

PLANT DIVERSITY OF MEDITERRANEAN-TYPE ECOSYSTEMS WITH AN EMPHASIS
ON CULTIVATED SPECIES

by

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DEDICATION

To my parents and my brother “Remon” who have supported me throughout my graduate studies. May God bless them.

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ABSTRACT

The Mediterranean Basin is an important biodiversity hotspot. Unfortunately, only 5% of its original vegetation remains intact because people have managed and transformed the landscape for the past 2000 years. In the last century, humans overused the semi-natural habitats which had a negative impact on the area more than earlier times. This is in addition to the mechanization of agriculture which had a negative impact on the area as well (Puddu, Falcucci, and Maiorano 2011). Mediterranean-type ecosystems (MTEs) are as plant diverse as tropical ecosystems. This biodiversity is larger than expected considering the relatively high latitude and the low productivity of the region. This makes these areas a good case study to examine the processes affecting plant diversity. Five MTEs are described as biodiversity hotspots due to the high numbers of endemic plant species. Scientists are working to decrease the biodiversity loss in the Mediterranean area. Here we will discuss biodiversity, cultivated species, and threats to Mediterranean-type ecosystems. Moreover, we will present the adaptation of these species to biotic and abiotic stresses, in addition to scientists' efforts to develop cultivars well-adapted to these stresses.

.

CHAPTER ONE

INTRODUCTION

Biodiversity hotspots are described as areas in which the endemic species experience exceptional habitat loss. The Mediterranean region contains about 25,000–30,000 flowering plants and was described as one of the biodiversity hotspots in the world. In this region, there are 25 independent nations, in which there are 10–11 hotspots. These hotspots form about 22% (515,000 km²) of the Mediterranean Basin total surface area and contain about 5500 endemic plants (Bacchetta, Farris, and Pontecorvo 2011).

Mediterranean-type ecosystems (MTEs) are located in southwestern Australia, South Africa Cape Region, Mediterranean Basin, California, and central Chile. These MTEs contain a large number of plant species. These ecosystems possess iconic Mediterranean-type shrublands, deciduous and evergreen woodlands in addition to evergreen forests, herblands, and grasslands all of which are considered as different vegetation structures (Rundel et al. 2016).

The term biodiversity describes all varieties of living life-forms. Biodiversity of crops is described by a series of historical genetic bottlenecks that happened to crop plants throughout domestication and breeding of plants, i.e. crucial moments have decreased this diversity. After multiple selections for desired traits, only a subset of the diversity of the wild species remained as a result of crop domestication. People only focus on specific species which are considered the most important for their food supply and they put pressure on these species to get certain phenotypes. As a result, there is a decrease in the number of species used as well as a decrease in allelic diversity (Elia and Santamaria 2013).

Fire persistence has been considered as one of the driving factors for speciation in Mediterranean-type ecosystems (MTEs). It is crucial to study the regional patterns of plant species diversity among the 5 different MTEs regions. This includes the interactions of geologic and climatic histories for each of the 5 regions in addition to the ecological factors which enhanced the diversification (Rundel et al. 2016).

Ancient seafaring colonists, on the farming enclaves, in Mediterranean region have developed many technologies for better growth of cultivated species (Zeder 2008). Grass crops and legume crops are the most popular cultivated species in the Mediterranean Basin because of their economic importance. Grass crops include: wheat, barley, rye, and cheatgrass. While cereal crops include: peas, and lentils. These crops are used in human food, animal fodder, and many industries. Therefore, scientists are developing breeding programs to produce new cultivars with improved traits such as high yields, yield stability, as well as tolerance to biotic and abiotic stress. These traits make the plants capable of adapting to global climate change. We will discuss each of these crops in detail in chapter three.

CHAPTER TWO

MEDITERRANEAN-TYPE ECOSYSTEMS

The Mediterranean-type ecosystems (MTEs) have a distinctive Mediterranean-type climate (MTC) showing warm dry summers and mild wet winters. Therefore, there is international interest to perform comparative studies on both ecosystem and evolutionary dynamics (Rundel et al. 2016).

The MTEs consist of five regions all over the world (Figure 1) which are California, central Chile, the Mediterranean Basin (MB), South Africa Cape Region (the Cape), and southern Australia [specifically southwestern Australia (SWA)]. In the summer, rainfall is rare and the temperatures are high because these regions consist of subtropical high-pressure cells which make clear skies and generate dry descending air masses. In the winter, the climate is affected by the polar jet stream and the accompanied prevalent westerlies which produce rain at low elevations, and snow at the high elevations. There is a moderation in the temperature because of the cold ocean currents off the west coast of the five regions. This allows the plants to grow in the late winters and early springs (Rundel et al. 2016).

MTC regions contain a large number of plant communities. In all five MTE regions there are winter-deciduous and evergreen forests and woodlands, however they are not abundant in the Cape. There are some montane and alpine vegetation in all five regions except SWA. On the other hand, the regions of winter-rainfall desert have been removed from MTE boundaries. In spite of the large scale of this plant community structure, evergreen sclerophyll shrublands compose the iconic mediterranean-type vegetation

(MTV) and represent biggest diversity of plant species. These shrublands are named as maquis in the MB, matorral in Chile and California, fynbos in the Cape, and kwongan in SWA (Rundel et al. 2016).



Figure 1. The five Mediterranean-climate regions are: southwestern Australia, South Africa Cape Region, Mediterranean Basin, California, and central Chile. Figure courtesy of the U.S. National Park Service (Rundel et al. 2016).

Mediterranean-Type Ecosystems and Biodiversity

Global conservation assessments identified the Mediterranean biome to be of a high priority for conservation among the world's biodiversity hotspots. It is important to study the location, magnitude and threats along with their relationship to the important species to be conserved. This helps create good future efforts and plans for conservation in this biome. The number of threats to Mediterranean biodiversity is different among the five areas of the MTEs. For instance, the rates of plant extinction are known to be linked to large-scale western colonization age and duration. Therefore, there are low rates of extinction in the Mediterranean Basin (1.1%) in comparison with Western Australia (6.6%). The Mediterranean Basin, which is considered as the old world, has hosted agriculture for a few millenniums and plant coevolution with people is one of the reasons for the high plant diversity in this biome (Underwood et al. 2009).

Among all of the Mediterranean biomes, the Mediterranean Basin is considered as the most important biodiversity hotspot. It has about 25,000 plant species (of which 13,000 are considered endemic species), 4.3% of worldwide plant species (which are estimated to have 300,000 total species), mammals, birds, reptiles, and endemic amphibians (Table 1). With regard to plants, the Mediterranean area is considered as a hotspot for wild species diversity as well as cultivated plant diversity. The fear about biodiversity loss should be coupled with the fear for agro-biodiversity loss. This is because it is important for agriculture as a result of agro-ecosystem loss, species loss and the loss of populations within each species. Crop wild relatives in addition to landraces are at great danger among plant genetic resources and should be conserved a top priority (Pacicco et al. 2018).

Table 1. This table shows the five Mediterranean-type ecosystems worldwide with their biogeographic and plant diversity traits. Table adapted from (Rundel et al. 2016).

Region	Area (10 ⁶ km ²)	Native plant species	Endemism (%)	Modal natural fire frequency (years)
Southwestern Australia	0.31	8,000	70	10–15
Cape Region	0.09	9,000	68	10–20
Mediterranean Basin	2.30	25,000	50	30–100
California	0.32	5,000	60	30–100
Central Chile	0.16	2,900	30	Fire absent

The Floras in Mediterranean-Type Ecosystems

There is no known theory that can elucidate both the overall and regional plant species diversity patterns among the five MTEs. It is important in each region to study the complexity of geologic and climatic histories. It is also crucial to study the ecological factors that have enhanced the diversification in the regions (Rundel et al. 2016).

Mediterranean Basin (MB)

The MB contains a large number of flora, including about 25,000 species which are spread across 75% of the entire MTE surface area. This consists of abundant floristic clades that have Pliocene and Quaternary origin in addition to a small number of ancient lineages that came from pre mediterranean epochs. Moreover, the Mediterranean Sea by itself has been considered as an important geographical barrier to prevent the dispersal of plants between Europe and North Africa (Rundel et al. 2016). Figure 2 & 3 represent the areas with high plant endemism incidences and the hot spots in the Mediterranean Basin respectively.

California

In California, the origin of flora with a high plant diversity is due to the new proto-mediterranean climate as well as the existence of fire regime in the middle Miocene which is about 15Ma (mega-annum) (Keeley et al. 2012). In addition to that, on the Pacific Coast there was the emergence of the cold California Current. Many of the different clades have developed from a wide collection of North American lineages since that era (Rundel et al. 2016).

Central Chile

In central Chile, the overall diversity of plant species is small compared to the other MTC floras. It is estimated to be 2,900 species and accordingly a limited number of species and generic richness compared to other MTCs on an equal surface area. However, Chile's moderate oceanic climate has helped many woody lineages to exist, which makes the woody flora larger when compared to that of California (Arroyo et al. 1995).

Southwestern Australia

In Southwestern Australia, many of the families that have their SWA origins in the middle to late Cretaceous are still existing. For example, the Myrtaceae, Proteaceae, and Haemodoraceae, as well as the tropical rainforests that contain conifers, ferns, and dicot trees are still existing on a large surface area in Australia. This pattern was persistent into the Paleogene with the developing of sclerophyll element which was withdrawn to the continent's dry west side at the time of the Middle Eocene Climatic Optimum (Lamont and He 2012).

Cape Region

Today in the Cape Region, the fynbos flora is a result of gradual diversification which was accompanied by low rates of extinction and it is not due to the climate change which triggers quick and new radiations. The upland fynbos flora, nowadays, is linked to Cenozoic lineages and associated with an aseasonal and mesic climate (Verboom et al. 2015). These lineages contain small and isolated heathland shrub families such as Bruniaceae, Geissolomataceae, Grubbiaceae, and, Penaeaceae. On the other hand, the lowland fynbos flora is known to have younger lineages with fast evolutionary radiation which started in the late Miocene 8–7 Ma (Hoffmann, Verboom, and Cotterill 2015).

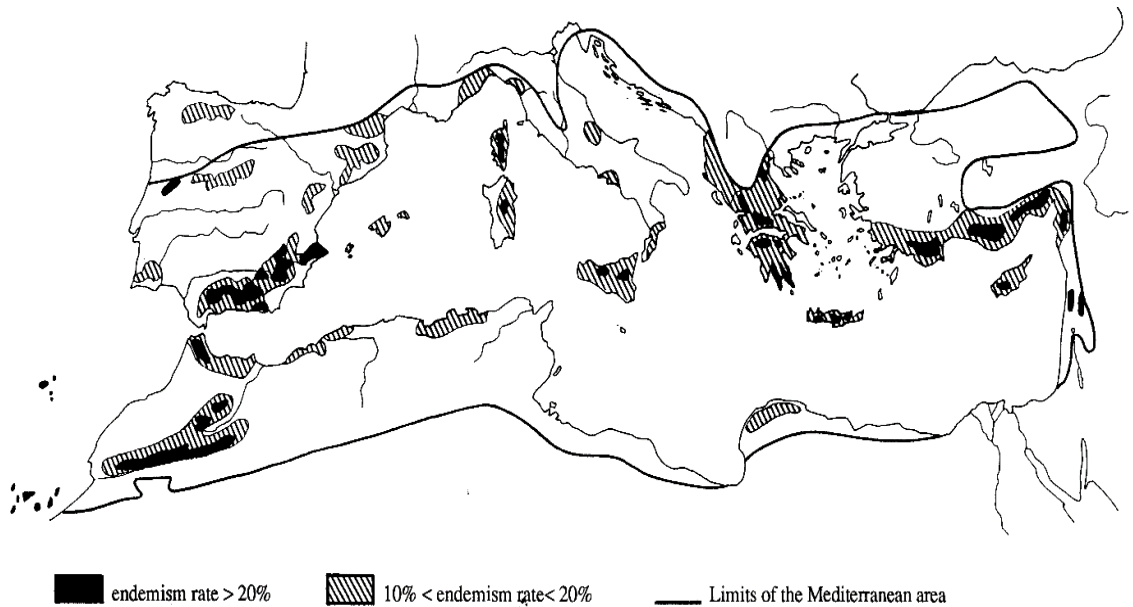


Figure 2. Biogeographical sectors that have high incidences for plant endemism in the Mediterranean area (Medail and Qu ezel 1997).



Figure 3. Hot spots in the Mediterranean area 1: Canaries and Madeiran archipelagos. 2: High and Middle Atlas Mountains. 3: Baetic-Rifan complex. 4: Maritime and Ligurian Alps. 5: Tyrrhenian islands. 6: Southern and Central Greece. 7: Crete. 8: Anatolia and Cyprus. 9: Syria-Lebanon-Israel. 10: Mediterranean Cyrenaic. The limits of the Mediterranean area is presented by the thick line (Medail and Quezel 1997).

Biodiversity Loss

In an era where there are many human activities, many changes in global environment, loss of habitat and extinction of species, conservation strategies are an important step in order to decrease biodiversity loss. For example, acidification of oceans and land use are increasing in many places, which has negative and irreversible impacts on biodiversity. In spite of some criticism, biodiversity hotspots can be used as a tool in decision-making for conservation priorities in order to preserve biodiversity. This approach which is based on biodiversity hotspot areas can be used in many geographical locations. It is known to be a great approach for maintaining world biodiversity on large and small scales. In the modern world, it is well understood that biodiversity is not only about the species number in a region, and that conservation strategy shouldn't be determined only by the taxa number existing in each ecosystem (Marchese 2015).

Land-use/land-cover change is one of the big factors that leads to biodiversity loss. The Mediterranean region has been subjected to huge disturbances throughout many years. Accordingly, many significant alterations have occurred in the Mediterranean hotspots and made it the most altered hotspot worldwide (Falcucci, Maiorano, and Boitani 2006).

Wildfires in Mediterranean-Type Ecosystems

Recently there has been an increase in both the number and the intensity of wildfires in the Mediterranean climate area (western USA, Mediterranean basin, Chile, South Africa and southeast Australia) which have been linked to the increase of human population in these regions. On the other hand, decreasing the fire frequencies in the area could be critical for maintaining water quality, water supplies, soil integrity, and biodiversity, which will affect the choice of management practices that can be employed. Moreover, plants in Mediterranean ecosystems have evolved a series of adaptations to protect them from fire and sometimes these plants become dependent on fire for reproduction. This happens because of the frequent exposure to fire over long time periods (Bradshaw et al. 2011).

In fire-prone ecosystems, there are changes in rainfall after fire which affect seeders and result in long-lasting effects on the vegetation. In the Mediterranean region, global climate change will cause decreased precipitation, increase the summer drought and therefore cause an increase in the fire danger. During the post-fire regeneration stage, it is crucial to study the sensitivity of plant life to changes in rainfall in order to understand the effects of climate change on Mediterranean-type areas all over the world (Parra and Moreno 2018).

CHAPTER THREE

CULTIVATED SPECIES IN THE MEDITERRANEAN-TYPE ECOSYSTEMS

The advanced cultivation and domestication of plants in the Mediterranean area are due to the use of advanced methods in documenting the plant diversity in this region. The first step of plant domestication in the Eastern regions of the Mediterranean Sea was about 12th Millennium cal B.P (calibrated Before Present). Approximately 1,000 years before the utilization of morphological changes to document domestication, there have been evidences for cultivation of crops. Various species have been domesticated in various regions of the Mediterranean Basin and the Fertile Crescent. Genetic analyses have been used to identify different domestic lineages of different species. Studies have proved that, the reason of domestication expansion and increased agricultural economies in the Mediterranean Basin was the presence of many groups of seafaring colonists who settled down around the Mediterranean Sea. Another reason was domesticate adoption and domestic technology adoption as well as the local domestication of different endemic species. These technologies were used by indigenous populations. However, the use of sustainable agricultural practices, in the Mediterranean region, have assisted in keeping high plant biodiversity since the Neolithic. (Zeder 2008)

Olives

The cultivated olive (*Olea europaea* L. subsp. *europaea* var. *europaea*) is the most iconic tree in the Mediterranean Basin. It has origins related to the development of the ancient civilizations, approximately six millennia ago. In the ancient times, olive cultivation was adopted in new places and became highly cultivated in the Mediterranean Basin (Infante - Amate et al. 2016). In the recent times, many varieties of olives are cultivated to yield high-quality fruits for oil use and table utilization. However, there is still debate about the origins of olives. Therefore, the linkages are unclear between the wild Mediterranean olives [*Olea europaea* subsp. *europaea* var. *sylvestris* (Mill.) Leh.] and the cultivated ones.

The production of olives worldwide is estimated to be about 20 million tonnes per year on 9.6 million hectares. It is also estimated that 97% of the production and 92% of the area are located in the Mediterranean Countries. Spain comes in the first place followed by Italy and Greece as the most important producers. In Italy, 16% of worldwide olive production is produced on 12% of the entire production area. Whereas Apulia, Italy possesses about 33% (373.00 ha) of the Italian olive production area and about 30% (1,000,000 tonnes) of the Italian olive production. It is important to mention that in this area the olive tree is highly adapted to the climatic conditions and thus produces olive oil with a high quality. This makes olive cultivation an important economic and employment resource in the country (Sardaro et al. 2016).

There are multiple uses of wild olive trees and cultivated ones, such as in human food, wood and cattle fodder. This was the reason for the spread of olive groves with the

growth of human civilization. It was challenging for researchers to understand the domestication history of olives because this species has dual nature, first being Mediterranean vegetation wild elements and second being a cultivated crop. Moreover, it is still challenging to differentiate between wild Mediterranean olives and feral ones (escaped from cultivation), even though the use of the recently developed genetic and phenotypic traits to help differentiation. This fragile domestication syndrome is the main factor which has influenced research performed not only on olive domestication, but also on date palms, grapes, and many woody crops in the Mediterranean areas (Zohary et al. 2012).

For the above mentioned reasons, there is always an estimation about olives' origin and their history of domestication mainly considering botanical data. The new collection of archeological, paleobotanical, molecular, and historical data (Rugini et al. 2016) has provided the researchers with important information about wild olives biogeography and their cultivation history in a timely fashion. However, many issues in olive domestication history still need to be studied. Further research is needed to explain the processes attached to olive primary domestication and its following secondary diversification. Furthermore, our knowledge about human selection for olive agronomic and adaptive phenotypic traits is limited. Thus, it is crucial to study wild and cultivated olive ecology in order to understand their domestication history and know more about their future flexibility to changes of global climate (Holliday et al. 2017). Afterwards, it is also necessary to study interactions between olives and the environment both on the biotic and abiotic levels. In recent times, our knowledge about pathogens and pests that have spread is still limited. An

example of the appearance of a pathogen is *Xylella fastidiosa* which is a bacterium spread in olive groves of South-East Italy by native vector insects whereas the pathogen was introduced from America. These kinds of outbreaks represent major threats to wild and cultivated olives (Saponari et al. 2014). The results of this kind of research should help maintain germplasm management for the cultivated olive to be used in the programs of future breeding. It can also be used in the programs of wild olive population conservation, especially during the changes in the global climate (Besnard, Terral, and Cornille 2018).

Pines

Mediterranean pines have common life-history traits. They can be found in different altitudinal levels all over the Mediterranean Basin. Their range extends from sea level to high elevation mountains, passing through hot dry to cold wet climates. Mediterranean pines are known to have the highest levels of differentiation all over the world. This is despite the fact that their genetic diversity is greatly enhanced from west to east and that their diversity decreases in the species of low-elevation. (Fady 2012).

Mediterranean pines have some life history traits in common. They exist in all altitudinal levels surrounding the Mediterranean Basin, starting from sea level and ending at mountains with high elevation. They are also found in hot and dry bioclimates as well as wet and cold bioclimates. However, they have a distribution pattern that can be regionally widespread or narrow. They sometimes show extensive, dense populations or can have small populations of dispersed individuals. Humans have used them a lot for millennia for their civilizations (Fady 2012).

There are 109 species identified as native to the Northern Hemisphere biomes, however pines (genus *Pinus*) are known to be the biggest and most widespread conifers all over world (Farjon 2008). The Mediterranean biome, in addition to Central America and Eastern Asia, constitute a large number of species representing this diversity. Pines are found on about 1.8 % of terrestrial habitats of the world (Fady and Médail 2004), despite that the Mediterranean regions of the Northern Hemisphere contain about 28 pine species (which represents 25 % of all species of pine). In the Mediterranean Basin, there are 11 species, while in California there are 17 species. In the other areas of Mediterranean climate (the Cape Province of South Africa, South-Western Australia, Central Chile, all of which represent 0.2 % of the terrestrial habitats all over the world), pines demonstrate an example of a successful invasive tree genus (Rejmánek, Richardson, and Pysek 2013). Therefore, research has been highly performed on pines because of their high importance both economically and ecologically (Fady 2012).

Black pine is a geographically widespread species in the Mediterranean area (*Pinus nigra* J.F. Arnold). In Turkey, the Turkish black pine (*Pinus nigra* subsp. *nigra* var. *caramanica*) is found on about 4.2 million hectares, and it is considered a very common and important native conifers economically to the country (Atalay and Efe 2012). Moreover, it is highly used in dendro-climatological studies in the region. However, this species is sensitive to drought and easily influenced by the change in climate in late decades and the coming global climate change (Janssen et al. 2018).

As mentioned above, Mediterranean pines have life history traits in common, including common distribution patterns and stand structure. Moreover, there is a common

interaction history between pines and human civilizations. As it is known, they are found on an important ecological area which is characterized by its severe climatic conditions, climatic differences, and landscapes in the Mediterranean Biome. Genetic differences existing among groups of ecologically close species and in the habitats they are found in, could suggest changes in their evolutionary history because of severe environmental effectors (Fady 2012).

Grass Crops (Cereals)

Wheat

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide and it was reported to grow in an area of about 222.28 million hectares producing about 724 million tonnes. It represents about 25% of total global cereal yield (Manjunatha et al. 2018) (Liu et al. 2018). The current global production doesn't meet the demand of the human population worldwide. Moreover, the wheat yields are negatively affected by the infecting pathogens and the increasing climatic variations (Riaz et al. 2018) (Liu et al. 2018). The yield and grain quality of wheat production are strongly affected by water availability, temperature, presence or absence of pathogens, and many other environmental factors (Wang et al. 2018).

Wheat is estimated to provide humans with about 18% of their daily calories in addition to about 20% of proteins. In the beginning, it was domesticated in the Fertile Crescent, afterwards, wheat has been one of the most important staple foods in Europe, West Asia as well as North Africa. The area where wheat is grown in the Mediterranean Basin is estimated to be 27% of the arable land, and this region counts for 60% of the total

area for durum wheat cultivation (which is used for making pasta). There are many changes that have happened to the wheat plant, shifting the cultivation process to plants with high quality standards and productivity that represent the modern varieties. Natural and human selections have influenced wheat varieties since ancient Wheat cultivars migration from the east of the Mediterranean Basin to its west. This leads to the emergence of local landraces that possess high genetic diversity and are known to be resistant to abiotic stresses. In the twentieth century, the breeding activities of wheat that were performed in the Mediterranean Basin have led to huge genetic gains both in quality and yield. However, new wheat varieties are needed to be developed in the Mediterranean Basin with more resistance to climate change impacts such as increased temperature and water shortage (Royo, Soriano, and Alvaro 2017).

It is expected that the human population will be about 10 billion by 2050. Scientists have reported that these increases in the yields can be obtained by controlling the pathogens that decrease the yield upon infecting the crops. Wheat rusts are major threats affecting wheat cultivation. For instance, stem rust epidemics happened in the United States between 1919 and 1954 and caused significant yield losses (Chen et al. 2018) (Wu et al. 2018).

Therefore, wheat breeding programs that provide high yield in addition to good quality are considered as a crucial step towards satisfying food demand of the world. Unfortunately, wheat diseases such as leaf, stem, and stripe rusts indicate serious danger for the production of common wheat. The use of chemical control has the side effects of environmental pollution and health threats. Therefore, using host resistance is

environmentally friendly and gives more effective results regarding the control of these diseases (Liu et al. 2018).

Origin and Evolution of Wheat. The origin of bread wheat (*Triticum aestivum*; AABBDD) has been widely discussed in the scientific community in the last decades (El Baidouri et al. 2017). Wheat is an allohexaploid species (*Triticum aestivum* L. $2n = 6 \times = 42$), which has three sets of related homeologous subgenomes (A, B, and D), each of which has seven pairs of chromosomes (Huo et al. 2018). Scientists have reported the donors of the subgenomes A and D while the donor of subgenome B hasn't been identified yet. The goatgrass *Aegilops speltoides* (genome SS) has been considered as the possible candidate donor of subgenome B because it is the closest ancestor of the wheat subgenome B (Gou et al. 2018). Nonetheless, the reported comparative analyses of different gene loci across the *Triticum* and *Aegilops* species have not revealed evidences to support that conclusion. In other words, the *Ae. speltoides* S genome was reported to be considered evolutionarily closer to the wheat subgenome B than to the subgenomes A and D, but its candidacy as the ancestor of subgenome B is still unclear. Moreover, subgenome B contains higher genetic variability than subgenomes A and D. Based on that, scientists stated the hypothesis that assumes subgenome B has diverged from its ancestor through many genomic modifications (Gou et al. 2018).

Towards this direction, polyploidization is a natural process that has an important role in the evolutionary history of plants especially the agriculturally important crops such as bread wheat (Huo et al. 2018). It is also known as whole genome duplication (WGD) in which a single genome can be duplicated to create autopolyploids that have more than two

homologs representing each chromosome. In addition, multiple genomes can be duplicated after the hybridization between two or more species to create allopolyploids with multiple pairs of homologs from different ancestral genomes, known as homoeologs. As a result of WGD, many copies of duplicated genes might be lost, diverge in function, or be silenced by a phenomenon known as “diploidization”. Following WGD, changes in the architecture of different traits have been reported because of rapid genomic rearrangements and epigenetic changes (Jighly et al. 2018).

With regard to polyploidization, it was reported that the allohexaploid wheat species has originated as a result of two independent polyploidization events. The first event happened 0.36 to 0.5 million years ago; which included the hybridization of two diploid progenitors, which are the ancestor of *Triticum urartu* ($2n = 2 \times = 14$, genome AA) and the unconfirmed species (BB genome) that is related to *Aegilops speltoides* ($2n = 2 \times = 14$, genome SS), which resulted in the allotetraploid emmer wheat (*T. turgidum* ssp. *dicoccum*, $2n = 4 \times = 28$, genomes AABB). On the other hand, the second event occurred 8,000~10,000 years ago, which included the ancestor of the diploid *Aegilops tauschii* (DD genome) that hybridized with the allotetraploid to create a hexaploid wheat ($2n = 6 \times = 42$). However, recent studies have hypothesized that the subgenome D has originated from a complex history of many rounds of hybridizations between ancestral A and B diploid species (Huo et al. 2018).

The successful speciation of an allopolyploid always gives the new species a better adaptation to a wide range of climates because the heterogeneity from the subgenomes gives genetic advantage (hybrid heterosis) when compared to the parental species.

Furthermore, the addition of the subgenome D in allohexaploid wheat gives unique viscoelastic properties that are needed for the bread-making process (Huo et al. 2018).

Taxonomy of Wheat. Tetraploid wheats have an important role in human history. Durum (tetraploid wheat) is the wheat used to produce pasta and semolina. Furthermore, it is the second most cultivated wheat after bread wheat (*Triticum aestivum* L.) that is considered the most cultivated wheat. Moreover, emmer (tetraploid wheat) is considered as a ‘relic’ crop today, however, it is used for bread making, animal feed and, as a genetic resource to improve durum and bread wheat varieties. In addition, rivet or cone (tetraploid wheat) is a wheat variety that has a broader cultivation tolerance range compared to durum, where it grows in northern latitudes such as the UK (Oliveira et al. 2012).

Tetraploid wheats are genetically and morphologically different and their evolution has not been fully understood. Significantly, studies have reported that cultivated emmer has evolved from the tetraploid wild emmer around the 8th millennium BC. Whereas, the tetraploid wheats such as durum and rivet appeared shortly after emmer in the near east region and it has been reported that they have evolved from the domesticated emmer stands as well. Furthermore, studies have reported that durum wheat evolved after emmer in the eastern Mediterranean region. Free-threshing wheats were cultivated in the western Mediterranean basin when agriculture started in this region, while emmer was the staple crop in ancient civilizations until durum was introduced in the Hellenistic period (Oliveira et al. 2012).

It is important to mention that nowadays the durum varieties that grow in various environments are of a great importance for grain production in the Mediterranean basin.

Scientists have reported that durum wheat history was associated with a decreased level of genetic diversity, starting from the wild ancestor and ending with the most recent modern varieties. Moreover, the different free-threshing subspecies show differences mainly in spike traits but can't be genetically distinguished (Sahri et al. 2014).

Cultivated Species of Wheat. Wheat is one of the most important cultivated crops. It is used to make a satisfactory pasta and leavened bread with its unique grain properties. Wheat nutritional value and its downstream use are usually determined by grain starch and storage protein constitution in the cultivated and natural-growing species (Uhlmann and Beckles 2010).

Diploid Wheat. Einkorn (*Triticum monococcum* L.) is an A-genome diploid wheat that is used to understand the biology, genomics and proteomics in *Triticeae*, in addition to discovery of novel genes. The reason is that it has a small genome size as well as a high level of polymorphism and easy cultivation procedure. Studies have shown that it was domesticated about 7500 BC. Although it became a relic crop, it still grows in the lands of South Europe, Minor Asia, Caucasus and North Africa to produce enough yields on poor soils. Nowadays, einkorn is being used in the wheat breeding programs to have useful traits such as resistance to pests and tolerance to abiotic stresses as well. Researchers use many transgenic technologies such as RNAi-based gene silencing and chloroplast transformation in the diploid model to further understand wheat genomics (Miroshnichenko et al. 2017). Einkorn is also known for its nutritional properties because it has high protein and high carotenoid contents (Bonnot et al. 2017).

Wild diploid wheat, *T. Urartu* ($2n=2\times=14$; AA), which is the A-genome donor of cultivated tetraploid ($2n=4\times=28$; genome AABB) and hexaploid wheat ($2n=6\times=42$; AABBDD), has a great role concerning the evolution of cultivated bread wheat. Despite *T. urartu* having subgenome A, as well as its presence in bread wheat, the genetic diversity of *T. urartu* has not been well studied as in einkorn wheat (*T. monococcum*), which is another diploid progenitor. In the recent times, the genetic diversity of wheat cultivars has been reduced as a result of domestication and breeding processes, therefore scientists are applying new genes to improve wheat crop traits such as agronomic characteristics, grain quality and biotic stress tolerance (Wang et al. 2017).

Tetraploid Wheat. Durum wheat is most cultivated in semiarid climates and counts for 5 to 8% of total wheat production worldwide. Canada comes in the second place after the European Union in durum wheat production with about 4.4 million tonnes annually (Kumar et al. 2018).

Towards this extent, recent studies have reported that the domesticated tetraploid wheats have originated from a mixed set of wild emmer populations. Upon the increase in chromosome ploidy from diploid to hexaploid during the evolution of wheat, scientists have noticed that there is a significant increase in the yield and harvest index. This means, the efficiency of the resource utilization such as water and nutrients, has enhanced in hexaploid wheat compared to tetraploid wheat (Pandey, Lal, and Vengavasi 2018).

Hexaploid Wheat. Studies have documented that hexaploid common wheat (*Triticum aestivum* L.) possesses enhanced adaptability to the stressful environments compared to its tetraploid wheat progenitor, for instance, its tolerance to low-nitrogen that

appeared immediately after allohexaploidization. Polyploidy played an important role in the domestication of many crops including wheat, canola, potato, sugarcane and cotton. It can cause genetic and epigenetic alterations at both total and homeolog-specific levels. It was also reported that polyploidy may cause physiological and morphologic variations such as increased photosynthetic capacity, changes in flower color, and increased tolerance to biotic and abiotic stresses; these changes are considered as a result of the adaptive evolution in polyploids (Yang et al. 2018).

Durum Wheat. Durum wheat ($2n = 28$, AABB, *Triticum turgidum* L. ssp. durum) is an allotetraploid wheat. It was reported that it originated in the Mediterranean region for making pasta and semolina products. Based on the recent studies, it is documented that 75% of durum wheat still grows in the Mediterranean basin that represents about 50% of the worldwide production. However, climate change is affecting the Mediterranean region; temperatures are expected to increase by 3–5°C, in addition to a 4–27% expected decrease in the annual precipitation during the cropping season. Moreover, it is also expected that there will be an increase in the frequency and duration of dry spells and heat waves in dryland areas. As a result, the drought and heat stresses will have a negative impact on wheat grain weight and yield (Sukumaran, Reynolds, and Sansaloni 2018).



Figure 4. Differences in the morphology of durum wheat spikes of the Mediterranean landraces (Royo, Soriano, and Alvaro 2017).

Hard Red Spring Wheat. Hard red spring (HRS) wheat flour is known with its superior flour quality and baking characteristics, and it is used for production of refrigerated dough (Simsek et al. 2011). Bread wheat (*Triticum aestivum* L.) can be classified as hard or soft depending on the endosperm hardness or texture. Hard wheat, compared to soft wheat, needs more energy to mill and a bigger number of starch granules are destroyed. Flour with the destroyed starch granules can absorb more water during mixing and baking which changes the bread-making properties of the flour, and consequently there is an increase in the loaf volume. Thus, hard wheat is generally used

for bread making, while soft wheat is preferred for cookies and pastries. Therefore, scientists are working to identify genes that influence quality traits such as endosperm texture, grain or flour protein content, and water absorption (Tsilo et al. 2011).

Hard White Wheat. Pre-harvest sprouting (PHS) of wheat (*Triticum aestivum* L.) can negatively affect end-use quality and viability of the seed at planting. The international markets prefer white over red wheat, therefore white wheat with PHS tolerance is more desirable for worldwide wheat production. Whereas, red wheat is more tolerant than white wheat in sprouting. Hard red winter wheats are enormously produced in the Great Plains of North America from the time the modern agriculture started in that region. In addition, in late 1980s, hard white winter wheat development and production started in that region. It was reported that white wheats give more flour yield and lighter color of whole wheat flour compared to red wheats. Therefore, in order to improve wheat marketing potential, it is necessary to develop adapted white wheat cultivars to be tolerant to PHS (Fakthongphan et al. 2016). For instance, products obtained from whole hard white wheat flour, including pan bread, tortillas, and flat bread, have a more pleasing appearance and flavor compared to those produced from red wheat (Jiang et al. 2011).

Soft White Wheat. The end-use quality of wheat (*Triticum aestivum* L) can be differentiated by Kernel texture (hardness), water absorption, protein (gluten) strength, and milling quality. In general, hard wheat flours are known for their higher gluten strength, damaged starch, and non-starch polysaccharides, all of which cause an increase in water absorption capacity. On the other hand, soft wheat flours are known for their lower gluten

strength, damaged starch, and non-starch polysaccharides, all of which cause a decrease in water absorption capacity (Jernigan et al. 2018).

Barley

Barley (*Hordeum vulgare* L.) is one of the most cultivated crops in marginal regions all over the world (Baum et al. 2007). Barley is also a very common crop (15 million ha per year) grown in the Mediterranean basin's driest regions. It is considered as an income source for many people in the area, hence it is very important to perform breeding programs to increase its yield. Breeding programs have been performed from landraces using old genotypes as well as new ones, however, all the used genotype sets are still cultivated in the Mediterranean basin. Landraces are tolerant to abiotic stress, and have elevated levels of yield stability. They also possess an intermediate level of yield in comparison with the old and new genotypes upon using reduced level of input agriculture. The new genotypes are known to show increased yield capacity upon using advanced cultivation techniques and conditions (Zeven 1998). Barley landraces are estimated to yield between 25% and 61% more than the new cultivars when exposed to stress conditions, whereas the new varieties are estimated to yield between 6% and 18% more than landraces in West Asia when exposed to optimum conditions (Pswarayi et al. 2008).

Barley is one of the most popular crops in dry-farming areas because of its ability to adapt to abiotic stresses (Baum et al. 2007). Therefore, barley has been used in the selection and breeding procedures in order to obtain varieties with certain abiotic stress adaptation in different geographical areas around the world. The genetically different germplasms that are adapted to various environmental conditions around the world can be

used for breeding programs and germplasm exchange. The International Center for Agricultural Research in the Dry Areas (ICARDA), which is located in Syria, has done its research in West Asia and Northern Africa (WANA), both marginal regions. They produced barley germplasm which was well adapted to the dry environments of Southern Australia as well as West Asia and Northern Africa regions (Shakhathreh et al. 2001).

Moreover, this germplasm can be used to understand the genetic basis underlying the stress adaptation in the different genetic genotypes. Barley stress adaptation has been related to the species' flexibility of morphological characteristics including peduncle extrusion, plant growth, biomass production, and tiller number (Shakhathreh et al. 2010). Responses to stress which are related to growth are avoidance strategies that make the plant keep a homeostasis in spite of any environmental changes. Furthermore, the genetic changes in some physiological parameters has been identified in barley, including chlorophyll fluorescence under stress and relative water content. These variations represent the differences in the processes of stress-tolerance that make the plant capable of keeping its cellular activities under biotic and abiotic stress (Bartels and Sunkar 2005).

It is difficult to predict rainfall in the Mediterranean environment, and this leads to variable environmental conditions which affect crop growth as well as plant genotypes through interaction with the environment (GE). GE, is known as the difference in proportional behavior of genotypes in various environments (Cooper and Byth 1996), and is critical in plant breeding programs. GE makes it difficult to test and select the good genotypes, slowing down the process of genetic progress. Two kinds of GE are known, called quantitative and qualitative (Pswarayi et al. 2008).

Quantitative interaction is the variation of the value of differences among genotypes in various test conditions without having variations in the rank. Whereas qualitative interaction is the variation in the rank orders, or crossover interaction, and it is considered very critical in plant breeding programs. Qualitative interaction inhibits prediction of genotype behavior on various locations (genotype by location interaction, GL), in various years (genotype by year interaction, GY) or on both of them (genotype by location by year interaction, GYL) (Baker 1988). GL can be repeatable or non-repeatable and is the changed response of the genotype on various spots.

Rye

Rye (*Secale cereale*) is a diploid genome species containing 2 sets of 7 chromosomes ($2n = 14$, RR) and it is also an open-pollinating species. It is a very heterogeneous species, and is well known to possess a high tolerance to many conditions of biotic and abiotic stress. Therefore, some of these rye characteristics have been transferred to other important crops, such as wheat, in order to gain tolerances to the conditions of biotic and abiotic stress. For example, tolerance to many pathogens and diseases as well as high yield improvement was moved to wheat when centric translocations of rye chromosome short arm 1R were used in breeding programs of wheat (Lukaszewski 2000). Whereas, D-genome chromosomes of wheat were introduced into triticale (hybrid of wheat and rye) to substitute a few chromosomes of the rye genome in order to have better agronomic traits for triticale and better quality characteristics for the end-use as well (Budak et al. 2004).

Rye is also an important crop in Europe and it is grown in Northern and Eastern regions. As mentioned above, rye has a big tolerance toward abiotic and biotic stresses, and it successfully grows in some countries despite the change in global climate. It is currently being used to produce whiskies and beer in many countries. It is also characterized by its tolerance to cold weather and its resistance to many diseases and pathogens in addition to its capability of growing well in poor soils. For all these reasons, it is considered as one of the most popular cereal crops which grows in northern Europe (Haffke et al. 2015).

In addition to its significant use in the distillery and brewing industries, rye is also highly used in human food and animal fodder. Our increased knowledge about health-related benefits as well as many industrial applications that use rye, encourage scientists to develop new techniques to increase its production. However, the current advanced technology and our developed knowledge have resulted in more rye productivity and cultivars with better quality to face the increased demand of the industry and consumers (Haffke et al. 2015).

Molecular analysis has been used greatly to understand both rye evolutionary history and its genome diversity. Rye's varieties consist of 2 major categories which are winter varieties and spring varieties (Ma et al. 2004). Cultivated rye (*Secale cereale*) is believed to have its origin from either *S. montanum* which is a wild species grown in southern Europe and some regions of Asia, or from *S. anatolicum* which is a wild rye grown in Iran, Armenia, Syria, the Kirghiz Steppe, and Turkistan (Isik et al. 2007).

Research has shown that *S. cereale* has its origin from its wild weedy relatives. This is based on the results coming from the 3 most repeated rye DNA sequences, as well as information from the DNA sequence of 5S ribosomal pTa794. The 3 most repeated sequences are probes pSc119.2, pSc74, and pSc34 (Cuadrado and Jouve 1997). Moreover, rye genotypes' genetic diversity has been studied using many molecular biology techniques such as single nucleotide polymorphisms (SNPs), amplified fragment length polymorphisms (AFLPs), and random amplified polymorphic DNAs (RAPDs) (Isik et al. 2007).

Cheatgrass

Cheatgrass is found in Europe and Asia as well as the Central Asian former Soviet Republics, in addition to its existence in the Mediterranean area including Spain and North Africa. However, it is not considered to be native to these regions in the same way we identify plants to be native to the range-lands of North America (Young and Allen 1997). Cheatgrass and close brome grass relatives prosper only in North American regions with a Mediterranean climate: hot dry summers and mild wet winters that are thus productive to plant growth.

One of the ongoing issues globally is the introduction and propagation of invasive species which has a bad effect on biodiversity, ecosystem integrity, as well as ecosystem services which are used by humans. Invasive species have impacts on the processes of ecosystem and huge competitive impacts with native species. In the United States, the invasion of exotic species is considered the second reason for the decrease in biodiversity after habitat loss and decay (Wilcove et al. 1998). One of these species is the annual grass

Bromus tectorum L. (cheatgrass) which colonized tens of millions of acres in the cold desert shrublands about a century ago. Therefore, *B. tectorum* invasion can negatively affect the options of land management in addition to creating challenges to restore the desirable species (Davies et al. 2011).

Cheatgrass was easily spread across North America because it is a contaminant of crop-seed. Alfalfa (*Medicago sativa* L.) was one of the crops to be contaminated by cheatgrass. To prevent the spread of this contaminant, there was a process of collecting cheatgrass in some states such as, Pennsylvania in 1861, Washington in 1893, Utah in 1894, Colorado in 1895, and Wyoming in 1900. One of the reason that cause the spread of cheatgrass is the development of the steam-powered grain thresher which moved from one place to another (Young and Allen 1997).

Bromus tectorum die-off is a common phenomenon, however, it is not fully studied. The seed bank of *B. tectorum* is not able to yield a stand of living plants, in spite of getting precipitation which is enough for establishment. There are many regions that experience die-off for many years, however, some other areas recover to produce a good quantity of *B. tectorum* in the next years (Baughman 2014). The factors that are responsible for *B. tectorum* die-off are still under study, although the current research has shown the involvement of many fungal pathogens which showed high pathogenicity under laboratory conditions. In the previous literature, there was not this kind of naturally occurring loss of dominant species both in wildlands of arid and semi-arid regions. Moreover, there is an occurrence of similar processes in agricultural settings compared to the previously

mentioned die-off, such as maize streak virus of corn, syndrome of sudden death for soybeans, and wheat fungus (Bithell et al. 2011).

The presence of these pathogens that resulted in agricultural system stand failure indicates that this mechanism is also applicable in low density, high diversity, and annual systems including *B. tectorum* near monocultures. The die-offs of *B. tectorum* not only show an unexpected and temporary reduction of a very competitive exotic, they could also offer a chance for restoration if native species are able to establish themselves in such changed conditions. After the die-offs, soils demonstrate a several-fold increase in the mineral nitrogen (N) of the soil compared to the neighboring soils that didn't experience die-off (Blank et al. 2011). The increased nitrogen in soils and the decreased competition with *B. tectorum* in die-offs could lead to native establishment. On the other hand, the causal agents of the die-off could result in native species death. This method of investigating restoration opportunity could be utilized in many situations including new agricultural abandonment, wildfire, useful biocontrol applications, and herbicide applications (Baughman et al. 2016).

There are many challenges to restoring the communities of native plants to lands which are invaded by *B. tectorum*. This is because of the existence of the invader, as well as our lack of knowledge that guides management practices in many common regions. Local adaptation, which is known as higher fitness, of the local genotypes is very common in some plant communities such as the Great Basin, when examined in local conditions, compared to non-local genotypes (Johnson, Hellier, and Vance-Borland 2013). However, the market demand for seeds in the Great Basin is directly proportional to the presence of

native seeds. Native seeds are commercially-produced by programs trying to produce genotypes that can be widely-adapted (Baughman et al. 2016).

Unfortunately, the parts of the Great Basin that are at high degradation rates partially overlap with collection locations of some of the known commercial seed lots (Jensen and Stettler, 2012). Hence, for a big portion of the Great Basin, seeds that the scientists utilized in restoration processes don't have traits for adaptation to the conditions of local biotic or abiotic stresses, including the phenomenon of die-off which was mentioned above. Therefore, it is crucial to perform more research in order to study the success of local native plants compared with nonlocal native plants in the Great Basin. Research should focus on the modified systems and the highly invaded ones, including those that have *B. tectorum* near monocultures (Baughman et al. 2016).

Legume Crops (Pulses)

Peas

Dry pea (*Pisum sativum* L.) is the second-most cultivated temperate grain legume all over the world and it is the most cultivated legume in Europe. This is because it is a versatile and cheap source of protein to feed animal as well as having a well-known advantageous function in cropping systems (Nemecek et al. 2008). Despite these benefits, there has been a constant decrease of dry pea acreage in the whole world. In 1962, it covered 10.3 million ha while in 2012, it covered 6.3 million ha (Rubiales and Mikic 2015).

Peas have a limited adaptability as well as a low tolerance to the conditions of biotic and abiotic stress. This leads to insecurity and variability of the yield, which are considered the main issues for peas within areas and between cultivation seasons (Jacobsen et al.

2012). Research has been performed to develop good breeding programs for peas' adaptability to different conditions both on the continental and oceanic levels. Whereas, limited research has been conducted to promote peas adaptability to the conditions of the Mediterranean environments. These environments possess moderate winters and dry springs, in which spring pea are dispersed and suffered from many stresses (Rubiales et al. 2009).

Accordingly, cultivation of pea in the Mediterranean Basin is limited and the newly released pea varieties have a limited adaptation to the conditions of the Mediterranean environments (Iglesias-García et al. 2017). This is a little bit unexpected because pea diversity primarily centers in the Eastern Mediterranean region and the region of West Asia. In those areas, wild varieties such as *P. sativum*, *P. fulvum* Sm. and subsp. *elatius* (M. Bieb.) Asch. and Graebn are still being cultivated in recent times. Also in those areas, pea highly contributed to human diets. This was proved by old DNA extraction from the peas, the first documented use of DNA extraction performed on any legume species (Medović et al. 2011).

With regard to field conditions, it is very important to develop pea genotypes that provide stable and elevated levels of seed yield (Smýkal et al. 2012), although some desired characteristics such as elevated level of biomass and a small phenological cycle are also important (Hebblethwaite et al. 2013). Scientists use statistic models to understand the processes underlying flowering date, grain yield, and aerial biomass in different conditions in the field. For example, it is important to study genotype x environment interactions

(GEIs) within time and space in field experiments in order to further study cultivars' stability. Therefore, this is very useful in breeding programs (Iglesias-García et al. 2017).

Research also focuses on the stability of the yield and other important agronomical traits in pea varieties that grow in regions of Southern Mediterranean and Northern Africa. These breeding programs aim at producing widely well-adapted cultivars with steady performance in many locations as well as cultivars that have steady performance in certain areas (Iglesias-García et al. 2017).

Pea cropping environments in the southern countries of Europe are known to have big climatic differences among different areas, and among different years as well as within the same cropping year. There are severe terminal drought and heat stress in southern Europe. Italy is an example, with its typical Mediterranean climate. This explains the huge anxieties to produce crop yields with high stability (Ranalli 1995).

Winter death is significant not only in regions showing subcontinental climate, for example northern areas of Italy, but also in the areas showing Mediterranean climate. In Mediterranean climates, plants are not entirely hardened or to some extent dehardened and are at risk of frost situation with a limited time period and seriousness (Annicchiarico and Iannucci 2008).

As mentioned above, crop adaptation to the stress conditions biotically and abiotically could be enhanced using breeding programs. Scientists could select the high yield cultivars, specific traits in certain environments, and specific traits of secondary phenotypes. Scientists could then use some genomic techniques and methods to achieve the results (Fleury et al. 2010). For example, the cultivated peas in Australia are facing

water shortage and increased temperature at their crucial stages of development which negatively affects crop yield. In order to improve peas' yield in these regions, scientists study the interaction between yield and two other traits which are growth rate in a severe conditions and seed abortion. Therefore, scientists study the physiological behavior of these traits, the balance achieved between adaptation to stress conditions, and yield in the appropriate conditions. Finally they use quick and cheap methods of screening in the breeding programs to obtain the results (Sadras et al. 2013).

Lentils

Lentil (*Lens culinaris* Medikus subsp. *culinaris*) is a diploid ($2n=2x=14$) slender short plant. It is also an annual legume which was domesticated in the ancient times in the Near East Fertile Crescent region (Sarker and Erskine 2006). The cultivation of lentil worldwide covers about 3.85 million hectare which produce about 3.59 million tonnes. The main regions that produce lentils with a percentage of the whole production are: South Asia and China (44.3%), North America (41.0%), Central and West Asia and North Africa (6.7%), Sub-Saharan Africa (3.5%) and Australia (2.5%). There are two main groups of the cultivated lentils, the microsperma which is the small-seeded and the macrosperma which is the large-seeded (Shrestha et al. 2006). In the areas where lentils are cultivated, the lentil crops face the condition of drought stress which is a harmful factor and leads to a decrease in the crop yield (Mishra et al 2014). Therefore, plants usually have two strategies to protect themselves from such stresses. These strategies are avoidance of drought and tolerance to drought condition (Mishra et al. 2016).

Avoidance strategy keeps high water level in plant tissue and utilizes mechanisms which decrease the loss of water from the tissue because of transpiration control in the stomata. Avoidance strategy also involves intensive water uptake using the expansive root system. Dehydration tolerance is the capability of the plants to resist and survive the low level of water in the tissue. Stress happening in the crucial growth period is very harmful for crop development and its production. Lentil crop in autumn or winter is exposed to irregular drought during their vegetative growth period at many stages in the countries of South Asia and in Mediterranean regions. It is also exposed to terminal drought during their reproductive stages once there is an increase in temperatures and a decrease in rainfall (Yusuf et al. 1979).

Research indicated that lentil is very sensitive to the shortage of water at its stages of seedling and flowering, whereas other research indicated that it is negatively affected by the condition of drought stress at its stages of pod formation and flowering. Other research suggested that lentil genotypes acquire avoidance and tolerance strategies, based on each genotype, to survive in drought stress conditions (Vadez et al. 2011).

In order to identify the responses of each genotype to drought, it is important to screen different genotypes of lentil for drought stress. This screening takes into consideration grain yield, yield components and biomass gain. It is also important to study the physiological and biochemical processes of the genotypes in the conditions of drought stress at various phenophases to support the preliminary results (Mishra et al. 2016).

However, scientists find difficulties in determining genotypes that are resistant and sensitive to drought stress because of huge variations in seed yield of the genotypes which

were collected at different conditions in different environment. However, scientists recently used drought indices to resolve this problem. Drought indices are measured based on a mathematical relationship between optimal seed yields and stressed seed yields in the environment (Mitra 2001). Although, these parameters are useful in screening of crop plants in the condition of drought stress, their usefulness has not been estimated in various lentil groups (Mishra et al. 2016).

Lentil has a positive impact on health enhancement of humans, animals, and soil. Its seed is considered a great source of minerals (K, P, Fe, Zn), vitamins, and protein used in human diet (Savage 1988), while its straw is considered an important animal fodder. Moreover, it makes an equilibrium in essential amino acids in the human diet when consumed with rice or wheat. This is because it has an elevated level of tryptophan and lysine content. When it is cultivated, there is an improvement in the status of soil carbon, nitrogen and organic matter, hence enhancing the systems for sustainable crop production (Sarker and Erskine 2006).

CHAPTER FOUR

DISCUSSION

Many of the different Mediterranean hotspots are located in eastern and southern countries of the Mediterranean Sea such as Israel, Turkey, Jordan and Lebanon and in the nearby Mediterranean islands. Research has indicated that these areas are at risk. Many of these areas are not protected, representing a big threat for many species showing endemic evolutionary history in these regions. Hence, those areas are in danger because they might lose a large number of species representing phylogenetic diversity in the region. Therefore, further research is needed at various scales in addition to studying the data-deficient species status to improve our understanding of the danger affecting the evolutionary history (Veron, Clergeau, and Pavoine 2016).

One of the main targets of conservation processes in the Mediterranean biomes is to make sure that species are well protected after being threatened. Moreover, scientists should exert more efforts to protect more species from the any possible future threats (Underwood et al. 2009).

On the other hand, future change in the global climate as well as changes in the population, could have a negative effect on the food supply in the countries of the Mediterranean region. Therefore, recent studies recommended more intensification of grazing and production of crops along with an increase in the cultivated lands in the Mediterranean region. However, no specific study indicated the effect of global climatic change throughout the whole region and no study has taken into consideration the effects of the restricted availability of water. Whereas, the Mediterranean region is subjected to

severe climatic changes, such as elevated temperatures, reduced precipitation, and many other climatic change extremes (Malek et al 2018)

It is important to consider priority for hotspots with the highest level of biodiversity and lowest cost during the conservation process. It is crucial not only to consider the habitats and wild species, but also the genetic resources, certain landraces and the crop wild relatives at danger (Pacicco et al. 2018).

The hotspot approach is an important tool to direct conservation efforts as well as its major role to make decisions for the cost of conservation strategies. However, some scientists have criticized the hotspot approach to some extent. Nowadays it is crucial, in the conservation strategies, to determine the areas with rich biodiversity. Species richness (SR) is always used in the conservation strategies because of the easiness of data interpretation and quantification as well as being considered the major focus of conservation studies. Furthermore, conservation strategies used richness information along with various irreplaceability measurements, such as. endemism or rarity, in order to prioritize certain areas such as biodiversity hotspots. It was reported that the main factors used in the analysis were (a) endemic numbers and the ratios of endemic species/area of plants, and (b) loss of habitats. The vascular plants were used as an endemism metric because they are necessary for animal life. For example, desert ecosystems constitute about 17% of landmass in the world and contain a significantly high biodiversity. Unfortunately, the scientific community did not highly support these conservation projects financially (Durant et al. 2014).

Therefore it is necessary to have a more advanced and wider vision for biodiversity conservation. Scientists along with decision-makers in non-governmental and governmental organizations should put more attention towards conservation priorities. They should stop repeating ineffective efforts, and make useful collaborations (Maury et al. 2013) to obtain good results from biodiversity conservation strategies. Since biodiversity conservation management is a very complicated topic, and the fact that it is difficult to predict changes in global climate, there is not a conclusive praxis to successful and powerful conservation. However this needs to integrate interdisciplinary research (Pohl and Hirsch Hadorn 2008) which is essential nowadays as never in the past (Marchese 2015).

Pines of the Mediterranean Biome, especially the Mediterranean Basin, demonstrate complicated biogeographic manners at their gene level which assists in tracing their evolutionary history. Despite having similar biological features, there are some differences in geographical, historical, demographic, and ecological processes. Identifying habitats of noticeably big and small genetic diversity is important for studying the critical factors influencing gene diversity. They can also be used in the Mediterranean biome for profiling areas with big value of conservation. However, single species analysis demonstrated by solitary case studies make it so risky to generalize for other species (Fady 2012).

Recent studies showed that barley acquires some adaption to non-lethal drought through using avoidance processes. This includes the decrease in growth that make the plants keep a cellular homeostasis as noticed in photosynthesis and proteome constancy in

drought conditions. On the other hand, heat has an effect on photosynthesis, and floret fertility, which resulted in a quick turnover of the proteins that are related to photosynthesis. Due to the observed variations in the protein, it is suggested that critical processes of heat-tolerance involve *de novo* synthesis and protein quality control. This resulted in more need of energy as noticed in the upregulation of the pathways that produce ATP. The decreased availability of CO₂ that resulted from stomatal shutting down in the heat conditions was counter-balanced by the induction of Rubisco by an enzyme called Rubisco activase B. The suppression of photosynthesis reactions that are independent of light have resulted in radical oxygen species generation as shown in the detoxifying and scavenging enzyme elevation level. Moreover, the changes in genetic phenotypes and genotypes in response to stress, such as photosynthesis, growth, and spike fertility, could be used in future research and breeding programs (Rollins et al. 2013).

Rye is found in various severe environmental conditions such as drought stress, which happened in the previous decade in the Central and Eastern regions of Europe. Recent research has shown that it is possible to have rye with increased yield stability as well as increased grain yield. Upon studying the molecular and phenotypic data, scientists were able to achieve a good understanding of the genetic mechanisms. Results have shown that there are many genotypes which produce high yield, and there are some genotypes that are very stable in many environments. However, it is not crucial to have breeding programs specific to drought stress because there is less than 50% decrease in the yield of rye (Blum 2005). On the other hand, it is crucial to select the varieties with high yield stability, as only 20% of the varieties used in the breeding programs were less than yield stability

average. This could be achieved by using environments that have different soil fertility and rainfall, and include in the experiments some environments that have controlled drought stress (Haffke et al. 2015).

With regard to peas, breeding programs have produced genotypes such as HR1 that is widely well-adapted, and demonstrates a good stability and high yields in various environments. Moreover, another cultivar called Desso cultivar, demonstrated a good yield and endurance in the areas of Southern Mediterranean. Desso cultivar could be used as a genotype source for advanced drought investigations to understand the underlying molecular mechanisms of the tolerance to drought stress. In addition, it can be used in the breeding programs as a genetic variability source to develop cultivars adapted to climate change as there is a high demand for legume crop cultivars well-adapted to drought conditions (Graham et al. 2003). Meanwhile, more advanced physiological research should be performed in these genotypes using controlled conditions in order to reveal the process of tolerance to drought and sensitivity established in the genetic pool in each of the developed genotypes (Iglesias-García et al. 2017).

Before the advanced research in agriculture, farmers used to cultivate the local lentil cultivars which produced low yield and were susceptible to various conditions of biotic and abiotic stresses. With the advanced research and technology, there is a significant increase in lentil yield production worldwide. The utilization of germplasms resistant to pathogens and resistant to abiotic stresses, such as drought and cold, has resulted in production increase. Since the 1970s, it was estimated that there was a production increase of 58% worldwide from 611 to 966 kg/ha as well as an increase in the area being cultivated.

Further research should study molecular breeding in order to develop cultivars with numerous stress resistances, better nutritional quality and more production. Moreover, technology transfer should help decrease the gap between research yield and production of the farms (Sarker and Erskine 2006).

REFERENCES CITED

- Annicchiarico P. 2002. Genotype by Environment Interactions-Challenges and Opportunities for Plant Breeding and Cultivar Recommendations. Food and Agriculture Organization of the United Nations, Rome.
- Annicchiarico, Paolo, and Anna Iannucci. 2008. 'Adaptation strategy, germplasm type and adaptive traits for field pea improvement in Italy based on variety responses across climatically contrasting environments', *Field Crops Research*, 108: 133-42.
- Arroyo M.TK., Cavieres L., Marticorena C., Muñˆ N. M. 1995. Convergence in the mediterranean florasin Central Chile and California: insights from comparative biogeography. In *Ecology and Biogeography of Mediterranean Ecosystems in Chile, California, and Australia*, ed. MTK Arroyo, PH Zedler, MD Fox, New York: Springer-Verlag, pp. 43–88.
- Atalay I., Efe R. 2012. Ecological attributes and distribution of Anatolian black pine [*Pinus nigra* Arnold. subsp. *pallasiana* Lamb. Holmboe] in Turkey. *J. Environ. Biol.* 33, 509–519.
- Bacchetta, G., E. Farris, and C. Pontecorvo. 2011. 'A new method to set conservation priorities in biodiversity hotspots', *Plant Biosystems - An International Journal Dealing with all Aspects of Plant Biology*: 1-11.
- Baker R. J. 1988. Tests for crossover genotype-environmental interactions. *J. Plant Sci.* 68, 405—410.
- Bartels, Dorothea, and Ramanjulu Sunkar. 2005. 'Drought and Salt Tolerance in Plants', *Critical Reviews in Plant Sciences*, 24: 23-58.
- Baughman O.W. 2014. Will Native Plant Succeed where Exotic Invaders Fail? Cheatgrass Die-off as an Opportunity for Restoration in the Great Basin, USA (*M.S. thesis*). University of Nevada, Reno.
- Baughman, Owen W., Susan E. Meyer, Zachary T. Aanderud, and Elizabeth A. Leger. 2016. 'Cheatgrass die-offs as an opportunity for restoration in the Great Basin, USA: Will local or commercial native plants succeed where exotic invaders fail?', *Journal of Arid Environments*, 124: 193-204.
- Baum, Michael, Maria Von Korff, Peiguo Guo, Berhane Lakew, Aladdin Hamwieh, Samer Lababidi, Sripada M. Udupa, Haitham Sayed, Wafa Choumane, Stefania Grando, and Salvatore Ceccarelli. 2007. 'Molecular Approaches and Breeding Strategies for Drought Tolerance in Barley.' in, *Genomics-Assisted Crop Improvement*.

- Besnard, G., J. F. Terral, and A. Cornille. 2018. 'On the origins and domestication of the olive: a review and perspectives', *Ann Bot*, 121: 385-403.
- Bithell, S. L., R. C. Butler, S. Harrow, A. McKay, and M. G. Crome. 2011. 'Susceptibility to take-all of cereal and grass species, and their effects on pathogen inoculum', *Annals of Applied Biology*, 159: 252-66.
- Blank R., Morgan T., Clements D. 2011. Cheatgrass dead zones in northern Nevada. *Proc. Soc. Range Manag.* 64, 94.
- Blum, A. 2005. 'Drought resistance, water-use efficiency, and yield potential—are they compatible, dissonant, or mutually exclusive?', *Australian Journal of Agricultural Research*, 56.
- Bonnot, T., E. Bancel, D. Alvarez, M. Davanture, J. Boudet, M. Pailloux, M. Zivy, C. Ravel, and P. Martre. 2017. 'Grain subproteome responses to nitrogen and sulfur supply in diploid wheat *Triticum monococcum* ssp. *monococcum*', *Plant J*, 91: 894-910.
- Bradshaw, S. D., K. W. Dixon, S. D. Hopper, H. Lambers, and S. R. Turner. 2011. 'Little evidence for fire-adapted plant traits in Mediterranean climate regions', *Trends Plant Sci*, 16: 69-76.
- Budak H., Baenziger P.S., Beecher B.S., Graybosch R.A., Campbell B.T., Shipman M.J., Erayman M., Eskridge K.M. 2004. The effect of introgressions of wheat D-genome chromosomes into 'Presto' triticale. *Euphytica*, 137: 261–270. doi:10.1023/B:EUPH.0000041590.55511.d0.
- Chen, S., Y. Guo, J. Briggs, F. Dubach, S. Chao, W. Zhang, M. N. Rouse, and J. Dubcovsky. 2018. 'Mapping and characterization of wheat stem rust resistance genes SrTm5 and Sr60 from *Triticum monococcum*', *Theor Appl Genet*, 131: 625-35.
- Cooper M., Byth D. E. 1996. Understanding plant adaptation to achieve systematic applied crop improvement – a fundamental challenge. *Plant Adaptation and Crop Improvement*, 5—23. *CABI Publishing*, Wallingford, UK.
- Cuadrado A., Jouve N. 1997. Distribution of highly repeated DNA sequences in species of the genus *Secale*. *Genome*, 40: 309–317. PMID:9202411.
- Davies K.W., Boyd C.S., Beck J.L., Bates J.D., Svejcar T.J., Gregg M.A. 2011. Saving the sagebrush sea: an ecosystem conservation plan for big sagebrush plant communities. *Biol. Conserv.* 144, 2573e2584.

- Durant, S. M., T. Wachter, S. Bashir, R. Woodroffe, P. De Ornellas, C. Ransom, J. Newby, T. Abáigar, M. Abdelgadir, H. El Alqamy, J. Baillie, M. Beddiaf, F. Belbachir, A. Belbachir-Bazi, A. A. Berbash, N. E. Bemadjim, R. Beudels-Jamar, L. Boitani, C. Breitenmoser, M. Cano, P. Chardonnet, B. Collen, W. A. Cornforth, F. Cuzin, P. Gerngross, B. Haddane, M. Hadjeloum, A. Jacobson, A. Jebali, F. Lamarque, D. Mallon, K. Minkowski, S. Monfort, B. Ndoassal, B. Niagate, G. Purchase, S. Samaïla, A. K. Samna, C. Sillero-Zubiri, A. E. Soultan, M. R. Stanley Price, N. Pettorelli, and David Richardson. 2014. 'Fiddling in biodiversity hotspots while deserts burn? Collapse of the Sahara's megafauna', *Diversity and Distributions*, 20: 114-22.
- El Baidouri, M., F. Murat, M. Veyssiere, M. Molinier, R. Flores, L. Burlot, M. Alaux, H. Quesneville, C. Pont, and J. Salse. 2017. 'Reconciling the evolutionary origin of bread wheat (*Triticum aestivum*)', *New Phytol*, 213: 1477-86.
- Elia, Antonio, and Pietro Santamaria. 2013. 'Biodiversity in vegetable crops, a heritage to save: the case of Puglia region', *Italian Journal of Agronomy*, 8.
- Fady, Bruno. 2012. 'Biogeography of neutral genes and recent evolutionary history of pines in the Mediterranean Basin', *Annals of Forest Science*, 69: 421-28.
- Fady B., Médail F. 2004. Mediterranean forest ecosystems. Burley Encyclopedia of forest science. Elsevier, London, pp 1403–1414.
- Fakthongphan, J., G. Bai, P. St Amand, R. A. Graybosch, and P. S. Baenziger. 2016. 'Identification of markers linked to genes for sprouting tolerance (independent of grain color) in hard white winter wheat (HWWW)', *Theor Appl Genet*, 129: 419-30.
- Falcucci, Alessandra, Luigi Maiorano, and Luigi Boitani. 2006. 'Changes in land-use/land-cover patterns in Italy and their implications for biodiversity conservation', *Landscape Ecology*, 22: 617-31.
- Farjon A. 2008. A natural history of conifers. *Timber Press*, Portland.
- Fattorini, Simone. 2006. 'Detecting Biodiversity Hotspots by Species-Area Relationships: a Case Study of Mediterranean Beetles', *Conservation Biology*, 20: 1169-80.
- Fleury D., Jefferies S., Kuchel H., Langridge P. 2010. Genetic and genomic tools to improve drought tolerance in wheat. *J. Exp. Bot.* 61, 3211–3222.
- Gou, X., Y. Bian, A. Zhang, H. Zhang, B. Wang, R. Lv, J. Li, B. Zhu, L. Gong, and B. Liu. 2018. 'Transgenerationally Precipitated Meiotic Chromosome Instability Fuels

- Rapid Karyotypic Evolution and Phenotypic Diversity in an Artificially Constructed Allotetraploid Wheat (AADD)', *Mol Biol Evol*, 35: 1078-91.
- Graham P.H., Vance C.P. 2003. Legumes: importance and constraints to greater use. *Plant Physiology* 131, 872-877.
- Haffke, Stefan, Peer Wilde, Brigitta Schmiedchen, Bernd Hackauf, Steffen Roux, Marlen Gottwald, and Thomas Miedaner. 2015. 'Toward a Selection of Broadly Adapted Germplasm for Yield Stability of Hybrid Rye under Normal and Managed Drought Stress Conditions', *Crop Science*, 55.
- Hebblethwaite P.D., Heath M.C., Dawkins T.C. 2013. 'The pea crop: a basis for improvement' (Butterworth-Heinemann).
- Hoffmann, V., G. A. Verboom, and F. P. Cotterill. 2015. 'Dated Plant Phylogenies Resolve Neogene Climate and Landscape Evolution in the Cape Floristic Region', *PLoS One*, 10: e0137847.
- Holliday J., Aitken S., Cooke J., et al. 2017. Advances in ecological genomics in forest trees and applications to genetic resources conservation and breeding. *Molecular Ecology* 26: 706–717.
- Huo, N., T. Zhu, S. Altenbach, L. Dong, Y. Wang, T. Mohr, Z. Liu, J. Dvorak, M. C. Luo, and Y. Q. Gu. 2018. 'Dynamic Evolution of alpha-Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat', *Sci Rep*, 8: 5181.
- Iglesias-García, R., E. Prats, F. Flores, M. Amri, A. Mikić, and D. Rubiales. 2017. 'Assessment of field pea (*Pisum sativum* L.) grain yield, aerial biomass and flowering date stability in Mediterranean environments', *Crop and Pasture Science*, 68.
- Infante-Amate J., Villa I., Aguilera E., et al. 2016. The making of olive landscapes in the south of Spain. A history of continuous expansion and intensification, Environmental history. Biocultural diversity in Europe, Vol. 5. Cham: *Springer*, 157–179.
- Isik, Z., I. Parmaksiz, C. Coruh, Y. S. Geylan-Su, O. Cebeci, B. Beecher, and H. Budak. 2007. 'Organellar genome analysis of rye (*Secale cereale*) representing diverse geographic regions', *Genome*, 50: 724-34.
- Jacobsen S.E., Jensen C.R., Liu F. 2012. Improving crop production in the arid Mediterranean climate. *Field Crops Research* 128, 34-47.

- Janssen, Ellen, Vincent Kint, Jean-Daniel Bontemps, Kürşad Özkan, Ahmet Mert, Nesibe Köse, Bilgin Icel, and Bart Muys. 2018. 'Recent growth trends of black pine (*Pinus nigra* J.F. Arnold) in the eastern mediterranean', *Forest Ecology and Management*, 412: 21-28.
- Jensen S., Stettler J., 2012. In: Applying provisional seed zones to plant materials development in the Great Basin, and cultural practices. Great Basin Native Plant Selection and Increase Project Annual Meeting. UT, Salt Lake City.
- Jernigan, K. L., J. V. Godoy, M. Huang, Y. Zhou, C. F. Morris, K. A. Garland-Campbell, Z. Zhang, and A. H. Carter. 2018. 'Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat', *Front Plant Sci*, 9: 271.
- Jiang, H., J. Martin, M. Okot-Kotber, and P. A. Seib. 2011. 'Color of whole-wheat foods prepared from a bright-white hard winter wheat and the phenolic acids in its coarse bran', *J Food Sci*, 76: C846-52.
- Jighly, A., R. Joukhadar, S. Singh, and F. C. Ogbonnaya. 2018. 'Decomposing Additive Genetic Variance Revealed Novel Insights into Trait Evolution in Synthetic Hexaploid Wheat', *Front Genet*, 9: 27.
- Johnson, R. C., Barbara C. Hellier, and Ken W. Vance-Borland. 2013. 'Genecology and seed zones for tapertip onion in the US Great Basin', *Botany*, 91: 686-94.
- Keeley J.E., Bond W.J., Bradstock R.A., Pausas J.G., Rundel P.W. 2012. Fire in Mediterranean Ecosystems: Ecology, Evolution and Management. *Cambridge, UK: Cambridge Univ. Press*.
- Kumar, S., R. E. Knox, A. K. Singh, R. M. DePauw, H. L. Campbell, J. Isidro-Sanchez, F. R. Clarke, C. J. Pozniak, A. N'Daye, B. Meyer, A. Sharpe, Y. Ruan, R. D. Cuthbert, D. Somers, and G. Fedak. 2018. 'High-density genetic mapping of a major QTL for resistance to multiple races of loose smut in a tetraploid wheat cross', *PLoS One*, 13: e0192261.
- Lamont B.B., He T. 2012. Fire-adapted Gondwanan angiosperm floras evolved in the Cretaceous. *BMC Evol.Biol.* 12:223.
- Liu, W., Y. Naruoka, K. Miller, K. A. Garland-Campbell, and A. H. Carter. 2018. 'Characterizing and Validating Stripe Rust Resistance Loci in US Pacific Northwest Winter Wheat Accessions (*Triticum aestivum* L.) by Genome-wide Association and Linkage Mapping', *Plant Genome*, 11.
- Lukaszewski A.J. 2000. Manipulation of the 1RS.1BL translocation in wheat by induced homologous recombination. *Crop Sci.*40: 216–225.

- Malek Ž., Verburg P. H., Geijzendorffer I. R., Bondeau A. , Cramer W. 2018. Global change effects on land management in the Mediterranean region, *Elsevier*, 50, pp.238-254.
- Manjunatha, C., S. Sharma, D. Kulshreshtha, S. Gupta, K. Singh, S. C. Bhardwaj, and R. Aggarwal. 2018. 'Rapid detection of Puccinia triticina causing leaf rust of wheat by PCR and loop mediated isothermal amplification', *PLoS One*, 13: e0196409.
- Marchese, Christian. 2015. 'Biodiversity hotspots: A shortcut for a more complicated concept', *Global Ecology and Conservation*, 3: 297-309.
- Ma R., Yli-Mattila T., Pulli S. 2004. Phylogenetic relation Ships among genotypes of worldwide collection of spring and winter ryes (*Secale cereale* L.) determined by RAPD-PCR markers. *Hereditas*, 140: 210–221. doi:10.1111/j.1601-5223.2004.01844.x. PMID:15198711.
- Maury, O., K. Miller, L. Campling, H. Arrizabalaga, O. Aumont, Ö Bodin, P. Guillotreau, A. J. Hobday, F. Marsac, Z. Suzuki, and R. Murtugudde. 2013. 'A global science–policy partnership for progress toward sustainability of oceanic ecosystems and fisheries', *Current Opinion in Environmental Sustainability*, 5: 314-19.
- Medail, F., P. Quezel. 1997. Hot-spots analysis for conservation of plant biodiversity in the Mediterranean Basin, *Ann. Missouri Bot. Gard*, 84: 112-127.
- Medović A., Mikić A., Čupina B., Jovanović Ž., Radović S., Nikolić A., Stanisavljević N. 2011. Pisum & Ervilia Tetovac - made in Early Iron Age Leskovac. Part one. Two charred pulse crop storages of the fortified hill fort settlement Hissar in Leskovac, South Serbia. *Ratarstvo i povrtarstvo* 48, 219-226.
- Miroshnichenko, D., I. Chaban, M. Chernobrovkina, and S. Dolgov. 2017. 'Protocol for efficient regulation of in vitro morphogenesis in einkorn (*Triticum monococcum* L.), a recalcitrant diploid wheat species', *PLoS One*, 12: e0173533.
- Mishra B.K., Srivastava J.P., Lal J.P. 2014. Drought stress resistance in two diverse genotypes of lentil (*Lens culinaris* Medik.) imposed at different phenophases, *J. Food Legume*, vol. 27, pp. 307–314.
- Mishra, B. K., J. P. Srivastava, J. P. Lal, and M. S. Sheshshayee. 2016. 'Physiological and biochemical adaptations in lentil genotypes under drought stress', *Russian Journal of Plant Physiology*, 63: 695-708.

- Molina-Venegas, R., A. Aparicio, F. J. Pina, B. Valdes, and J. Arroyo. 2013. 'Disentangling environmental correlates of vascular plant biodiversity in a Mediterranean hotspot', *Ecol Evol*, 3: 3879-94.
- Nemecek, Thomas, Julia-Sophie von Richthofen, Gaëtan Dubois, Pierre Casta, Raphaël Charles, and Hubert Pahl. 2008. 'Environmental impacts of introducing grain legumes into European crop rotations', *European Journal of Agronomy*, 28: 380-93.
- Nieto, Héctor, Inmaculada Aguado, Mariano García, and Emilio Chuvieco. 2012. 'Lightning-caused fires in Central Spain: Development of a probability model of occurrence for two Spanish regions', *Agricultural and Forest Meteorology*, 162-163: 35-43.
- Oliveira, H. R., M. G. Campana, H. Jones, H. V. Hunt, F. Leigh, D. I. Redhouse, D. L. Lister, and M. K. Jones. 2012. 'Tetraploid wheat landraces in the Mediterranean basin: taxonomy, evolution and genetic diversity', *PLoS One*, 7: e37063.
- Pacicco, L., M. Bodesmo, R. Torricelli, and V. Negri. 2018. 'A methodological approach to identify agro-biodiversity hotspots for priority in situ conservation of plant genetic resources', *PLoS One*, 13: e0197709.
- Pandey, R., M. K. Lal, and K. Vengavasi. 2018. 'Differential response of hexaploid and tetraploid wheat to interactive effects of elevated [CO₂] and low phosphorus', *Plant Cell Rep.*
- Parra, A., and J. M. Moreno. 2018. 'Drought differentially affects the post-fire dynamics of seeders and resprouters in a Mediterranean shrubland', *Sci Total Environ*, 626: 1219-29.
- Pausas, Juli G., and Millán M. Millán. 2019. 'Greening and Browning in a Climate Change Hotspot: The Mediterranean Basin', *BioScience*, 69: 143-51.
- Pohl, Christian, and Gertrude Hirsch Hadorn. 2008. 'Methodological challenges of transdisciplinary research', *Natures Sciences Sociétés*, 16: 111-21.
- Pswarayi, A., F. A. van Eeuwijk, S. Ceccarelli, S. Grando, J. Comadran, J. R. Russell, E. Francia, N. Pecchioni, O. Li Destri, T. Akar, A. Al-Yassin, A. Benbelkacem, W. Choumane, M. Karrou, H. Ouabbou, J. Bort, J. L. Araus, J. L. Molina-Cano, W. T. B. Thomas, and I. Romagosa. 2008. 'Barley adaptation and improvement in the Mediterranean basin', *Plant Breeding*, 127: 554-60.

- Puddu, G., A. Falcucci, and L. Maiorano. 2011. 'Forest changes over a century in Sardinia: implications for conservation in a Mediterranean hotspot', *Agroforestry Systems*, 85: 319-30.
- Ranalli, P. 1995. 'Improvement of pulse crops in Europe', *European Journal of Agronomy*, 4: 151-66.
- Rejmánek, Marcel, David M. Richardson, and Petr Pyšek. 2013. 'Trees and shrubs as invasive alien species - 2013 update of the global database', *Diversity and Distributions*, 19: 1093-94.
- Riaz, A., N. Athiyannan, S. K. Periyannan, O. Afanasenko, O. P. Mitrofanova, G. J. Platz, E. A. B. Aitken, R. J. Snowdon, E. S. Lagudah, L. T. Hickey, and K. P. Voss-Fels. 2018. 'Unlocking new alleles for leaf rust resistance in the Vavilov wheat collection', *Theor Appl Genet*, 131: 127-44.
- Rocchi, Lucia, Luisa Paolotti, Carla Cortina, and Antonio Boggia. 2016. 'Conservation of Landrace: The Key Role of the Value for Agrobiodiversity Conservation. An Application on Ancient Tomatoes Varieties', *Agriculture and Agricultural Science Procedia*, 8: 307-16.
- Rollins, J. A., E. Habte, S. E. Templer, T. Colby, J. Schmidt, and M. von Korff. 2013. 'Leaf proteome alterations in the context of physiological and morphological responses to drought and heat stress in barley (*Hordeum vulgare* L.)', *J Exp Bot*, 64: 3201-12.
- Royo, Conxita, Jose Miguel Soriano, and Fanny Alvaro. 2017. 'Wheat: A Crop in the Bottom of the Mediterranean Diet Pyramid.' in, *Mediterranean Identities - Environment, Society, Culture*.
- Rubiales D., Fernández-Aparicio M., Moral A., Barilli E., Sillero J.C., Fondevilla S. 2009. Disease resistance in pea (*Pisum sativum* L.) types for autumn sowings in Mediterranean environments. *Czech Journal of Genetics and Plant Breeding* 45, 135-142.
- Rubiales D., Mikic A. 2015. Introduction: legumes in sustainable agriculture. *Critical Reviews in Plant Sciences* 34, 2-3.
- Rugini E., Baldoni L., Muleo R., Sebastiani L. 2016. The olive tree genome. Cham: Springer International Publishing AG.
- Rundel, Philip W., Mary T. K. Arroyo, Richard M. Cowling, Jon E. Keeley, Byron B. Lamont, and Pablo Vargas. 2016. 'Mediterranean Biomes: Evolution of Their Vegetation, Floras, and Climate', *Annual Review of Ecology, Evolution, and Systematics*, 47: 383-407.

- Sadras, V. O., L. Lake, A. Leonforte, L. S. McMurray, and J. G. Paull. 2013. 'Screening field pea for adaptation to water and heat stress: Associations between yield, crop growth rate and seed abortion', *Field Crops Research*, 150: 63-73.
- Sahri, A., L. Chentoufi, M. Arbaoui, M. Ardisson, L. Belqadi, A. Birouk, P. Roumet, and M. H. Muller. 2014. 'Towards a comprehensive characterization of durum wheat landraces in Moroccan traditional agrosystems: analysing genetic diversity in the light of geography, farmers' taxonomy and tetraploid wheat domestication history', *BMC Evol Biol*, 14: 264.
- Saponari, M., G. Loconsole, D. Cornara, R. K. Yokomi, A. De Stradis, D. Boscia, D. Bosco, G. P. Martelli, R. Krugner, and F. Porcelli. 2014. 'Infectivity and transmission of *Xylellua fastidiosa* by *Philaenus spumarius* (Hemiptera: Aphrophoridae) in Apulia, Italy', *J Econ Entomol*, 107: 1316-9.
- Sardaro, Ruggiero, Francesco Bozzo, Francesco Petrillo, and Vincenzo Fucilli. 2017. 'Measuring the financial sustainability of vine landraces for better conservation programmes of Mediterranean agro-biodiversity', *Land Use Policy*, 68: 160-67.
- Sardaro, Ruggiero, Stefania Girone, Claudio Acciani, Francesco Bozzo, Alessandro Petrontino, and Vincenzo Fucilli. 2016. 'Agro-biodiversity of Mediterranean crops: farmers' preferences in support of a conservation programme for olive landraces', *Biological Conservation*, 201: 210-19.
- Sarker, A., and W. Erskine. 2006. 'Recent progress in the ancient lentil', *The Journal of Agricultural Science*, 144: 19-29.
- Savage G. P. 1988. The composition and nutritive value of lentils (*Lens culinaris*). *Nutrition Abstracts and Reviews (Series A)* 58, 319–343.
- Shakhatreh Y., Haddad N., Alrababah M., Grando S., Ceccarelli S. 2010. Phenotypic diversity in wild barley(*Hordeum vulgare* L. ssp. *spontaneum*(C. Koch) Thell.) accessions collected in Jordan. *Genetic Resources and Crop Evolution* 57(1), 131–146.
- Shakhatreh Y., Kafawin O., Ceccarelli S., Saoub H. 2001. Selection of barley lines for drought tolerance in low rainfall areas. *Journal of Agronomy and Crop Science* 186, 131–146.
- Shrestha, R., N. C. Turner, K. H. M. Siddique, D. W. Turner, and J. Speijers. 2006. 'A water deficit during pod development in lentils reduces flower and pod numbers but not seed size', *Australian Journal of Agricultural Research*, 57.

- Simsek, S., K. L. Whitney, J. B. Ohm, J. Anderson, and M. Mergoum. 2011. 'Refrigerated dough quality: effect of environment and genotypes of hard red spring wheat', *J Food Sci*, 76: S101-7.
- Skeels, A., and M. Cardillo. 2017. 'Environmental niche conservatism explains the accumulation of species richness in Mediterranean-hotspot plant genera', *Evolution*, 71: 582-94.
- Smýkal P., Aubert G., Burstin J., Coyne C.J., Ellis N.TH., Flavell A.J., Ford R., Hýbl M., Macas J., Neumann P., Mcphee K.E., Redden R.J., Rubiales D., Weller J.L., Warkentin T.D. 2012. Pea (*Pisum sativum* L.) in the Genomic Era. *Agronomy* 2, 74-115.
- Sukumaran, S., M. P. Reynolds, and C. Sansaloni. 2018. 'Genome-Wide Association Analyses Identify QTL Hotspots for Yield and Component Traits in Durum Wheat Grown under Yield Potential, Drought, and Heat Stress Environments', *Front Plant Sci*, 9: 81.
- Tsilo, T. J., S. Simsek, J. B. Ohm, G. A. Hareland, S. Chao, and J. A. Anderson. 2011. 'Quantitative trait loci influencing endosperm texture, dough-mixing strength, and bread-making properties of the hard red spring wheat breeding lines', *Genome*, 54: 460-70.
- Uhlmann, N. K., and D. M. Beckles. 2010. 'Storage products and transcriptional analysis of the endosperm of cultivated wheat and two wild wheat species', *J Appl Genet*, 51: 431-47.
- Underwood, Emma C., Joshua H. Viers, Kirk R. Klausmeyer, Robin L. Cox, and M. Rebecca Shaw. 2009. 'Threats and biodiversity in the mediterranean biome', *Diversity and Distributions*, 15: 188-97.
- Vadez, Vincent, Jens D. Berger, Tom Warkentin, Senthold Asseng, Pasala Ratnakumar, K. Poorna Chandra Rao, Pooran M. Gaur, Nathalie Munier-Jolain, Annabelle Larmure, Anne-Sophie Voisin, Hari C. Sharma, Suresh Pande, Mamta Sharma, Lakshman Krishnamurthy, and Mainassara Abdou Zaman. 2011. 'Adaptation of grain legumes to climate change: a review', *Agronomy for Sustainable Development*, 32: 31-44.
- Verboom, G. A., N. G. Bergh, S. A. Haiden, V. Hoffmann, and M. N. Britton. 2015. 'Topography as a driver of diversification in the Cape Floristic Region of South Africa', *New Phytol*, 207: 368-76.

- Wang, B., J. Wei, N. Song, N. Wang, J. Zhao, and Z. Kang. 2018. 'A novel wheat NAC transcription factor, TaNAC30, negatively regulates resistance of wheat to stripe rust', *J Integr Plant Biol*, 60: 432-43.
- Wang, X., G. Luo, W. Yang, Y. Li, J. Sun, K. Zhan, D. Liu, and A. Zhang. 2017. 'Genetic diversity, population structure and marker-trait associations for agronomic and grain traits in wild diploid wheat *Triticum urartu*', *BMC Plant Biol*, 17: 112.
- Wilcove D.S., Rothstein D., Dubow J., Phillips A., Losos E. 1998. Quantifying threats to imperiled species in the United States. *Bioscience* 48, 607-615.
- Wu, J., Q. Zeng, Q. Wang, S. Liu, S. Yu, J. Mu, S. Huang, H. Sela, A. Distelfeld, L. Huang, D. Han, and Z. Kang. 2018. 'SNP-based pool genotyping and haplotype analysis accelerate fine-mapping of the wheat genomic region containing stripe rust resistance gene Yr26', *Theor Appl Genet*.
- Yang, C., Z. Yang, L. Zhao, F. Sun, and B. Liu. 2018. 'A newly formed hexaploid wheat exhibits immediate higher tolerance to nitrogen-deficiency than its parental lines', *BMC Plant Biol*, 18: 113.
- Young J. A., Allen F. L. 1997. Cheatgrass and range science: 1930-1950, *J. Range Management* 50:530-535.
- Young J. A. and Allen F. L. 1997. Cheatgrass and range science: 1930-1950. *J. Range Manage.* 50:530-535
- Yusuf M., Singh N.P., Dastane N.G. 1979. Effect of frequency and timings of irrigation on grain yield and water use efficiency of lentil, *Ann. Arid Zone*, vol. 18, pp. 127–134.
- Zeder M. A. 2008. Domestication and early agriculture in the Mediterranean Basin: Origins, diffusion, and impact. *J. PNAS* vol. 105 no. 33 11597–11604.
- Zeven A. C. 1998: A review of definitions and classifications. *Euphytica* 104, 127—139.
- Zohary D., Hopf M., Weiss E. 2012. Domestication of plants in the Old World: the origin and spread of cultivated plants in Southwest Asia, Europe, and the Mediterranean Basin. Oxford: *Oxford University Press*.