

Short Communication

Gene Expression in Leaves and Epidermis of Arabidopsis under Salt and Drought Stress

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Abstract: Gene expression induced by drought and salt stress also, difference genes in different time are induced with different stresses. Plants of Arabidopsis were divided into groups one under salt stress and others are to drought for 6h. Most genes are expression in both leaves and epidermis under both treatments. However, DREB2A was more highly expression in leaves at control and epidermis at 2h of drought stress as compared with other treatments.

Keywords: Salt, Arabidopsis

INTRODUCTION

Severe environmental stress can be responsible for up to 65% of decreases in plant yield, and salt and drought stresses are two of the major factors which cause this [1]. Drought and salt stresses can be connected because drought can cause soil to become salty directly or indirectly through irrigation. Growth rates are lower and biomass accumulates more slowly in roots under salt stress. For example, when barley was exposed to 100 mM NaCl and 0.1mM Ca⁺ growth and development were reduced, including reduced root hair density and root thickening compared with control plants [2]. The most obvious factors to explain the reduced growth in plants exposed to salt are osmotic stress and Na⁺ toxicity, including effects on mineral nutrition [3]. Expression some genes have been shown to increase in response to salinity, cold, drought and oxidative stress [4].

Gene expression is often different between organs and between stresses. For example *DREB2A* and *DREB2B* genes are highly expressed in roots in response to high salt and dehydration and in stems only in response to dehydration. Both had weak expression in leaves of Arabidopsis while *RD29a* was highly expressed in roots, stems and leaves after 5 hours dehydration. Also the expression of *DREB2A* and *DREB2B* was weak in flowers and siliques, and the expression of *COR78/RD29a* was also observed [5].

MATERIALS AND METHODS

Plants of *Arabidopsis thaliana* L.(Heyn) ecotype Columbia were grown in the control condition for about 5 to 6 weeks from sowing. The temperature used was 20°C /15°C for day/night. Samples were collected for analysis at the same time when plants were transferred to other treatments (time 0). The samples were collected in 1.5 ml micro centrifuge tubes, frozen in liquid nitrogen, and stored at -80°C until needed. For salt treatment, compartments containing plants growing in soil were immersed in solution containing 250 mM NaCl for 15-20 minutes. For drought treatment, the leaves were collected in Petri dishes and the leaves were weighed immediately after cutting from the plants.

Epidermis or peeled leaves were used. Lower epidermis was peeled off using tweezers. Samples of peeled epidermis or whole leaf were collected and put it in micro tubes. About 15-25 mg was collected from epidermis and 100-150mg from leaves and used to analyze different periods of exposure to salt and drought stress. RNA extracted using TRI reagent and gene expression analysis by PCR

RESULTS AND DISCUSSION

Shows gene expression for constitutively expressed reference genes *Actin* and *EF1 α* and also for transcription factor *COR* and *LTP* genes at 2 h and 6 h during drought and at 2 h, 6 h and 24 h under salt stress. The *actin* gene was expressed in both leaves and epidermis. The expression was lower in the epidermis at control, epidermis 2 h salt and epidermis 6 h salt. However, *EF1 α* was expressed in most samples but it was undetectable in epidermis at 2 h drought and was weak in epidermis at 2 h of salt.

DREB2a was expressed in control leaves and leaves at 2 h and 6 h of drought and 2 h, 6h and 24 h under salt stress (Fig 1). It was highly expressed in epidermis at 2 h under drought much more than in leaves under drought. It was undetectable at 2 h and 6 h salt in epidermis. On the other hand it was detectable at 24 h in epidermis under salt. *CBF1* was expressed under drought stress in epidermis at 6 h and in leaves at 2 h compared with control levels. *CBF1* had a higher expression in epidermis at 24 h in salt and in leaves at 24 h in salt compared with the control. *CBF3* was detectable in all samples. It showed higher expression in the epidermis at 6 h and in leaves at 2 h than other samples in drought stress. It had a higher expression in leaves than epidermis under salt stress. *COR78* was expressed when plants were exposed to drought in both leaves and epidermis at 2 h but expression decreased at 6 h in both leaves and epidermis (Fig 1). However, the expression was higher in leaves than epidermis under salt stress.

Most researchers have analysed acclimation in whole plants and organs but gene expression induced by cold is different in different tissues, for example epidermis and vascular transition zone in cereals [6]. In plants, about 60 to 77% of the genes do not have a strict tissue expression [7]. Many genes are coordinately regulated by salt and drought stress, supporting a high degree of cross talk between these types of stresses [8, 9].

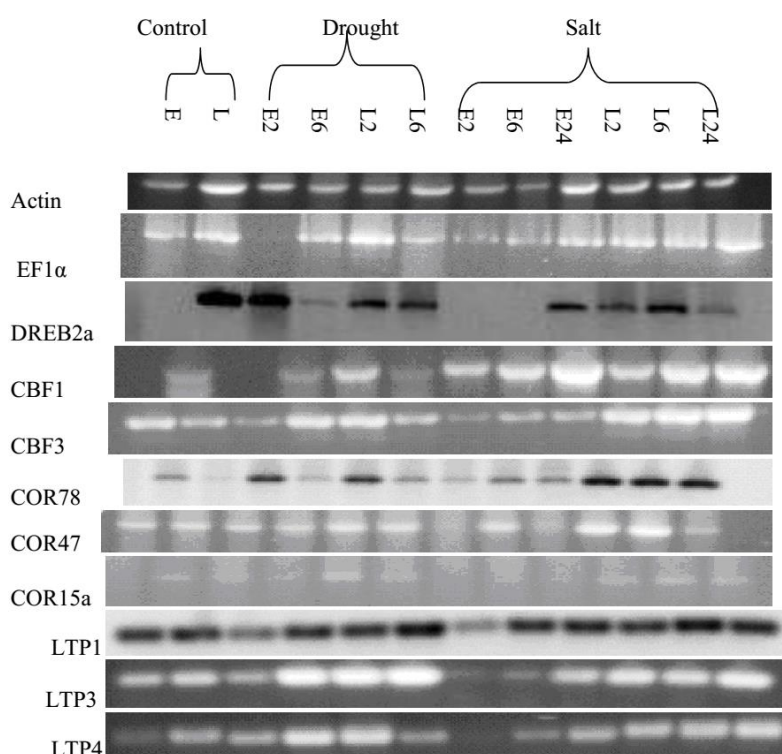


Fig-1: PCR products using cDNA from 100ng total RNA extracted from epidermis and leaves from Arabidopsis exposed to 2 h and 6 h drought or exposed to salt for 2 h, 6 h and 24 h. E= epidermis, L= leaves.

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