

## FvKex2 is required for development, virulence and mycotoxin production in *Fusarium verticillioides*

Limin Wu<sup>1</sup>, Wenyin Bian<sup>2</sup>, Yakubu Saddeeq Abubakar<sup>2</sup>, Jiayi Lin<sup>3</sup>, Huijuan Yan<sup>4</sup>, Fang zhang<sup>4</sup>, Zonghua Wang<sup>2</sup>, Changbiao Wu<sup>1</sup>, WonBo Shim<sup>4\*</sup>, Guo-dong Lu<sup>2\*</sup>

<sup>1</sup>Fujian Vocational College of Bioengineering, Fuzhou 350002, China

<sup>2</sup>Key Laboratory of Bio-pesticide and Chemical Biology, Fujian Agriculture and Forestry University, Fujian, Fuzhou 350002, China

<sup>3</sup>Guangzhou University of Chinese Medicine, Guangzhou 510006, China

<sup>4</sup>Department of Plant Pathology and Microbiology, Texas A&M University, College Station 77843-2132, TX, USA

\*Corresponding author:

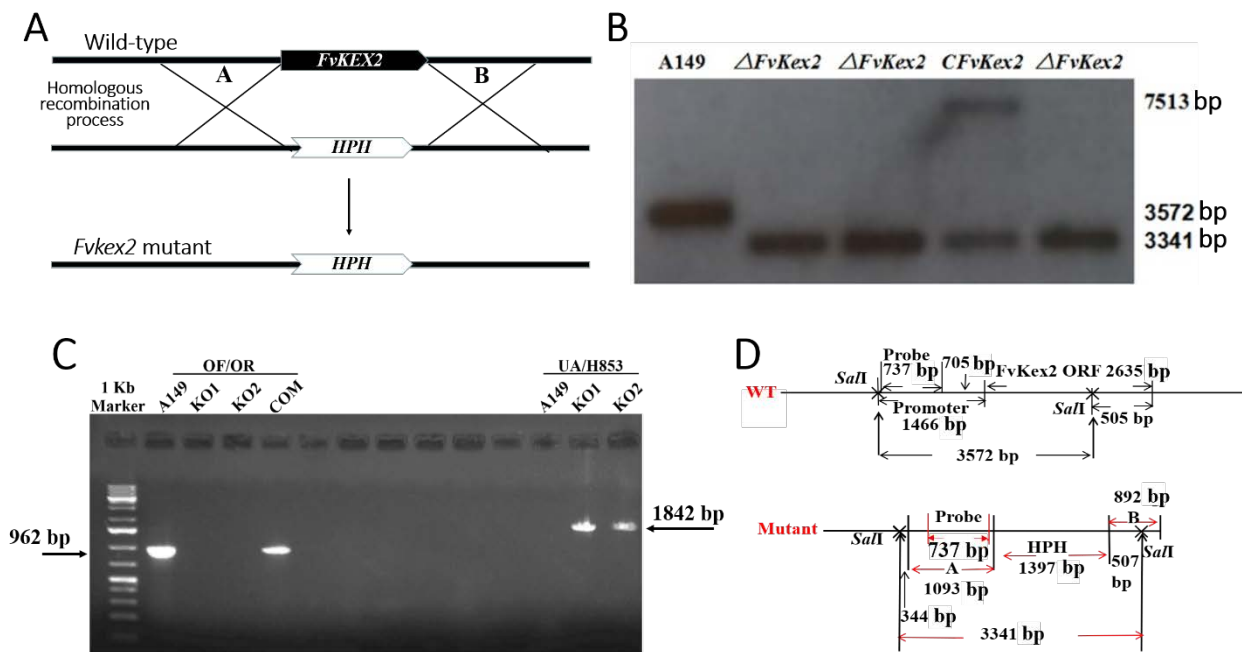
Won Bo Shim E-mail address: wbslim@tamu.edu,

Guo-dong Lu

Tel: +86-13950480067 Fax: +86-591-83768251

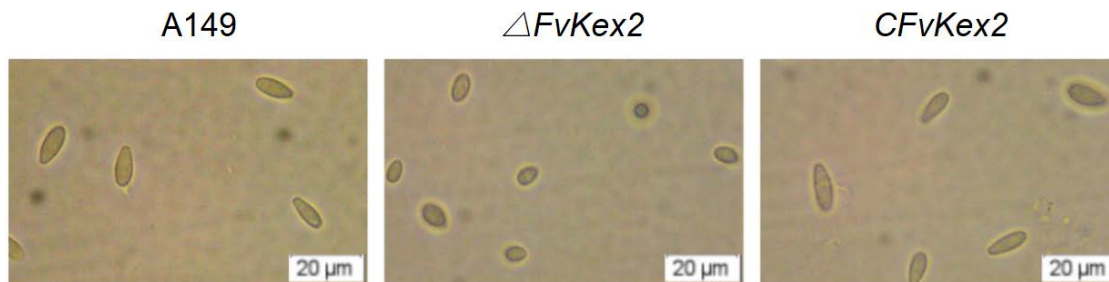
E-mail address: lgd@fafu.edu.cn

## Supplemental Figures



**Fig. S1: Targeted *FvKEX2* gene deletion in *F. verticillioides***

(A) Targeted gene deletion strategy for the *FvKEX2* gene. The *FvKEX2* gene (962 bp) was replaced by the hygromycin phosphotransferase (*HPH*) gene in the mutant. (B) Southern blot analysis was used to confirm the *FvKEX2* gene deletion and complementation. Genomic DNA from the indicated strains was digested with *SalI* and separated on a 1% agarose gel. The target bands of 3572, 3341 and 7513 bp were observed in the wild-type A149, mutant and complemented strain, respectively. (C) Confirmation of *FvKEX2* gene deletion by PCR. The FvKOF and FvKOR primers were used to amplify a 962 bp fragment of the gene ORF (open reading frame) using genomic DNA from the indicated strains; the band could not be amplified from the mutant DNA. Also, the primers FvKUA (which anneals upstream of the A fragment) and H853 (which anneals within the *HPH* fragment) gave positive bands of 1842 bp in the mutants, which the band was absent in the wild-type. (D) A map showing the digestion fragments for Southern blot assay. *SalI* digestion produces 3573 bp and 3341 bp fragments in the wild-type and mutants, respectively.



**Fig. S2: Morphology of *Fvkex2* mutant conidia.**

The  $\Delta Fvkex2$  mutant has shorter conidia than A149 and *CFvKex2*