



Agronomic characterization, genetic diversity and association analysis of cotton cultivars using simple sequence repeat molecular markers

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ABSTRACT. Cotton is the most important textile plant in the world and is one of the most important crops for the production of oilseed. Because of its worldwide economic importance, new cultivars are constantly being released in the world and consequently in the Greek market, as Greece is the largest producer in Europe. We used simple sequence repeat (SSR) markers for the identification and the phylogenetic analysis of the most widely cultivated cotton cultivars in Greece. Initially, we used 12 pairs of SSR molecular markers for the analysis of 29 cultivars of *Gossypium hirsutum* and an interspecific hybrid (*G. hirsutum* x *G. barbadense*). Of the 12 pairs of SSR primers, 11 amplified polymorphic products, while one pair did not amplify any product. Globally, 17 polymorphic marker loci were identified. Two to four different alleles were amplified at each genomic locus, with a mean of 2.53 alleles per locus. Among the 30 genotypes that we analyzed,

the polymorphism information content ranged from 0 to 0.548, with a mean of 0.293. Three main groups were formed among the 30 genotypes when a phylogenetic analysis was performed using UPGMA. Computational analysis of each molecular marker separately showed an association of SSR markers with agronomic traits such as fiber quality. To our knowledge, this is the first in-depth molecular analysis of cotton cultivars grown in Greece using SSR markers. An analysis of association of SSR markers with fiber quality traits of 29 cotton cultivars is reported for the first time.

Key words: *Gossypium hirsutum*; SSR; Association; Fiber