

Chinese scientists clarify a molecular module to regulate rice tillering

Rice tillering is a multigenic trait that influences grain yield, but up to now its regulation network is poorly understood. Dr. Chong Kang's Lab reported a miMTD (miRNA/MADS/TCP/D14) regulation network to control rice tillering. At the same time, a novel function in tiller and axillary bud development has been uncovered for OsMADS57, a member of the highly conserved MADS-box transcription factors family.

Data both *in vivo* (ChIP) and *in vitro* (EMSA, yeast one-hybrid, transcriptional repression activity assay) suggested that OsMADS57 directly bounded *D14*, a gene encoding the receptor of new phytohormone strigolactone, and suppressed its expression. The interaction of OsMADS57 with OsTB1 reduced OsMADS57's inhibition on *D14* transcription. Furthermore, the *OsMADS57* gene is negatively targeted by miR444a. The discovery of this miMTD regulation mechanism for tillering not only uncovered the novel function of MADS-box transcription factors, but also deepens our understanding of the molecular regulation mechanism of tillering and axillary bud development. It has great potential application in efforts to increase yields through rice molecular breeding programs. It has been published on *Nat Commun* (2013, 4:1566). This work was supported by NSFC.

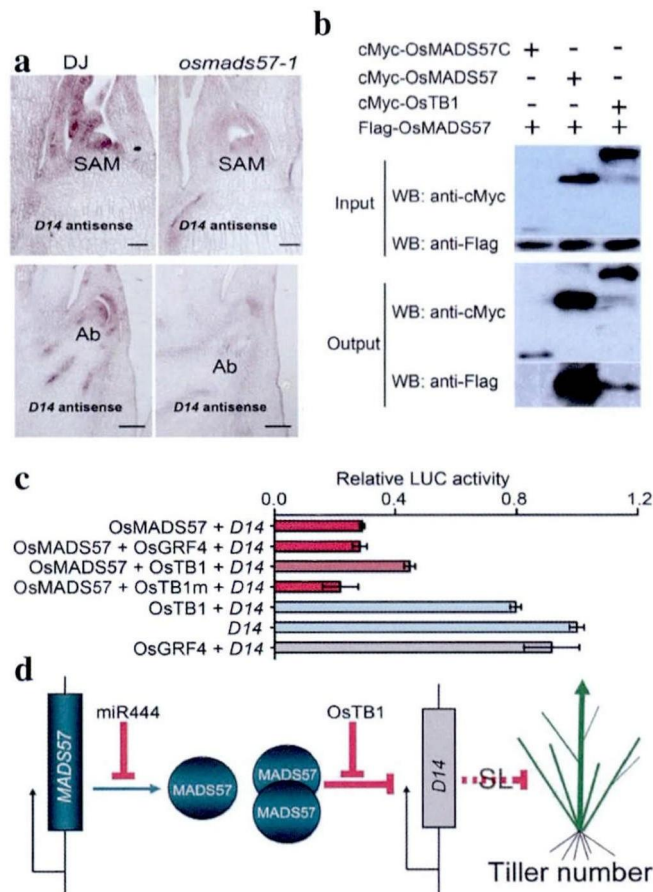


Figure OsMADS57-mediated tillering regulation mechanism. a. *D14* expression was reduced in *osmads57-1*, a gain-of-function mutant; b. OsMADS57 interacted with OsTB1; c. OsMADS57 negatively regulated *D14*, OsTB1 could partially reduce this negative regulation; d. Model of the OsMADS57-mediated network for control of tillering.