Assessment of the phylogenetic relationships within the spondylidine branch of Spondylidinae (Coleoptera, Cerambycidae)

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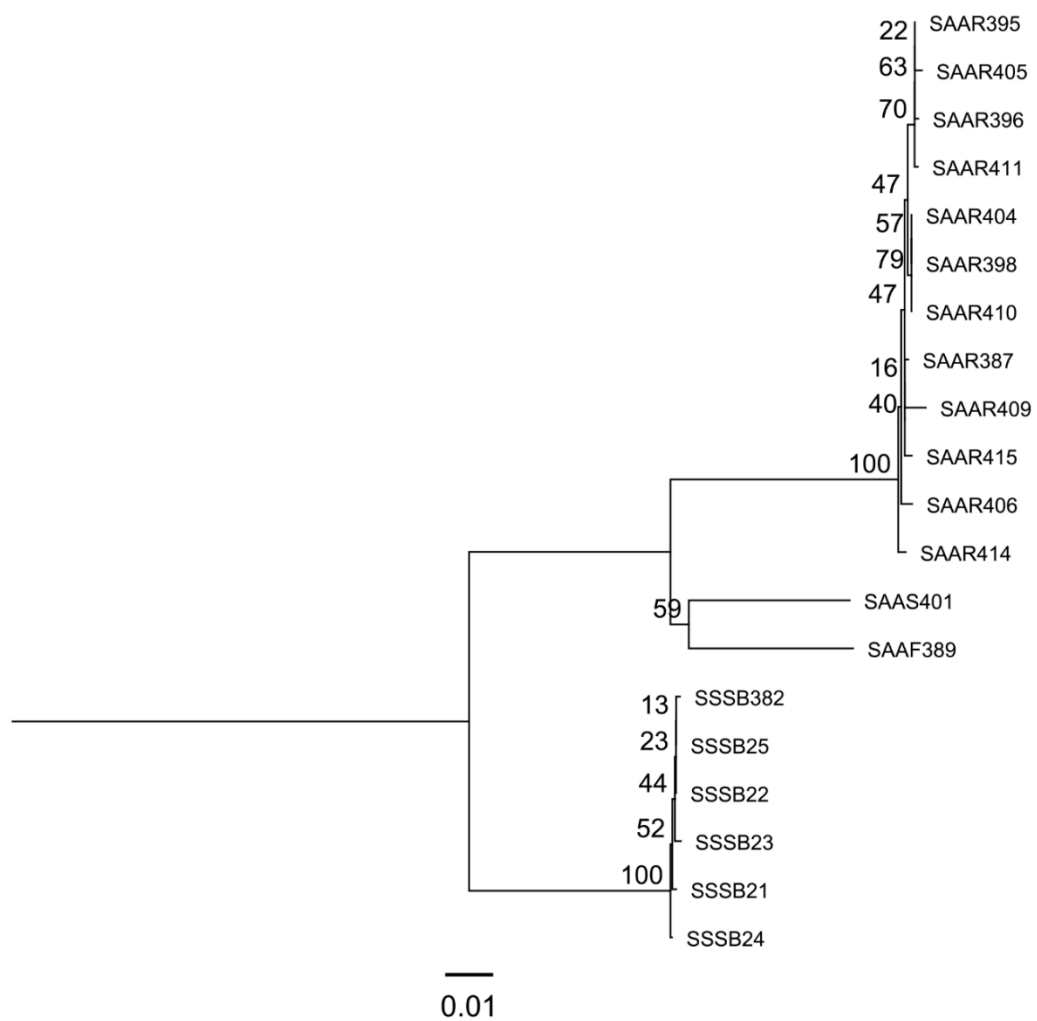*Corresponding author; e-mail: havvasoydabas@gmail.com

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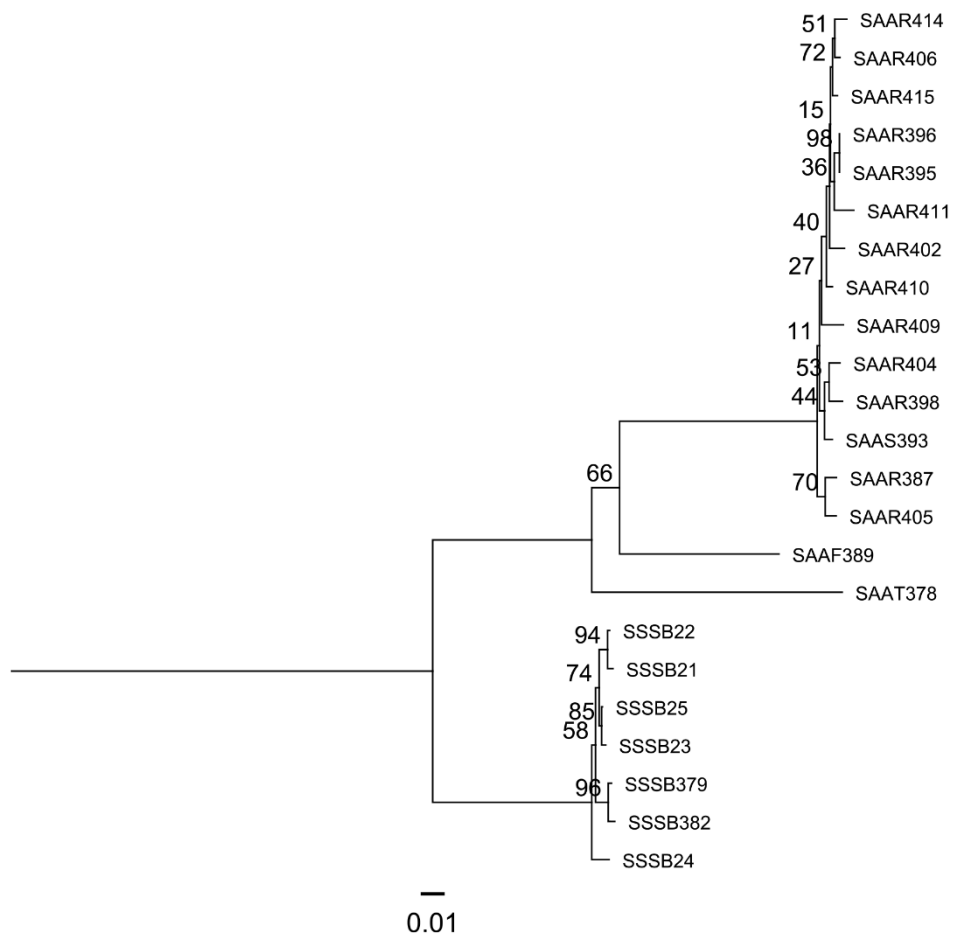
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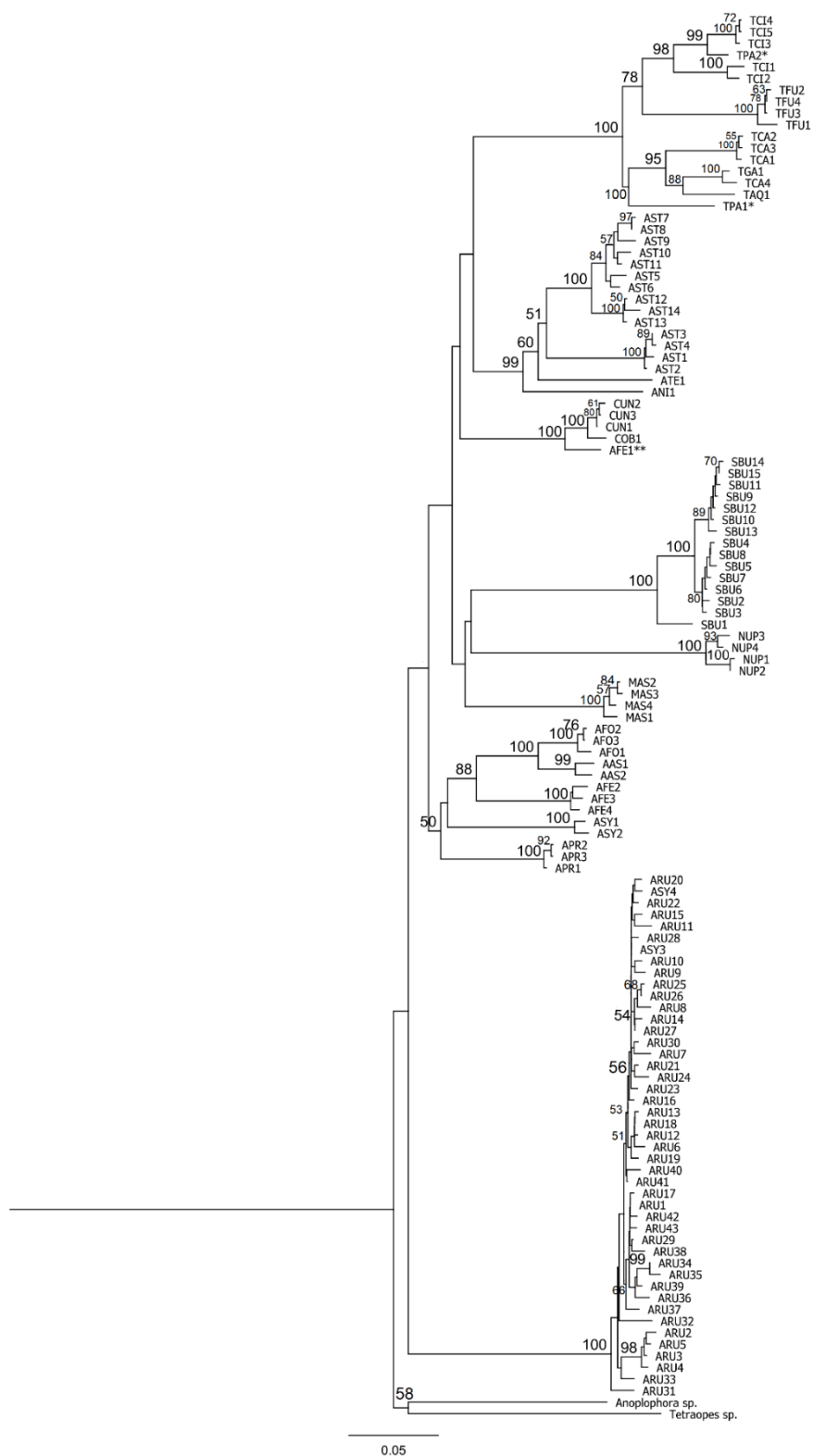
Fig. S1. Maximum Likelihood (ML) phylogenetic tree based on *COI* haplotypes (658 bp).

Bootstrap supports equal to or higher than 50% were shown on the nodes.

Fig. S2. Maximum Likelihood (ML) phylogenetic tree based on the binary combination of COI+28S rRNA D1-D2 gene regions. Bootstrap supports were shown on the nodes.

Fig. S3. Maximum Likelihood (ML) phylogenetic tree based on the binary combination

of *COI+16S rRNA* gene regions. Bootstrap supports were shown on the nodes.