

SUPPLEMENTARY FIG. 1. Bayesian 50% majority rule consensus phylogenetic tree based of combined data set of *SSU* rRNA, *LSU* rRNA, *TEF*, *RPB1* and *RPB2* of *Cordyceps* species that parasitize Orthoptera. Bayesian posterior probabilities and ML bootstrap support are given respectively at first and second position, above or below the branches. *Glomerella cingulata*, Bionectriaceae, Nectriaceae and Hypocreaceae were used as the outgroup taxa based on previous phylogenetic analyses (Castlebury et al. 2004, Sung et al 2007a, Kepler et al 2011).