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AtEF1a, a translational elongation factor 1a from *Arabidopsis*, functions as molecular chaperone and confers resistance to salt stress in yeast and plant

Dongjin Shin, Hyo-jung Lee, and Dae-Jin Yun'

Division of Applied Life Science, Graduate School of Gyeongsang National University, Jinju 660-701, Korea

Objectives

We have isolated and characterized an Arabidopsis gene that confers NaCl tolerance to yeast

Materials and Methods

1. Material

Yeast-Saccharomyces cerevisiae Plant-Arabidopsis thaliana plants

2. Methods

Arabidopsis genes that can functionally complement salt-sensitive phenotype of a calcineurin (CaN)-deficient yeast mutant (cnb, regulatory subunit null mutant) was isolated and characterized.

Results and Discussion

An Arabidopsis cDNA clone that encodes putative translational elongation factor 1a (EF1a) was isolated by functional complementation of yeast cnb mutant. The amino acid identities of AtEF1a with the known proteins from human, yeast were 82.6%, and 81.2% The transformants harboring full length cDNA or truncated form of EF1a (deleted 24 amino acids) complemented the NaCl sensitive phenotype of cnbD cells. Because EF1a is known to regulate protein fidelity in protein elongation step, we made two point mutants related to protein fidelity and examined this activity is related to salt stress. However, the activity of EF1a was not important to salt tolerance in yeast. Interestingly, AtEF1a showed chaperone activity in a dose-dependant manner in vitro. Deletion analysis indicated that the chaperone activity of central domain of EF1a (DS3) was significantly higher than that of full length EF1a. Consistent with this observation, DS3 domain was required for NaCl tolerance of cnbD cells, but N- or C-term of EF1a was not. compared with wild-type, knock-out plant of AtEF1a from ABRC stock center was more Furthermore, transgenic plant overexpressing EF1a was more sensitive to NaCl stress. tolerance to NaCl than wild-type. Taken together, we suggest that AtEFla functions as molecular chaperone in the cell, and this activity is required for NaCl tolerance in yeast and plants. [Supported by EB-NCRC and Biogreen 21 program]

^{*} Corresponding author: Dae-Jin Yun, TEL: 055-751-6256, E-mail: djyun@gsnu.ac.kr