



34 0- or 1-septate, and 6.7-23.1  $\mu\text{m}$  in length ( $n>30$ ); macroconidia were straight to slightly curved, 3- or 5-  
 35 septate, and 30.8-53.9  $\mu\text{m}$  in length ( $n>30$ ). Genomic DNA, extracted from six isolates, was amplified  
 36 with three pairs of primers, ITS1 and ITS4 (White et al. 1990), EF1-728F and EF1-986R (Carbone and  
 37 Kohn 1999), and fRPB2-5F and fRPB2-7cR (Liu et al. 1999). The amplicons from all six isolates were  
 38 sequenced and identical sequences obtained. The sequence of one representative isolate was uploaded to  
 39 NCBI (National Center for Biotechnology Information) and analyzed with BLASTn in the Fusarium  
 40 MLST database (<https://fusarium.mycobank.org>). The sequence of the internal transcribed spacer 1  
 41 (ITS1) region (GenBank MN944550) showed 99.1% (449/453 bp) identity to *Fusarium solani* strain  
 42 NRRL 53667 (syn: *Neocosmospora solani*, GenBank MH582405). The sequence of the translation  
 43 elongation factor-1 (EF-1) gene (GenBank MN938933) showed 97.8% identity (263/269 bp) to *F.*  
 44 *solani* strain NRRL 32828 (GenBank DQ247135). The sequence of the second largest subunit of RNA  
 45 polymerase II (RPB2) gene (GenBank MW002686) showed 98.7% identity (810/821 bp) to *F.*  
 46 *solani* strain NRRL 43441 (GenBank MH582407). Based on a multilocus phylogenetic analysis of the  
 47 ITS1, EF-1 and RPB2 sequences, coupled with the morphological characteristics, the isolate (designated  
 48 as NsPed1) was considered to be *Neocosmospora solani* (syn: *Fusarium solani*) (Crespo et al. 2019).  
 49 Subsequently, three-month-old healthy seedlings and 45-day-old cuttings of *P. edulis* 'Mantianxing'  
 50 plants were inoculated with the isolate NsPed1 to test its pathogenicity. Stems were wounded,  
 51 approximately 1-2 mm deep, in the collar region of plants at 2 cm above the soil. A disk (9 mm in  
 52 diameter) of NsPed1-colonized PDA was placed on the wound. Sterile PDA served as controls. All plants  
 53 were kept in a growth chamber with 28-30°C, 60% relative humidity, and 16/8-h light/dark photoperiod.  
 54 Fifteen plants were used for each treatment and replicated three times. Two weeks after inoculation, the  
 55 stems of the inoculated plants turned brown with a lesion, 2-5 cm in length, and the leaves wilted. These  
 56 symptoms were similar to those of the diseased plants in the field. The control plants were asymptomatic.  
 57 *N. solani* NsPed1 was re-isolated from the infected plants, satisfying Koch's postulates. Taken together,  
 58 *N. solani* NsPed1 was identified as the causal pathogen of collar rot in *P. edulis* 'Mantianxing'.  
 59 Knowledge of the causal organism of collar rot in purple passion fruit will lead to improved measures to  
 60 prevent and control the disease in China and other countries.

## 61 **Acknowledgements**

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## 63 **Reference:**

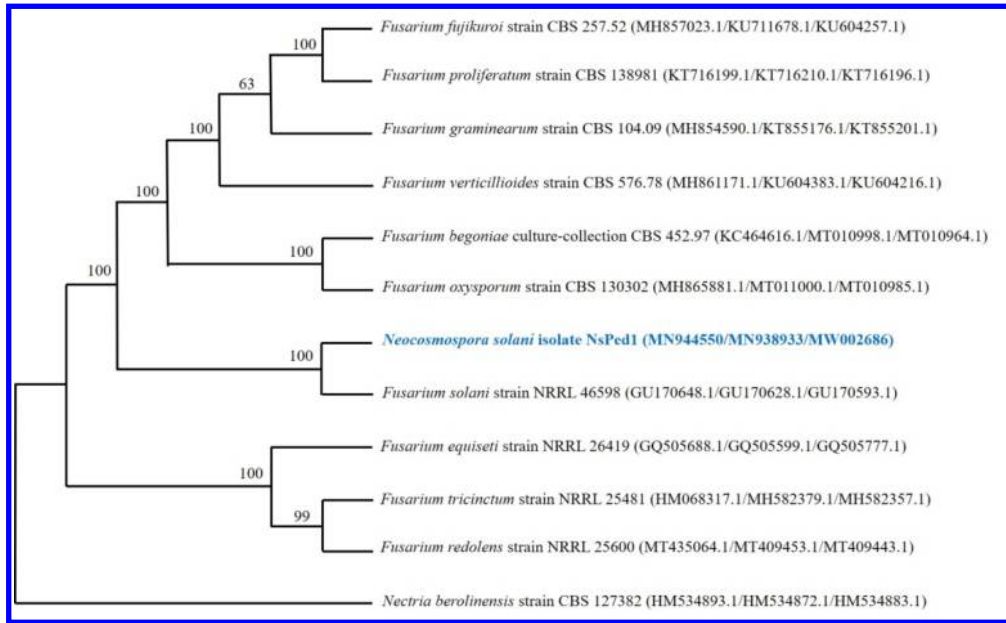
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Supplementary Figure 1 The symptoms of collar rot in purple passion fruit (*P. edulis* 'Mantianxing') and morphological characters of *Neocosmospora solani* isolate NsPed1. A, The symptoms of collar rot in purple passion fruit in the field. B, Transections (up) and longitudinal section (down) of stems of healthy (left) and infected (right) plants in the field. C, Colony morphology of *N. solani* NsPed1 observed from the top of a PDA Petri dish. D, Colony morphology of *N. solani* NsPed1 observed from the bottom of a PDA Petri dish. E, Macroconidia and microconidia of *N. solani* NsPed1 on synthetic nutrient agar (SNA) medium. Red arrows indicate macroconidia and green arrows indicate microconidia. F to H, 90-day-old seedlings of purple passion fruit were inoculated with sterile PDA (the two plants or stems on the left) and *N. solani* NsPed1 (the two plants or stems on the right) after two weeks. I to K, 45-day-old cuttings of purple passion fruit were inoculated with sterile PDA (the two plants or stems on the left) and *N. solani* NsPed1 (the two plants or stems on the right) after two weeks. All scale bars are 10 mm, except that in panel E is 50 μm.

255x191mm (350 x 350 DPI)



Supplementary Figure 2 The phylogenetic tree for *Neocosmospora solani* isolate NsPed1 and related *Fusarium* genus based on the combined sequence data sets for ITS1, EF-1 and RPB2 genes, constructed by neighbor-joining method using MEGA-X software (<https://megasoftware.net/>). *Nectria berolinensis* was used as the outgroup. Numbers at the branch nodes indicate bootstrap values based on 1000 replications.

303x185mm (350 x 350 DPI)