

# Analysis of expressed sequence tags from mulberry (*Morus indica*) roots and implications for comparative transcriptomics and marker identification

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**Abstract** Mulberry (*Morus indica*) serves as the most commercially valuable plant of the sericulture industry and has the unrealized potential to influence rural economy directly. Despite the poised economic importance of mulberry, there is a dearth of genomic or transcriptomic data available for mulberry; therefore, in the present study, efforts were initiated to produce transcriptomic data about mulberry roots to aid selective breeding and biotechnology for stress tolerance in this important tree species of the sericulture industry. Knowledge of the mulberry root transcriptome is an important step and will contribute to a better understanding of molecular information of this important cash crop. A total of 2,400 expressed sequence tags were sequenced from the roots of *M. indica* cv. K-2 and assembled into 148 contigs and 1,420 singletons. Functional categorization of mulberry unigenes revealed conservation of genes involved in diverse cellular processes. Comparative transcriptomic studies undertaken from the leaf and root tissues of mulberry exposed to a variety of abiotic stress conditions revealed overlapping and specific patterns of transcript expression. The utility of expressed sequence tag (EST)-based simple sequence repeats (SSRs) prompted us to perform a bioinformatics analysis for SSR detection in the EST repertoires of

mulberry leaf and root. The identification of expressed transcripts generated from this effort has the unrealized potential as cornerstones of functional genomics studies, and candidate genes relevant to the interest of the sericulture industry may represent important molecular tools to mulberry research groups.

**Keywords** Expressed sequence tags (ESTs) · Mulberry · Roots · Simple sequence repeats (SSR) · Transcriptomics

## Introduction

Mulberry (*Morus indica*), a member of the family Moraceae (Rosales), is an extremely important plant determining the profitability of the sericulture industry as its foliage is the sole diet for monophagous silkworm (*Bombyx mori*). The genus is distributed widely from tropical to temperate climates in a wide range of areas around the world. India is the second largest producer of mulberry silk with an estimated annual production of about 16,000 metric tons. Indeed, mulberry is an important source of income-earning livelihood for many in developing countries. Four mulberry species (*M. indica*, *Morus alba*, *Morus laevigata*, *Morus serrata*) have been reported from India (for a review on mulberry, see Khurana and Checker 2011). Genomic endeavors in mulberry research have been undertaken recently, with the characterization of the mulberry chloroplast genome (Ravi et al. 2006) and generation of expressed sequence tags (ESTs) from native and water-stressed leaves (Lal et al. 2009; Gulyani and Khurana 2011). These ESTs provided a source of elite, stress-specific clones as targets of transgenic approach, and their subsequent transfer to

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