

Biometrical Identification of Gene Actions and QTLs Linked to Agronomic and Fiber Quality Traits in Cotton

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THE MAJORITY of cotton fiber quality and agronomy traits are quantitatively inherited traits that jointly influence the utility of cotton. Identification of mode of inheritance and loci of quantitative traits for agronomic and fiber traits in Egyptian cottons and their allelic association would be of great interest to both cotton breeder and molecular biologist. This study employed several biometrical models to analyze the effects and mode of gene action in several populations derived from the cross between two cotton lines, *i.e.*, Egyptian cotton G89 (*Gossypium barbadense*) used as female parent and TAMCOT (*Gossypium hirsutum*) as male parent. The study also analyzed QTLs associated with agronomic and fiber traits across 103 F₂ plant families. The implemented statistical models provided estimates of additive and dominance genetic effects as well as the direction of the effects of alleles from both parents and predicted gain. With the current set of probes, the results identified eighteen QTLs controlling fiber quality properties closer to designated markers. Fiber length, strength, elongation, fineness, uniformity and yellowness were influenced by 3, 3, 3, 4, 3, and 2 QTLs, respectively. Cotton yield traits showed very limited insignificant QTLs, Maximum likelihood locations such as those obtained in this study do not necessarily represent physical distances. The results indicated more dominance than additive effect in gene mode of action. It could be concluded that selection procedures based on breeding backcrossing populations proved to be effective in shifting favorable gene frequency under the current gene action and genetic variation and would be successful in improving these traits. Investigating the correlation between traits and DNA markers linked to specific yield and/or fiber quality QTLs will facilitate marker-assisted selection in cotton breeding programs as well as for cloning genes for transformation. Locating the used markers that proved to be diagnostic for identification the assigned traits with such a physical map linkage groups will be, practically, very useful for cotton breeder and producer.

Keywords: Egyptian cottons, QTLs, Gene actions, Variances partition, Heritabilities, MAS, Genetic gain .