Figure S1. Phylogenetic tree of *Gnomoniopsis smithogilvyi* isolates, for the *TEF1-α* partial gene. The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree is shown. The tree is drawn to scale, with branch lengths (next to the branches) in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method [2] and are in the units of the number of base substitutions per site. This analysis involved 32 nucleotide sequences with 619 positions. Evolutionary analyses were conducted in MEGA11 [3]. *Gnomoniopsis paraclavulata* Sogonov was used as the tree root.

[1] Saitou, N.; Nei, M. The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **1987**, *4*, 406-425.
[2] Kimura, M. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *J. Mol. Evol.* **1980**, *16*, 111-120.
[3] Tamura, K.; Stecher, G.; Kumar, S. MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. *Mol. Biol. Evol.* **2021**. https://doi.org/10.1093/molbev/msab120.