



Supplementary Fig. S1. A phylogenetic tree of 61 strains used in this study and the related strains of *Aspergillus* sect. *Nigri* by maximum likelihood method based on sequences of calmodulin gene, with algorithm of the General Time Reversible plus discrete Gamma distribution with five rate categories, and by assuming that a certain fraction of sites was evolutionarily invariable (GTR+G+I), which was calculated as the highest likelihood for this dataset. The numbers on the branch nodes represent bootstrap values >70% based on 1000 replications are shown. *Aspergillus flavus* NRRL 1957 was used for an outgroup.