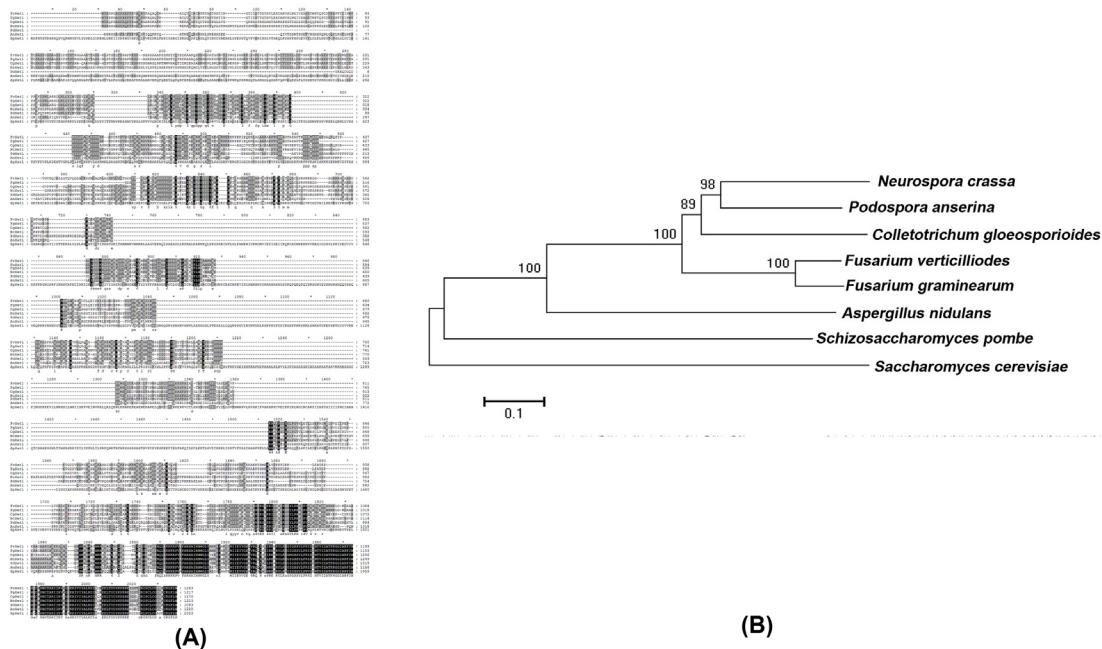


# Supplementary Materials: Involvement of FvSet1 in Fumonisin B1 Biosynthesis, Vegetative Growth, Fungal Virulence, and Environmental Stress Responses in *Fusarium verticillioides*

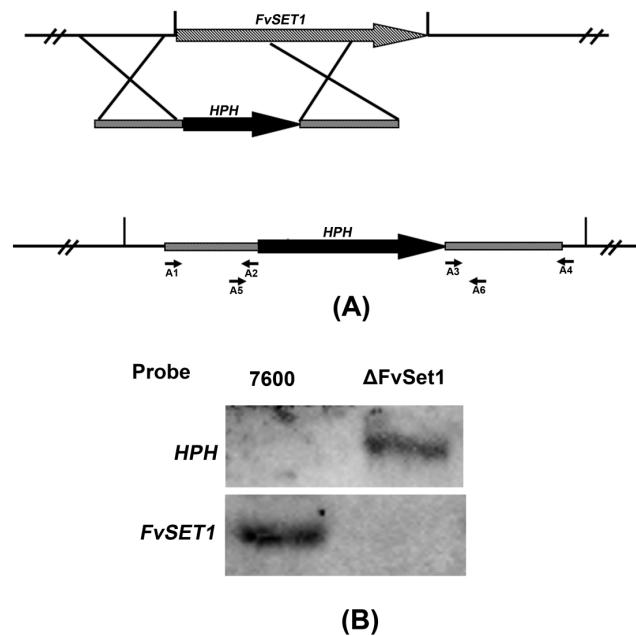
**Qin Gu, Hafiz Abdul Samad Tahir, Hao Zhang, Hai Huang, Tiantian Ji, Xiao Sun, Liming Wu, Huijun Wu and Xuewen Gao**

**Table S1.** Primers used in this study.

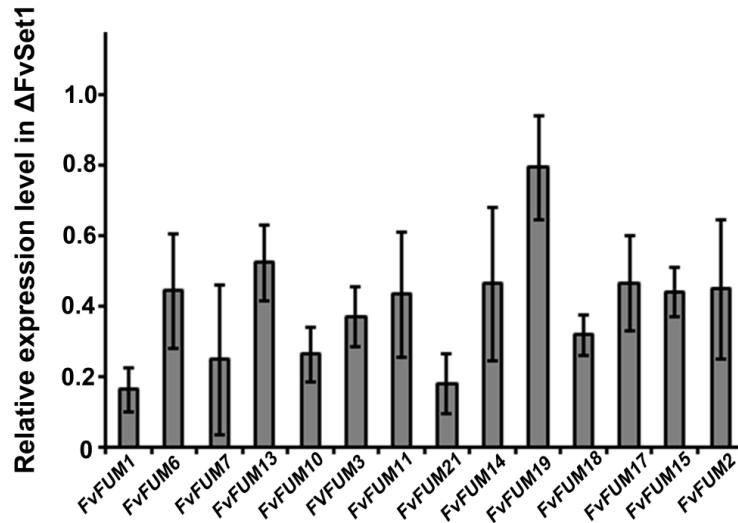
| Primer     | Sequence (5'-3')   | Application   |
|------------|--|---|
| A1         | CGATGAAGAGGAGGGAGTTGA  |   |
| A2         | CAAAATAGGCATTGATGTGTTGACCTCCG<br>GAAATTGGTGGGAGAATGA           | A pair of PCR primers for amplification of the upstream sequence of the <i>FgSET1</i> gene for construction of the gene deletion vector   |
| A3         | CTCGCCGAGGGCAAAGGAATAGAGTAG<br>AATGATTAGGACGATGACGCC           | A pair of PCR primers for amplification of the downstream sequence of the <i>FgSET1</i> gene for construction of the gene deletion vector |
| A4         | ATATCGGGCTCGGGATT  |   |
| A5         | AAGCGAGCGTCAACTCCTTG   |   |
| A6         | ATTGATATAACCGAGGGGACCC   | A pair of PCR primers for identification of <i>FgSET1</i> deletion mutants  |
| FvSet1-C-F | CAGATCTGGCTTCGTAGGAACCCAATC<br>TTCAATGACTCGCCCGCCA             | A pair of PCR primers to amplify <i>FgSET1</i> fragment used for construction of the FgSet1-C vector                                      |
| FvSet1-C-R | CACCACCCGGTAAACAGCTCCTCGCCCT<br>TGCTCAC GTT GAGGAAGCCCTTGCAGTT |   |
| HPH-F      | GGAGGTCAACACATCAATGCCTATT                                      | Amplify <i>HPH</i> sequence   |
| HPH-R      | CTACTCTATTCTTTGCCCT  |   |
| FvActin-F  | TGCTCCTGAGGCTCTCTTCCA  | Quantitative real-time PCR primers for analysis of the reference gene actin expression level  |
| FvActin-R  | AAGCAAGAATAGAACCCACCGA   |   |
| FUM1-F     | TGCTGCCCTGTATCACAACCA  | Quantitative real-time PCR primers for analysis of <i>FUM1</i> gene expression level  |
| FUM1-R     | AATGTGCGCTTGATCCAGTT   |   |
| FUM6-F     | TCTCTGTTCTTGGCTGTCG  | Quantitative real-time PCR primers for analysis of <i>FUM6</i> expression level   |
| FUM6-R     | TCAATTCTAGCAGCATCGG  |   |
| FUM7-F     | GCATGGAGAGACAAGTTGCA   | Quantitative real-time PCR primers for analysis of <i>FUM7</i> expression level   |
| FUM7-R     | TCTGATGAAACTGGCTTCGT   |   |
| FUM21-F    | AGCTTGTCAACCCAGCAGATA  | Quantitative real-time PCR primers for analysis of <i>FUM21</i> expression level  |
| FUM21-R    | TCAACTATAGTCCCAGCATCA  |   |
| FUM10-F    | TTTGGAACCCAATGGCGAT  | Quantitative real-time PCR primers for analysis of <i>FUM10</i> expression level  |
| FUM10-R    | TTTCGGCAGGGCTGATTTTT   |   |
| FUM11-F    | AAGGGGGAAGATAGGCACT  | Quantitative real-time PCR primers for analysis of <i>FUM11</i> expression level  |
| FUM11-R    | ATTACGAGTCTAGCGAGCGA   |   |
| FUM13-F    | AAACCATGGATGGTATCAGG   | Quantitative real-time PCR primers for analysis of <i>FUM13</i> expression level  |
| FUM13-R    | TTTCTGCTGAGCCGACATCAT  |   |
| FUM14-F    | AAGAGGTGCTAAAGACAGCCA  | Quantitative real-time PCR primers for analysis of <i>FUM14</i> expression level  |
| FUM14-R    | ACTCAGGAGCTGCGACTGATA  |   |
| FUM15-F    | TATGCCCTGGAAAAGCTTG  | Quantitative real-time PCR primers for analysis of <i>FUM15</i> expression level  |
| FUM15-R    | TCTGTGGGTCCATTCAATA  |   |
| FUM17-F    | CTCACGATATCAGTGACCTTT  | Quantitative real-time PCR primers for analysis of <i>FUM17</i> expression level  |
| FUM17-R    | AGCCATATGATGTTGAGGGT   |   |
| FUM18-F    | TCCTCTCCTGTTCTGACGA  | Quantitative real-time PCR primers for analysis of <i>FUM18</i> expression level  |
| FUM18-R    | TTGTAGTTGAGATTGCTGCCA  |   |
| FUM2-F     | AAGTGCTGGGGAGCGGGTT  | Quantitative real-time PCR primers for analysis of <i>FUM2</i> expression level   |
| FUM2-R     | TCGGGGCATAACTCTATATCG  |   |
| FUM3-F     | ACTGATTCACCGAGGCCAA  | Quantitative real-time PCR primers for analysis of <i>FUM3</i> expression level   |
| FUM3-R     | AGCGGACCGGAAGCTTCT   |   |



**Figure S1.** FvSet1 is homologous to those counterparts from yeasts and other filamentous fungi. **(A)** alignments of amino acid sequences of Set1 orthologs from *Fusarium verticillioides* (FvSet1), *Saccharomyces cerevisiae* (ScSet1), *Schizosaccharomyces pombe* (SpSet1), *Neurospora crassa* (NcSet1), *Podospora anserina* (PaSet1), *Colletotrichum gloeosporioides* (CgSet1), *Aspergillus nidulans* (AnSet1), and *Fusarium graminearum* (FgSet1). Boxshade program was used to highlight identical (black shading) or similar (grey shading) amino acids; **(B)** phylogenetic tree generated using the neighbour-joining method with Mega 4.1 software (<http://www.megasoftware.net/>) on the basis of the deduced amino acid sequences of FvSet1 from *F. verticillioides* strain 7600 and those from *S. cerevisiae*, *S. pombe*, *N. crassa*, *C. gloeosporioides*, *P. anserine*, *A. nidulans*, and *F. graminearum*. The bootstrap values are indicated on the phylogenetic tree.



**Figure S2.** Schematic representation of the *FvSET1* disruption strategy and Southern blotting analyses of the deletion mutants. **(A)** Schematic diagram of the *FvSET1* gene, and gene replacement construct; **(B)** Southern blot analysis of *Dra* I-digested genomic DNA of the wild type 7600 and  $\Delta$ FvSet1 mutant hybridized with the *FvSET1* gene and *HPH* probes, respectively.



**Figure S3.** Relative expression of *FUM* genes in the  $\Delta$ FvSet1. The relative expression levels of *FUM* genes in  $\Delta$ FvSet1 are the relative amounts of mRNA of the gene in the wild-type progenitor. The expression level of the actin gene was used as an internal reference for each sample. Line bars in each column denote standard errors of three repeated experiments.