2005 Beltwide Cotton Conferences, New Orleans, Louisiana - January 4 - 7, 2005

QTL MAPPING OF COTTON YIELD COMPONENTS

Gerald Myers
LSU
Baton Rouge, LA
Baogong Jiang
LSU AgCenter
Baton Rouge, LA
Muhanad W. Akash
Iowa State University
Ames, IA

Abstract

Cotton (*Gossypium spp.*) is an important world crop. Cotton yield is still the most important trait for breeders to improve. Fully understand the genetics background of yield component traits will greatly help breeders for the improvement of yield. This paper reported the results of the QTL analysis of cotton yield and yield components that conducted on an $F_{2:3}$ population derived from the intraspecific cross. A previously developed linkage map was used based on same population covering 1733.2 cM (37.7%) cotton genome (4700 cM). A total of 47 markers associated with yield and yield component traits were detected. Nine and seven QTL detected by interval mapping (IM) and composite interval mapping (CIM) methods, respectively, four of which were detected by both methods. For lint yield, two main QTL, explaining 27% of variation, were detected via CIM method. No QTL was detected for bolls per plant by IM method and one QTL explaining 8.56% variation was detected by CIM method. For number of fibers per seed, 23.7 % of variation was explained by two main QTL detected by both IM and CIM methods. For mean weight per fiber, two QTL were detected via CIM. No QTL was detected for seed number per boll via either method.