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**Record 1 of 1****Title:** Whole Mitochondrial and Plastid Genome SNP Analysis of Nine Date Palm Cultivars Reveals Plastid Heteroplasmy and Close Phylogenetic Relationships among Cultivars**Author(s):** Sabir, JSM (Sabir, Jamal S. M.); Arasappan, D (Arasappan, Dhivya); Bahieldin, A (Bahieldin, Ahmed); Abo-Aba, S (Abo-Aba, Salah); Bafeel, S (Bafeel, Sameera); Zari, TA (Zari, Talal A.); Edris, S (Edris, Sherif); Shokry, AM (Shokry, Ahmed M.); Gadalla, NO (Gadalla, Nour O.); Ramadan, AM (Ramadan, Ahmed M.); Atef, A (Atef, Ahmed); Al-Kordy, MA (Al-Kordy, Magdy A.); El-Domyati, FM (El-Domyati, Ftooh M.); Jansen, RK (Jansen, Robert K.)**Source:** PLOS ONE **Volume:** 9 **Issue:** 4 **Article Number:** e94158 **DOI:** 10.1371/journal.pone.0094158 **Published:** APR 9 2014**Times Cited in Web of Science Core Collection:** 7**Total Times Cited:** 7**Usage Count (Last 180 days):** 1**Usage Count (Since 2013):** 33**Cited Reference Count:** 55**Abstract:** Date palm is a very important crop in western Asia and northern Africa, and it is the oldest domesticated fruit tree with archaeological records dating back 5000 years. The huge economic value of this crop has generated considerable interest in breeding programs to enhance production of dates. One of the major limitations of these efforts is the uncertainty regarding the number of date palm cultivars, which are currently based on fruit shape, size, color, and taste. Whole mitochondrial and plastid genome sequences were utilized to examine single nucleotide polymorphisms (SNPs) of date palms to evaluate the efficacy of this approach for molecular characterization of cultivars. Mitochondrial and plastid genomes of nine Saudi Arabian cultivars were sequenced. For each species about 60 million 100 bp paired-end reads were generated from total genomic DNA using the Illumina HiSeq 2000 platform. For each cultivar, sequences were aligned separately to the published date palm plastid and mitochondrial reference genomes, and SNPs were identified. The results identified cultivar-specific SNPs for eight of the nine cultivars. Two previous SNP analyses of mitochondrial and plastid genomes identified substantial intra-cultivar (= intra-varietal) polymorphisms in organellar genomes but these studies did not properly take into account the fact that nearly half of the plastid genome has been integrated into the mitochondrial genome. Filtering all sequencing reads that mapped to both organellar genomes nearly eliminated mitochondrial heteroplasmy but all plastid SNPs remained heteroplasmic. This investigation provides valuable insights into how to deal with interorganellar DNA transfer in performing SNP analyses from total genomic DNA. The results confirm recent suggestions that plastid heteroplasmy is much more common than previously thought. Finally, low levels of sequence variation in plastid and mitochondrial genomes argue for using nuclear SNPs for molecular characterization of date palm cultivars.**Accession Number:** WOS:000334339000083**Language:** English**Document Type:** Article**KeyWords Plus:** PHOENIX-DACTYLIFERA; BIPARENTAL INHERITANCE; CHLOROPLAST DNA; CYTOPLASMIC INHERITANCE; AFLP MARKERS; SAUDI-ARABIA; ISSR MARKERS; L. CULTIVARS; GENERATION; PLANTS**Addresses:** [Sabir, Jamal S. M.; Bahieldin, Ahmed; Abo-Aba, Salah; Bafeel, Sameera; Zari, Talal A.; Edris, Sherif; Shokry, Ahmed M.; Gadalla, Nour O.; Ramadan, Ahmed M.; Atef, Ahmed; Al-Kordy, Magdy A.; El-Domyati, Ftooh M.; Jansen, Robert K.] King Abdulaziz Univ, Dept Biol Sci, Jeddah 21413, Saudi Arabia.

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**Publisher:** PUBLIC LIBRARY SCIENCE**Publisher Address:** 1160 BATTERY STREET, STE 100, SAN FRANCISCO, CA 94111 USA**Web of Science Categories:** Multidisciplinary Sciences**Research Areas:** Science & Technology - Other Topics**IDS Number:** AE9PC**ISSN:** 1932-6203**29-char Source Abbrev.:** PLOS ONE**ISO Source Abbrev.:** PLoS One**Source Item Page Count:** 13**Funding:**

Funding Agency	Grant Number
Deanship of Scientific Research (DSR), King Abdulaziz University, Jeddah	1-3-1432/HiCi

This project was funded by the Deanship of Scientific Research (DSR), King Abdulaziz University, Jeddah, under Grant no. (1-3-1432/HiCi). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Open Access:** gold**Output Date:** 2017-07-26

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