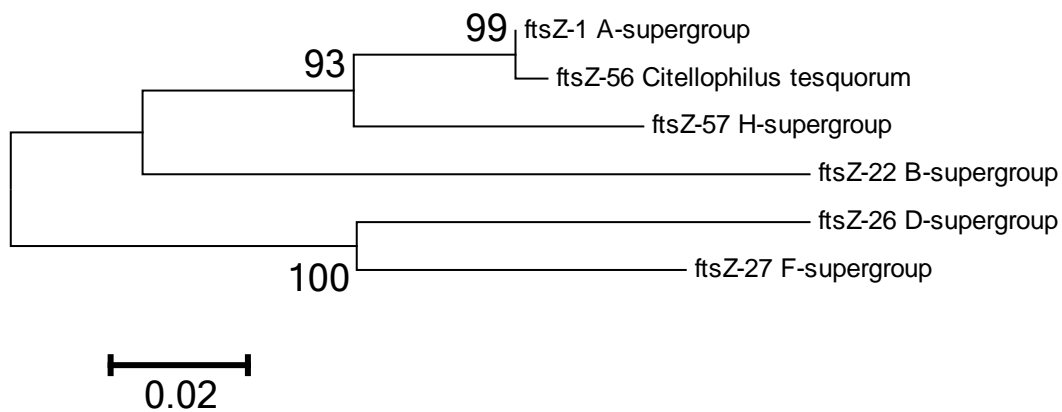
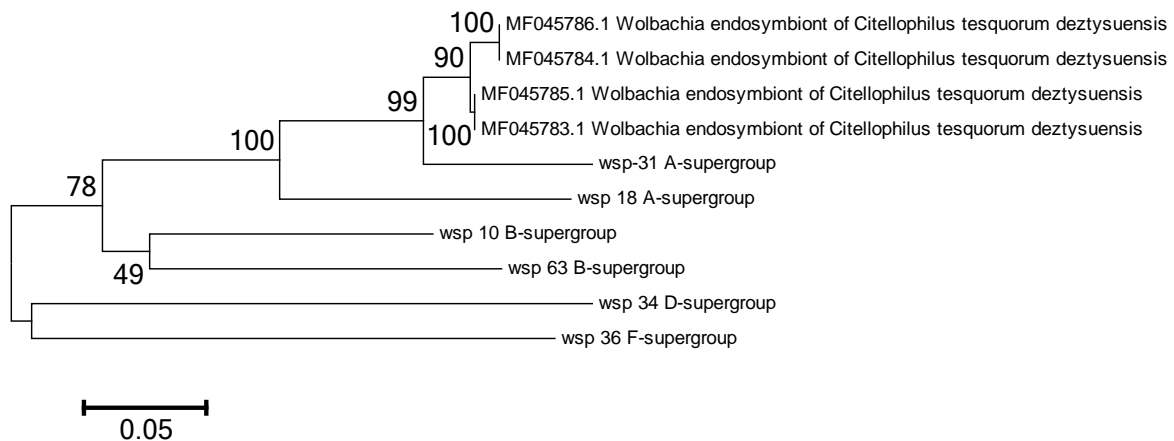


Figure S1. Diagnostic characteristics of *Citellophilus tesquorum* subspecies. Abdomen: clasper (cl), membranous appendage (ma) and sternum VIII (8st) (A) *C. t. altaicus* (from: Ioff *et al.*, 1965, fig. 196), (B) *C. t. dzetysuensis* (from: Ioff *et al.*, 1965, fig. 197), (C) *C. t. sungaris* (from: Ioff *et Scalon*, 1954, fig. 121), (D) *C. t. mongolicus* (from: Ioff *et Scalon*, 1954, fig. 122). Abdomen: sternum VII (E) *C. t. altaicus*, (F) *C. t. dzetysuensis* (from: Ioff *et al.*, 1965, fig. 199), (G) *C. t. sungaris* with modifications (from: Ioff *et Scalon*, 1954, fig. 123), (H) *C. t. mongolicus* (from: Goncharov *et al.*, 1989, fig. 75). Scale bars = 0.1 mm.



(A)



(B)

Figure S2. (A) Maximum likelihood phylogenetic tree of *ftsZ* alleles of *Wolbachia* symbionts was reconstructed with Mega6 [Tamura et al., 2013]. The *Wolbachia* isolate of *Citellophilus tesquorum* belong to supergroup A. (B) Maximum likelihood phylogenetic tree of *wsp* alleles of *Wolbachia* symbionts was reconstructed with Mega6 [Tamura et al., 2013]. The *Wolbachia* isolates of *Citellophilus tesquorum dzetysuensis* are clustered into supergroup A.

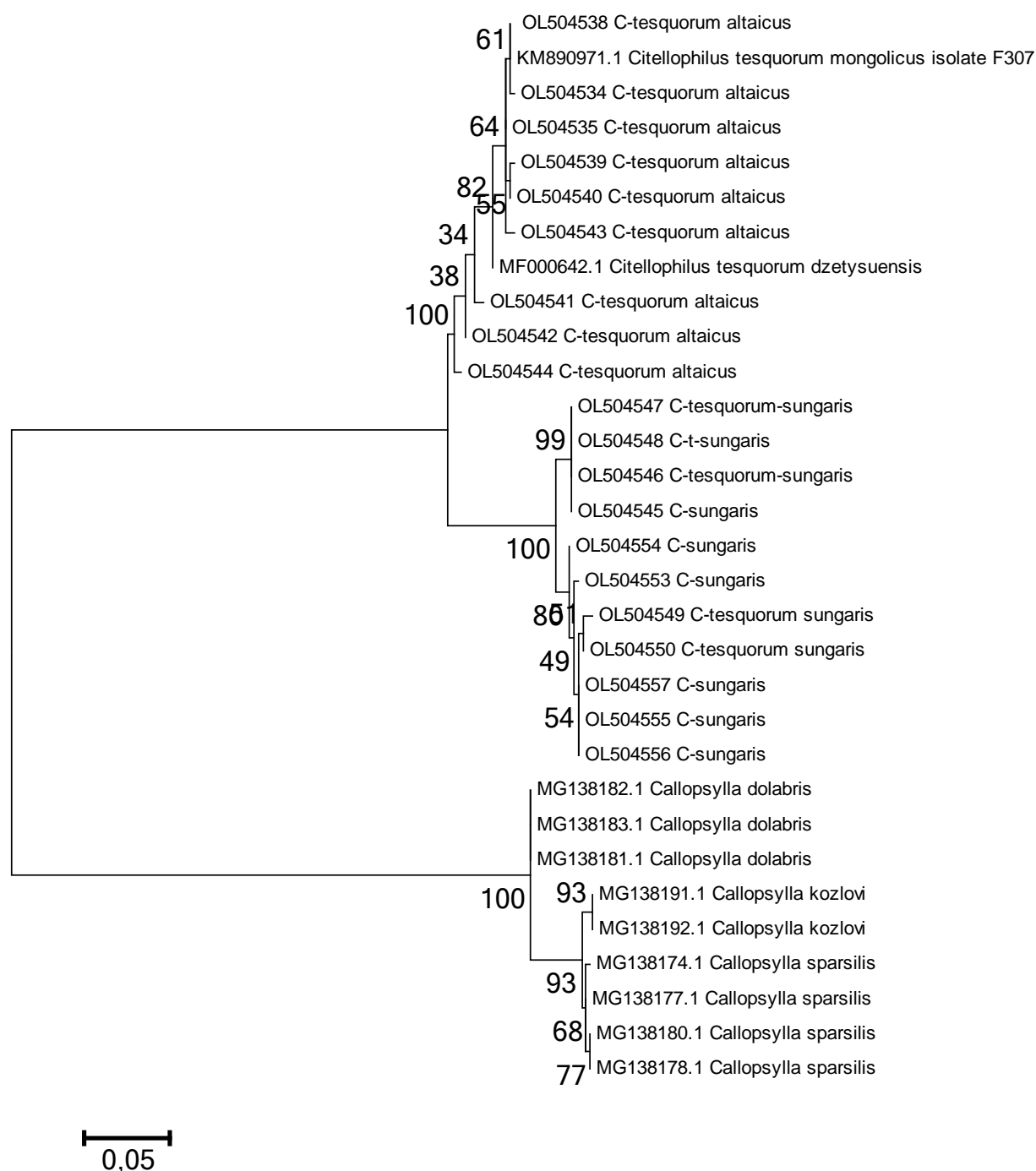


Figure S3. Molecular phylogenetic tree of 404 bp part of COI gene is reconstructed by Maximum Likelihood method based on the T92+I model. All bootstrap (100 iterations) values are indicated.

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