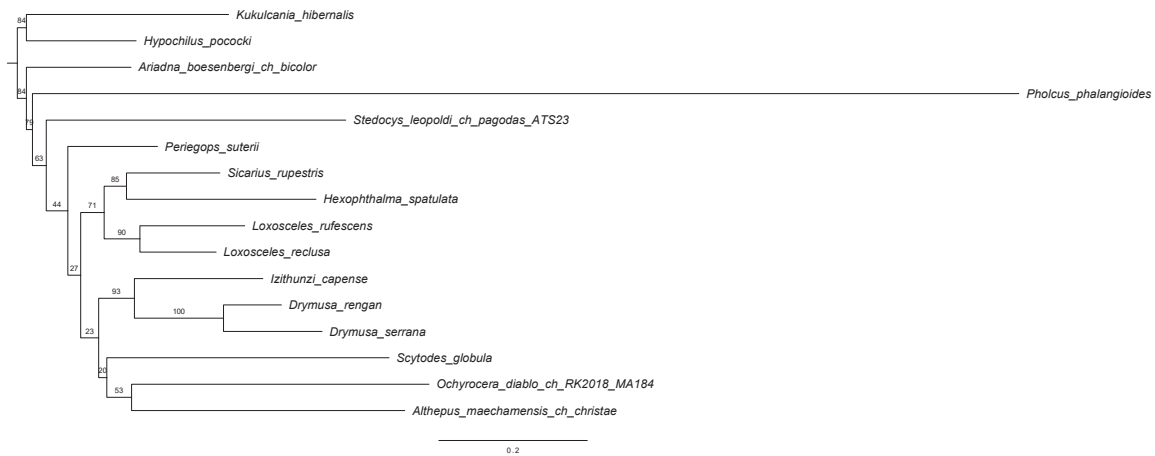


## Supplementary Figures

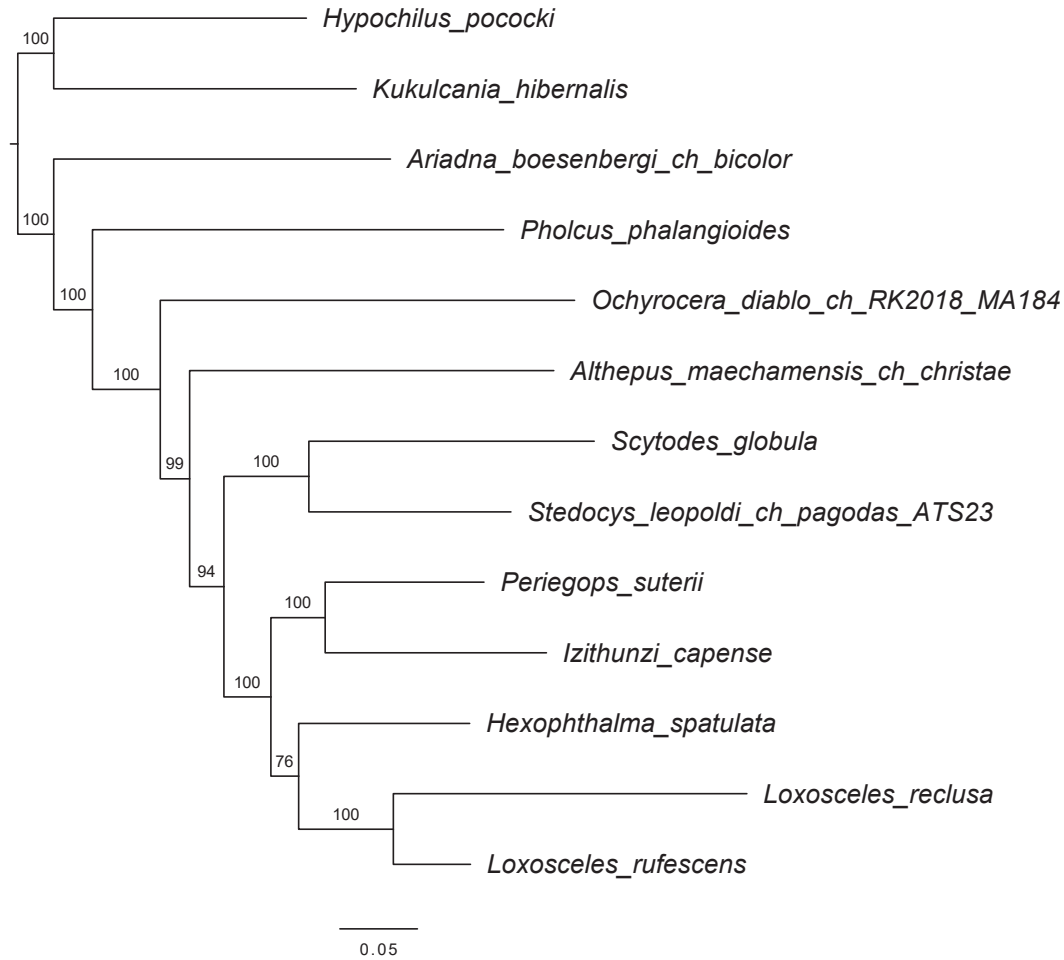
### Revision of recluse spiders (Sicariidae: *Loxosceles*) preserved in Dominican amber and a total-evidence phylogeny of Scytodoidea reveal the first fossil Drymusidae

Ivan L. F. Magalhaes, Abel Pérez-González, Facundo Labarque, Martín J. Ramírez, Martín Carboni, Jörg U. Hammel, Robin Kunz, Mónica M. Solórzano-Kraemer

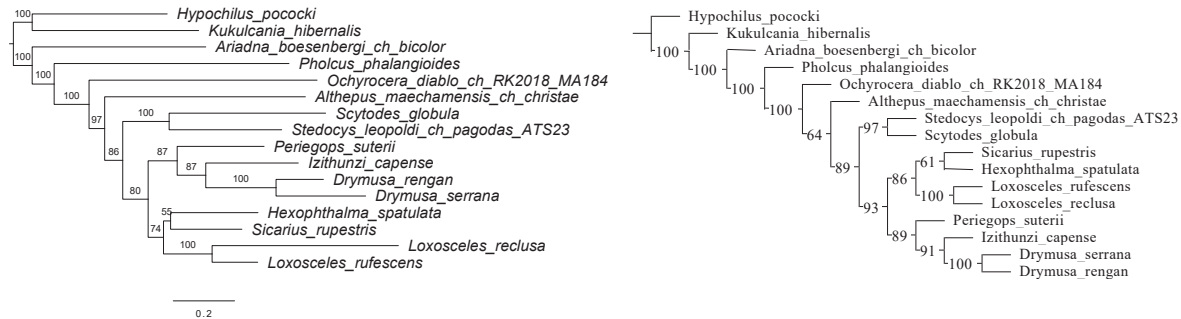
#### *Arthropod Systematics and Phylogeny*



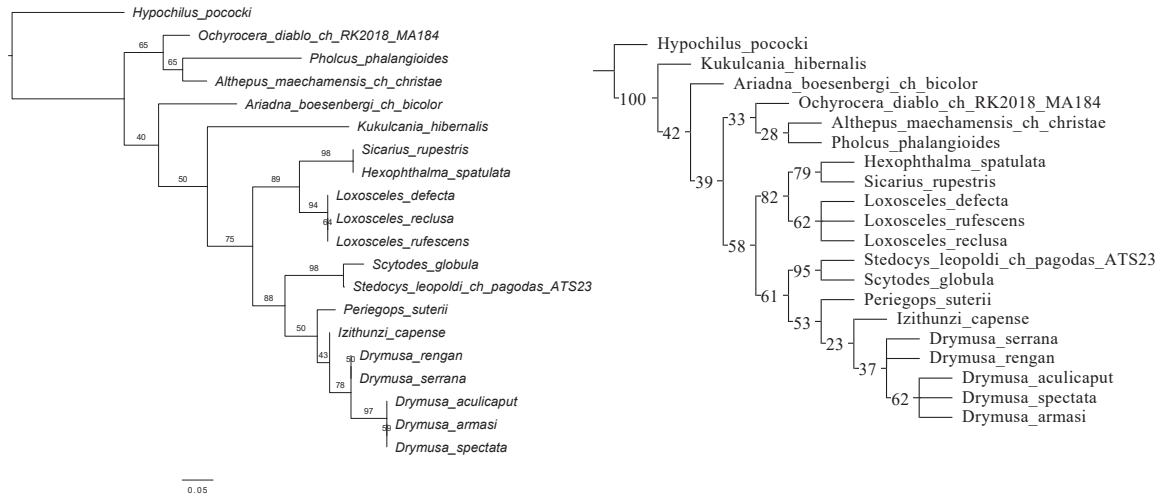
**Figure S1.** Maximum likelihood tree from target-gene molecular markers (12S, 16S, COI, H3, 18S, 28S), estimated with IQ-TREE, with 1000 ultrafast bootstrap rounds.



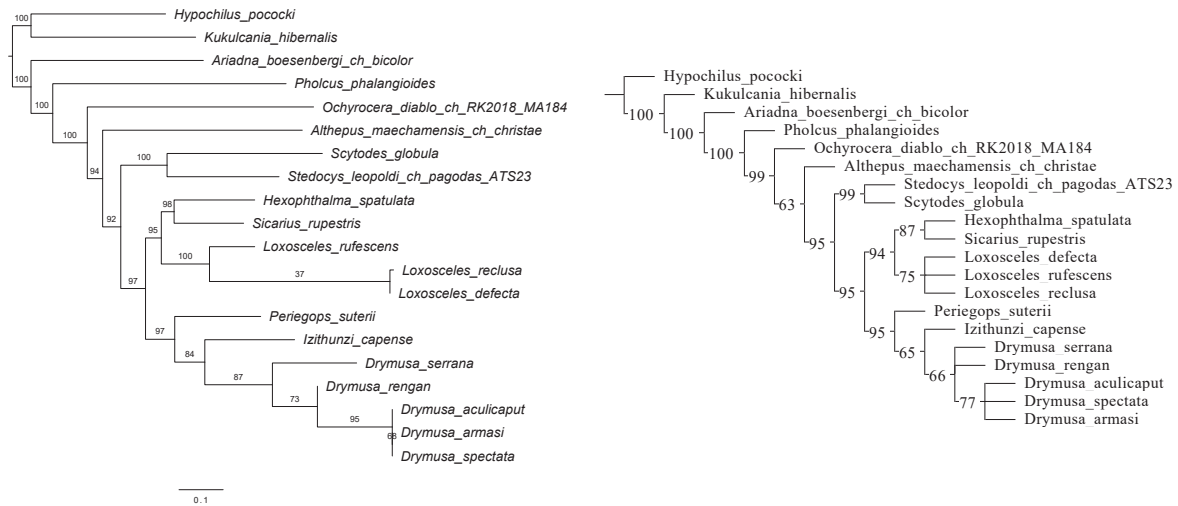
**Figure S2.** Maximum likelihood tree from the UCE genomic dataset, estimated with IQ-TREE, with 1000 ultrafast bootstrap rounds.



**Figure S3.** Trees from the molecular partition (UCE + target-genes). Left, maximum likelihood tree estimated with IQ-TREE, with 1000 ultrafast bootstrap rounds. Right, maximum parsimony tree estimated with TNT, with 1000 bootstrap rounds.



**Figure S4.** Trees from the morphological partition. Left, maximum likelihood tree estimated with IQ-TREE, with 1000 ultrafast bootstrap rounds. Right, maximum parsimony consensus tree estimated with TNT, with 1000 bootstrap rounds.



**Figure S5.** Total evidence dataset. Left, maximum likelihood tree estimated with IQ-TREE, with 1000 ultrafast bootstrap rounds. Right, maximum parsimony tree estimated with TNT, with 1000 bootstrap rounds. Note: the branches resolved in the ML tree (but not in the MP tree) are not supported by any synapomorphy, molecular or morphological, and have been collapsed for Fig. 6.