Molecular cloning and expression analysis of \textit{GhLOF} genes in upland cotton (\textit{Gossypium hirsutum} L.)

T.C. Dai\textsuperscript{1,2} and Z.M. Wang\textsuperscript{1,2}

\textsuperscript{1}Plant Science Department, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai, China
\textsuperscript{2}Key Laboratory of Urban Agriculture (South), Ministry of Agriculture, Shanghai, China

Corresponding author: Z.M. Wang
E-mail: zmwang@sjtu.edu.cn

Received July 14, 2014
Accepted November 27, 2014
Published May 4, 2015
DOI http://dx.doi.org/10.4238/2015.May.4.16

\textbf{ABSTRACT.} Shoot branching, i.e., the timing and position of shoot growth, determines to a large extent the pattern of plant architecture, and is the result of the integration of a plant’s genetic background and environmental cues. Many genes that are involved in the formation and outgrowth of axillary buds have been cloned, but the exact mechanism is still unclear. Branching pattern is an important agronomic trait in many crops, including cotton. In the present study, we cloned four genes from cotton, and designated them as \textit{GhLOF1/2/3/4}. Sequence analysis revealed that all four genes shared conserved protein domains with \textit{LATERAL ORGAN FUSION (LOF)} from \textit{Arabidopsis} and \textit{TRIFOLIATE (Tf)} from tomato. Phylogenetic analysis revealed that \textit{GhLOF3} and \textit{GhLOF4} were close to \textit{Tf} because of their similar expression patterns, whereas \textit{GhLOF1} and \textit{GhLOF2} were differentially expressed.

\textbf{Key words:} \textit{Gossypium hirsutum} L. (upland cotton); \textit{GhLOF} genes; Shoot branching; RACE; Expression patterns