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COMMENT

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A breakthrough in cotton transformation technology

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A new cotton transformation method was developed by Ge and colleagues at Institute of Cotton Research of Chinese Academy of Agricultural Sciences, and this work was published in a recent issue of the Journal of Integrative Plant Biology (Ge et al. 2023; https://doi.org/10.1111/jipb.13427). This method is a milestone progress in the development of cotton transformation technologies, as it can be used to transform different genotypes and species of cotton such as *Gossypium hirsutum*, *Gossypium barbadense*, and *Gossypium arboreum*. This method is fast, user friendly, and the transformation efficiency is equivalent to or superior to other cotton transformation methods. Ge et al. named this technique the shoot apical meristem (SAM) cells-mediated transformation system (SAMT), which can also be applied to transform other dicot crop species such as soybean and cucumber. The invention of the SAMT method represents a seminal achievement in crop transformation technology, and it will facilitate genetic improvement in elite cotton varieties as well as in other dicot crops that have been hitherto recalcitrant to transformation.

Agrobacterium-mediated cotton transformation was first accomplished in late 1980s and early 1990s (Firoozabady et al. 1987; Umbeck et al. 1987; Bayley et al. 1992). Among the pioneers, Trolinder and Goodin at Texas Tech University developed a highly reproducible cotton regeneration system based on somatic embryogenesis (Trolinder and Goodin 1987). Then Trolinder and Chen (1989) identified Coker 312 as the most suitable donor plant for cotton somatic embryogenesis, which led to a reliable cotton transformation method (Bayley et al. 1992). This breakthrough technology was significant in the field of cotton biotechnology as it opened up possibilities for introducing novel genes into cotton for improving resistance to pests and herbicides, as well as increased tolerance to environmental stresses. However, because it is highly genotype-dependent, subsequent attempts to adapt the protocol to other upland cotton varieties or other cotton species have been challenging. Zhixian Chen, a visiting scientist from Shanxi Province of China, became the first Chinese scientist who could transform cotton, followed by sharing this knowledge to many Chinese scientists. For the last 30 years, Chinese scientists have steadily advanced the state of the art in cotton transformation. Specifically, a vast collection of cotton cultivars were screened for improving transformation efficiency as well as reducing the regeneration time (Jin et al. 2005 and 2006; Li et al. 2019a and 2019b; Xu et al. 2013).

While cotton transformation technology is being developed in China, the Trolinder method has been used by scientists worldwide since its invention. Although this approach was very reproducible, it typically takes two years to obtain transgenic cotton. Coker 312 and its closely related old cotton cultivars (such as Coker 201 and Coker 210) are the only ones that work with this technique; therefore, the Trolinder method could not be used to transform other types of cotton, including the elite modern upland cotton cultivars and the highly sought-after sea island cotton, which is superior in fiber quality. Since there is currently no public cotton transformation service in the United States and only a small

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number of laboratories are capable of performing cotton transformation, cotton transformation has become a major bottleneck in introducing genes into cotton.

The new cotton transformation method developed by Ge et al. (2023) takes an average of nine months to obtain transgenic cotton from seeds to seeds, while the traditional methods would take between 12 and 24 months. The SAMT method can be used to transform *G. barbadense* and *G. arboreum*, while it is uncertain whether other transformation methods can be used to transform cotton species other than *G. hirsutum*. Transgenic cotton obtained using the SAMT method was verified by DNA blot analysis, and the phenotype of transgenic cotton was consistent with the function of the introduced gene. The transformation rate was comparable with most existing methods, and the chimera ratio was not particularly high compared with other methods, including those currently used in many American laboratories. Hence, the SAMT method represents a substantial advance and contributes significant value to the global cotton community, promising to usher in a new era of cotton basic biology research, the discovery of functional genes in cotton, and genetic engineering cotton for higher yield and better quality in the future.

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