

## The Sequence Analysis of Histone3 Gene Segments in Cultivated Tetraploid Cotton and Their Diploid Progenitors

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**Abstract:** Histone is important component of the plant genome. The universal primer for amplifying conserved sequence of Histone3 gene in different cotton species have been designed based on registered Histone3 with whole length of 686 bp cDNA sequence (Genbank Accession No. AF024716) in GenBank. Four studied cotton species include cultivated tetraploid (AD-genome) TM-1 (*G. hirsutum*) and Hai7124 (*G. barbadense*), and their diploid progenitors *G. herbaceum* (A-genome) and *G. raimondii* (D-genome). The gene segments amplified from different cotton species also consist of two introns, partial exon and 3'-end untranscribed region. The lengths of the conserved sequence are 602 bp (from *G. herbaceum*, called as A), 600 bp (from *G. raimondii*, called as D), 609 bp (from A-subgenome of *G. barbadense*, called as A<sub>TB</sub>), 598 bp (from D-subgenome of *G. barbadense*,

called as D<sub>TB</sub>), 602 bp (from A-subgenome of *G. hirsutum*, called as A<sub>TH</sub>), and 599 bp (from D-subgenome of *G. hirsutum*, called as D<sub>TH</sub>), respectively. By sequences comparison, 77 SNP (single nucleotide polymorphism) loci are found, which 9 in exon, 21 in intron I, 22 in intron II and 25 in 3'-end untranscribed region, respectively. SNP differences in exon didn't affect transcription and translation of Histone3 gene by inferred based on AF024716 sequence. Phylogenetic analysis showed detail evidence of orthologous (A vs D with similarity 91.6%, A vs A<sub>TH</sub> with 95.2%, A vs A<sub>TB</sub> with 95.8%, D vs D<sub>TH</sub> with 98.0%, D vs D<sub>TB</sub> with 98.5%) and homoeologous (A<sub>TB</sub> vs D<sub>TB</sub> with 92.5%, A<sub>TH</sub> vs D<sub>TH</sub> with 91.0%) relationship. The gene trees recovered reproduced the organismal history of diploid divergence followed by allotetraploid. The truth that genetic divergence between A<sub>T</sub> and D<sub>T</sub> is equal to that between A and D shows the evolutionary rates in diploids and polyploids are equivalent. In this paper, we also discuss that similarity analysis in different cotton species can not only be used to study evolution relationship, but also to find SNP loci with the species.

**Key words:** cotton; species; Histone3 gene; sequence analysis