



**Supplementary Figure S2.** Phylogenetic tree (log-likelihood: -7,026.633) resulting from the analysis of *tub2* from 48 *Sporocadaceae* isolates. Numbers represent maximum-likelihood/maximum-likelihood bootstrap values, respectively. Values represented by an asterisk were less than 70%. Scale bar represents the expected number of substitutions per site. The tree was rooted to *Beltrania rhombica* (CBS 123.58).