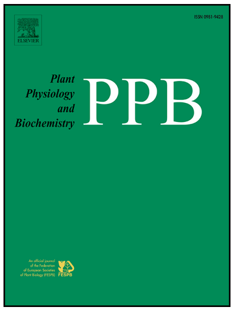

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PII: S0981-9428(18)30216-X

DOI: 10.1016/j.plaphy.2018.05.016

Reference: PLAPHY 5263

To appear in: *Plant Physiology and Biochemistry*

Received Date: 29 January 2018

Revised Date: 9 May 2018

Accepted Date: 9 May 2018

Please cite this article as: T. Cheng, D. Wang, Y. Wang, S. Zhang, C. Zhang, S. Liu, Y. Xi, F. Sun, Identification and functional characterization of a *MAX2* ortholog from switchgrass (*Panicum virgatum* L.), *Plant Physiology et Biochemistry* (2018), doi: 10.1016/j.plaphy.2018.05.016.

Identification and functional characterization of a *MAX2* ortholog from switchgrass (*Panicum virgatum* L.)

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Abstract

Switchgrass (*Panicum virgatum* L.) is a sustainable cellulosic energy crop with high biomass yield on marginal soils. Tillering, an important agronomic characteristic related to biomass production in gramineous plants, is regulated by complex interacting factors, such as plant hormones. Strigolactones (SLs) comprise a novel class of plant hormones that inhibit shoot branching. The *MORE AXILLARY GROWTH2 (MAX2)*/*DWARF 3 (D3)*/*RAMOSUS (RMS4)* genes encode proteins involved in the SL signaling pathway in various plants. The switchgrass tetraploid genome likely contains two high-similarity *MAX2* homologues, one of which is 6 bp longer than the other. The longest is named *PvMAX2* and is the ortholog of *MAX2* in Arabidopsis, *D3* in rice, and *RMS4* in petunia. *PvMAX2* is expressed ubiquitously in switchgrass tissues, with higher expression levels observed in the stem and shoot. *PvMAX2* gene expression is upregulated by GR24, a synthetic SL analog. Ectopic expression of *PvMAX2* in the Arabidopsis *max2* mutant rescued the dwarf and bushy phenotypes and small leaf size in the mutant, suggesting that functions of *AtMAX2* in Arabidopsis are conserved in *PvMAX2*. Ectopic *PvMAX2* expression also restored the wild-type primary root and hypocotyl length phenotypes and restored the response to GR24. These results indicate that *PvMAX2* may play an important role in switchgrass tillering through the SL pathway.

Key words: Switchgrass, *PvMAX2*, Strigolactones, root, tillering