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## *Capsicum annuum* homeobox 1 (CaHB1) is a nuclear factor that has roles in plant development, salt tolerance, and pathogen defense

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### ABSTRACT

Homeodomain-leucine zipper (HD-Zip) family proteins are unique to plants, but little is known about their role in defense responses. CaHB1 is a nuclear factor in peppers, belonging to subfamily II of HD-Zip proteins. Here, we determined the role of CaHB1 in the defense response. CaHB1 expression was induced when pepper plants were challenged with *Phytophthora capsici*, a plant pathogen to which peppers are susceptible, or environmental stresses such as drought and salt stimuli. CaHB1 was also highly expressed in pepper leaves following application of SA, whereas ethephon and MeJA had a moderate effect. To further investigate the function of CaHB1 in plants, we performed gain-of-function study by overexpression of CaHB1 in tomato. CaHB1-transgenic tomatoes showed significant growth enhancement including increased leaf thickness and enlarged cell size (1.8-fold larger than control plants). Microscopic analysis revealed that leaves from CaHB1-transgenic plants had thicker cell walls and cuticle layers than those from controls. Moreover, CaHB1-transgenic plants displayed enhanced resistance against *Phytophthora infestans* and increased tolerance to salt stress. Additionally, RT-PCR analysis of CaHB1-transgenic tomatoes revealed constitutive up-regulation of multiple genes involved in plant defense and osmotic stress. Therefore, our findings suggest roles for CaHB1 in development, salt stress, and pathogen defense.

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### 1. Introduction

The homeodomain leucine zipper (HD-Zip) family of proteins in plants is a group of transcription factors that regulate development in response to environmental or external stresses [1,2]. The family is classified into four subfamilies (HD-Zip I-IV) by DNA-binding, conserved motif, and function [2]. The genes in subfamily I and II are involved in adaptation to external stimuli such as drought and salinity [3,4]. The H52 protein in tomato, a member of the HD-Zip family, limits cell death during pathogen infection [5]. Silencing of H52 in tomatoes resulted in cell death, which spread to uninfected neighboring plant parts during infection [5].

Osmotic treatment induced the expression of a number of HD-Zip family genes, namely *Arabidopsis thaliana* HB6 (*AtHB6*), *Barssica napus* HB6 (*BnHB6*), and *Oriza sativa* *hox22* (*Oshox22*) [6–8]. These genes were up-regulated by various environment

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stresses and by externally applied abscisic acid (ABA) or salicylic acid (SA) [6–8]. Zhang et al. [8] demonstrated that overexpression of *Oshox22* reduced tolerance to salt stress at the rice seedling stage through an ABA-mediated signaling pathway. However, there is no available information about the *Homeobox* (HB) gene-mediated defense response to pathogen attack.

Recently, we described the *NbHB1* gene, which encodes an HD-Zip protein from *Nicotiana benthamiana* [9]. Using transient or virus-induced gene silencing in *N. benthamiana*, we showed that *NbHB1* positively regulated pathogen-induced cell death. In our studies, expression of *NbHB1* following inoculation with pathogens and various other treatments was enhanced [9]. Ectopic expression of *NbHB1* accelerated cell death following abiotic stresses or bacterial pathogen inoculation [9]. According to protein databases, the *NbHB1* protein belongs to subfamily II with an N-terminal variable region and C-terminal conserved CPSCE motif [1,9]. We also identified *Capsicum annuum* *homeobox 1* (*CaHB1*), an HD-Zip II family gene, in pepper plants infected with a bacterial pathogen [9]. However, the role of *CaHB1* in disease resistance is unknown.

Here, we describe the role of *CaHB1* in plant defense against pathogens using gain-of-function studies in transgenic tomato (*Solanum lycopersicon* L. cv. ‘MicroTom’) plants overexpressing

*CaHB1*. We believe these results will considerably enhance understanding of the role of HD-Zip genes in defense against pathogens and environmental stresses.

## 2. Materials and methods

### 2.1. Plant materials

For tomato (*S. lycopersicon* L. cv. 'MicroTom') transformation, seeds were surface-sterilized in 1% (v/v) NaOCl, followed by wash with sterilized distilled water. Seeds were then germinated on MS agar medium and kept in a plant growth chamber under a 16-h photoperiod at 25 °C for 2 weeks before being used for transformation [10]. Tomato and pepper plants (cv. Bugang) were grown in pots and maintained under a 16-h photoperiod at 25 °C.

### 2.2. Agrobacterium-mediated transformation of tomato

A method for generation of transgenic plants was used as described by Oh et al. [10]. Briefly, cotyledons from 2-week-old tomato seedlings germinated on MS medium were used for co-cultivation with *Agrobacterium* to generate transgenic plants [10]. Kanamycin-selected transgenic plants were grown in a greenhouse, and then transgenic plants were further selected by measuring the expression of the nopaline synthase terminator by PCR with a primer set (Table S1).

### 2.3. Evaluation of *CaHB1*-transgenic tomato resistance to *Phytophthora infestans*

Four-week-old T3-tomato plants were inoculated with the zoospores of *P. infestans*. *P. infestans* infection of tomato plants were performed using zoospores inoculations as described by Oh et al. [10]. Disease symptoms appeared within 2 to 3-DAI from 5–6 independent infected plants. The index of *Phytophthora* infection was determined visually based on the necrotic leaf area [10].

### 2.4. Chlorophyll content analysis

For the leaf disk assay, tomato leaf disks with a diameter of 10 mm ( $n=5$ ) were prepared from tomato leaves of identical development stage of both vector-control and transgenic plants and floated on solutions of different NaCl concentrations for 3-days. After treatment with NaCl (0.5 and 1.0 M), chlorophyll was extracted from transgenic or control only transgenic-tomato leaves according to the method of Hu et al. [11], and then the chlorophyll content was calculated by the method of Lichtenthaler [12]. The photographs were taken at 3 days, and the experiments were repeated at least twice.

### 2.5. Microscopic analysis

Microscopic analysis was carried out following the methods as described by Sarowar et al. [13]. Leaves of one-month-old control or *CaHB1*-transgenic plants were observed under a light microscope and a transmission electron microscope (TEM).

### 2.6. Chemical treatment and pathogen inoculation

To determine the expression of the *CaHB1* transcripts after treatment of 5 mM SA, 5 mM ethephone, 100  $\mu$ M MeJA, or 100  $\mu$ M ABA, leaves of pepper plants were sprayed with chemicals as described in Oh et al. [10].

### 2.7. Subcellular localization of *CaHB1* protein

A construct, *CaHB1*-smGFP under the control of CaMV-35S promoter, was made for *CaHB1* expression in *N. benthamiana* protoplast. The fusion constructs were introduced into *N. benthamiana* protoplasts prepared from young leaves by the polyethylene glycol-mediated transformation Oh et al. [10]. Expression of the fusion constructs was observed at 40 h after transformation using a confocal laser scanning microscope (Carl Zeiss LSM 510), and the image was captured with a cooled charge-coupled device camera. The filter sets were used as described in Oh et al. [10].

### 2.8. RT-PCR analysis

Total RNA samples were extracted from pepper using TRI reagent according to the manufacturer's instructions (Invitrogen). RT-PCR was performed to detect the endogenous levels of several genes using the primer sets listed in Supplemental Table S1. The expression of the *PiEF1a* gene was controlled with a primer pair specific for the constitutively expressed tomato *Actin* gene (Table S1).

## 3. Results

### 3.1. Expression and cellular localization of *CaHB1*

We isolated *CaHB1* using genome-wide screening, which identifies genes up-regulated during pepper-bacterial pathogen interaction [9,14]. This gene's (NCBI accession No. EU998972) open reading frame encodes 272 amino acid residues (Fig. S1) and, according to protein databases, contains an N-terminal variable region, an HD-Zip domain, and a C-terminal conserved CPSCE motif. Therefore, it belongs to subfamily II of the HD-Zip family [1,9]. The overall structure of *CaHB1* is similar to other HD-Zip family plant proteins, especially NbHB1, with which it shares 84% amino acid identity (Fig. S1).

The expression of *CaHB1* was determined in different tissues of the pepper plant. High levels of *CaHB1* transcripts were present in flowers and stems, while levels were low in leaves and roots (Fig. 1A). *CaHB1* was highly expressed during development in pepper leaves, indicating *CaHB1* regulates senescence (Fig. 1B).

HD-Zip proteins are transcription factors; therefore, we determined whether *CaHB1* is present in the nucleus. Although we did not find putative nuclear localization sequences in *CaHB1* with the PSORT II program (<http://psort.nibb.ac.jp>), other evidence indicates that it is localized in the nucleus. *CaHB1* was tagged at the C-terminal with soluble modified green fluorescent protein (smGFP) and constitutively expressed using the CaMV-35S promoter (Fig. 1C). The fused construct was transformed into protoplasts of *N. benthamiana*, and GFP fluorescence was localized in the nucleus (Fig. 1C). In contrast, with the 35S-smGFP control, GFP fluorescence was observed throughout the cytoplasm and the nucleus. Like other HD-Zip proteins, *CaHB1* appears to be a nuclear transcription factor.

### 3.2. Effect of biotic and abiotic stresses on *CaHB1* expression

To understand the function of *CaHB1* in stress, the expression levels of *CaHB1* were monitored in pepper plants treated with biotic and abiotic stress. *CaHB1* expression was strongly induced when pepper leaves were inoculated with the pepper pathogen, *Phytophthora capsici*. Likewise, *CaHB1* transcripts increased remarkably after inoculation, before disease symptoms were visible, and remained elevated until 72 h after inoculation (Fig. 1D). *CaPR-1* transcript, a marker gene, was detected 48 h after inoculation and remained high for 72 h (Fig. 1D).

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