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Analysis Of Date Palm Germplasm Phylogenetic Relationship Using Simple Sequence Repeat (SSR) Markers

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Abstract

Background:

Microsatellite (Simple Sequence Repeat) markers are very powerful tool especially in plant genome analysis because they are locus-specific, co-dominant, highly polymorphic and highly reproducible. However, in date palm only few microsatellite markers are available worldwide so far. Fortunately, more than 1000 new microsatellite markers were developed recently by a research group in ICARDA based on the date palm genome sequence generated by next generation DNA sequencing that is published by Weill Cornell Medical College in Qatar.

Objectives:

The aim of this work was to analyze the genetic diversity among most common cultivars of Qatari date palm and the genetic variation within each cultivar using simple sequence repeat markers. In addition, the study aimed to develop a detailed understanding of the genetic and molecular relationships of Qatari date Palm cultivars

Methods:

A new set of hundred genomic DNA microsatellite primer pairs was used to assess the genetic diversity of the 47 collected Date palm samples that are representing 17 genotypes from two genetic resource fields (Rodat Alfaras Germplasm field and Qatar University Experimental Farm). Bands were precisely measured by Gel documentation System software and scored for each genotype. Each reproducible polymorphic DNA band at particular position on the gel was treated as a separate character and scored as present (1) or absent (0) to generate a binary data matrix. Results:

The results revealed that out of 100 SSR primers 27 primers showed exact expected size band and 62 primers showed clear polymorphism. In addition 11 over 100 did not show clear bands.in the whole set of 47 Date palm samples. Total of 538 bands were generated using the 100 SSR primers for the 15 Date palm date palm cultivars. On average, each primer generated 5 bands per genotype. The number of amplified bands varied from cultivar to cultivar and primer to primer.

Band pattern data was converted into a binary data in excel work sheet and was analyzed using Powermaker program to calculate similarity coefficient values according to Jaccard (1908). A similarity matrix between Qatari date palm cultivars (Figure 5) showed an average genetic distance range from 0.000 to 0.4769. The cultivars studied here were highly divergent at the DNA level. The highest genetic distance value was observed between Lulu -3 and both Khadrawy-2and Khadrawy-3 cultivars (0.4769) which seem to be the most far three varieties. . Conclusions:

In this study, SSR markers have been used to assess the molecular characterization and the phylogenic relationships of Qatari date palm cultivars. Our results provide evidence of a genetic diversity among the studied Qatari date genotypes and the ability of SSR markers to detect the genetic diversity in date palm. We may conclude that all date-palm genotypes are interrelated in spite of their agronomic



