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The roles of a transcription factor ICE1 in plant ABA-dependent signaling pathways

Key words: signal transduction in plants, membrane proteins, Arabidopsis

To cope with ever-changing environment which is determined by temperature, light and water, plants employ a signal transduction network that enable the survival and growth. This signal network also monitors the status of growth and metabolism in the plants. The core of this network is usually comprised by a diverse of transcription factors that directly control the genes required for the plant responses. Some of the transcription factors can receive signals from more than one source. Both ABA-dependent pathways and ABA-independent pathways play roles in this stress response network [4]. We have studied the functions of a novel membrane protein, HHP1, from Arabidopsis. First, we identified HHP1 as a negative regulator in plant responses to osmotic stresses via an ABA-dependent pathway [2]. Further, the N-terminus of HHP1 was found to interact with a transcription factor, ICE1 [1]. Recently, we reported that ICE1 is involved in sugar responses in an ABA-dependent pathway [3]. Following to our discovery on the interaction of HHP1-ICE1, a similar interaction between HHP2/CAMTA3 or HHP3/ICE2 has been reported by another research group. This implied that such interaction between membrane protein and transcription factor should play a new molecular mechanism in plants.

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