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Monitoring of the cell wall modification related genes by permissive high temperature treatment in Chinese cabbage

Kyung Ae Yang¹, Chan Ju Lim¹, Joon Ki Hong¹, Nguyen Duong Nha¹, Woo Sik Chung¹, Kyun Oh Lee¹, Young Ju Choi², Sang Yeol Lee¹, Chae Oh Lim^{1*}.

¹Division of Applied life Science (BK21), Environmental Biotechnology National Core Research Center, Gyeongsang National University, Jinju 660-701, Korea

²Department of Food and Nutrition, Silla University, Busan 617-736, Korea

Objectives

Plant can acquire enhanced tolerance to otherwise lethal high temperature, if it is subject to a permissive-high temperature. This phenomenon is termed as acquired thermotolerance. In this study, to understand the acquired thermotolerance mechanisms, we monitored the global transcriptome changes using *Brassica rapa EST 6.4K* microarrays with probes derived from the time courses of permissive-high temperature exposure.

Materials and Methods

1. Materials

- Plant: One-week old Chinese cabbage (*Brassica campestris* L. ssp. *perkinensis* cv. Jangwon) seedlings incubated at 37°C for 0 h, 0.25 h, 1 h, 3 h, and 12 h

- Microarray: *Brassica rapa EST 6.4K*

2. Methods

- Microarray hybridization, analysis and data mining

- Histochemical staining: ① Monitoring H₂O₂ generation using tetramethylbenzidine reagent
② Cell wall observation using Aniline Blue.

Results and Discussion

By permissive-high temperature treatment, Chinese cabbage seedlings obtained the acquired thermotolerance; microarray analyses showed that about 20% of total microarray elements were positively regulated during heat treatment. It included several antioxidant genes and cell wall modification genes as well as many heat shock proteins (HSPs) and heat shock factors (HSFs). Similar to transcriptome changes, histochemical staining proved the induction of the heat-mediated oxidative stress generating hydrogen peroxide (H₂O₂) and the cell wall modification during heat treatment. In addition, several cell wall modification related genes (e.g. xyloglucosyl transferase) were induced by H₂O₂ (Genevestigator D/B; <https://www.genevestigator.ethz.ch/>). These results indicate that synthesis of HSPs and HSFs were involved in acquiring thermotolerance, but also the cell wall modification under the oxidative stress induced by permissive-high temperature is an important resource to acquire thermotolerance.

* Corresponding author : Chae Oh Lim, TEL: 055-751-6255, E-mail: colim@gsnu.ac.kr.