S5 Fig. Maximum likelihood tree of *M. oryzae* Zn(II)$_2$Cys$_6$ cluster proteins. Proteins containing Zn(II)$_2$Cys$_6$ domain were identified in the *Magnaporthe* database using PFAM pHMM zn_clus_ls.hmm. The unrooted phylogenetic tree was constructed using an alignment of 119 zinc cluster *M. oryzae* sequences. Asterisks in the clades denote high LRT support values (* LRT > 80%).