

# Complete mitochondrial genome sequence of historical olive (*Olea europaea* subsp. *europaea*) cultivar Mehras in Jordan

Prof. Mohammad Brake  
Biology Department  
Jerash University

Prof. Monther Sadler  
Department of Horticulture  
and Crop Science  
Jordan University

## Background:

- Jordan is considered along others countries in the Fertile Crescent region core of origin for olive domestication and cultivation.
- Olives are major economic trees grown for both healthy oil and fruits in Jordan.
- 70% of tree cultivated areas are olive orchids
- 20 Million trees grown in 250000 Acres.

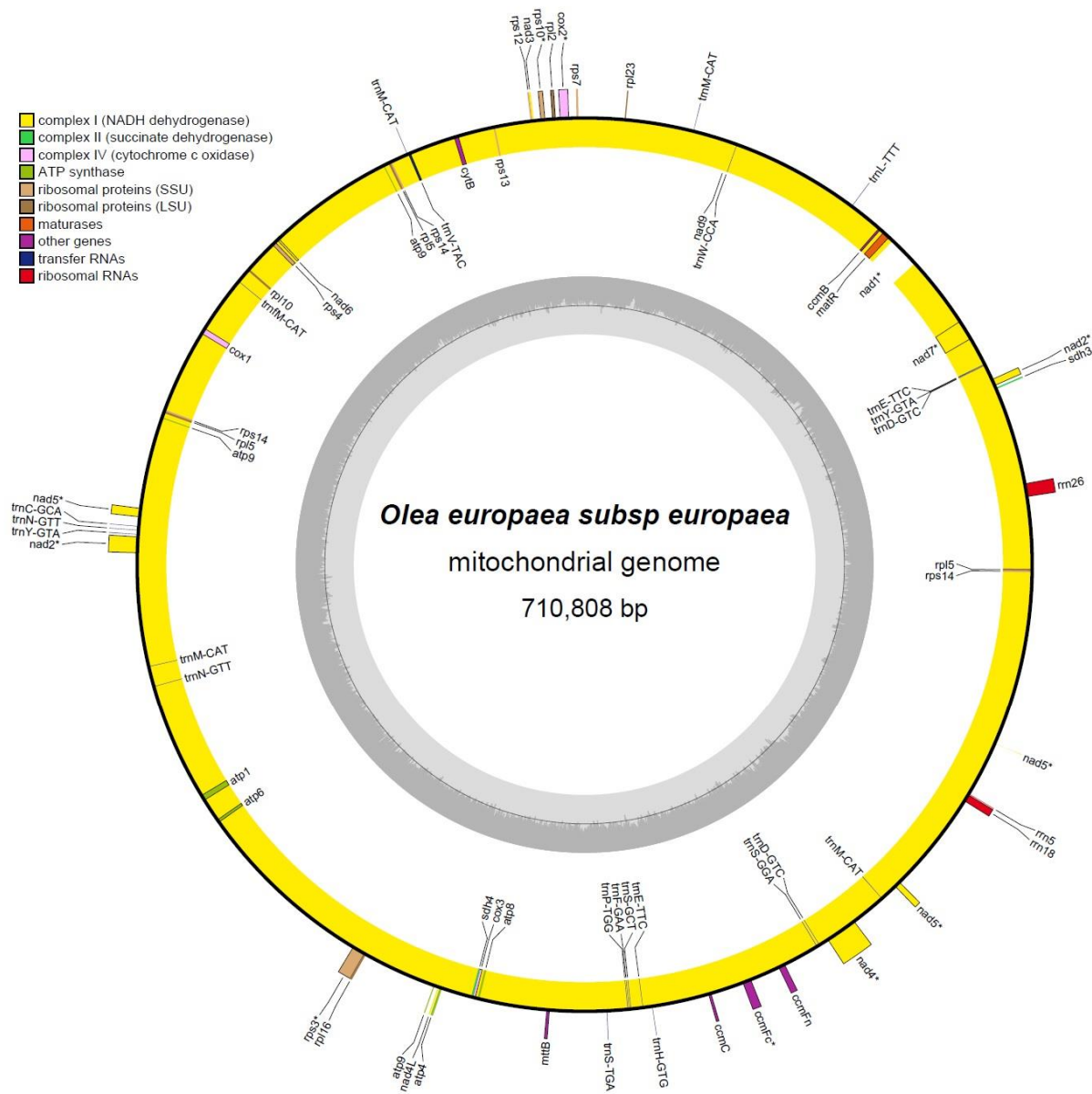
# Mehras



- Illumina HiSeq sequencing technology to sequence the mitochondrial genome.
- CLC Genomics Workbench (USA) to assemble the mitochondrial genome of Mehras.
- The complete mitochondrial genome sequence deposited into GenBank database (Accession Number: MW262896).
- The mitochondrial genome was illustrated using OGDRAW (Greiner et al., 2019).
- Selected regions of mitogenome sequences were aligned using the multiple sequence alignment (CLC Genomics Workbench, USA).
- PHYLIP software were used to construct phylogenetic tree.

- The complement mitochondrial genome of Mehras was 710,808 bp length of circular form.
- The mitochondrial genome contained 70 genes (44 protein-coding, 23 tRNA, and 3 rRNA).
- GC content was 44.7%.
- Some mitogenome gene in Mehras are missing start codons.

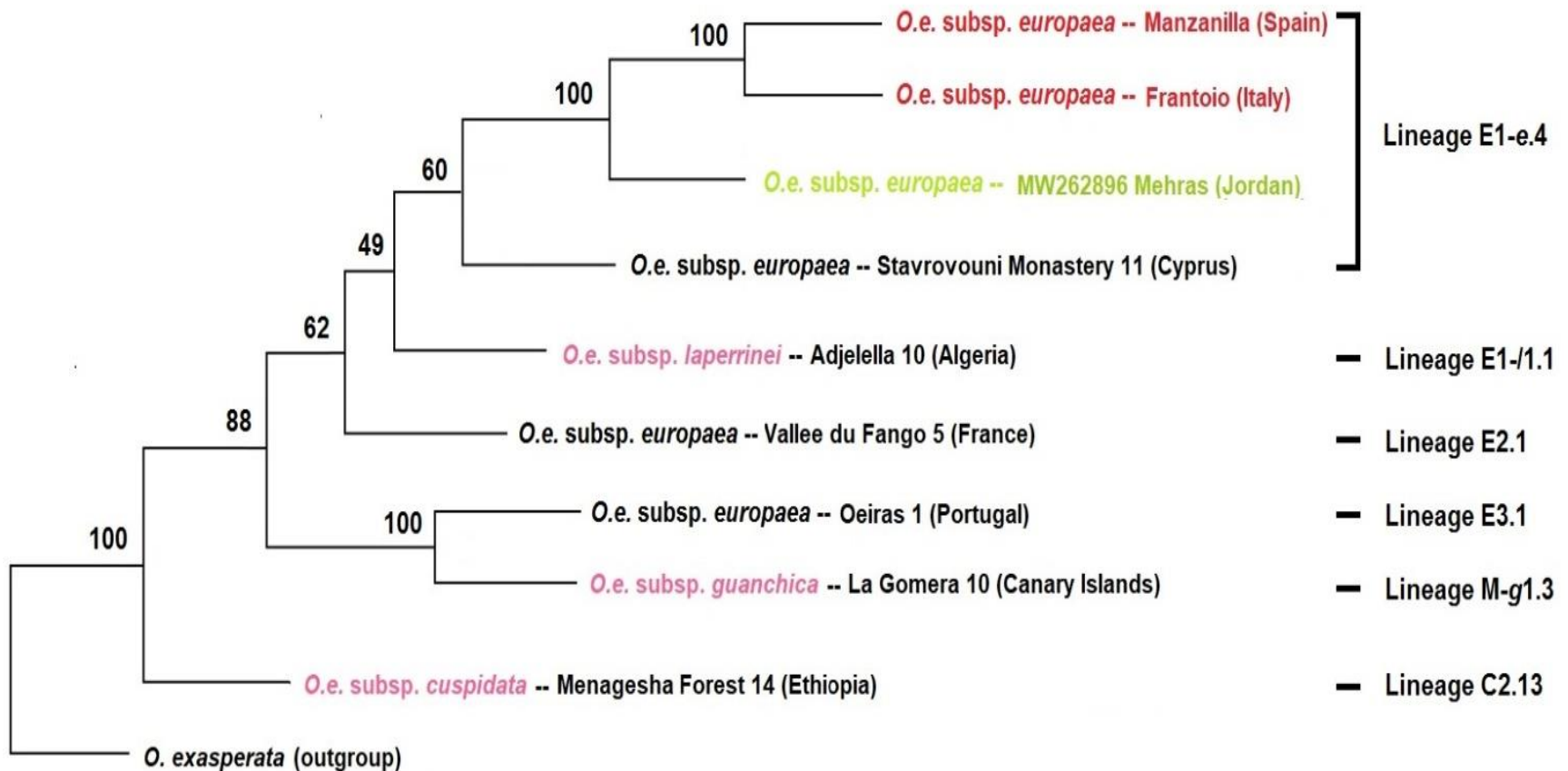




- The entire mitogenome of *O.e. subsp. europaea* cultivar Mehras (Jordan) and related cultivar Stavrovouni Monastery 11 (Cyprus) were aligned.

Region	Gene name	Gene product	SNPs	InDels (bases)							
				1	2	3	4	5	6	7	8
Intergenic			564	23	10	5	7	5	5	3	1
Intragenic	rrn26	26S ribosomal RNA	189	2	1		1				
	rrn18	18S ribosomal RNA	120	1							
	trnW-CCA	tRNA-Trp	1								
	rpl23	ribosomal protein L23	2								
	trnV-TAC	tRNA-Val	4	1							
	trnM-CAT	tRNA-Met	1								
	trnN-GTT	tRNA-Asn	3								
	atp1	ATPase subunit 1	15								
	atp4	ATPase subunit 4	1								
	trnS-TGA	tRNA-Ser	13			2					
	trnF-GAA	tRNA-Phe	5	1							
	trnH-GTG	tRNA-His	3								
	trnS-GGA	tRNA-Ser	3								
	trnD-GTC	tRNA-Asp	1								
Total			925								68

- The constructed phylogenetic trees shows that *O. e. subsp. europaea* cultivar Mehras has a common ancestor with cultivars Frantoio from Italy and Manzanilla from Spain






## MITOGENOME ANNOUNCEMENT

 OPEN ACCESS  Check for updates

# Complete chloroplast genome sequence of historical olive (*Olea europaea* subsp. *europaea*) cultivar Mehras, in Jordan

Nizar Haddad<sup>a</sup> , Hussein Migdadi<sup>a,b</sup>, Mohammad Brake<sup>c</sup>, Salam Ayoub<sup>a</sup>, Wisam Obeidat<sup>a</sup>, Yahya Abusini<sup>a</sup>, Abeer Aburumman<sup>a</sup>, Banan Al-Shagour<sup>a</sup>, Eman Al-Anasweh<sup>a</sup> and Monther Sadder<sup>d</sup>

<sup>a</sup>National Agricultural Research Center – NARC, Amman, Jordan; <sup>b</sup>College of Food and Agricultural Sciences, King Saud University, Riyadh, Saudi Arabia; <sup>c</sup>Science Faculty, Jerash University, Jerash, Jordan; <sup>d</sup>School of Agriculture, The University of Jordan, Amman, Jordan

### ABSTRACT

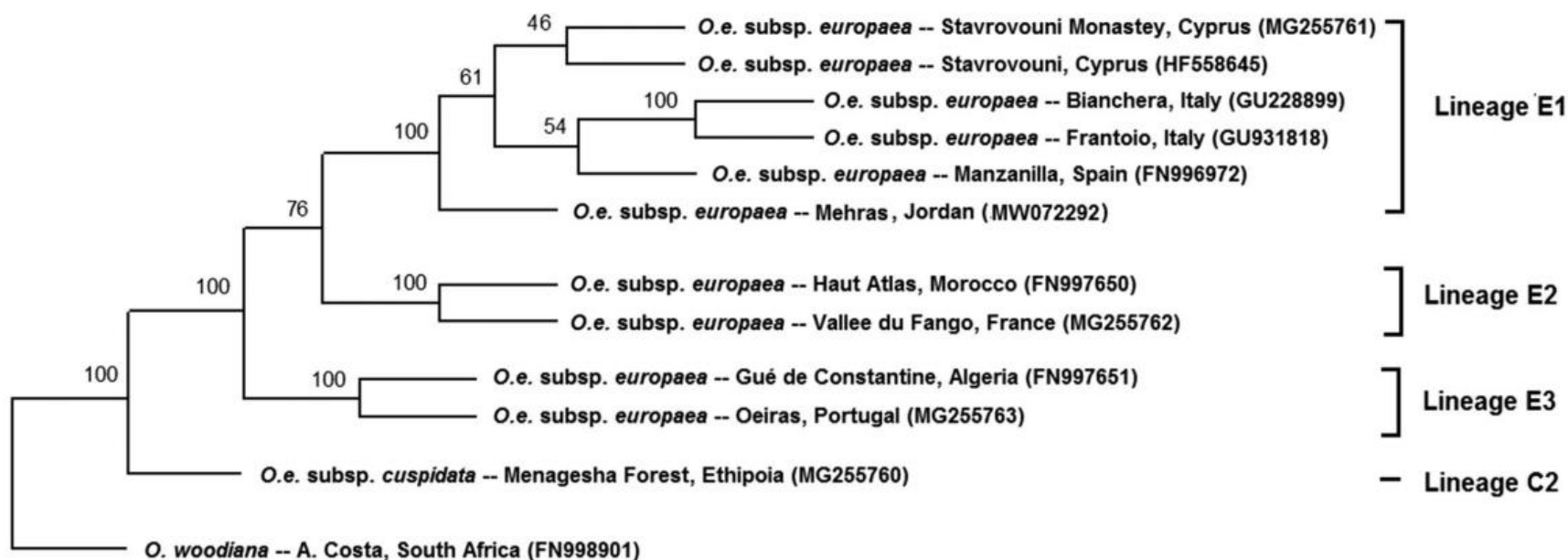
The complete chloroplast genome sequence of *Olea europaea* subsp. *europaea* cultivar Mehras was determined using high-throughput sequencing technology. Chloroplast genome was 155,897 bp in length, containing a pair of 25,742 bp inverted repeat (IR) regions, which were separated by large and small single-copy regions (LSC and SSC) of 86,622 and 17,791 bp, respectively. The chloroplast genome contained 130 genes (85 protein-coding, 37 tRNA, and eight rRNA). GC content was 37.8%. We performed phylogenetic analysis with other isolates. The analysis showed that *O. e.* subsp. *europaea* cultivar Mehras has an ancient common ancestor with cultivated olives in Italy, Spain, and Cyprus.

### ARTICLE HISTORY

Received 17 October 2020  
Accepted 27 November 2020

### KEYWORDS

Mehras; olive; plastome

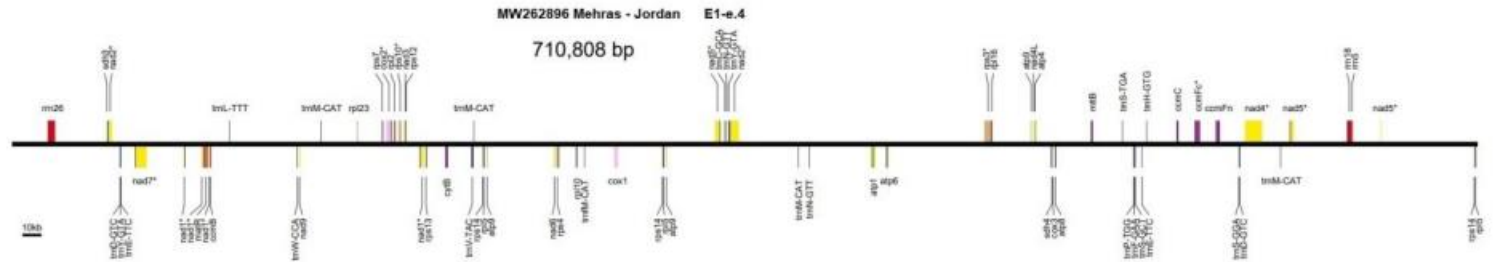
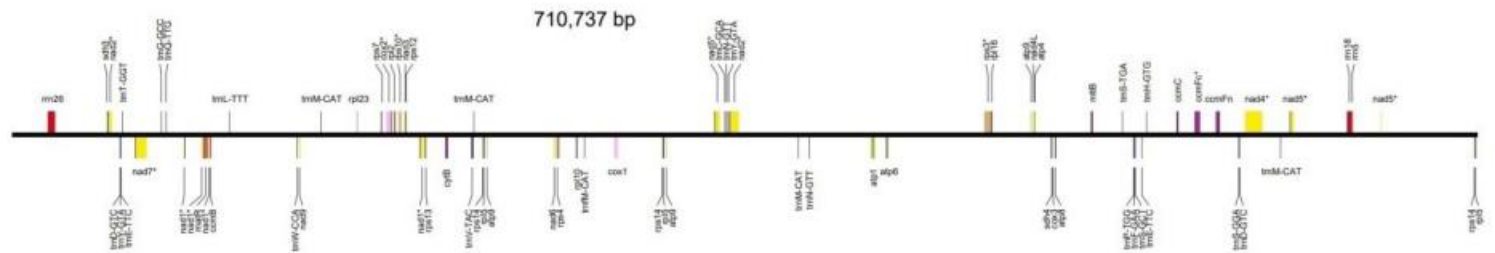
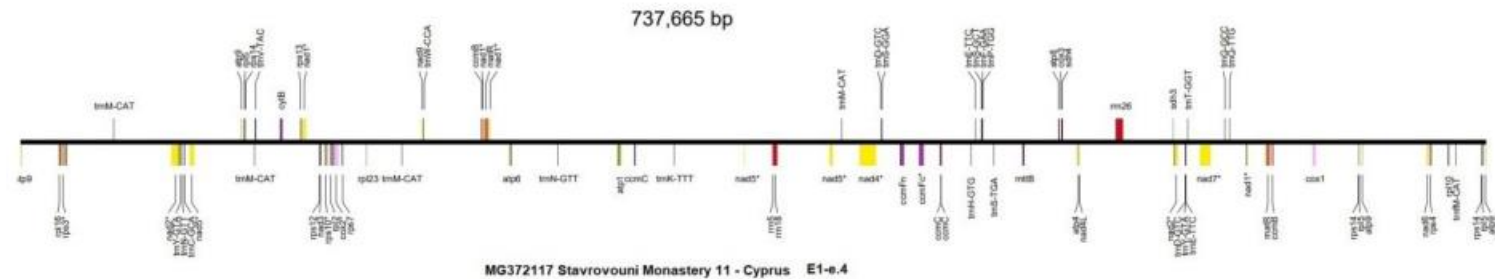
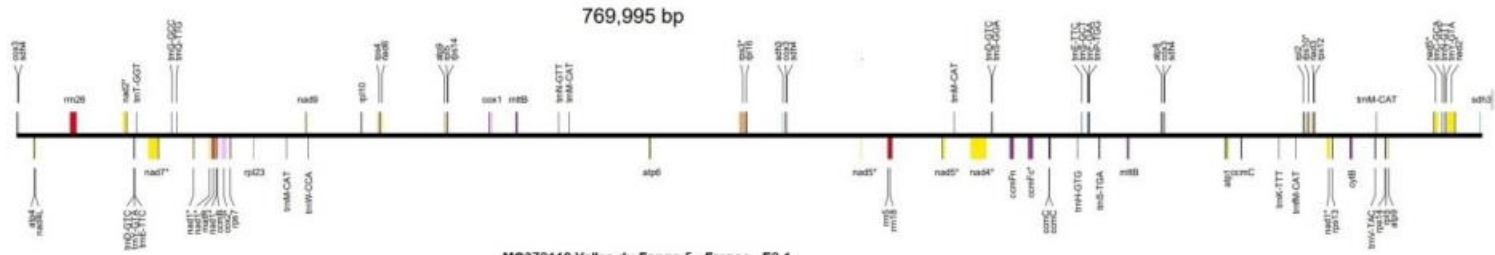


**Figure 1.** Plastid DNA maximum-likelihood phylogenetic tree of *Olea europaea* subsp. *europaea* cultivar Mehra along with other isolates. Bootstrap values are given on each branch (1000 replicates). *O. e. subsp. cuspidata* and *O. woodiana* were used as out-groups. Olive plastid lineages were based on Besnard et al. (2011).

- The gene order and reading direction was compared using aligned linear forms of four mitochondrial genomes.
- The alignment shows almost a complete synteny between in order and gene reading directions between Stavrovouni Monastery 11 and Mehras.
- The alignment shows apparent differences among two cultivars; Oeiras 1 and Vallee du Fango 5.

*Olea europaea subsp europaea* mitochondrial genome

MG372119 Oeiras 1 - Portugal E3.1



In the near future:

1. Analysis of nuclear genome.

Purposes:

- Using detecting SNPs and genetic variations in the whole genome be used in marker assisted selection programs.
- Studying phylogeny and evolution of Mehras cultivar.
- Identifying genes correlated with desirable traits specially for abiotic stress tolerance.

2. Studying the performance of cultivar Mehras under abiotic stress conditions like drought, salinity, and heat.

## Innovation:

1. The last years the price of olive oil of Mehras was augmented by 50%.
2. More investigation at the molecular level like full genome sequences analysis could leads to discovery of novel genes unique to Mehras cultivar which in turn will:
  - increase the farmer's income.
  - Increase areas cultivated by cultivar Mehras.



Thanks