DNA fingerprinting and genetic diversity in Lentil Germplasm using SSR markers

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ABSTRACT

Molecular markers are useful tools for evaluating genetic diversity and DNA fingerprinting. The purpose of this study was to evaluate the genetic diversity within lentil germplasms microsatellite markers. The observed variability from morphological and SSR analysis among 110 lentil accessions is important for varietal improvement in Bangladesh. However, such information is not available for Bangladesh lentils. The genetic diversity in 121 lentil accessions comprising landraces, modern popular cultivars, selected advanced lines and phenologically adapted exotic accessions was assayed by nine primer combinations. A total of 104 alleles were detected across all microsatellite loci and the number of alleles per locus ranged from 4 (SSR340) to 22(SSR33), with an average of 11.56 alleles. The frequency of the most common allele at each locus ranged from 12.50% (SSR33) to 86.49% (SSR340). On an average, 44.21 % of the 121 lentil accessions shared a common major allele at any given locus. The genetic diversity varied from 0.24 (locus SSR 340) to 0.93 (locus SSR33) with a mean of 0.69. Polymorphism Information Content (PIC) values ranged from 0.23 to 0.93 with an average of 0.66. Cluster analysis based on SSR amplification products grouped genotypes into three clusters with 54, 40 and 27 accessions each and substantial association between molecular diversity and origin was evident.

Key words: Fingerprinting, Lentil, diversity, germplasm