Colletotrichum jacksonii versus C. echinochloae

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Colletotrichum jacksoni J.A. Crouch et al., published Mycologia 100 (5), 26 Aug 2009 [ex type culture MAFF 305460]
Colletotrichum echinochloae Moriwaki & Tsukib., published Mycoscience 50 (4), 25 July 2009 [ex type culture MAFF 511473]

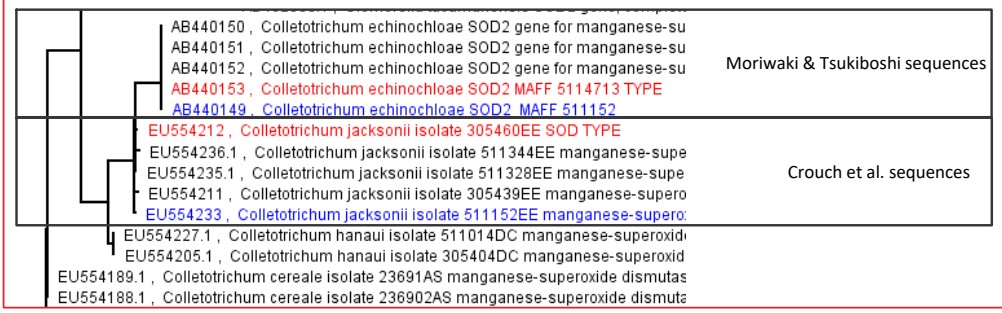
Both are pathogens of Japanese millet (E*chinochloa esculenta* (= *E. utilis*)), described from specimens collected from Japan, by Crouch et al. (2009) and Moriwaki & Tsukiboshi (2009) respectively.

The only gene sequenced in common across the two studies is SOD. Sequences of the isolates included in the phylogenies in the two studies are identical, except for a non-coding region from bases 16 to 78 near the start of the fragment sequenced. For this non-coding region, all isolates in the Crouch study have one haplotype, and all isolates in the Moriwaki & Tsukiboshi study have a second haplotype.

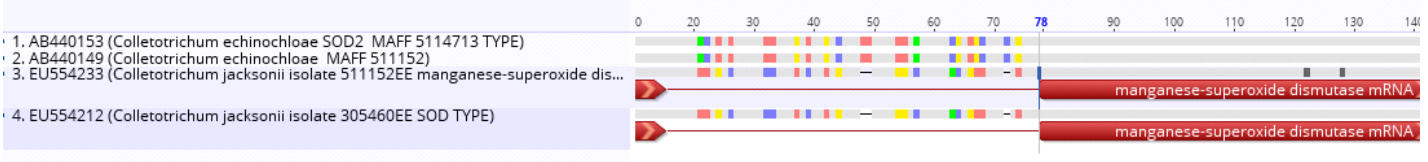
One isolate, MAFF 511152 (blue in tree below), was sequenced in both studies - the non-coding haplotypes for this isolate differ between the studies. This suggests the different haplotypes reported in the non-coding region from the two studies are the result of some sequencing artifact.

Based on the genetic data available, together with the ecological and geographic match acrosss the two species, it is highly likely these names are synonyms; *C. echinochloae* has priority, published one month before *C. jacksonii*.

SOD phylogeny



SOD alignment including ex-type specimens of *C. jacksonii* and C. *echinochloae*, as well as MAFF 511152 sequences from the Crouch et al. (2009) and Moriwaki & Tsukiboshi (2009) studies, showing differences in the non-coding region near the start of the fragment sequenced.



P.R. Johnston, 28 Feb 2019