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Research Progress of Gramineae Cellulose Synthase Gene in Cellulose Synthesis Regulation

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Abstract

Gramineae, such as Zea mays, Oryza sativa, Sorghum bicolor and Miscanthus, has a high cellulose content in the cell wall. Cellulose synthase gene (CesA) plays an important role in the process of plant growth and cell wall morphogenesis. In this paper, the related research results of CesAs in Gramineae was summarized, and the role of CesAs in regulating cellulose synthesis was analyzed.

Keywords: Gramineae; Cellulose; Cellulose synthase gene

Abbreviations: CesA: Cellulose Synthase; CesA: Cellulose Synthase Gene; CSC: Cellulose Synthase Complex; GT2: Glycosyltransferase 2; PCW: Primary Cell Wall; SCW: Secondary Cell Wall

Introduction

Gramineae have more than 500 genus and more than 8,000 species, which are widely distributed in different ecological environments around the world [1]. Gramineae include important grain or sugar crops such as *Oryza sativa, Triticum aestivum, Zea mays and Saccharum officinarum*, as well as important biomass ingredients crops such as *Miscanthus* and *Panicum virgatum*. Gramineae usually have a high cellulose content [2], and the stability and great ductility of cellulose make it an ideal raw material for manufacturing many fiber products [3,4].

Biosynthesis of Cellulose

Cellulose is one of the important components of the higher plants mature cell walls. As a structural polysaccharide, it accounts for 30-40% of the total cell wall polysaccharides [5]. The basic unit of cellulose is pyranoid D-glucose, which is connected by β-1,4 glucoside bonds and usually exists in the form of microfibrils, and its structure has a specific hydrogen bond structure between molecules [6]. Studies have shown that the pathway of cellulose biosynthesis is mainly divided into three steps (Figure 1), and CesA plays an important role in the program [7]. CesA is a membrane-bound transmembrane protein a member of the glycosyltransferase 2 (GT2) family that catalyzes the formation of β bonds between glycosylates. CesA is a hexagonal lotus shaped enzyme with a diameter of 25-30nm, it can be assembled into a Cellulose Synthase Complex (CSC) with a sixfold symmetrical rosette structure on the cell membrane [8]. The amount of CSC in plants is positively correlated with the final synthesis amount of cellulose. The number of rosette structures of the Arabidopsis mutant rsw1 is significantly less than that of the wild type, which caused β-1,4-glucan to accumulate in an amorphous form and the cellulose content is reduced [9].

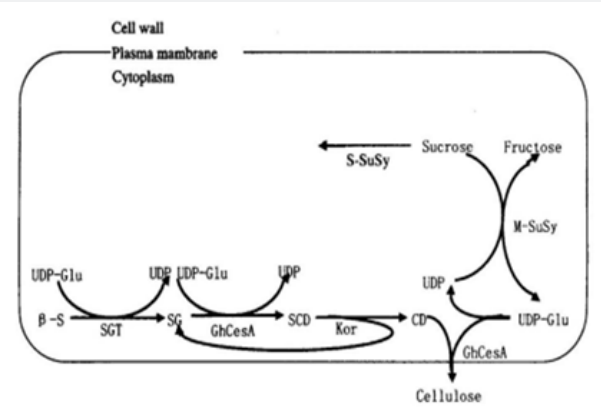

Figure 1: Plant cellulose biosynthesis process diagram [7].

Cellulose Synthase Gene (*CesA*)

The length of *CesAs* sequence is between 3.5~5.5 kb, containing approximately 9~13 introns and encoding 985~1,088 amino acid [10]. In 1982, Benziman [11]. cloned *CesA* in vitro bacteria for the first time [11]. In 1996, Peal et al. cloned the β-1,4-glucosidyltransferase gene encoding the catalytic CesA subunit from cotton for the first time by random sequencing and sequence analysis from a cDNA library [12]. Since the discovery of *CesA* in cotton, *CesAs* had been successively cloned in *Arabidopsis thaliana* [13], *Oryza sativa* [14], *Zea mays* [15], *Populus trichocarpa* [16], *Boehmeria nivea* [17] and *Phyllostachys edulis* [18]. In the studies of Gramineous *CesAs*, it was found that *OsCesA4, 7,9* of rice were all involved in the formation of SCW, forming a complex regulatory network of SCW cellulose biosynthesis. These three *CesA* genes can be expressed cooperatively in rice seedling stage, young stem, immature panicle and root development, but relatively little expression in mature leaves [19]. The missense mutation of *OsCesA7* caused the decrease of cellulose level and cell wall damage in S1-24 mutant rice; at the heading stage, compared with wild-type, S1-24 mutant rice has a lower mechanical strength and a relatively slower growth rate [20]; however, the expression of *OsCesA7* could be directly up-regulated by regulating the MYB transcription factor *OsMYB58/63* of rice [21]. When *OsCesA9* has a missense mutation, it will cause plant dwarfing and extremely low fertility [22]. In *Panicum virgatum* L., *PvCesA4* and *PvCesA6* genes have different expression levels in different parts. After the overexpression and/or knockout of *PvCesA4* and *PvCesA6*, the cellulose content of the transgenic plants decreased, while the xylan content increased. The increase of xylan content would lead to the decrease of crystallinity of cellulose, which would affect the synthesis of cellulose Therefore, the expression of *CesAs* had changed cell wall composition and cellulose crystallinity [23]. The *CesAs* of *Miscanthus × giganteus* has been reported. *MgCesA10*, *MgCesA 11* and *MgCesA 12* may participate in the formation of SCW and form an equal proportion of CSC. *MgCesA5* and *MgCesA6* are constitutively expressed genes that cooperate with *MgCesA2*, *3, 4, 7* and *8* to regulate the formation of PCW. However, except for *MgCesA5*, the expression of other *CesA* genes in leaves was reduced due to senescence. The expression of genes involved in the formation of *Miscanthus × giganteus* PCW varies depending on the location [24].

Different Regulation Levels of Gramineae *CesA*

Cellulose synthesis can be regulated at the transcriptional level by *CesAs*. The biggest difference between *CesAs* is the presence and location of introns in the coding sequence [13]. For example, *wheat CesA1, 2* and *6* have 13 introns, while *CesA4, 7* and 8 have 7, 12 and 9 introns respectively; *CesA1, 2* and *6* participate in the formation of PCW, while *CesA4, 7* and *8* participate in the formation of SCW [25]. This indicated that the number of introns of *CesAs* in the formation of wheat PCW was higher than that of *CesAs* in the formation of SCW. Previous studies have shown that genes containing introns have higher transcription levels [26]. This also indicates that transcription levels of *CesAs* participate in wheat PCW formation are higher than those of *CesAs* participate in SCW formation. In addition to the regulation of cellulose synthesis at the transcriptional level of *CesAs*, the post-transcriptional level of *CesAs* also affects the synthesis of cellulose. Daniel et al. found that the small RNA produced by *HvCesA6* can selectively attenuate the expression of *CesA* gene, therefore, the expression of genes that affect cell wall formation can greatly influence the content of barley cellulose [27].

Conclusion

Cellulose is the most important component of plant cell walls, and cellulose synthase plays a key role in cellulose biosynthesis. In the studies of Gramineae *CesAs*, it was found that *CesA* gene family was involved in cell wall morphogenesis, forming a complex regulatory network of cellulose biosynthesis. Transcriptional or post-transcriptional regulation of *CesA* genes can change plant cell wall composition, change cellulose content and cellulose crystallinity, so as to provide a strong theoretical basis for the high value utilization of cellulosic feedstock crops.

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