

# Molecular and functional characterization of mulberry EST encoding *remorin* (*MiREM*) involved in abiotic stress

Vibha G. Checker · Paramjit Khurana

Received: 28 May 2013 / Revised: 15 July 2013 / Accepted: 15 July 2013 / Published online: 14 August 2013  
© Springer-Verlag Berlin Heidelberg 2013

## Abstract

**Key message** Group1 remorins may help the plants to optimize their growth under adverse conditions by their involvement in mediating osmotic stress responses in plants.

**Abstract** Mulberry (*Morus indica*), a deciduous woody tree, serves as the cardinal component of the sericulture industry. Genomic endeavors in sequencing of mulberry ESTs provided clues to stress-specific clones, but their functional relevance remains fragmentary. Therefore in this study, we assessed the functional significance of a remorin gene family member that was identified in leaf ESTs. Remorins represent a large, plant-specific multigene family gaining importance in recent times with respect to their role in plant–microbe interactions, although their role in response to environmental stresses remains speculative as in vivo functions of remorin genes are limited. Mulberry remorin (*MiREM*) localizes to plasma membrane and is ubiquitously present in all plant organs. Expression analysis of *MiREM* by northern analysis reveals that its transcript increases under different abiotic stress conditions especially during dehydration and salt stress, implicating it in regulation of stress signaling pathways. Concomitantly, transgenic *Arabidopsis* plants overexpressing heterologous remorin show tolerance to dehydration and salinity at the

germination and seedling stages as revealed by percentage germination, root inhibition assays, fresh weight and activity of photosystem II. This study predicts the possible function of group 1 remorin gene in mediating osmotic stress thus bringing novel perspectives in understanding the function of remorins in plant abiotic stress responses.

**Keywords** Abiotic stresses · *Arabidopsis* · Group1 remorin · Mulberry

## Introduction

Plants adapt and acclimatize rapidly to changing environmental conditions by inducing coordinated responses involving hundreds of genes including stress sensors, signaling molecules and output proteins (Knight and Knight 2001; Mittler and Blumwald 2010). Substantial progress has been achieved in the last decade concerning identification and characterization of novel stress-responsive genes in model species (Cushman and Bohnert 2000; Sreenivasulu et al. 2007). Formidable genomic approaches reveal a multitude of gene families conferring improved productivity and adaptation to abiotic stresses (Jewell et al. 2010). However, despite the importance of non-model species, there is dearth of information on functional genomics of mulberry (*Morus indica*), a tree species of immense importance in the Indian economy. Reduction of the losses caused by biotic and abiotic environmental factors can help to improve mulberry productivity, thereby influencing the economics of sericulture. Success of transgenesis has been demonstrated in mulberry, indicating the potential of this approach (Lal et al. 2008; Das et al. 2011; Checker et al. 2012a). Generation of expressed sequence tags (ESTs) from native and abiotic stressed

Communicated by A. Dhingra.

**Electronic supplementary material** The online version of this article (doi:10.1007/s00299-013-1483-5) contains supplementary material, which is available to authorized users.

V. G. Checker · P. Khurana (✉)  
Department of Plant Molecular Biology, University of Delhi  
South Campus, Dhaula Kuan, New Delhi 110021, India  
e-mail: paramjitkhurana@hotmail.com