

Plant Genomics 2019: Genetic diversity of Omani date palm (*Phoenix dactylifera* L.) cultivars and its relationships with 'exotic' cultivars using SSR markers- Al-Ghaliya H Al-Mamari, Ministry of Agriculture & Fisheries, Oman

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The present study investigated the genetic diversity of one hundred and ninety-four date palm accessions from Oman and forty-eight accessions from Italy, USDA-ARS, France, Iraq, Libya, Sudan and Iran using SSR molecular markers. Around 300 varieties of date palm are grown throughout the Sultanate and this study has provided the first molecular identification key, which enables the unambiguous discrimination of Omani date palm accessions. The genetic analysis showed that the Omani accessions were closely related to each other and there was no clear genetic differentiation between female and male cultivars. There was a quite high degree of genetic differentiation observed between germplasm from Oman, Sanremo, Bordighera, USDA-ARS, France, Iraq, Libya, Sudan and Iran as measured by F_{st} (19.7 %) compared with the genetic differentiation observed among the Omani accessions (2.1%) of the total variation, which probably reflects the homogeneous nature of the Omani date palm used in this study comparing to the divergent sets of other germplasm. The study also confirms that the Europe-Africa (Sanremo, Bordighera, France, Libya and Sudan) accessions are distinguished from West-Asia (Oman, Iraq and Iran) accessions, have their own autochthonous origin, a finding which was strongly validated by bootstrap consensus tree test. The genetic diversity in the date palm germplasm of 59 female accessions representing 12 cultivars from different locations in Qatar was investigated using 14 loci of simple-sequence repeat (SSR) primers. A total of 94 alleles, with a mean of 6.7 alleles per locus, were scored. The number of alleles per locus varied from 3 (primer mPdCIR090) to 11 (primers mPdCIR010 and mPdCIR015). The amplified SSR band sizes ranged from 104 to 330 bp. The

mean gene diversity was 0.66 and ranged from 0.39 (locus mPdCIR093) to 0.86 (locus mPdCIR015), indicating that the Qatari date palm collection has a high degree of genetic diversity. The heterozygosity ranged from 0 (marker mPdCIR090) to 98% (marker mPdCIR010). Forty-four percent of the variability is explained at the inter-population level, while 56% of the variability is maintained within individuals. However, the loci mPdCIR044, mPdCIR057, mPdCIR090, and mPdCIR093 revealed that the total gene diversity is explained at the inter-population level. The Qatari populations Khalas, Shishi, Barhi, Hillali, Khnaizi, Gar, and Jabri showed significant differentiation compared to all other populations. The average fixation index was 0.24814, showing that about 24.81% of the genetic variation was present among populations, which correlated with analysis of molecular variance. The most common characteristics that are used to identify different cultivars of date palm are the morphology of leaves, spines, and fruit, which are mainly based on the characterization of introduced date palm cultivars in California (Nixon, 1950). However, morphological traits are often unreliable or imprecise indicators of plant genotype because they are influenced by environmental conditions and vary with the developmental stage of plants. Over the years, many date palm cultivars have been transplanted to areas other than the area of their origin, and they may have been given different names. As a result, a variety may have different names in different areas, or two genetically different varieties may have the same name. This may reduce the genetic diversity of the cultivars, making them vulnerable to biotic and abiotic stresses.