

QTL MAPPING OF AGRONOMIC AND FIBER QUALITY TRAITS IN COTTON USING AFLPS

M.W. Akash

Department of Agronomy

Iowa State University

Ames, IA

G.O. Myers

Department of Agronomy and Environmental Management

Louisiana State University

Baton Rouge, LA

Abstract

A genetic linkage map of Upland cotton (*Gossypium hirsutum* L.) was constructed with amplified fragment length polymorphism (AFLP) markers using 138 $F_{2,3}$ lines developed from the intraspecific cross of Paymaster 54 and Pee Dee 2165. A new DNA isolation protocol was established, which allows high quality DNA to construct a genetic map with AFLP markers. A total of 32 *EcoRI/MseI* primer combinations were screened for parental polymorphism. Twenty primer combinations were selected to assay the mapping population and to provide 200 polymorphic loci. Linkage analysis was performed at a LOD score of 4.0 and a maximum recombination fraction of 0.34. The genetic linkage map comprised 143 markers assembled into 25 linkage groups and covered 1773.2 cM, 38% of the estimated genome size, with a mean interlocus spacing of 12.4 cM and no dense clustering of loci. The 143 linked markers were assigned to 13 major and 15 minor linkage groups. The 13 major groups ranged from 50.3 to 205.1 cM in length and each group carried 3 to 19 markers. The 15 minor groups ranged from 7.5 to 49.3 cM in length and each group carried 2 to 6 markers. Significant deviations from the expected Mendelian segregation ratio were observed for 67 loci. This map provides a useful tool for of QTL identification for agronomic and fiber quality traits in Upland cotton which will be the primary target.