Remarks on genetic diversity and relationship of Punica protopunica and P. granatum assessed by molecular analyses

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Abstract:

Here, two Punica species, viz., P. protopunica Balf. fil., reported as native to Socotra, and P. granatum L., were compared for the first time. Analysis of one P. protopunica and eleven P. granatum accessions was performed using three molecular markers, i.e., sequence related amplified polymorphism (SRAP), target region amplification polymorphism (TRAP), and intron targeted amplified polymorphism (ITAP), along with analysis of pgWD40 sequences, a gene involved in anthocyanin biosynthesis. All markers revealed the relationship between the two species and placed them at 33% similarity. SRAP, TRAP, and ITAP generated a total of 299, 260, and 160 bands, respectively. Of these, 78, 74, and 41 bands were specific for P. protopunica, and 92, 85, and 57 bands, respectively, were shared between both species. Sequence analysis of pgWD40~870 bp amplicons exhibited 100% identity among P. granatum accessions and 98% identity to that of P. protopunica. Phylogenetic analysis of WD40 sequences from monocot and dicot species, including both Punica species confirmed the relation between P. protopunica and P. granatum, supporting earlier reports that P. protopunica could be an ancestral species of P. granatum. Furthermore, the genetic diversity among and within P. granatum accessions from Egypt (3), Mexico (5), and Yemen (3) was assessed. Molecular marker-based relationships among region-bulked accessions was approximately the same (~90% similarity), whereas the degree of genetic variation was altered within each region. Specific bands (alleles) for accessions of each region along with those shared among them were identified. Thus, these bands could be used for pomegranate genotyping and breeding programs.

Keywords:

Anthocyanin Genetic diversity Molecular marker Pomegranate Punica granatum Punica protopunica

Published In:

Genetic Resources and Crop Evolution , 65 , 577-590