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The introgression of two sub-populations and their highly divergent regions

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Understanding the genetic diversity and population structure of existing germplasm is important for selecting and utilizing parents in crop breeding. The genomic changes during upland cotton domestication and improving process are still mysterious and the available genetic resources within improved cotton cultivars are very limited. By using restriction site associated DNA markers sequencing (RAD-seq) technology in 582 tetraploid cottons, we totally detected 106 domesticated regions harbored 314 genes, and two distinct genomic signatures on chromosome A06 and A08 within modern improved upland cotton population. Integrating pedigree, previously reported QTLs, introgression and transcriptome analysis, we suggest that two divergent genomic regions on chromosome A06 and A08 resulted by introgressing exotic lineage from *G. hirsutum* race and related wild species, might be the typical genomic characteristic for two specific subpopulations including Central Asia ecotype cotton (Group-2) and the offspring of interspecific hybridization in southern China(Group-1), respectively. Meanwhile, both two genomic regions are located at putative centromere regions, implying its application difficulties and challenges. Depending on density SNP markers, our study reveals the genetic diversity and population structure of tetraploid cottons, as well as provides new insights for understanding the genomic basis of exotic introgressions in modern cotton cultivars.

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