

# Comparative analysis of expressed sequence tags (ESTs) from *Triticum monococcum* shoot apical meristem at vegetative and reproductive stages

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**Abstract** *Triticum monococcum* has recently drawn the attention of biologists to discover and utilize novel genes and alleles. To explore the molecular features of the genetic network governing floral transition in shoot apical meristem (SAM) of spring growth habit *T. monococcum*, two expressed sequence tag (EST) libraries containing 3,031 ESTs from vegetative SAM (VS) and 2,647 ESTs from early reproductive SAM (RS) were analyzed. Assembly of ESTs resulted in 2,303 unigenes for VS library (368 contigs and 1,935 singletons) and 1,890 unigenes (337 contigs and 1,553 singletons) for RS library. The 67.05 % of VS unigenes and 66.30 % of RS unigenes showed significant similarity with genes of known, putative and or unknown function, whereas the remaining 32.95 % of the VS unigenes and 33.7 % of RS unigenes displayed no significant match with the public protein database. The 1,064 and 866 unigenes of VS and RS libraries were assigned to functional categories using Pageman ontology tool. Further analysis revealed that the switch from VS to

RS caused significant changes in the abundance of unigenes assigned to some functional categories. A total of 37 genes were identified which were significantly differentially expressed between vegetative and reproductive stages of *T. monococcum* SAM. Investigation of the differentially expressed genes revealed the importance of the genes involved in energy metabolism, ubiquitin/26S proteasome system, polyamines biosynthesis and signaling of reactive oxygen species in SAM differentiation towards floral transition in *T. monococcum*.

**Keywords** *Triticum monococcum* · Shoot apical meristem · Floral transition · EST analysis · Functional annotation

## Introduction

The shoot apical meristem (SAM) contains a reservoir of pluripotent stem cells that differentiate and then form plant aerial organs (Haerizadeh et al. 2009). Throughout the life cycle of a plant, the SAM undergoes three phases of development; vegetative, inflorescence and floral identities (Trevaskis et al. 2007). The shift of SAM identity from vegetative to inflorescence triggers floral transition, the most dramatic phase change in plant life cycle (Araki 2001). Despite the important role of SAM in floral transition, little is known about the molecular mechanisms controlling its functions.

Temperate cereals such as winter wheat exhibit distinct, but connected, floral pathways which often respond to a combination of day length, vernalization and temperature to optimize timing of flowering (Greenup et al. 2009). In wheat, variation in requirement of vernalization, exposure to a prolonged period of low temperature, is mainly controlled by

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