



Overexpression of *Prunus mume* Dehydrin Genes in Tobacco Enhances Tolerance to Cold and Drought

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Dehydrins, known as group 2 or D-11 family late-embryogenesis-abundant (LEA) proteins, play important roles in plant growth and stress tolerance. Six dehydrin genes were previously identified from the genome of *Prunus mume*. In this study, five of them (*PmLEA8*, *PmLEA10*, *PmLEA19*, *PmLEA20*, and *PmLEA29*) were cloned from cold-resistant *P. mume* 'Beijingyudie'. Real-time RT-PCR analysis indicated that all these genes could be up-regulated by one or several treatments (ABA, SA, low temperature, high temperature, PEG, and NaCl treatments). The results of spot assay demonstrated that the expression of all these dehydrins, except *PmLEA8*, conferred improved osmotic and freezing-resistance to the recombinant *Escherichia coli*. So four dehydrin genes, *PmLEA10*, *PmLEA19*, *PmLEA20* and *PmLEA29* were chosen for individual overexpression in tobacco plants. The transgenic tobacco plants showed lower relative content of malondialdehyde, relative electrolyte leakage and higher relative content of water than control plants when exposed to cold and drought stress. These results demonstrated that *PmLEAs* were involved in plant responses to cold and drought.

Keywords: *Prunus mume*, dehydrins, LEA proteins, cold stress, drought tolerance

INTRODUCTION

Dehydrins, which are also known as group 2 or D-11 family late-embryogenesis-abundant (LEA) proteins, are a family of highly hydrophilic, glycine-rich, heat-stable, and intrinsically unstructured proteins (Soulages et al., 2003; Hundertmark and Hincha, 2008; Banerjee and Roychoudhury, 2016). They have been reported in a wide range of organisms, including higher plants, mosses, fungi, algae, and cyanobacteria (Close and Lammers, 1993; Cuming et al., 1994; Li et al., 1997; Saavedra et al., 2006; Pochon et al., 2013). Dehydrins typically accumulate in the late stages of seed maturation and in vegetative tissues in response to drought, salinity, low temperature, or abscisic acid (ABA) treatment (Battaglia et al., 2008). Dehydrins are characterized by the presence of one or several conserved, lysine-rich K segment (EKKGIMDKIKEKLPG) (Rorat, 2006). This segment can fold into an amphipathic α -helix structure that may interact with lipid membrane or partially denatured proteins (Koag et al., 2009) to protect the cell against damage caused by stress. Apart from the K segment that can be found in all dehydrins, some dehydrins may possess S segment (serine cluster) and Y segment (DEYGNP). Based on the arrangement of these three segments, dehydrins can be classified into five subclasses: YnSKn, SKn, Kn, YnKn, and KnS (Close, 1996, 1997).