THE MYSTERY SOLVED: A-GENOME ORIGIN OF CULTIVATED DIPLOID AND TETRAPLOID COTTONS

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Abstract

Controversial concepts surrounding A-genome origins have hindered effective exploitation of cultivated diploid and tetraploid cotton genomes. The conflicting knowledge was developed with a limited number of morphological, genetic, cytogenetic, and/or molecular markers that reside in different regions of the cotton genomes. Recently our complete genomes of the four cultivated cotton species opened the door to solve the mystery of evolutionary history and phylogenetic relationship for more effective utilization. The detailed genomic analysis revealed that the speciation of diploids A_1 (*G. herbaceum*) and A_2 (*G. arboreum*) evolved independently after the formation of tetraploids AD_1 (*G. hirsutum*) and AD_2 (*G. barbadense*). Neither diploid cotton was the true donor of A-genome to tetraploid cottons during its preceded hybridization. All existing A-genomes may have originated from a common ancestor (A_0) which was more related to A_1 than A_2. Our study also included re-sequencing a representative collection of A-genome and AD-genome accessions, and the population analysis confirms the divergence between A_1, A_2 and AD cotton species, with our sequenced var. *africanum* being the only living ancestor for A_1 cotton accessions. This talk will present novel genomic insights and abundant sequence resources for cotton genetic improvement.