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GENETIC STUDIES ON EGYPTIAN COTTON USING MOLECULAR MARKERS

Thesis

Submitted for partial fulfillment of the requirements for M.Sc. in Botany-Microbiology

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Faculty of Science Cairo University 2001 AB-1422 AH I dedicate this modest thesis to my parents,
my unique brother,
and to my dear sisters.

ACKNOWLEDGMENT

I thank Allah for all gifts He has given me

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NOTE

Beside the work carried out in the thesis the author has attended and passed successfully the following postgraduate courses:

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- 3. Bacteriology.
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ABSTRACT

The genetic variability and relationships among 12 Egyptian cotton varieties (G. barbadense) and one G. hirsutum off-type genotype (Hindi) were estimated using 49 RAPD, 14 ISSR, 8 SSR and 6 AFLP primers/primer combinations. The level of polymorphism among all genotypes as revealed by RAPD, ISSR, SSR and AFLP was 30.4%, 53%, 68%, and 56.3%, respectively. While, the variability levels among the 12 Egyptian genotypes were 24.9%, 44.4%, 58.9%, and 43.1%, respectively. The topology of the dendrograms derived from different marker types was unique with evident similarities. All dendrograms clearly discriminate between the Hindi off-type genotype belonging to G. hirsutum and the Egyptian genotypes belonging to G. barbadense. Both RAPD and AFLP clusters separated the variety G45 from all the other G. barbadense varieties. The reshuffling in the position of the remaining G. barbadense varieties in the different dendrograms revealed that they share common genetic background. Variety-specific DNA markers characterized different genotypes and therefore, were used to generate unique fingerprint for each genotype. The RAPD, ISSR, SSR and AFLP revealed 26, 16, 2, and 70 variety-specific DNA markers, respectively. The Hindi off-type was characterized by the highest number of putative speciesunique DNA markers (101) followed by G45, which was characterized by 38 variety-specific markers. Comparison of the applied DNA marker techniques reflected the superiority of AFLP over other types. AFLP showed the highest multiplex ratio (71.3%), effective multiplex ratio (241), sum effective number of alleles (150.9), expected heterozygosity (0.19) and marker index (45.79). Four new microsatellite sequences were identified by cloning, in E. coli (JM109) host, and sequencing of microsatellite enriched ISSR-PCR products. These new motifs were perfect simple dinucleotide repeats [(AG)₁₈ and (TC)₁₇] and imperfect simple dinucleotide repeats [(GA)₁₆CNACA(GA)₂ and (TC)₁₀TA(TC)₆TA].

Key wards:

DNA markers, RAPD, AFLP, Microsatellite, Inter Simple Sequence Repeats (ISSR), Simple Sequence Repeats (SSR), Cotton, G. barbadense, G. hirsutum, E. coli (JM109), Genetic relationships, Variety-specific DNA markers, Cluster Analysis, Sum Effective Number of Alleles (SENA), Expected heterozygosity for polymorphic loci (H_{(av)P}), Marker Index (MI), Effective multiplex ratio (E).

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