



Category: Plant Genomics

Does epigenome is influenced by allopolyploidisation during the evolution of *Gossypium hirsutum*

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Abstract

In ecological and evolutionary time scale, Darwinian selection acts on each nucleotide to shape the whole genome. Beside nucleotide diversity, epigenetic modifications seem to be conserved in intra and inter-species during evolution. *Gossypium hirsutum* (A₁D₁) is an allotetraploid crop plant which was evolved from morphologically different diploid ancestors by polyploidisation event expected to occur around 1 million year ago. Its progenitors are *Gossypium arboreum* (A) and *Gossypium ramondii* (D) and they are still available for study. We are keen to understand whether the epigenome structure of A- and D-subgenomes are conserved or influenced by polyploidisation? To understand the influence of polyploidisation on the epigenome, it is important to determine conserved DNA elements which are under purifying selection during evolution. We aligned whole genome sequences of *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium ramondii* and *T. cacao* by LASTZ aligner taking *T. cacao* as a reference genome. Our analysis revealed conserved DNA elements and their distribution in the A/D sub-genomes. The portion of the A/D sub-genome under purifying selection is also determined. Our future study on DNA methylome of *Gossypium arboreum* (A) and *Gossypium ramondii* (D) and AD-genome of *Gossypium hirsutum* and their correlation with conserved DNA elements will reveal influence of polyploidisation on epigenome.

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