



Genetic bottlenecks in Turkish okra germplasm and utility of iPBS retrotransposon markers for genetic diversity assessment

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ABSTRACT. Lack of requisite genetic variation in Turkish okra has necessitated the use of different types of markers for estimating the genetic diversity and identifying the source of variation. Transposable elements, present abundantly in plant genomes, generate genomic diversity through their replication and are thus an excellent source of molecular markers. We hypothesized that inter-primer binding site (iPBS)-retrotransposons could be the source of variation because of their genome plasticity nature. In the present study, genetic diversity of 66 okra landraces was analyzed using iPBS-retrotransposon markers. iPBS-retrotransposons detected 88 bands with 40.2% polymorphism and an average of 6.8 bands per primer. Gene diversity and Shannon's information index ranged from 0.01 to 0.13 and 0.02 to 0.21 for iPBS-retrotransposons and from 0.06 to 0.46 and 0.14 to 0.65 for simple sequence repeat (SSR) markers, respectively. Polymorphism information content value for retrotransposons varied between 0.12 and 0.99, while that for SSR was from 0.52 to 0.81. Neighbor joining analysis based on retrotransposons and SSRs divided all the accessions into

four clusters; however, SSR markers were more efficient in clustering the landraces based on their origin. Using the STRUCTURE software for determining population structure, and two populations (at the number of hypothetical subpopulations, $K = 2$) were identified among the landraces. Low genetic diversity in Turkish okra highlights the need for the introduction of plants from countries with greater genetic diversity for these crops. This study also demonstrates the utility and role of iPBS-retrotransposons, a dominant and ubiquitous part of eukaryotic genomes, for diversity studies in okra.

Key words: Population structure; *Abelmoschus esculentus*; Genetic diversity; Retrotransposons; Turkish landraces