



# Molecular marker redundancy check and construction of a high density genetic map of tetraploid cotton

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**Abstract:**

A consensus genetic map of tetraploid cotton was constructed using six high-density maps and after the integration of a sequence-based marker redundancy check. Public cotton SSR libraries (17,343 markers) were curated for sequence redundancy using 90% as a similarity cutoff. As a result, 20% of the markers (3,410) could be considered as redundant with some other markers. The marker redundancy information had been crucial part of the map integration process, in which the six most informative interspecific *Gossypium hirsutum* x *G. barbadense* genetic maps were used for assembling a high density consensus (HDC) map for tetraploid cotton. With redundant markers being removed, the HDC map could be constructed thanks to the sufficient number of collinear non-redundant markers in common between the component maps. The HDC map consists of 8,254 loci, originating from 6,669 markers, and spans 4,070 cM, with an average of 2 loci per cM. The HDC map presents a high rate of locus duplications, as 1,292 markers among the 6,669 were mapped in more than one locus. Two thirds of the duplications are bridging homoeologous At and Dt chromosomes constitutive of allopolyploid cotton genome, with an average of 64 duplications per At/Dt chromosome pair. Sequences of 4,744 mapped markers were used for a mutual blast alignment (BBMH) with the 13 major scaffolds of the recently released *Gossypium raimondii* v2.1 genome (<http://www.phytozome.net/cotton.php>) indicating a high level of convergence between the diploid D genome and the chromosomes of the D genome of the tetraploid HDC genetic map. Overall, the HDC map will serve as a valuable resource for trait QTL comparative mapping, map-based cloning of important genes, and better understanding of the genome structure and evolution of tetraploid cotton. An update of the data and tools available from TropGeneDB (<http://tropgenedb.cirad.fr/tropgene/JSP/index.jsp>), including genetic and QTL maps, physical map, CMap, and GBrowse, will be reported.



CottonGen is developed by the [Mainlab](#) at [Washington State University](#).

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