

Genes Cloning and Bioinformatics Analysis of CUC2-like transcription factor in *Camellia azalea* and *Camellia japonica*

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Abstract: Leaf marginal shapes is an important ornamental character in Camellias, which can be described as entire, serrated and lobed. The CUC transcription factors have been found involved in the development of leaf serration or dissection. In this paper, two genes of CUC transcription factors were isolated from *Camellia azalea* (entire leaf margin) and *Camellia japonica* (serrated leaf margin) by homology cloning strategy. Bioinformatics analysis suggested that these two genes are homologous with the reported CUC2 gene sequence in many other plants, hence they were named *CaCUC2-like* and *CjCUC2-like*. The full coding region of *CaCUC2-like* is 1059 bp and encodes a polypeptide of 352 amino acids, while the full coding region of *CjCUC2-like* is 1056 bp and encodes a polypeptide of 351 amino acids. Further analysis showed that these two genes are highly similar in coding region. Above results revealed that the differences between smooth leaf margin and serrated leaf margin of Camellias may not due to gene structure.