# The Role of p38 MAPK, JNK, and ERK in Antibacterial Responses of *Chilo suppressalis* (Lepidoptera: Crambidae)

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### Abstract

The mitogen-activated protein kinases (MAPKs) are conserved signal transduction pathways and broadly responsible for bacterial infection from yeast to mammals, and virus, fungi, and bacteria, specifically *Bacillus thuringiensis*, to insects. But little is known about the MAPK pathways in antibacterial responses in *Chilo sup pressalis* (Walker), an important lepidopteran pest of rice. In this study, we used the bacteria of *Bacillus thuringiensis*, *Escherichia coli*, and *Staphyloccocus aureus* to infect *C. suppressalis* larvae, and the responses of MAPK pathways were analyzed. The results showed that *E. coli* infection induced the up-regulated expression of *Csp38* and *CsERK1* at 24 h postinfection (pi). Meanwhile, injection of *B. thuringiensis* and *S. aureus* resulted in strong activation of *CsJNK* phosphorylation at 3 h pi. These results suggest that MAPK signaling pathways play important functional roles in antibacterial responses in *C. suppressalis* larvae.

Key words: p38 mitogen-activated protein kinase, c-Jun N-terminal kinase, extracellular signal-regulated kinase, Chilo suppressalis, antibacterial responses

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Table 1. Specific primers used in the experiments

• m • m	• . ~ . <b>E E</b>	• 'm'' · · · · (5'-3')
<i>EF-1-</i> F	1.11	GAACCCCCA ACAGCGAA CC
EF-1_	At	C CCG GCCAACCAGAAA AGG
<i>Р38-</i> F	· · ·	CA ACGCGG GAG GCAA
P38	At	GCAAAC G CGA CGC GAA
JNK-F	· · ·	GGCAGC ACGA AC GGCA
JNK-	At	AC CCCGA G C GCG
ERK1-F		GCC GCC A A CGGCAAC
ERK1	At	CCGG GGAAGGG GAGG C
ERK2-F	· · ·	C GCG C G ACGGGAG G C
ERK2	Att	CGAACAG A GCCACCAGAAG

#### Materials and Methods

Insect Rearing

#### Real-Time Quantitative PCR

a marker elliptic presses A particulation m to E coli A , E to B , E to E coli A , E to E B to , to , to , to for  $(10,000, m, 4^{\circ}C) f = 5 m$  $\mathbf{t}_{\mathbf{v}} = \mathbf{c}_{\mathbf{v}} \mathbf{t}_{\mathbf{v}} (\mathbf{D}) \cdot \mathbf{f} \mathbf{1.0}, \quad \mathbf{2} \mu = \mathbf{t}_{\mathbf{v}} \mathbf{c}_{\mathbf{v}} \mathbf{c}_{\mathbf{v}} \mathbf{c}_{\mathbf{v}} \mathbf{w}_{\mathbf{v}} \mathbf{w}_{\mathbf{v}}$  $\begin{array}{c} \mathbf{x}_{1} = \mathbf{y}_{1} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{x}_{1} \mathbf{x}_{2} \mathbf{$  $( -1)_{w} \quad f : t = CB \quad f : t = (tt : t)_{www}$ m ....  $\ell$  ....  $\ell$  .... k )  $\ell$  .... C .... C suppressalis (1, t, ..., t, ..., 1, ..., $\begin{array}{c} & & \\ & &$ , a, alter a a C. ema, a dide at a par alter t, e sut eve v, D. A, er, un to 1µtt 🖕 A<sub>w</sub> , v  $\begin{aligned} \mathbf{t}_{\mathrm{const}} &= \left( \begin{array}{c} \mathbf{D} \\ \mathbf{A} \\ \mathbf{C} \\$ 2004; 2).

#### Western Blot Assays

 Table 2. Primer specifications for optimized qRT-PCR amplification

 of C. suppressalis

Gran m	Eff.	$R^2$	~• *
CsEF1	99.8%	0.992	-3.326
Csp38	100.9%	0.994	-3.300
ĊsJNK	103.9%	0.995	-3.235
CsERK1	99.9%	0.992	-3.325
CsERK2	103.5%	0.980	-3.242

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#### Data Analysis

 $ttt = \frac{1}{2} \frac{1}{2$ 

#### **Results and Discussion**

Effect of Bacteria on *C. suppressalis* p38 MAPK Pathway Activation



Fig. 1. Effects of bacterial treatment on *C. suppressalis* MAPKs. (A) Relative estimates of *Csp38* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (B) Relative estimates of *CsJNK* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (B) Relative estimates of *CsJNK* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (C) Relative estimates of *CsERK1* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (D) Relative estimates of *CsERK2* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (D) Relative estimates of *CsERK2* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (D) Relative estimates of *CsERK2* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. (D) Relative estimates of *CsERK2* transcripts from qRT-PCR of *C. suppressalis* larvae treated with bacteria for 0, 3, 6, 12, and 24 h. Relative amounts of genes transcript were normalized to the expression of *EF1*. Each symbol and vertical bar represents the mean  $\pm$  SE (n = 3). Asterisks indicate significant differences (P < 0.05; ANOVA).

# Responses of *C. suppressalis* JNK Pathway to Bacteria Challenge

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### Analysis of *C. suppressalis* ERK1/2 Pathways in Response to *S. aureus*, *B. thuringiensis*, and *E. coli* Immune Stimulations

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