 |
|----------|----------|----------|----------|----------|----------|
| EU414755 | | 97.5% | 97.5% | 97.3% | 94.1% |
| EU414757 | 97.5% | | 99.7% | 99.5% | 95.4% |
| EU414758 | 97.5% | 99.7% | | 99.8% | 95.4% |
| EU414759 | 97.3% | 99.5% | 99.8% | | 95.2% |
| EU414756 | 94.1% | 95.4% | 95.4% | 95.2% | |

SuppFig. 3. Intragenomic variation in ITS sequences among the five clones sequenced from isolate GE09. 18S boundary ends with GATCATTA and 5.8S begins with CAACTTT, according to the convention of Hibbett et al. (1995).