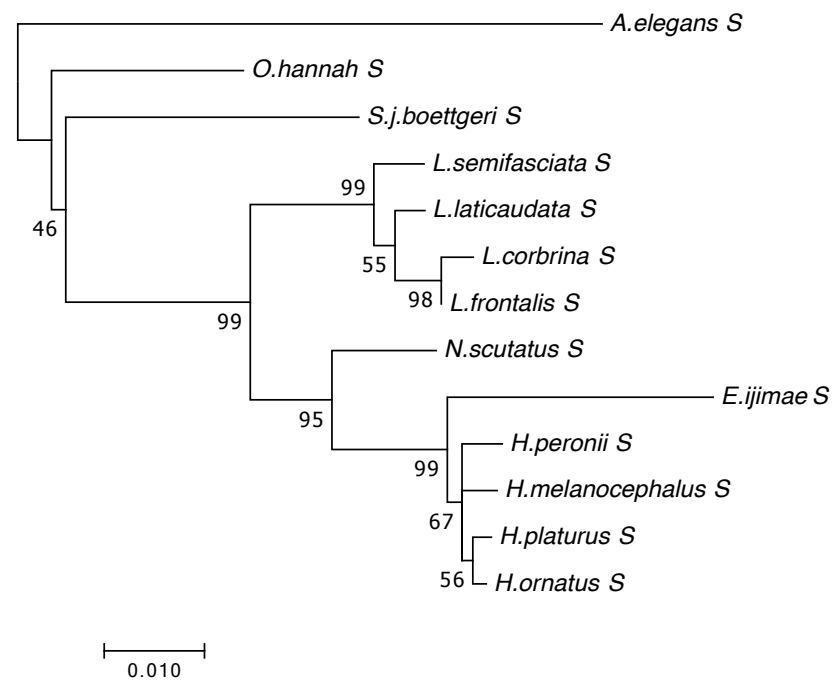
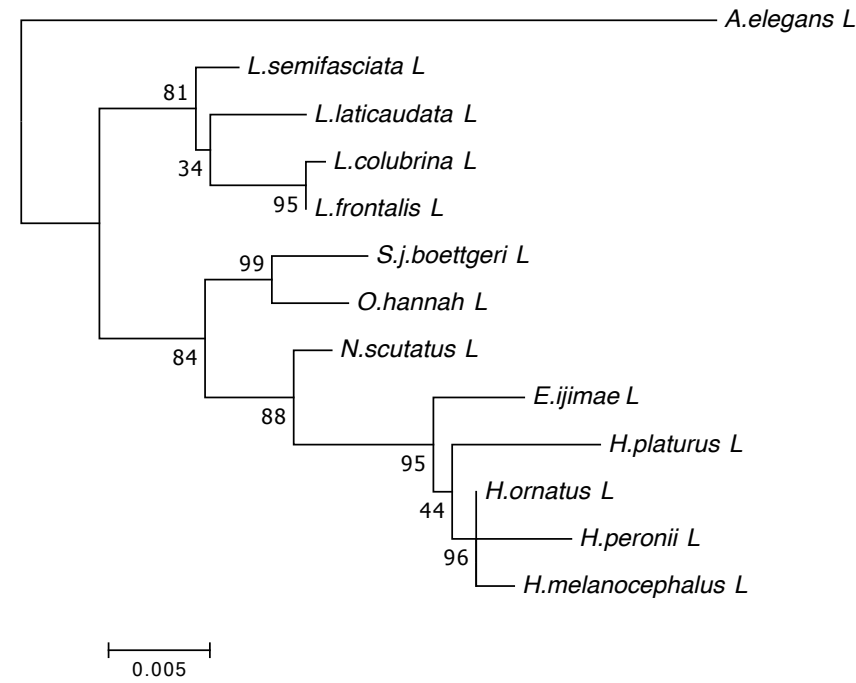


(a) *SWS1*



(b) *LWS*



(c) *RH1*

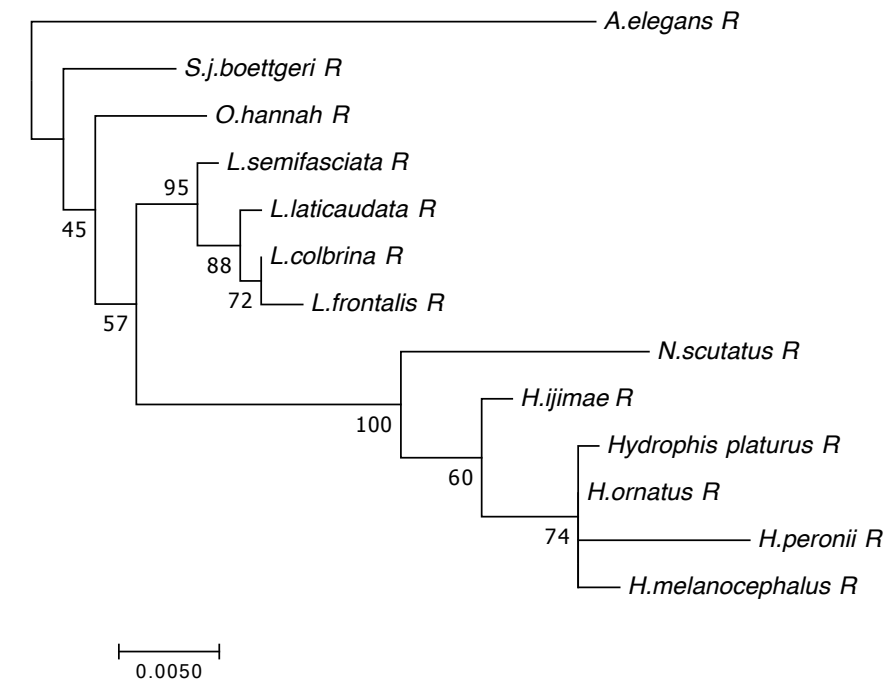


Fig. S2 Maximum Likelihood trees for (a) *SWS1*, (b), *LWS*, and (c) *RH1*

Bootstrap probability for each clade was obtained by 1,000 replicates and is shown next to each node. The scale bar represents 0.01 (*SWS1*) and 0.005 (*LWS* and *RH1*) substitutions per site.