

Review of: "An account of Colletotrichum species associated with anthracnose of Atractylodes ovata in South Korea based on morphology and molecular data"

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The disease note is written quite well. However, I recommend some improvements in the text and the figures. Furthermore, some additional information (e.g. used primers) are needed.

1. In "Sampling and isolation", were there any yellow halos surrounding the lesions?
2. In "DNA extraction, PCR amplification and sequencing", why were there so many strains only sequence ITS? Such as *C. fruticola* WHT112, *C. fruticola* M52, *C. gloeosporioides* WSH43, *C. siamense* M63, *C. sojae* T2B2 and *C. Plurivorum*.

Another question is whether the gene of ApMat was used in this paper?

3. In "Multi-locus phylogeny", there were some questions in Fig 4. Why do you think the isolates of M92 and SPL93 were clustered into the same clade of *C. kahawae*/*C. cigarro*? From the phylogenetic tree, isolate M92, even isolate SPL93 maybe a new clade differing with *C. kahawae*/*C. cogro*. What do you think about them?

The same question was occurred for isolates SPL2133, 213, 2136 and 2139.

4. In S1 Fig, is the strain of *Colletotrichum theobronmicola* CBS 124945 suitable to be used as the outgroup? *Colletotrichum theobronmicola* CBS 124945 was closed to one branch of *C. siamense* in Fig S1. So, please check the phylogenetic tree.
5. In S2 Fig, were the strains of *C. cigarro* not clustered into one branch? If not, could you make sure that the isolates of SPL93 and M92 were closed to *C. cigarro*?
6. For Fig 15, This part of analysis were no meaning for differ the species. We suggested to delete it.
7. In "Pathogenicity test", due to infection rate and the typical symptom of pathogenicity test, could you think all the seven species isolated from *Atractylodes ovata* were the pathogens? Please check the symptoms. If not same, some species of *Colletotrichum* maybe the saprophytic or endophytic. The field tests maybe need to supply.
8. Good luck to authors.

