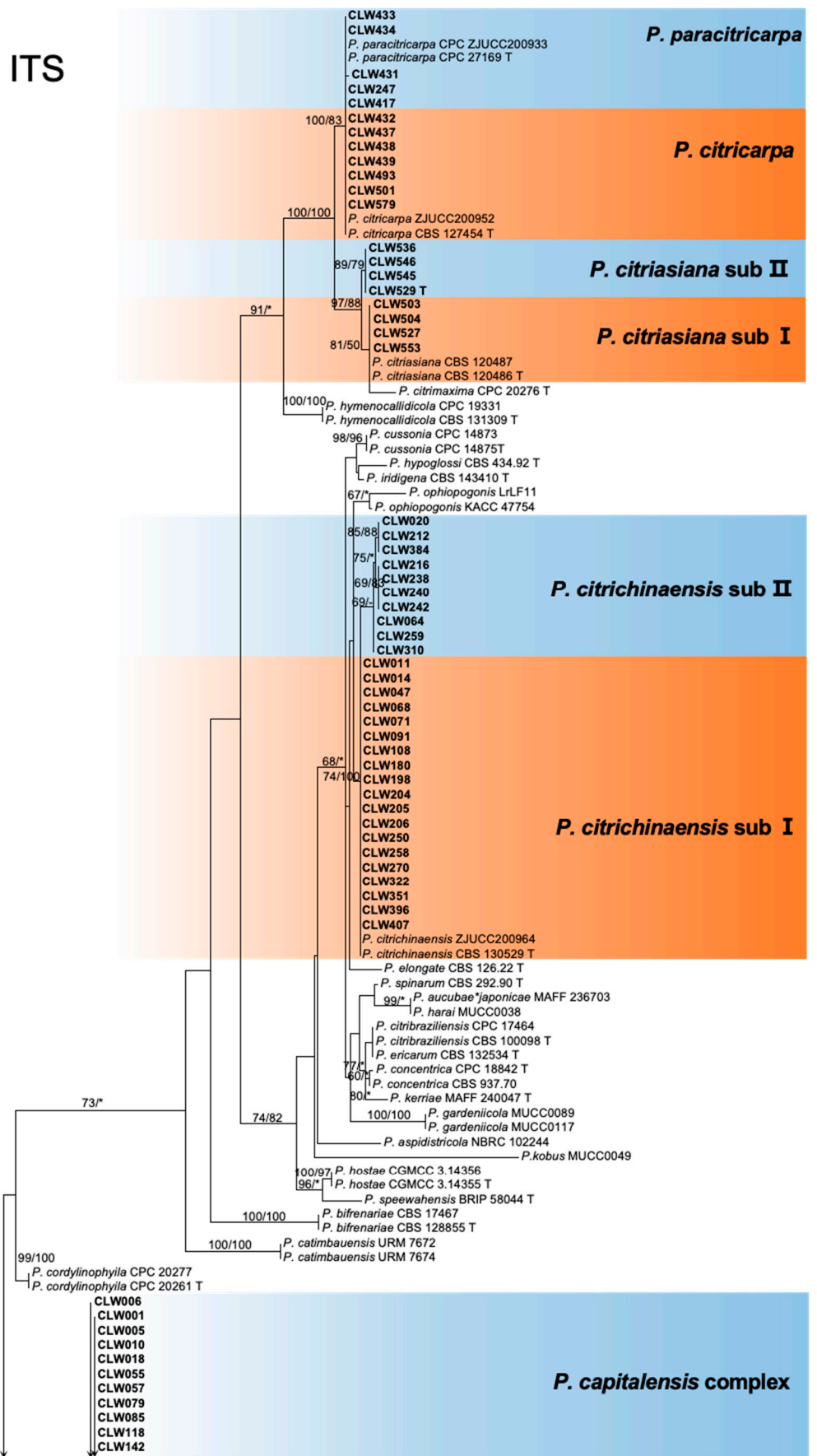


Figure S1 Symptoms of citrus fruit spots from which the *Phyllosticta* isolates were obtained. a *C. maxima* fruits, b *C. reticulata* cv. Nangfengmiju, c *C. reticulata* cv. Unshiu, d *C. limon*, e *C. sinensis* cv. Navel, f *C. sinensis* cv. Valencia.



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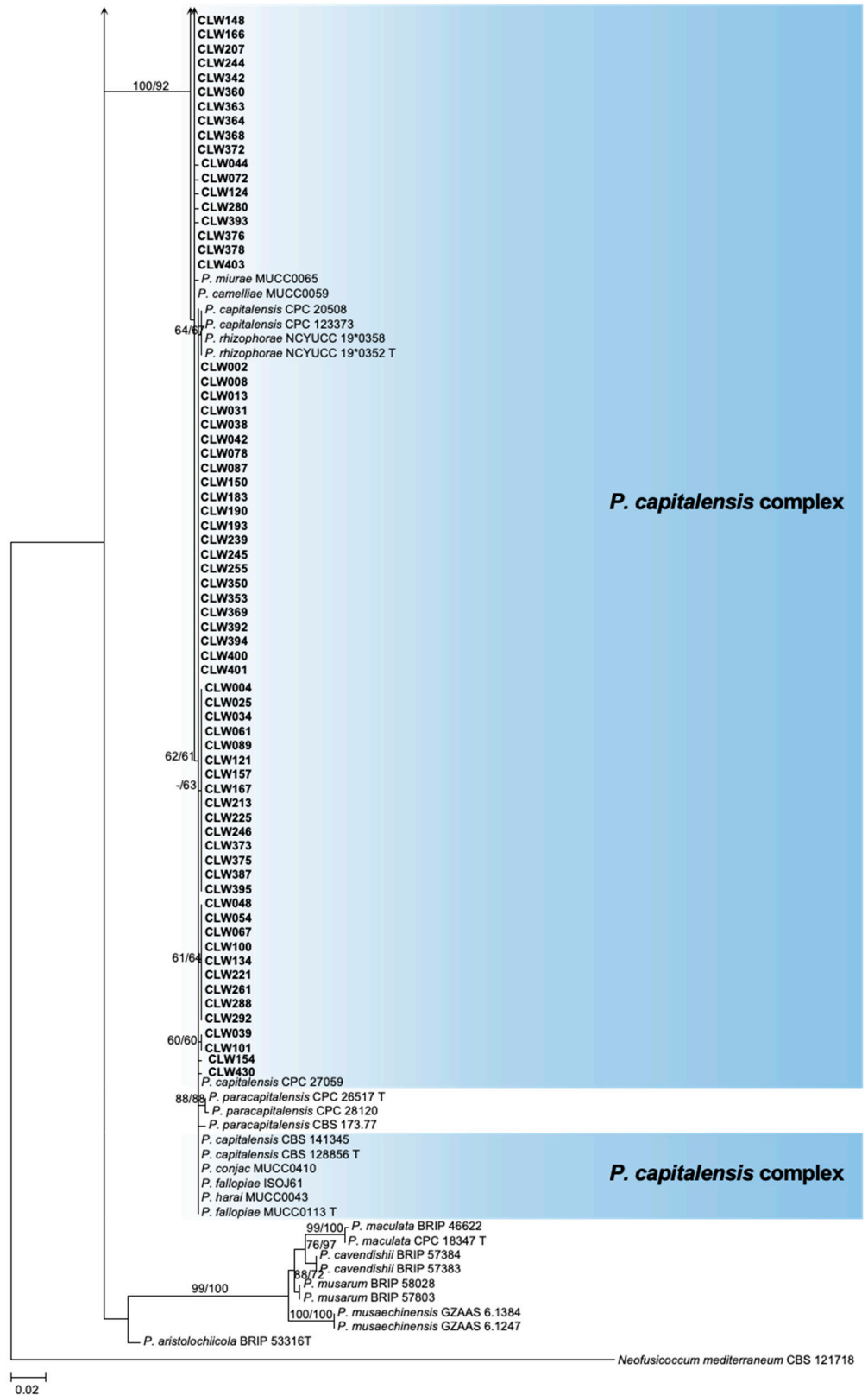
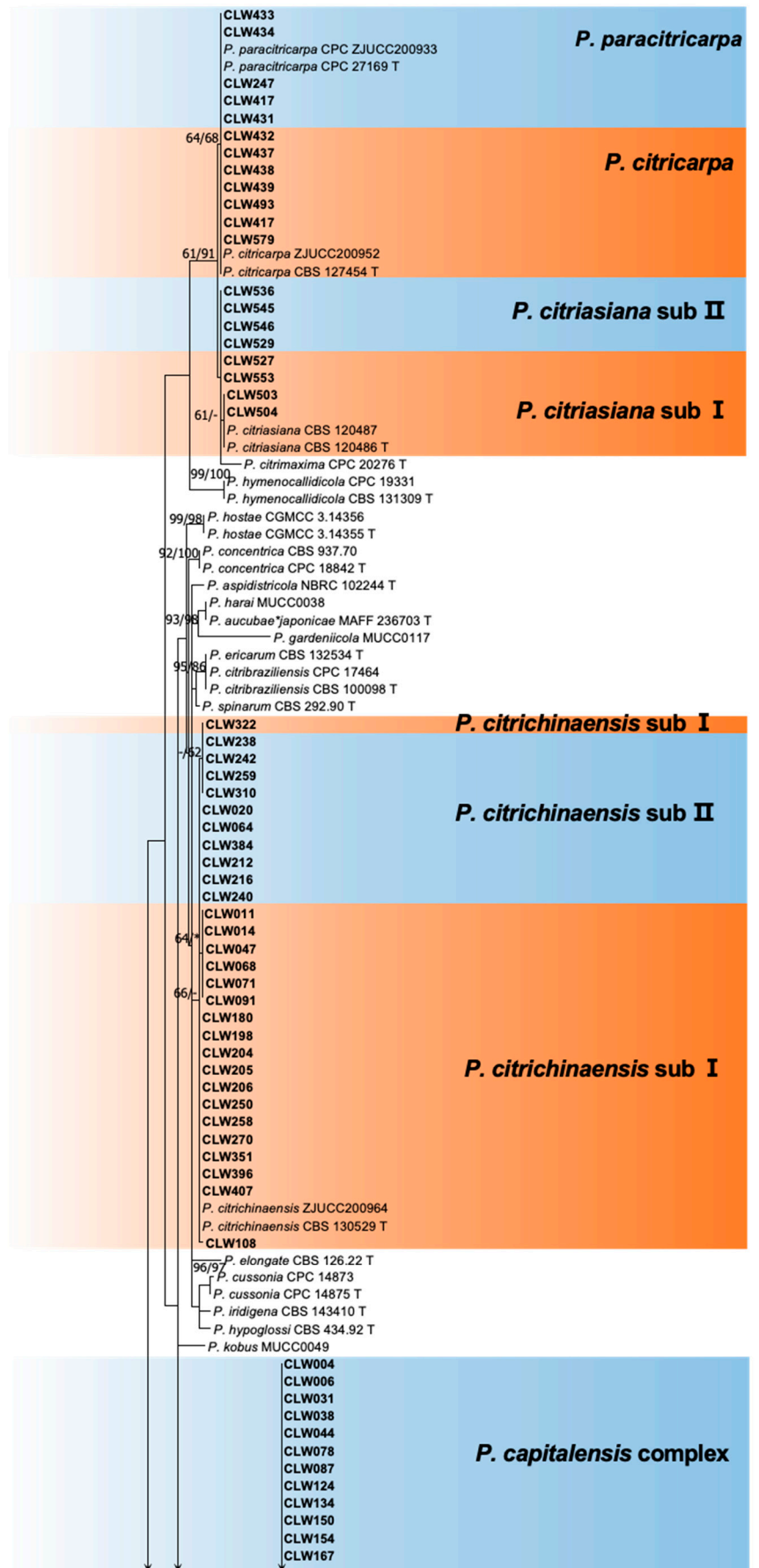


Figure S2. Maximum likelihood phylogeny of *Phyllostica* isolates related to citrus. 194 isolates of ITS tree.

actA



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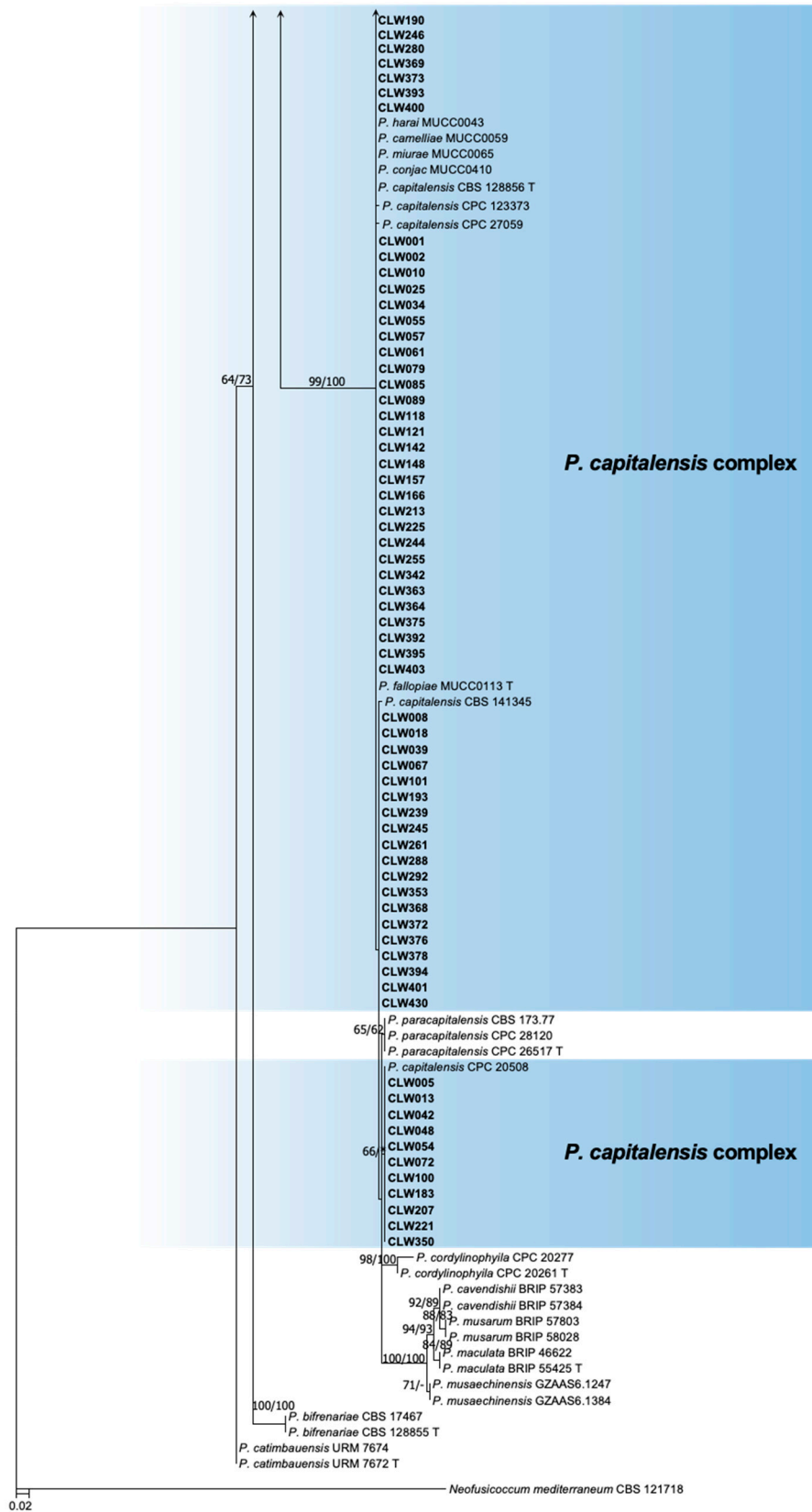
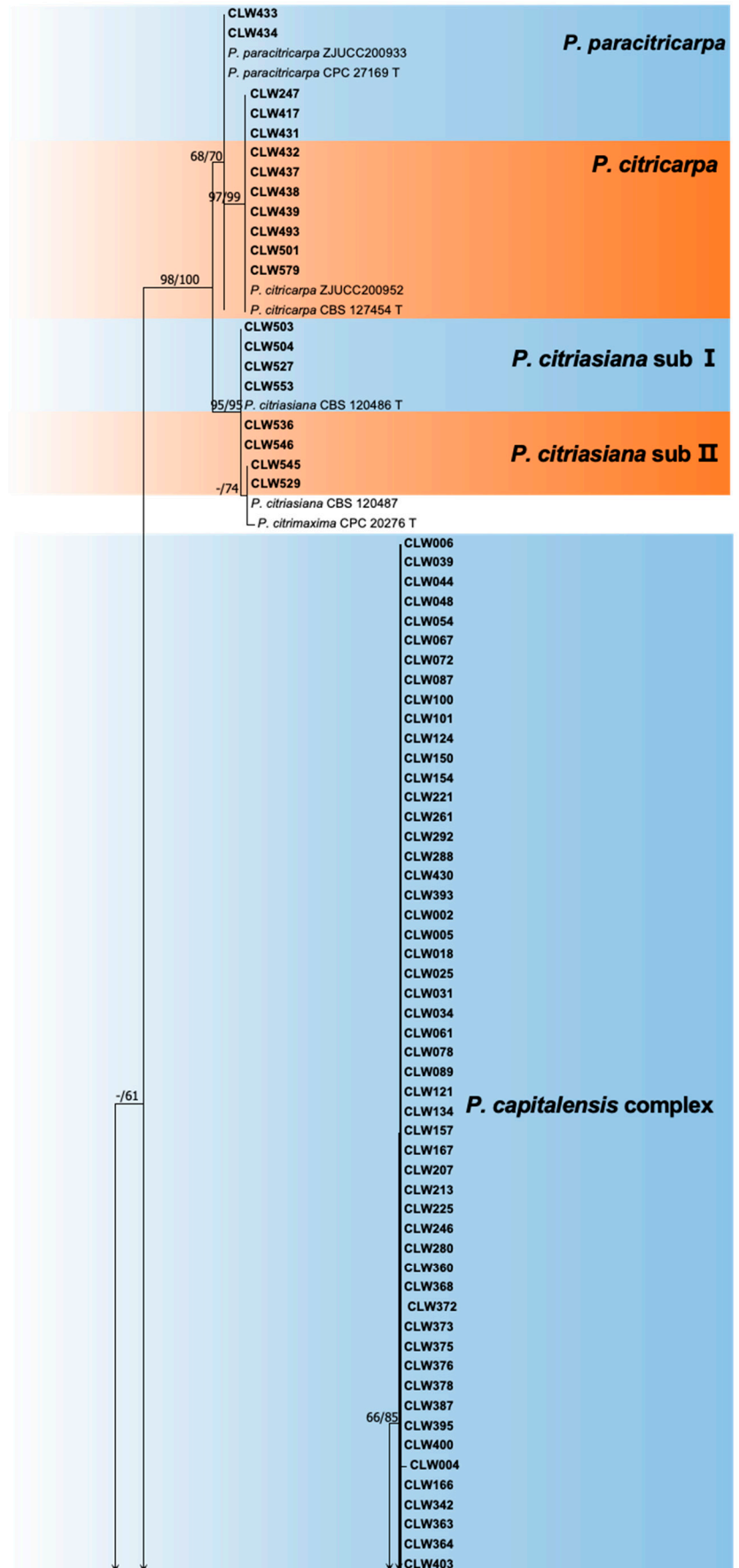


Figure S3. Maximum likelihood phylogeny of *Phyllostica* isolates related to citrus. 183 isolates of *actA* tree.

tef1



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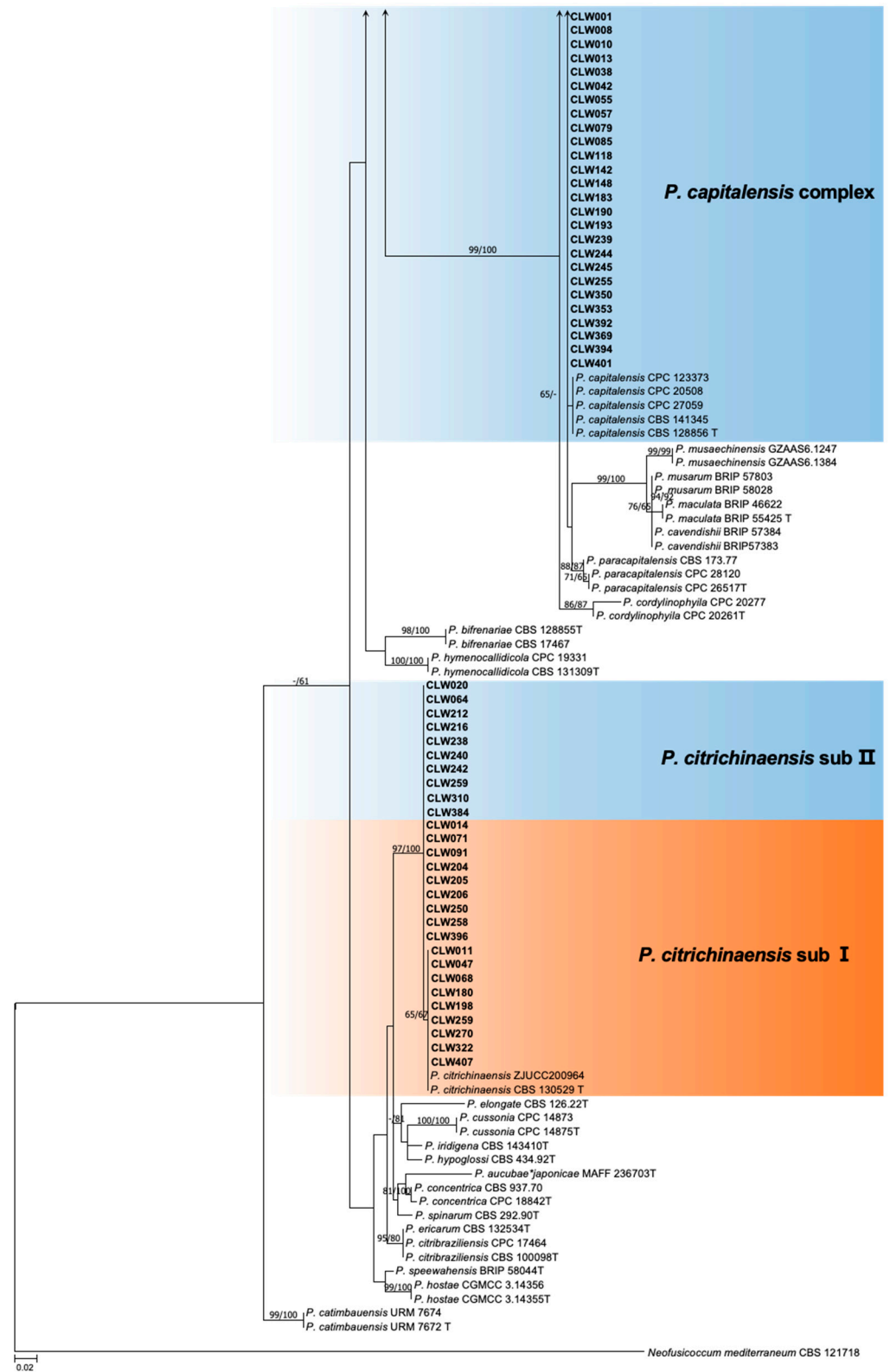
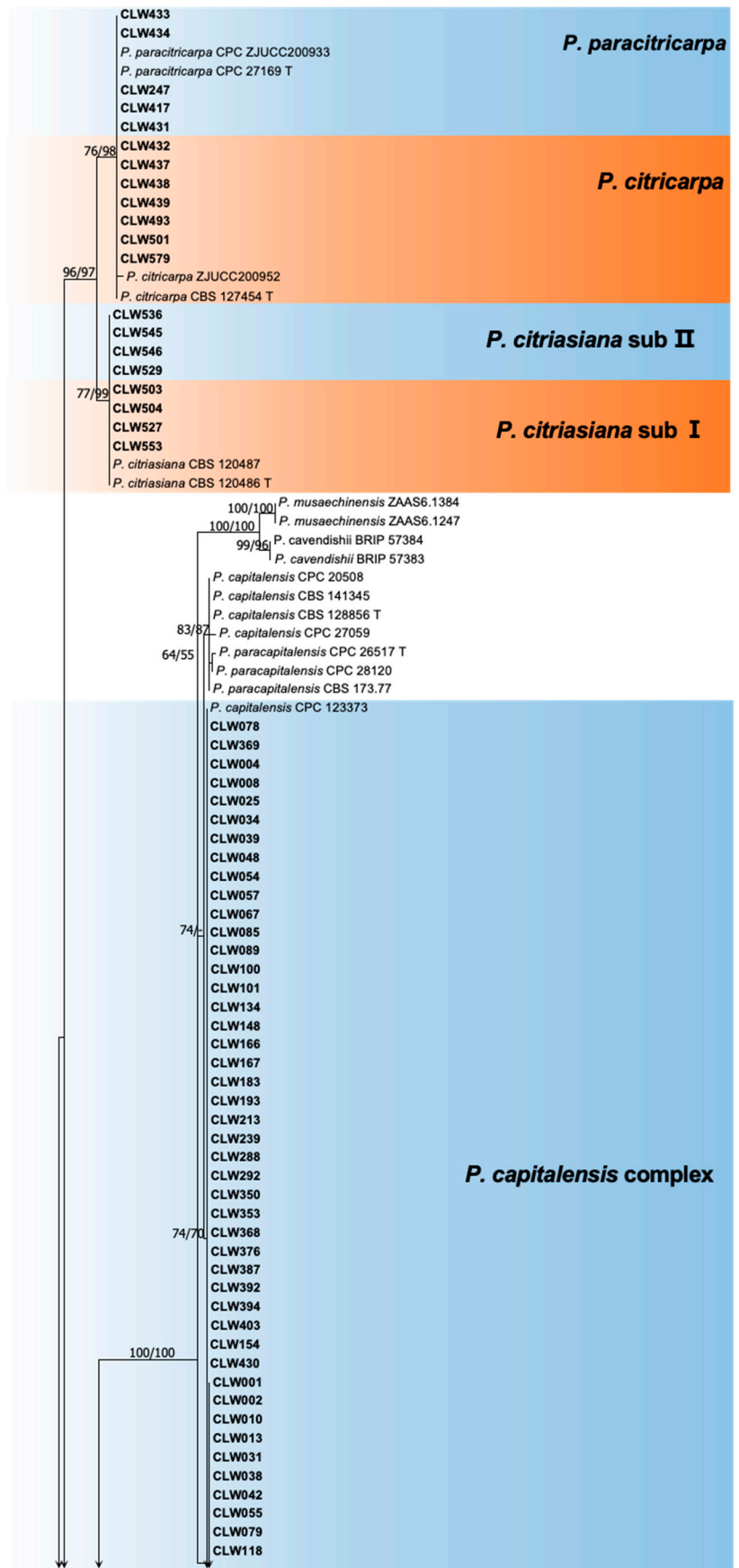


Figure S4. Maximum likelihood phylogeny of *Phyllostica* isolates related to citrus. 176 isolates of *tef1* tree.

gapdh



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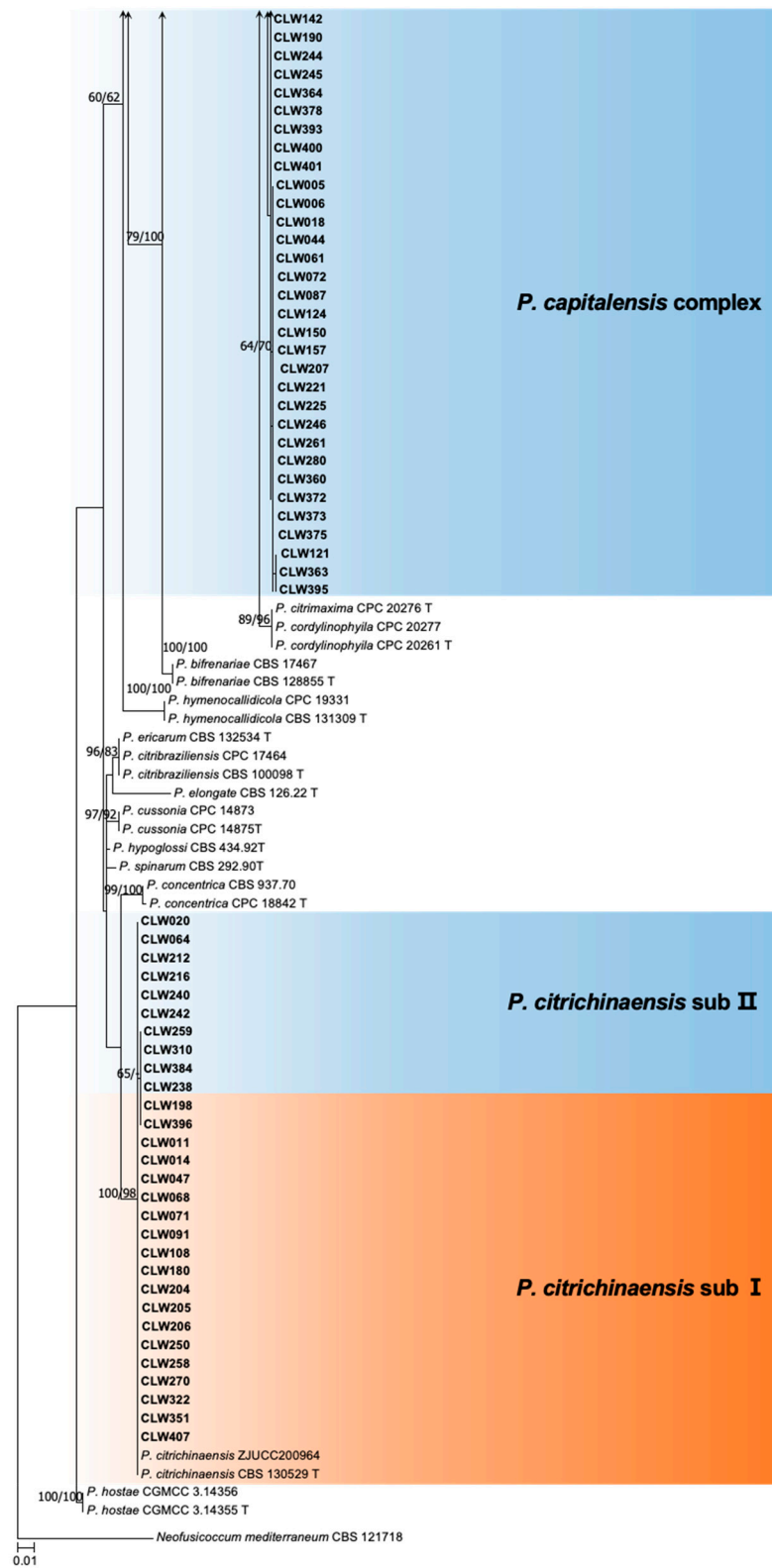
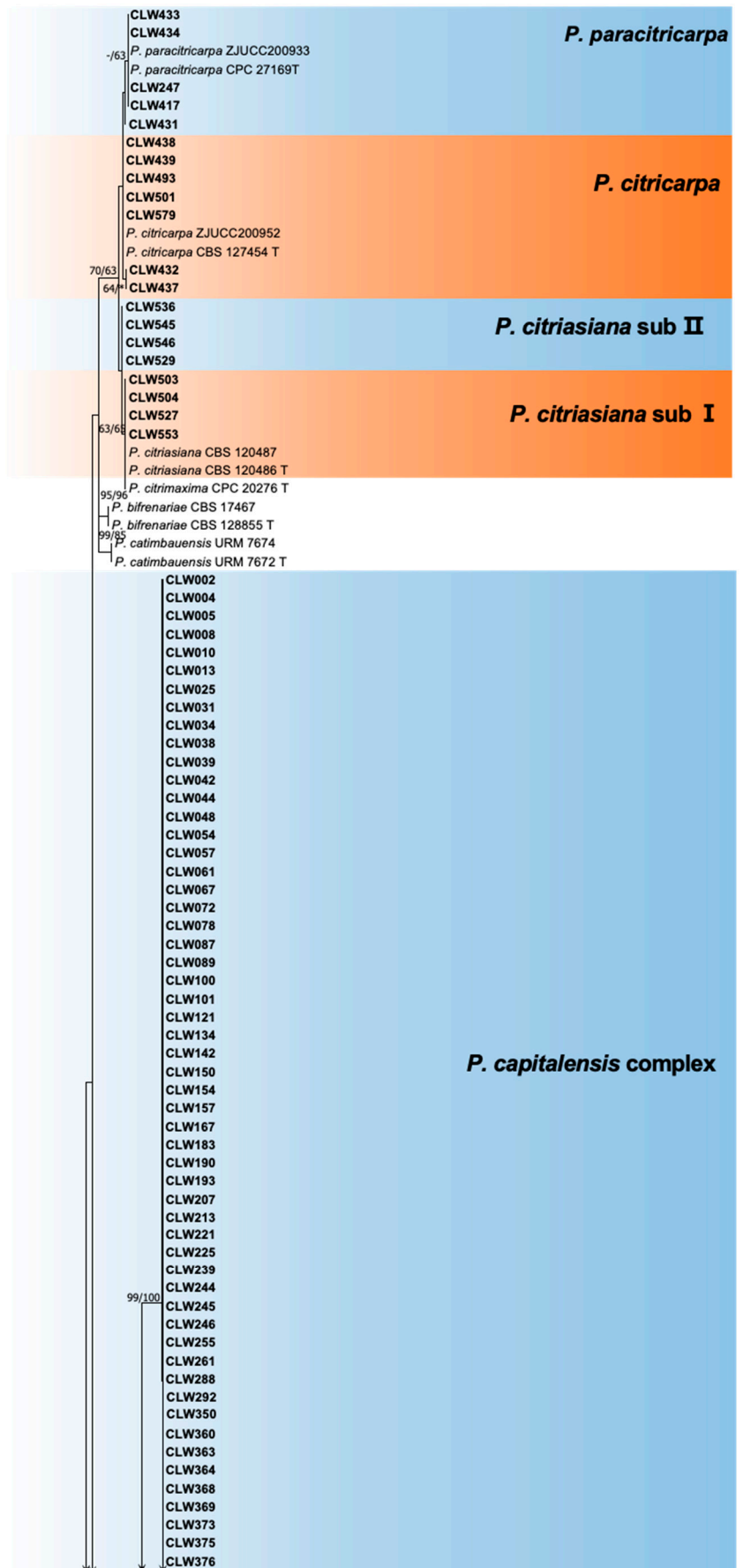


Figure S5 Maximum likelihood phylogeny of *Phyllosticta* isolates related to citrus. 166 isolates of *gapdh* tree.

LSU



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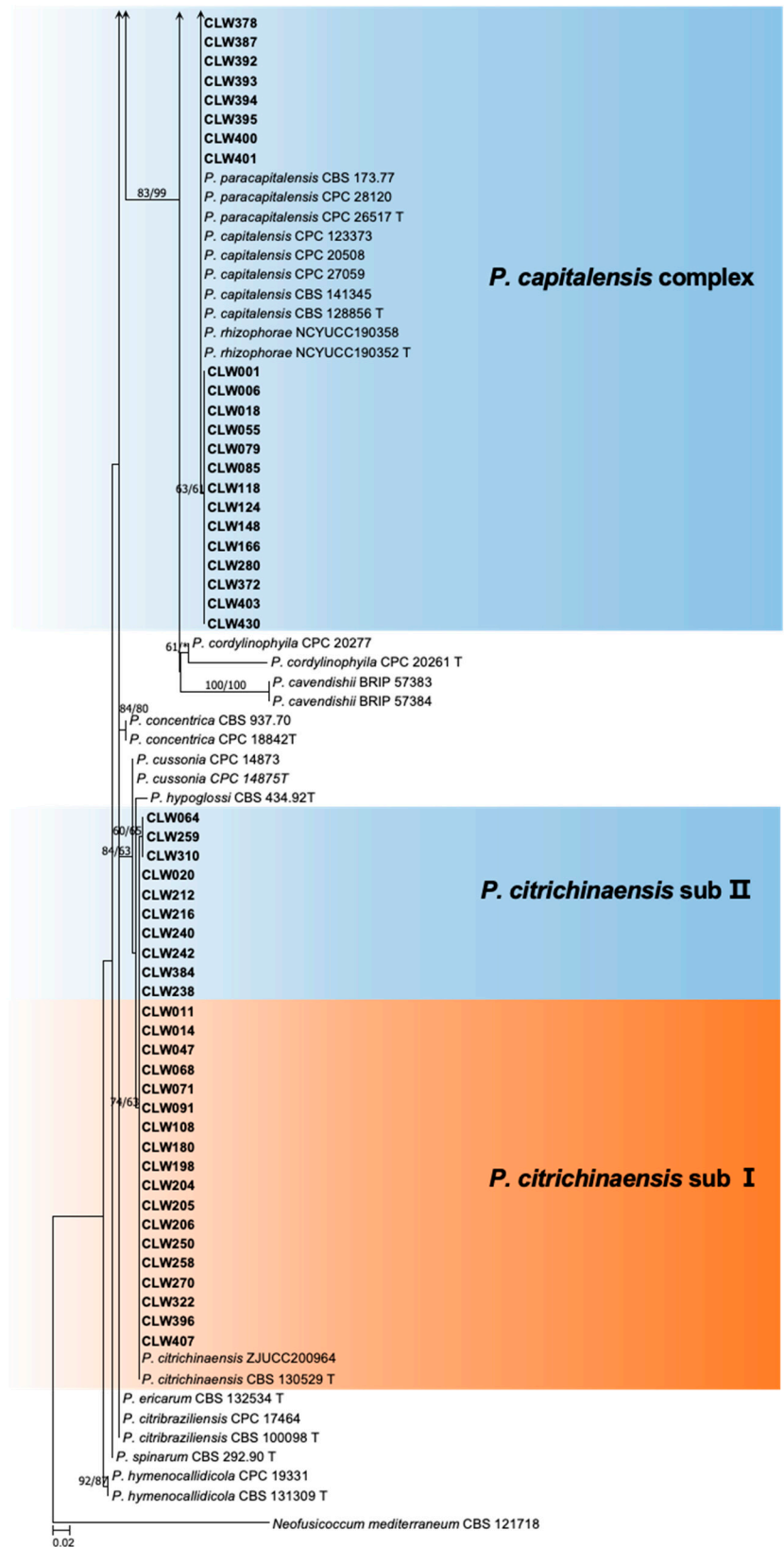
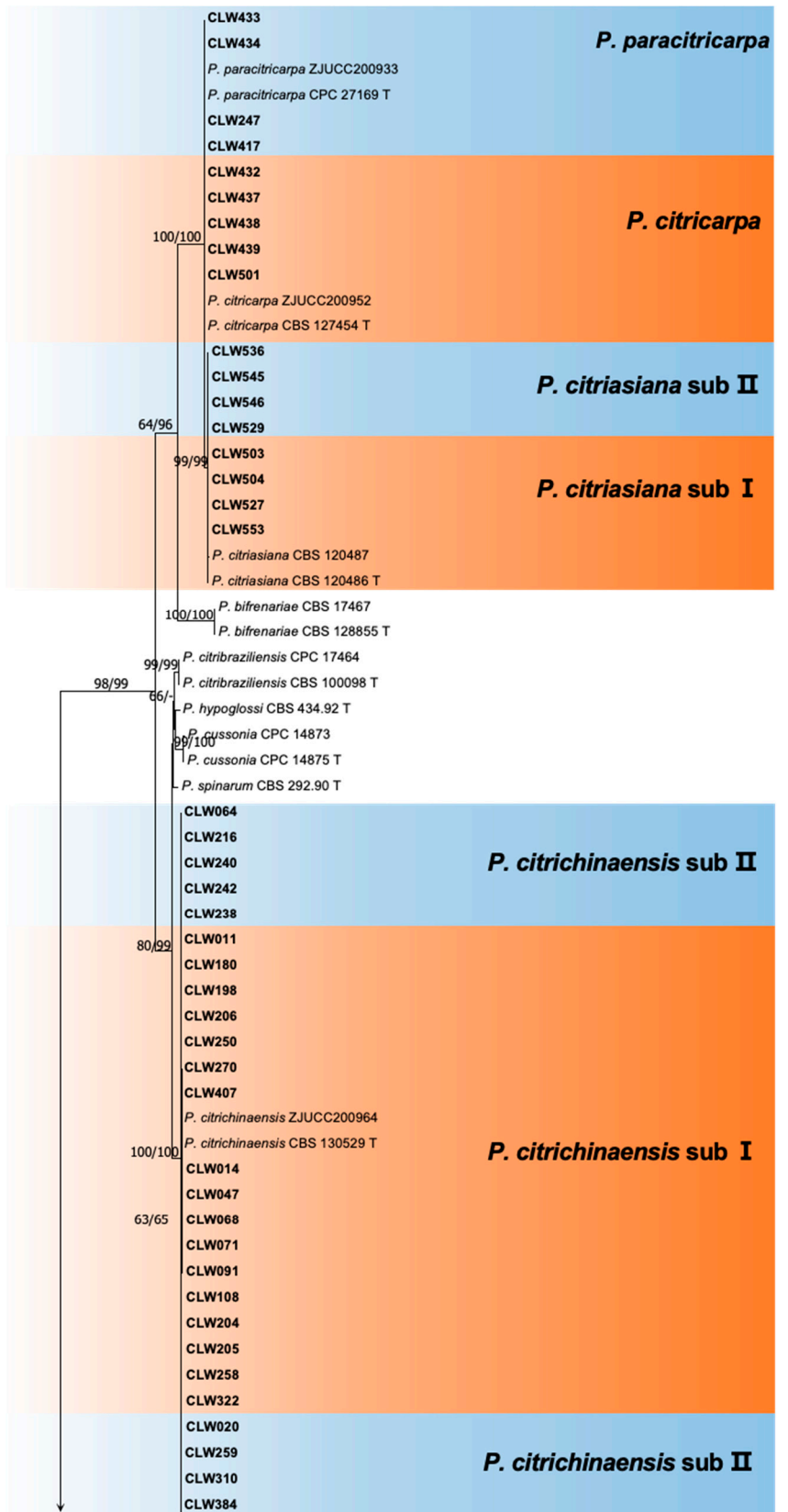


Figure S6 Maximum likelihood phylogeny of *Phyllostica* isolates related to citrus. 164 isolates of LSU tree.

rpb2



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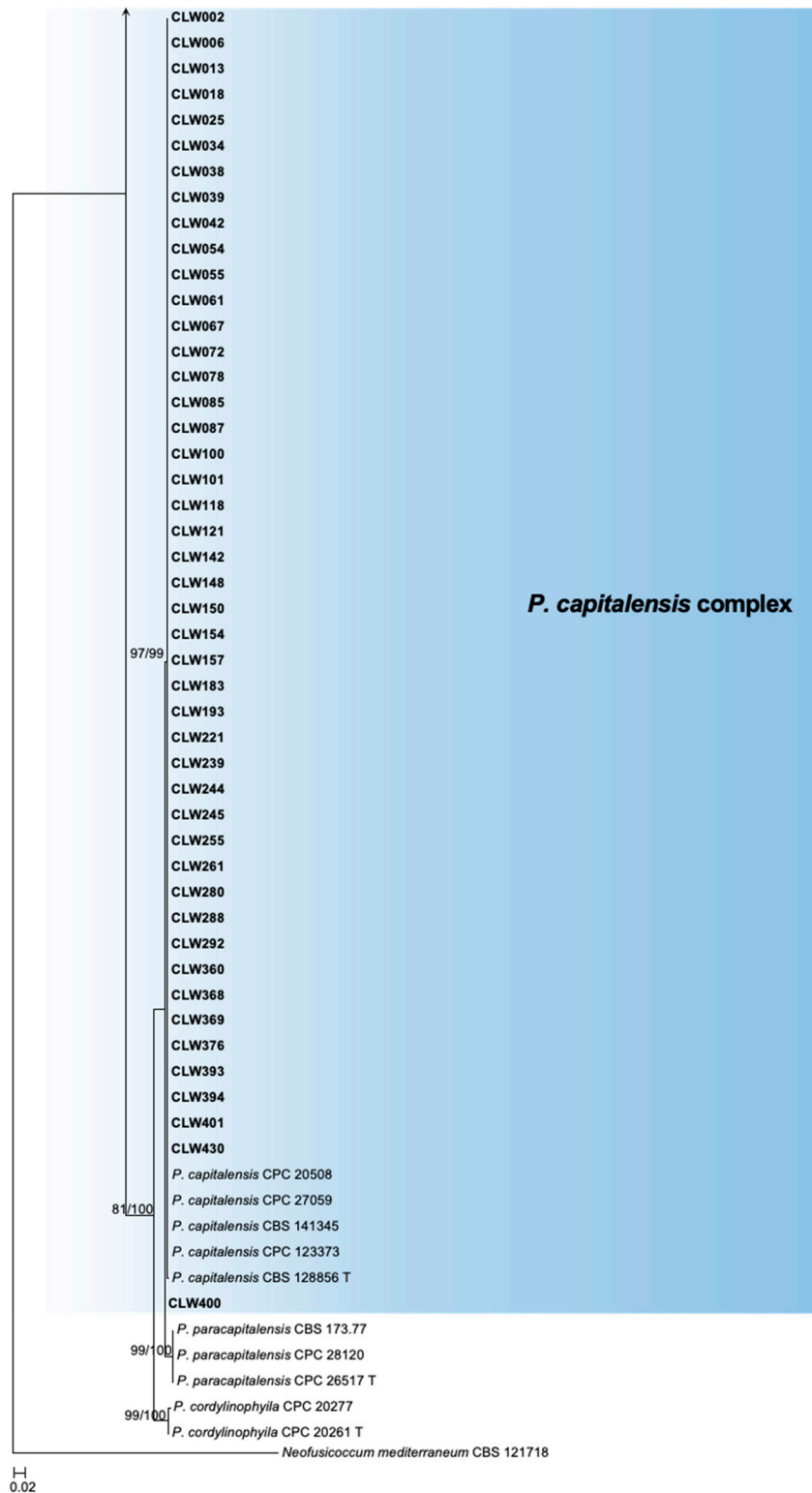


Figure S7 Maximum likelihood phylogeny of *Phyllostica* isolates related to citrus. 116 isolates of *rpb2* tree. S1-S6, Isolates sequenced in this study are in bold. Bootstrap support values $\geq 60\%$ for ML and MP are presented above branches as follows: ML/MP, bootstrap values $< 60\%$ are marked

with '-', and absent are marked with '*'. Ex-type isolates are marked with 'T'. The trees were rooted with *Neofusicoccum mediterraneum* (CBS 121718).

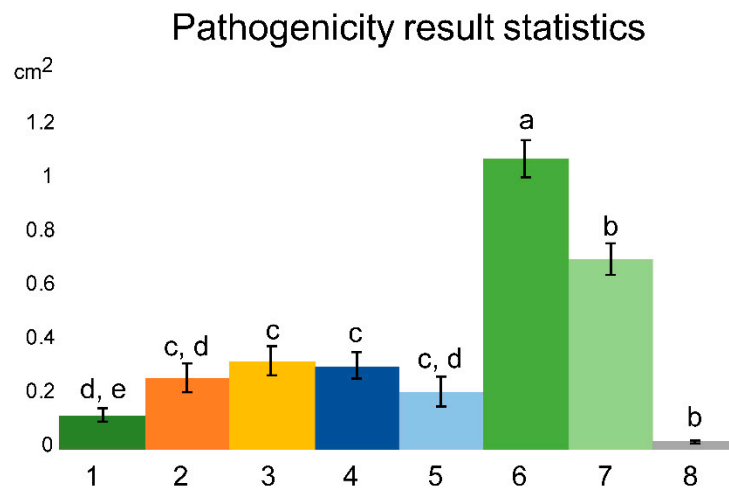


Figure S8 Column chart indicating the average lesion area produced each isolate of *Phyllosticta* spp. Bar topped with different letters indicate treatment means that are significantly different ($P = 0.05$). 1 to 7 represent average lesion area caused by isolates of *P. capitalensis*, *P. citriasiana* sub I & II, *P. citrichinaensis* sub I & II, *P. citricarpa* and *P. paracitricarpa*, 8 represent average lesion area caused by sterile water.