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Construct a high-density genetic map in upland cotton and its application to genetic regulation analysis for yield and fiber quality traits

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Notton (Gossypiumhirsutum L.) is widely grown in the world as it can provide renewable natural fiber resources for the global textile industry and human's life. Technological developments in the textile industry and improvements in human living standards have increased the requirement for supplies and better quality cotton. Upland cotton 0-153 is an elite cultivar harboring strong fiber strength genes. To conduct quantitative trait locus (QTL) mapping for fiber quality in 0-153, we developed a population of 196 recombinant inbred lines (RILs) from a cross between 0-153 and sGK9708. Three method, new SSR marker, cotton 63K chips and specific locus amplified fragment sequencing were used to construct a high-density genetic map with the RIL population. Map constructed by SSR markers harbored 997 markers with a total genetic distance of 4,110 cM with an average distance of 5.2 cM between adjacent markers. A total of 165 QTLs of fiber quality traits were identified with this map and 47 of them was stable ones which could be detected in at least three environments. a high-density genetic map was constructed by combining the three kinds of markers. This map harbored 8295 markers, spanned a total distance of 5056.96 cM and could cover the genome of upland cotton. The average distance between adjusts markers was 0.86cM. Based on the construction of the high density map, the genetic regulation and the relation of the fiber quality traits and the yield traits could be explained. Further study such as identifying the functioning genes, pyramiding breeding, could be facilitated. These could make a contribution to improving the yield and the fiber quality at the same time.



Biography

Youlu Yuan has been involved with studies related to cotton hybrid vigor and molecular marker assisted selection about fiber quality, focus on cotton variety molecular design, especially on excellent fiber quality variety development. Since 2013 worked as a Director of Bio-technology Research Department and PI of cotton variety molecular design unit.

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