CORRECTION



Correction to: Isolation and Mycotaxonomic Characterization of *Colletotrichum lillacola*: A Novel Species Causing Anthracnose of *Bergenia ligulata*

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In the original article, figure 3a was incorrectly published. The correct Fig. 3a is provided here.

The original article was corrected.

The online version of the original article can be found under doi: 10.1007/s40011-017-0903-7.



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Fig. 3 a Phylogenetic tree (neighboring joining tree) constructed using UPMGMA clustering method showing the relationship of isolates with other related fungal species retrieved from GenBank based on their sequence of the internal transcriber spacer regions ITS1 and ITS2 of the rDNA. Statistics on BioloMICS Ward's minimum variance tree: cophenetic coef. corr.: 0.13263N obs.: 1128.00000 DF: 1127.00000 T value: 4.49218 ND P: 0.415813 D P: 0.831627 OTUs in tree: 48. b Branches receiving <60% bootstrap support were collapsed to polytomies, and long branches were shortened by 50%, which is indicated with two diagonal slashes. Bootstrap values are given for branches among but not within cultures. The scale bar indicates the number of substitutions per site with the number '0.5' shows the length of branch that represents an amount genetic change of 0.5 indicated by green line at the bottom (color figure online)



