TOWARD IDENTIFICATION OF THE COMPLETE AQUAPORIN GENE FAMILY IN COTTON – A POSSIBLE WAY TO IMPROVE COTTON PRODUCTION

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Abstract

Cotton is the most important natural-fiber producing crop and represents a significant global agricultural commodity. Because of the significance of water to the quantity and quality of cotton production, efforts to decrease the amount of water applied and improvement of cotton water use efficiency are highly desirable. In this study, we aimed at studying the aquaporin protein at the molecular level as a potential target for manipulating water use efficiency. Aquaporin proteins are present across plant tissues where they function as membrane transport channels for water and other small molecules. The plant aquaporins consist of 5 subfamilies including plasma membrane intrinsic proteins (PIP), tonoplast intrinsic proteins (TIP), NOD26-like intrinsic proteins (NIP), small basic intrinsic proteins (SIP), and the recently discovered X intrinsic protein (XIP). In order to identify a complete set of aquaporin genes in cotton (*Gossypium hirsutum* L.), *in silico* and molecular cloning efforts and subsequent sequence analyses were performed. Here we report the identification of 71 cotton aquaporin genes, consisting of 28 and 23 highly homologous members in PIP and TIP subfamilies respectively, while also containing more divergent 12 NIP and 7 SIP members in addition to one member of the XIP subfamily. To explore the physiological roles of these aquaporin genes in cotton, semi-quantitative gene expression analysis was performed.