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Single nucleotide polymorphism associated with salinity stress tolerance in upland cotton (*Gossypium hirsutum* L.)

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Although much studies have been done on salinity tolerance in cotton crop, but little is known about genetic control based on single nucleotide polymorphism (SNPs) underlying salt tolerance of cotton plants at seedling stage. To gain an understanding of the genetic basis of upland cotton tolerance to salinity at seedling stage, a genome wide association study (GWAS) was conducted for salinity stress tolerance traits in a core collection of genetically diverse population comprising of 419 accessions. While a genetic map of 5178 SNP markers were developed from 277 F2:3 populations. The map spanned 4768.098 cM with an average distance of 0.92 cM. Next generation high throughput Illumina HiSeq platform was used for genome sequencing, which resulted in 6.45 Tb raw sequences with 150 -bp read length. After sequence quality and filtering process 6.35 Tb high quality SNPs were finally used for subsequent analysis. A total of 5655 SNPs associated with different traits were found. Finally, 15 candidate genes containing key SNPs, involved in different biological pathways for salt tolerance were found for further omics studies. We identified 18 single nucleotide polymorphs (SNPs) significantly associated with relative electrolyte conductivity ratio, 13 SNPs were found high association with REC, 5 SNPs with relative water content and 5 SNPs were found significantly associated with fresh weight. A total of 66 QTLs (quantitative-trait loci) for 10 traits related to salinity were detected in three environments (0, 110 and 150 mM salt treatment). Only 14 QTLs were consistent, accounting for 2.72% to 9.87% of phenotypic variation. Parental contributions were found to be in the ratio of 3:1, 10 QTLs from the sensitive and four QTLs from the resistant parent. Five QTLs were located in At and nine QTLs in the Dt sub-genome. Moreover, eight clusters were identified, in which 12 putative key genes were found to be related to salinity. The GBS-SNPs-based genetic map developed is the first high-density genetic map that has the potential to provide deeper insights into upland cotton salinity tolerance. The 12 key genes found in this study could be used for QTL fine mapping and cloning for further studies. The findings of our GWAS study provides new knowledge about genetic control of salt tolerance at seedling stage, which could aid in elucidation of genetic and molecular mechanism of salinity stress tolerance in cotton crop.

Recent Publications

1. Ma Z, He S, Wang X, Sun J, Zhang Y, Zhang G and Yan Y (2018) Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield. *Nature Genetics* 50:803-13.
2. Du X, Huang G, He S, Yang Z, Sun G, Ma X and Jia Y (2018) Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. *Nature Genetics* 50(6):796-802.
3. Lei Fang (2017) Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. *Nature Genetics* 49(7):1089-98.
4. Wenfang Gong (2017) iTRAQ-based comparative proteomic analysis of seedling leaves of two upland cotton genotypes differing in salt tolerance. *Frontiers in Plant Science* 8:2113.
5. Diouf L, Pan Z, He S P, Gong W F, Jia Y H, Magwanga R O and Du X (2017) High-density linkage map construction and mapping of salt-tolerant QTLs at seedling stage in upland cotton using genotyping by sequencing (GBS). *International Journal of Molecular Science* 18(12):2622.

Biography

Xiongming Du was the Vice Director of National Key Lab of Cotton Science and Dean of Cotton Germplasm Division in the Institute of Cotton Research at Chinese Academy of Agricultural Sciences (ICR, CAAS). He was also the Seventh Council Member of Academic Committee of Cotton in China since 2012 and he was the Fourth and Fifth Council Member of Branch Association of Genetic Resources under Association of Chinese Agronomy since 2000.

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