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Fungal endophyte misidentified as Neurospora crassa.

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Abstract
The endophytic fungus isolate, ZP5SE, recently described in Rehman et al. 2008 was misidentified identified as Neurospora crassa. The 28S ribosomal gene sequence of the isolate shows 100% sequence similarity with GenBank accession Neurospora crassa M38154.

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Fungal endophyte misidentified as Neurospora crassa.

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The endophytic fungus isolate, ZP5SE, recently described in Rehman et al. 2008 was misidentified identified as Neurospora crassa. The 28S ribosomal gene sequence of the isolate shows 100% sequence similarity with GenBank accession Neurospora crassa M38154. However, there are three additional 28S ribosomal gene sequences deposited in GenBank as N. crassa U40124 (culture NRRL 13141), N. crassa AF286411 (culture MUCL 19026), and N. crassa AY681158.1 (culture ICMP 6360). Phylogenetic analyses shows that these three additional sequences are closest relatives (100% similarity) and that this group is more distantly related to the ZP5SE and N. crassa M38154 sequences (88%-91% similarity). In phylogenetic analysis, the ZP5SE sequence and M38154 form a sister group to many Sordariaceae, including species of Neurospora, Gelasinospora and Sordaria (Figure 1). As a result, ZP5SE cannot yet be assigned to a particular genus or species on the basis of the 28S ribosomal gene sequence. In addition, we infer that the GenBank sequence M38154 must be incorrectly attributed to N. crassa.

Figure 1. Phylogenetic analysis comparing the fungal endophyte (ZP5SE) with related fungi using partial SSU and LSU rDNA sequences from Figure 4 of Rehman et al. 2008. N. crassa AY681158 represents three GenBank sequences of N. crassa (AY681158, U40124 and AF286411), and is nestled with Gelasinospora species, as expected. N. crassa M38154 is quite distant from the three other N. crassa sequences and likely is misattributed to N. crassa.

References: