



A genetic pathway for naturally colored cotton production

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Naturally colored cotton (NCC) results from pigmentation in developing fibers. Importantly, NCC serves as an environmental-friendly resource for human society because it does not require dyeing and bleaching during textile processing, and thus substantially reduces pollution and saves energy and water (Wen et al., 2018; Wang et al., 2022b). With the increasing demand for eco-friendly products, NCCs have attracted more interest from the textile industry. Currently, NCC yields are lower and the NCC fiber is usually shorter and weaker than regular cotton, limiting NCC's applications. There is an urgent need to understand the genetic basis of the natural brown cotton to improve the breeding of this green product (Yan et al., 2018).

Brown cotton fibers are the most frequently used NCCs, and the coloration is the result of excessive accumulation of anthocyanin and proanthocyanidin (PA). Biosynthesis, transport, and storage pathways of these pigments have been well characterized in *Arabidopsis* (*Arabidopsis thaliana*) (Martin et al., 1991; Holton and Cornish, 1995). However, only a few genes related to anthocyanin homeostasis have been cloned and functionally characterized in cotton (*Gossypium hirsutum*) (Wen et al., 2018; Yan et al., 2018). In this issue of *Plant Physiology*, Wang and colleagues report that the transcription factor MYB113 regulates anthocyanin biosynthesis in cotton. Ectopic expression of MYB113 activated anthocyanin and PA synthesis, resulting in red foliated cotton and brown fiber (Wang et al., 2022a).

The authors isolated a red foliated cotton mutant (designated as ReS11) from the backcross progenies between sea-island cotton and upland cotton. Map-based cloning identified a 288-bp insertion in the promoter region of

MYB113 in ReS11. The insertion contains a G-box, which caused increased expression of MYB113 in the mutant. The authors further demonstrated that ectopic overexpression of MYB113 under the control of the *Cauliflower Mosaic Virus* 35S promoter caused the red foliated cotton phenotype. The 35S:MYB113 overexpression transgenic plants developed red color in various organs, but the fiber remained white. Interestingly, fiber-specific over-expression of MYB113 resulted in brown mature fiber, and the color change was caused by overaccumulation of anthocyanin and PA. In addition, anthocyanin biosynthetic genes were highly induced in the MYB113 overexpression lines, which further established the direct connection between anthocyanin accumulation and brown fibers.

The authors conducted transcriptome analysis and co-expression network analysis to identify genes in the same genetic pathways as that of MYB113. As a result, a transcriptional regulatory network of MYB113 for the anthocyanin pathway was proposed and further validated by the dual-luciferase reporter system. In this network, phytochrome interacting factor 4 (PIF4) binds to the G-box region of the MYB113 promoter and drives the expression of MYB113, which transcriptionally activates genes in anthocyanin biosynthesis and metabolism, leading to increased anthocyanin synthesis. Consequently, the Re mutant with the G-box-containing insertion produces red foliated cotton (Figure 1).

The MYB113-anthocyanin module characterized by Wang et al. (2022a) offers an excellent strategy for molecular breeding of NCC. In-depth understanding of how other genetic factors associated with MYB113 function in this module will be crucial for expanding the molecular targets for

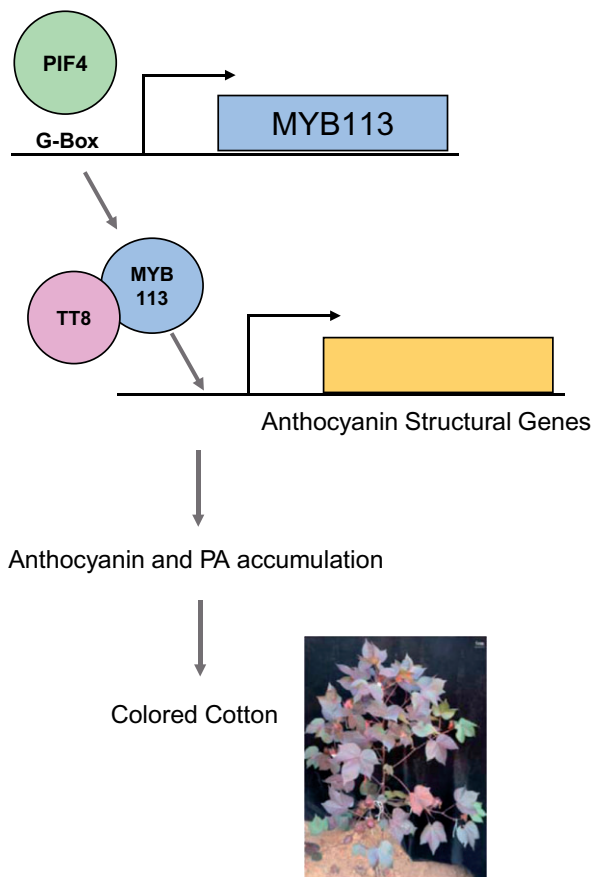


Figure 1 The regulatory model controlling brown coloration by the MYB113 transcription factor. Light-responsive factor PIF4 binds to the G-Box region in the promoter of *MYB113* to drive its expression. Afterward, MYB113 forms a protein complex with TT8 and activates the expression of anthocyanin biosynthesis genes, leading to the accumulation of anthocyanin and PA. The increased pigmentation produces red foliated cotton and brown fiber. Coding genes are depicted as bars with line and arrow showing promoter and transcription direction, respectively. Proteins are represented with circles.

colored cotton fiber breeding practices (Gonzalez et al., 2008). Another challenge ahead is to precisely control the expression of color-producing genes to find the balance between coloration and fiber quality and/or productivity, and thus reach the best economic benefit.

Conflict of interest statement. None declared.

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