Figure S1. Multiple sequence alignment of *SIX6* genes. Two sequences of F. hostae were obtained from the genome data by tBLASTn using sequence of *F. mindanaoense* (a; PD20-05, ACY39286) and *Fusarium oxysporum* f. sp. *lycopersici* (b; BFOL51, ACY39286) as queries. The predicted SIX6 of *F. mindanaoense* (PD20-05) is shown as a representative sequence. The hyphen means gap site. Predicted cleavage sites of signal peptides are indicated by vertical bars. The alignment was conducted by ClustalW implemented in MEGA7.