

BOOK OF ABSTRACT

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I. SESSION DESCRIPTION

ID: S8a

Title of session:

Conservation and utilization of Crop Wild Relatives (CWRs) under changing world

Hosts:

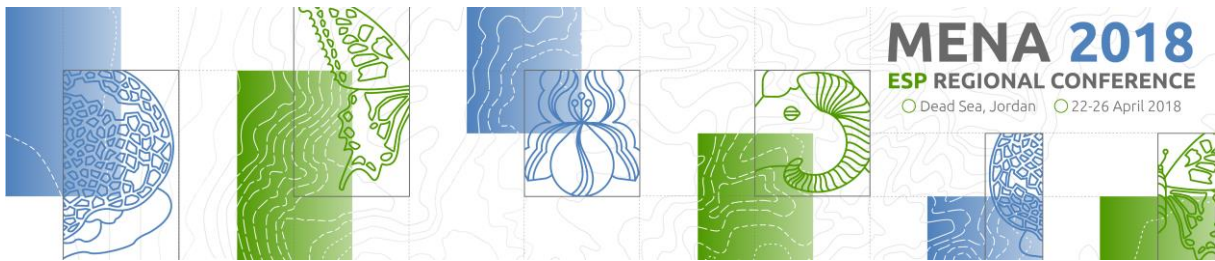
	Title	Name	Organisation	E-mail
Host:	Dr.	Khaled Abulaila	NCARE	kabulaila@gmail.com

Abstract:

Crop Wild Relatives (CWR) including progenitors of modern cultivated varieties are species genetically related to our food crops and the base of genetic diversity and so potential sources for useful traits, such as pest or disease resistance, and yield especially under changing conditions, that can be used now and in the future for secure food production of the globe, in other words they are the raw material used by researchers to improve the quality and productivity of our crops. Part of the local flora of Jordan is wild relatives of globally important crops of which wheat and barley are amongst the most famous crops. In addition, more than 14 wild relatives of global significance such as small grain cereals and many food legumes (lentil, chickpea), forage species (*Vicia*, *Medicago*), vegetables (lettuce, carrot) and fruit trees (olive, almond, pear, grape, pistachio, etc.) that have been domesticated over the last 10,000 years and have progressively spread to all over the world. Due to different threats, mainly urbanization and overgrazing as well as ongoing conflicts taking place in many countries of this region, many of the natural habitats and niches of CWRs critically endangered. Therefore, conservation and sustainable use of such natural wealth should be a major priority on the local as well as the regional levels.

Goals and objectives of the session:

Emphasise the importance of CWRs protection in achieving the strategic goals of improving food security in the face of climate and land use changes. Explore various steps and methods of CWRs utilization using conventional and modern approaches. Provide opportunities and measures that should be taken toward in situ and ex situ conservation of CWRs



Planned output / Deliverables:

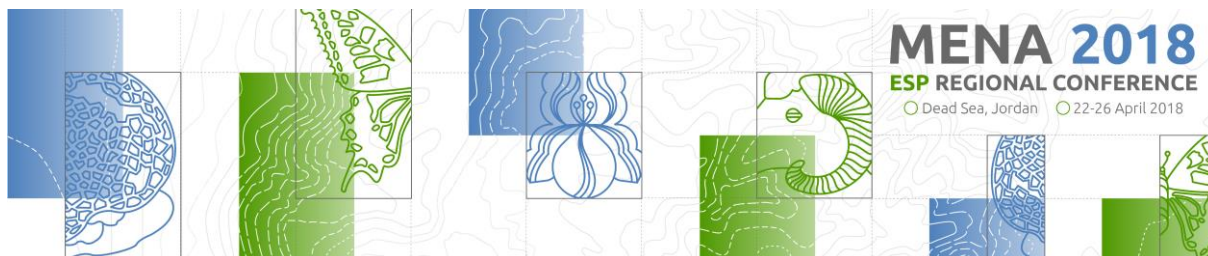
Insights about the importance of CWRs for food security on local as well as global levels
How protecting CWRs provides an integrated approach to improving both biodiversity and sustainable development, in accordance with global conventions and treaties. Promoting best approaches for sustainable and efficient utilization of CWRs

Voluntary contributions accepted:

YES

Related to ESP WG or NN:

[SWG 8A- Task Force on Agrobiodiversity](#)



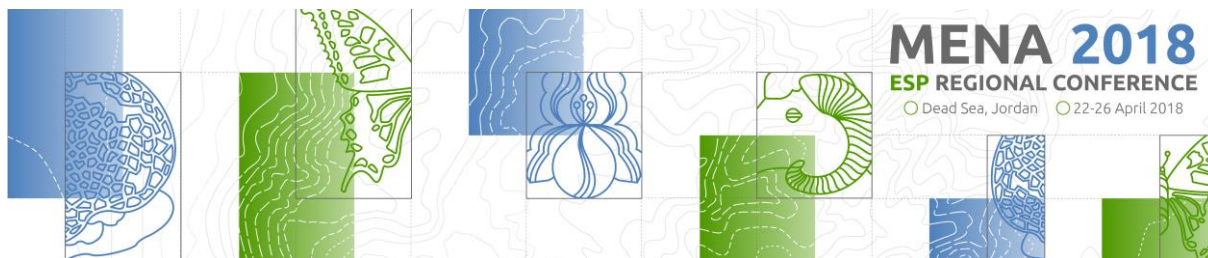
II. SESSION PROGRAM

Date of session: 23rd April 2018

Time of session: 10:30 - 12:30

Timetable speakers

Time	First name	Surname	Organization	Title of presentation
10:30 to 11:00	Khaled	Abulaila	NCARE	The value of Crop Wild Relatives
11:00 to 11:30	Nawal	Alhajaj	NCARE	Morphological characterization of wild Oat populations (<i>Avena sterilis</i> L.) from Jordan
11:30 to 12:00	Farshid	Talat	Azarbaijan Agricultural and Natural Resources Research and Education Center, AREEO, Urmia, Iran	Synonymous codon usage bias in chloroplast genomes of <i>Vitis vinifera</i> and two Caucasic Subspecies of grape fruit
12:00 to 12:30		General Discussion		



III. ABSTRACT

1. Type of submission: *Invited speaker abstract*

S. Sectoral Working Group sessions: S8a Conservation and utilization of Crop Wild Relatives (CWRs) under changing world

Morphological characterization of wild Oat populations (*Avena sterilis* L.) from Jordan

Author: Nawal Alhajaj

Other author: Israa Alhasanat

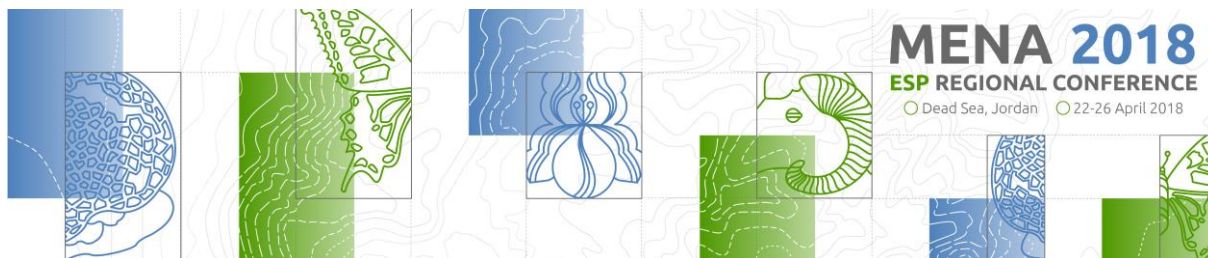
Affiliation: National Center for Agricultural Research and Extension (NCARE), Jordan

Contact: nawal@ncare.gov.jo

ABSTRACT

The wild ancestral form of Oat, *Avena sterilis* L., collection from oat center origin countries, is a valuable source for gene enrichment for oat crop improvement. It might be, this first study have been assessed the extent and pattern of morphological variation in the wild oat populations with respect to accessions passport data and to identify the major traits contributing to observed diversity in collection populations. Ten plant and spike agronomic traits were evaluated for forty-eight populations of *A. sterilis* L. collected from Jordan, to define the structure of the diversity. The studies populations showed a large variation for most of morphological traits evaluated. The highest variation was recorded for number of stems and number of spikelet, while the lowest was for awns length. The result of a cluster analysis did not show grouping on the basis of collection region. Considerable variation was observed, even between populations collected from nearby sites. This work provided an important contribution to morphological characterization of *A. sterilis* L. traits, and emphasized the importance of short distance sample collection to capture as much as variation as possible of the gene pool.

Keywords: diversity, characterization, morphology, Breeding, *Avena sterilis* L.



2. Type of submission: **Invited speaker abstract**

S. Sectoral Working Group sessions: S8a Conservation and utilization of Crop Wild Relatives (CWRs) under changing world

Synonymous codon usage bias in chloroplast genomes of *Vitis vinifera* and two Caucasia Subspecies of grape fruit

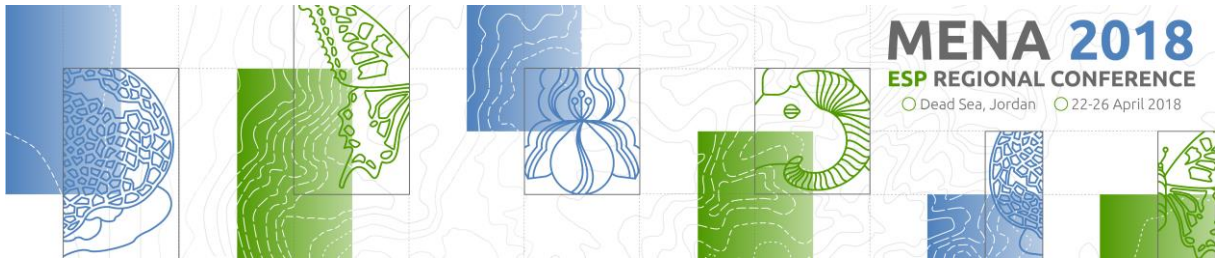
Author: Farshid Talat

Other authors: Sayna Shahdparvar , Jirayer Karapetian

Affiliation: West Azarbaijan Agricultural and Natural Resources Research and Education Center, AREEO, Urmia, Iran

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Chloroplast research have significant advantage of genomics and genome sequencing, and a new picture is emerging of how the chloroplast functions and communicates with other cellular compartments. Grape (*Vitis vinifera*) is a genus of trees in the family Vitaceae. *Vitis vinifera* species belongs to Eurasian grapes. The chloroplast genome is the most comprehensive genome in plants and has many features for evolution analyses due to the unique molecular structure and single-parent inheritance. Sequence and gene annotation was mainly performed by DOGMA. Map of chloroplast genome structure and gene distribution was carried out using OGDRAW V1.1. Relative synonymous codon usage (RSCU) of different codons in each gene sample was calculated by codonW in MobyE. An online version of REPuter was used to specify the repeat sequence and location. this research was targeted to study and compare the complete chloroplast genome sequences of Saperavi and Meskhuri mtsvane from caucasia subspecies with common grape (*Vitis vinifera*) and as well genome structure analysis, gene content, organization and repetitive sequences, codon usage and comparison among genomes. The chloroplast (cp) genome of *Vitis vinifera* is a circular DNA molecule of 160928 base pair (bp) which is longer than chloroplast genome of Saperavi and Meskhuri Mtsvane cultivars. Large and small unique regions are separated by two inverted repeat regions a, b. In all of three genomes, whole genome contains 131 genes which include 79 protein coding genes, 4 rRNA genes and 30 tRNA genes. In other words, there are totally 113 single-copy genes and 18 double-copy genes located in inverted repeat region (IR) in the three studied genomes. The SSRs of the chloroplast genomes were identified and the results indicated that the chloroplast genomes of *Vitis vinifera* and Saperavi both have 74 and Meskhuri mtsvane



has 73 SSRs. The cpSSRs are important and useful for genetic diversity studies. Low GC content is a significant feature of plastid genomes, which is possibly formed after endosymbiosis by DNA replication and repair.

Keywords: Chloroplast genome, complete sequence, *Vitis vinifera*