UNLOCKING THE GENETIC POTENTIAL OF UPLAND COTTON: INSIGHTS INTO TM-1 GENOME AND ITS SUB-GENOMES

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Abstract

Upland cotton (*Gossypium hirsutum* L.) is the result of concerted evolution and domestication. This important crop plant counts for more than 90% of natural fiber production in the world. Since the late last century, cotton growers have experienced a plateau in yields and other agronomic traits, and most commercial cultivars lack genetic diversity, making cotton vulnerable to natural threats. Until recently, the genetic potential of Upland cotton was barely explored due to its large and complex allotetraploid genome. Recent assembly and annotation of Upland cotton genetic standard TM-1 following its two extant diploid progenitors create unique opportunities to effectively unlock the genetic potential that is essential for cotton improvement. Decoding the allotetraploid TM-1 genome and its interactive sub-genomes provides molecular insights into Upland cotton evolution and spinnable fiber development. The new knowledge and advanced genomic tools will help researchers and breeders develop cotton cultivars with improved fiber qualities, higher yields and more tolerance to biotic and abiotic stresses due to global climate change.